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(l, d) [AOH16]. 1 [BHHR19]. 2
[ABF+04, CLR+05, EHK+02, GMS05, KMRG09b, OSC11, SSW20, YE02]. 3
[AT05, CFB+07, DSN14, GRM09, GWX18, HPR09, KMRG09a, PSCP09,
SVD14, Shi10a, ZLTS13]. 4 [CCJ09]. + [ACKK19]. 1 [LPW05, Rob96, XU97].
15 [JGL11]. 2 [HBD94, Lat99]. nd [PS11]. ′ [DS19]. th [Ber11]. 0 [LLD+16]. 50
[CN17]. $_{H1}$ [SKG+00]. A [TP11]. $A*$ [HMU06, LR00]. α
[BSB+05, cLcSwP+21, MXW+20, TS96]. β [IPH18, Tra19]. • [URB+19]. C
[SKG+00]. C_α [MN08]. C_L [SKG+00]. E [Met06, SBC+05]. ℓ_0 [LKL21]. ϵ
[RSM06]. γ [HLR14]. ≥ 4 [HR08]. K
[APC21, Ben21, BS98, CZNF19, JTL+10, ARS17, BHKM22, Che12, CHS17,
FPS22, HTY22, KVZ24, MSBR08, NM14, OB16, OYB18, Ore20, PPV20,
PFK17, PGV16, PNPC20, RM21, RC24, SBK22, TAA16]. $K*$ [JHLD20]. κ
[LZBK15]. L [LLD+16, WY11]. m [CGSW14, GSW16]. n [TZHR14]. n^2
[Fom16a, Fom16b, Fom19]. n^5 [CCJ09]. O [CCJ09]. $O(n \log n)$
[CDH+06, FHKR11, SRLM10]. P
[SS01, BFT04, Kei05, VY18, WG08b, WYLW21]. ϕ [MVP06]. ψ [MVP06]. q

[RSM06]. R [WCL18a, MKB+20, ROB+22]. S [YDN12]. t [DMP+06, VY18]. τ [SAL09]. $\times$ [TTTL17]. V_H [GKKS98]. V_L [GKKS98]. Z [BMWG04].

-Approximation [OSC11]. **-Blockers** [Tra19]. **-Chains** [CCJ09]. **-D** [Shi10a]. **-Dimensional** [YE02]. **-Dominant** [DS19]. **-Exemplar** [WZW15]. **-Gap** [DMP+06]. **-Gram** [RSM06]. **-Helical** [TS96]. **-Index** [MKB+20, ROB+22]. **-Interval** [CLR+05]. **-Knockdown** [cLcSwP+21]. **-Leaping** [SAL09]. **-Level** [SSW20]. **-Matches** [RSM06]. **-Mer** [FPS22, HTY22, NM14, RM21, RC24, SBK22, ARS17, PFK17, PGV16, PNPC20, Ben21]. **-Mers** [OYB18, PPV20, BHKM22, OB16, Ore20, TZHR14, APC21]. **-Mismatch** [TAA16]. **-Modes** [CZNF19]. **-Noncrossing** [HPR09]. **-Norm** [WYLW21]. **-Optimality** [TP11]. **-Pairs** [BHHR19]. **-Partite** [CHS17, JTL+10]. **-Planted** [AOH16]. **-Regular** [CGSW14, GSW16]. **-Regularized** [LKL21]. **-Robinson** [KVZ24]. **-Score** [BMWG04]. **-Squared** [WCL18a]. **-Stem** [MSBR08]. **-Strands** [IPH18]. **-Structures** [HLR14]. **-System** [YDN12]. **-Test** [VY18]. **-Time** [CDH+06]. **-tuple** [BS98]. **-tuples** [WY11]. **-Value** [BFT04, Kei05]. **-Values** [SBC+05, WG08b, Met06, SS01]. **-Values-Based** [VY18].

/Her [JSZ+20]. **/Her-2-** [JSZ+20]. **/VEGFA}** [MXW+20].

1 [BYL+20, CDC+11, HPVS96, SS04]. **1.375-Approximation** [CKdAHdF15]. **10.1089** [Ano22b]. **10.1089/cmb.2019.0110** [Ano22b]. **10.1089/cmb.2019.0224** [Ano20]. **10.1089/cmb.2020.0112** [Ano21b]. **101** [YBF19]. **10th** [JMR+21]. **11th** [BMM+23]. **1201** [XWJZ20]. **13th** [CSZ18]. **14** [Ber11]. **14th** [CSZ19]. **15th** [CSZ20]. **16S** [MP16, RPS02, RKTS14, CDH+16, DPSW20]. **16th** [CSPZ21a, CSPZ21b]. **17th** [CSZ22]. **1826** [XWJZ20]. **18th** [CSZ23b, CSZ23a]. **19** [BZB+22, LCG+23, MRG+24, MJCM22]. **19th** [Pat24, Pat25].

2} [Pat25, YLD+18, ALB+19, ABTP23, APC21, BBH+21, MMK+21, NKG+21, PS11, SS23, TM22, WCZ+18, ZSB+23]. **2'-O-Methylation** [YLD+18]. **2-Regular** [GJL+22]. **2.1** [TH17b]. **2000** [Sha00]. **2001** [Len02]. **2002** [Mye03]. **2003** [MV04]. **2004** [Gus05]. **2005** [Miy06]. **2008** [Ano09b]. **2009** [Ano10b]. **2011** [CKS12]. **2012** [CKS13, Cho13]. **2014** [CKS15]. **2015** [HHC17]. **2016** [Ano17]. **2017** [Sah18]. **2018** [DND+19, Ist20]. **2019** [Cow20]. **2020** [Sch21a, Sch21b]. **2021** [AHIV23, CSZ22, EN22, Pen22b]. **2022** [Pe'22a, Pe'22b]. **2023** [Edi24, Tan23]. **2024** [MS24]. **21** [Ano14]. **21/4** [Ano14]. **2OM** [YLD+18].

3 [Sel13]. **3'-to-5** [Sel13]. **3F** [DCV+07].

449a [WHLR20].

5 [HR12a]. **5'-3** [HR12a]. **5-Fluorouracil** [PIM23]. **550a** [XWJZ20]. **5p** [WHLR20, XWJZ20].

7th [HSHC15].

80th [Ano21a, IPSV22].

9th [HASL18, MMN+21].

A*0201 [ZYB+04]. **aBayesQR** [AV18]. **Aberration** [BG11, LRL+07]. **Abiotic** [JJY+20]. **Abnormal** [LYF+19]. **Abortion** [CCL+19]. **Absence** [KYSE10]. **Absolute** [LGS20]. **Abstraction** [ZM16]. **Abstracts** [Ano00]. **Abundance** [Elh01, EHC+13, GCB20, PLL16, WY11]. **Abundance-Based** [WY11]. **Abundant** [JÖNK17]. **Acaricides** [CLT+20]. **Accelerate** [KM08, SSTM19]. **Accelerated** [CFE+13, DBM09]. **Accelerates** [JHLD20]. **Accelerating** [LZL24, SM04]. **Acceptable** [ZHQS05]. **Access** [KP96]. **Accessibility** [WAPM05]. **Accessible** [DBM09, MRM+02, WZZU07]. **According** [BWGM17, DC16a, FCS12]. **Account** [BG15]. **Accumulated** [WT07]. **Accuracy** [CWR24, DBT11, HA12, HD98, KD13, TYSX19, WHJE19, XLZ13, ZZL23a, ZPG+24]. **Accurate** [AI12, ADPH15, DKK20, DG02, DBL+12, FB12, GWM+21a, HJD17, HLH04, HHP+09, JMPR23, KBS09, KBKF17, Kei05, LRD19, LRM11, ML22, NWN+10, NMH13, OAR+24, OYY+12, OMS13, PZH11, PWKAF16, RC15, SAL09, SEV09, WMK17, YW21, ZZC+24]. **Accurately** [Mye95, NVCW15]. **Acetylation** [LSY+05]. **Acetylcholinesterase** [SCB14]. **Achieved** [ZL22]. **Acid** [BET00, DSN14, Geo09, HZNF06a, HZNF06b, HHP+09, KC96, LMT01, MKKK+17, MNG+15, MV00, Ore20, RC07, STV96, TBB00, TDV24, TLK+06, VST03, VS98, XGD24]. **Acid-Based** [MKKK+17]. **Acid-Level** [XGD24]. **Acids** [CCJ09, CWYB16, CFH13, GC15, JMEB18, TS96, BIPD17]. **Acknowledgment** [Ano22a, Ano23, Ano24, Ano25]. **Acquisition** [DKC15]. **Across** [HKL07, JC22, KMCKS17, LWLJ10, NSA08, YCP16, LPW05, LM11]. **Act** [WHLR20]. **Action** [ITdB09]. **Activated** [MXW+20, VND17]. **Activation** [BGH+08, URB+19, UTD+20]. **Activator** [CASP10]. **Active** [LKC21, NSMV18]. **Activity** [EAM+17, FFSL22, GAWI19, KGN09, Kru17, LBDVF10, PKK97, RHS+21, RFH+25, SKP+12, SKS+09, TGTG19, ZZUPY06]. **Actomyosin** [Ben98]. **Acute** [DDK21, OSK+15, Tho21]. **Acyclic** [CJ23, KLR23, LL05a, Voo14]. **Acyl** [TS96]. **Adamantinomatous** [fZbMqW+20]. **Adaptation** [ZZZU20]. **Adaptive** [DK18, FPS22, GMY10, HLY25, KZE10, LCG+23, PSIM18, QMMW11, RKTS14, WP11, ZRGHJ08]. **Additive** [LQ23, MRM20, ML00, WG98, XWLJ08]. **Adenocarcinoma** [CYF+20, HXL+20, TYS+20, ZLL+20, ZQZ20]. **Adenocarcinomas** [BSB+05]. **Adenylation** [LSAD05]. **Adjacencies** [AFR+08, DKA+17, XJZ+21]. **Adjacency** [DLM10, YS10]. **Adjustable**

[WF12]. **Adjustment** [Hav06, SZSW09, YYA10]. **Admixed** [ACBM18, BG09, BG11]. **Admixture** [BG11]. **Admixtures** [RBEB13]. **Advanced** [Ila20]. **Advances** [BMM+23, JMR+21, MMN+21, WTE25]. **Advantage** [BL02]. **Advantages** [BG23]. **Adversarial** [GWA+21]. **Advising** [DKK20, KD13]. **Affected** [LGS20, LZY+23]. **Affiliation** [ODNW21]. **Affine** [PLSM+06]. **Affinity** [BÖB+23, HD16, LKC21, OJFD18, ÖBA+23, WlLK+12, ZYB+04]. **AFMDD** [ZLTZ25]. **after** [Gu01]. **Against** [GGKS95, LZHC15, SSW20, UBGFD+19, ZRNA20]. **Age** [HPL+20, MDWZ24, RYZ23, RDR12, Ves12]. **Age-Structured** [RYZ23]. **Aggregated** [RRKT07]. **Aggregation** [BCPS04, ISK99]. **Agility** [CL21b]. **Agonist** [CWRF15]. **Agreement** [HL13, KKS22, LTsL24, Prz98, Voo14]. **Agrobacterial** [GMVC20]. **ahead** [Ano20]. **AI** [QBA+25]. **AIDS** [EBS+22, HAM+22, RYZ23]. **AlCoB** [DMV17]. **ALFRED** [TCL+16]. **Algae** [JB10]. **Algebraic** [JTSB10, Lu15, NW12]. **Algorithm** [ABF+04, AI12, ACKK19, ARSW22, ABG+03, BMY01, BNA+12, BHHR18, BMR09, BZB+22, BRZH15, BFK+11, BMWG04, CCG06, CZNF19, CTC21a, CFB+07, CCJ09, CD11, CPR22, CFH13, CS15, Clo05, CDH+06, CKdAHdF15, Dew01, DFG06, DEH10, DCD19, EBK11, FYJ18, FHKR11, Fom16b, FNPP02, GLM+09, GP13, GBR17, GGM12, GZN16, GYZ19, Guo15, GMSZ12, HG11, HD16, HVPBK13, HHE13, HWH+13, HBK11, HBD94, HMU06, Hor01, HCC05, IW95, JDK+18, JR17, JRS19, Jen09, JJGD16, JHLD20, KEL15, KZE10, KLM11, KS11, KPS00, KBZ+05, KMM17, KLW96, KVK08, LSS01, LTsL24, LYL+04, Lat99, LR00, Li09, LDLZ12, LLWZ19, LZC+23, LSAD05, LS97, LLCT05, LC03a, LSHL04, LC03b, Lu15, LMSH03, MC08, Mal98, MYBK+11, MTH11, Mat10, MK06, MA13, ML10, MD03, NK07, NMG+05, NTMM06, OJFD18, PB18, PDZ+16, PZMM15, PU00, PZZ20]. **Algorithm** [RC15, RC07, SM20, SG15, Sal95, SSC23, SAL09, SB17, SLM15, SM16, SSLMW10, Sie03, SWR08, SMML24, TGT08, TAA16, TBJF01, TPSB19, TAY16, UMR11, VM06, WP11, WOG03, WMD06, WLYC12, WW18, WY21, WZW15, Wu96, WCC+06, WY11, Wu13, XJL+22, XWLJ08, XS07, XMU96, XJB07, Xu09, XZW15b, YLC+17, YL17, YM06, YK05, ZZS17, Zha94, ZSWM00, ZCH+13, ZRNA20, ZF05, ZFAS08, ZPB+10, ZWT18, ZUGVWS10, ZCK17]. **Algorithmic** [AS11, CS03, ES06, FJK+99, GKKS98, GI95, SMZ+12]. **Algorithms** [AFBS95, AMK00, AO08, And09, BSS11, Ber95, BST02, BGL24, Bry96, CFR12, CJ23, CJC01, CFS+08, CGI+07, CST20, CJS12, DMV17, DG02, DMB07, DHY02, EHK+02, EHFK24, EN22, GFE+16, GB08, GM07, GWX18, Gus01, HA12, HTZ+12, HHL06, JM97, JGT22, JZL+20, KS00, KAS09, Kle99, KSB98, KLR23, KABH15, LTCH11, LHC02, MT06, MS00, NCMS+21, NS18, PGV16, RBH05, RND+23, RLK+09, Ros05, SIKS06, Shi07, SCSA+16, SDG+07, SP97, TMfTK23, TPH+09, VUR11, fW23, Wil99, Wu08, WZW10, YzCW20, YW21, YFBK07, YWN11, ZHZ+16, ZFBK09]. **Aligned** [AS96, CL17, MBR+94]. **Aligning**

[AKK11, KKW10, NBC+11, PL06, RC14, RC15, YW21, ZPM97, ZSWM00].
Alignment
[AG98, AT05, BG02, BWS13, BH11, Ben97, Bun02, CL17, CHM94, CHS17, CB06, CST20, DSS+22a, DSC+22, Dew01, DLPH06, DHL00, Eli06, FND+09, GTT06, GWA+21, GTA22, GHM+10, GKG12, GWM+21a, GKS95, HDBZ08, HHX16, HlAM20, HB11, HWSH18, HSAEM13, HD98, Hor01, Hua08, JZGA20, JHS06, JDSB04, JD05, Jus01, KBS09, KTSS19, KD13, KC96, KX06a, KX06b, KS06, KJmZ+22, KKT+06, KPZU11, KMB+20, LRD19, vLKMR22, LNW01, LRV98, LR00, LKW04, LS08b, LMSH03, MTH11, MWRS16, McC09, MSZW11, MBVA07, MNG+15, MWB10, MSZM96, NSRR23, NMG+05, NL09, NK11, NBB18, PAC02, PB18, PM14, PRT08, PLSM+06, RCSW09, RLVCVR17, RLCVVR18, SF12, SDDI+08, SV97, SNW04, SYYH02, SPW22, SI97, SRZ+13, SM04, SLL+17, SP97, SLY06, Tay94, TCL+16, VLL+06, VV97, WOW+14, WRSW10, WJ94, War95].
Alignment [WFH18, WLS+11, WY12, WG08b, XJB07, YJ04, YK05, YS99, YH01, YJEP08, YA11, ZRHM94, ZW03, ZMppVN22, ZFAS08, ZWT18, ZF07, Zhu07, ZUGVWS10]. **Alignment-Free** [BWS13, DLPH06, HWSH18, LRD19, vLKMR22, RCSW09, SRZ+13, TCL+16, WRSW10]. **Alignments** [AM97, BMWG04, CCI+04, DBHC24, GKB00, GB06, HS14, HW01, KMMF20, KJmZ+22, LAP03, MWP00, Met06, MT99, NB94, New08, RK96, RDH04, SGSN12, SRS02, SS01, ZBM98]. **Aliphatic** [TS96]. **Aliquoting** [WS11]. **All-Atom** [KXL08, ZHY+20]. **Allele**
[JGB12, Lai12, RM18, WCM+08]. **Allele-Specific** [Lai12, WCM+08, RM18]. **Alleles** [BSKgG23, HKL07, YWN11]. **Alleles/Supertypes** [HKL07]. **Allowing** [SNW98]. **AllSome** [SHCM18]. **Almost** [CD11]. **Along** [ZCH+13, ZKT14]. **Alpha** [AEB+04, MMK+21]. **Alpha-Satellite** [AEB+04]. **Alphabet** [SBNS21]. **Alphabets** [Ris16]. **ALPHLARD** [HMY+19]. **ALPHLARD-NT** [HMY+19]. **Altered** [CPR22, RCER21]. **Altering** [ZZZU20]. **Alternate** [SGT15]. **Alternating** [LLWZ19]. **Alternative** [BBV+14, BMP+09, FDB18, MG06, Sam09, WXS14, XLZ+24, ZZ14b]. **Alu** [ZPC+18]. **Alzheimer** [BSKgG23, SCB14]. **AMASS** [KS99]. **Ambiguous** [GCB20, ZZL23a]. **Amino** [BET00, BIPD17, CWYB16, DSN14, Geo09, GC15, HZNF06a, HZNF06b, HHP+09, KC96, LMT01, MNG+15, MV00, Ore20, STV96, TBB00, TDV24, TS96, TLK+06, VST03, VS98, XGD24]. **Amino-Acid** [MNG+15]. **Amnesic** [AB00]. **Amoebots** [FPSD22]. **Among** [CZS15, RKTS14, TRS17, yWCF06]. **Amplicon** [BDN19, KABH15]. **Amplicon-Based** [BDN19]. **Analogs** [GAWI19]. **Analogy** [AK07]. **Analyses** [ARSW22, CKZL20, CD21, LSRR18, MSS+22, XXZ+21]. **Analysis** [ÅMR07, ABF+04, ADP+08, ACKK19, AEB+04, AN18, AO08, AFCN13, AHK+02, BSP+25, BR24, BHL+18, Bar04, BB15, BGTSB98, BB04, BG11, BCG+18, BFK+10, BG06, BZMM16, BS20, BFP13, CK11, CYF+20, CY10, CWRF15, CCL+19, CCH+19, CLT+20, CYY23, CC09, CRT04, CQG10, CHJ05, CLSW02, CDC+11, CM04, DMHM97, DLL+12, DMDR17, DKC15, DC16b, EHK+02, ES07, FZF+20, FDW20, FSW+20, FBJ04, FSZ02,

FP11, FCR+13, FJAOB18, FDDK07, GVMB24, GVTS04, GMF+08, Gel95, GSH17, GH16, GSCG19, GSV21, GSV+11a, GDL+15, HBRW06, HMY+19, HLK+13, HSD05, HXL+20, HWW+20, HZL22, Hua10, HJ14, ITSH00, IRCA21, JKG+04, JJY+20, JLmR+23, JSZ+20, JFLL20, KV17, KBZ+05, KCG+19, KV23, KMC00, Ker03, KX14, KAD+19, Kle99, KBČ19, KBCBS11, KL98, Lai12, LSBS18, LPW05, LYMD03, LDS12, LRSG07, LVC+04, LSG04].
Analysis [LZHC15, LGD+19, LL19b, LJCZ20, LJP20, LS97, LABD+06, LHC19, LL19c, LLZ19, LXL+20, LTL20, cLcSwP+21, LCD11, LBDVF10, LRNBJ10, LLL+20, LZX12, Mal98, MK11, MGW+07, MMHC98, MDL+18, MXW+20, MHL22, MM21, MSS21, NES22, NH08, NXGL20, NSH+23, NW05, OJOD+04, OH03, PD20a, PGAE04, PLSL18, PNMI15, PLL16, PSP21, PG03, Pic08, PSG+20, PPV+14, PRC+13, PZZ20, QQL+19, QP09, QbMyD+19, RLH13, RS13, SG10, SG15, SKGG17, SPD95, SMZ+12, SS07, SSC23, SDC03, SLL+23, SIK+05, SSV19, SBPS11, SM09, SJ18, SH04a, SZVM10, SFC11, SLYC09, SSZC95, SLZH15, SGCD19, SBTV10, TBL18, TZZY20, TE96, TBJF01, TTTA07, TPSB19, TS96, UGS19, WGL98, WSW15, WPL+19, WFL+20, WHK21, WLM21, WWH17, WV11, WSHB98, WNMB99, WMC04, WHC09, WZW10, XL18, XMWZ20, XSH+22, YS23, YHW18, YZWZ13, YLC+17, YHT+17, YDG+20, YcXyW+21, YYZ23]. **Analysis** [YMM+24, YYW14, YfZX+21, YLC+20, Yu24, ZMGN23, ZSB+23, ZPC+18, ZCY+20, Zha02, ZWQ19, ZLW+20, ZLB+20, ZZ20, ZLSY20, ZDG+20, ZW23, ZYD+19, ZZL+17, ZL22, fZbMqW+20]. **Analysis-Based** [BB15, PD20a]. **Analytic** [CH15, CKS06]. **Analytical** [DT12, DRT+25, KLC+11]. **Analytics** [SSR21]. **Analyze** [ADS03, FLNP00, PRC+24, WXY+13]. **Analyzing** [ABG+03, BSB+05, CJ22, DGH+01, DWS05, DAL+08, HHZ+18, LDB+07, PD20b, PFRD05, RH19, RHS+21, WZH+18, YHB+03, YL17, ZLTZ25]. **Ancestor** [QEk24]. **Ancestral** [AS10, AJA+16, ASL06, BLEM08, CHSY10, CGOT10, DR17, ET07, GM96, HSAEM13, JSN09, LTI10, MRR+08, ME12, Mos03, OR14, PMCB08, Par10, SZW+09, SH05, TBKR10, Wu08, XSS08, XJZ+21, YCP16]. **Ancestrally** [KWBN19]. **Ancestries** [BG09]. **Ancestry** [RBEB13]. **Anchored** [BCCHZU18]. **Anchoring** [HHC06, Sch97a]. **Anchors** [LZF+05]. **Ancient** [BBWE09]. **AND/OR** [ZWZ16]. **Angiosperm** [SZW+09]. **Angle** [KAC17]. **Angular** [LRSG07]. **Annihilate** [BMN+07]. **Annotated** [SZUP06, ZLU+22]. **Annotating** [SSB07]. **Annotation** [DCW+17, FPRV18, GVMB24, KMJ+20, KBČ19, LDBj22, PBS+99, PBMC17, RND+23, SK21, SBK22, ZW23]. **Announces** [Prz24]. **Annual** [Ano00]. **Anomalies** [NME+15]. **Anomalous** [BCVL17, IP09]. **Anopheles** [XSS08]. **Ant** [ZZL22, ZLP22]. **Anti** [Ami12, Ano21b]. **Anti-Cooperative** [Ami12]. **Anti-SARS-CoV** [Ano21b]. **Antibiotics** [MLY+11, PCS18]. **Antibody** [BP16, Jos96, MBK+03, YK19]. **Anticipation** [SAL09]. **Antigen** [HMY+19, YK19]. **Antiretroviral** [EBS+22]. **Antisense** [AKN+06]. **Antiviral** [Ano21b, MJCM22]. **Anytime** [Lat99]. **Apache** [HFUH19, LCG18]. **APOBEC3G** [DCV+07].

APOBEC3G/3F [DCV+07]. **APOE}** [RMC+05, BSKgG23]. **Apomorphine** [PD20b]. **Apomorphine-Mediated** [PD20b]. **Apoptosis** [JKG+04]. **App** [PBMC17]. **Applicable** [MKKK+17]. **Application** [ATLS07, BG11, BGJ+04, BZMM16, BSSz+20b, CRT+17, CHS17, DCL10, DBB+02, EVLZU19, GK18, GRM09, HKZ+04, JHS06, KLV+13, KS05, KSSK09, LNW01, LDLZ12, LCW16, LS23, LSAD05, LLCT05, LH03, LDB+07, LCL+17, MS00, MA13, MV19, MKBC05, MS03, MJCM22, NES22, NSRR23, NL09, OKKS21, PBMC17, PSP21, PSCP09, RRKT07, RMC+05, SKGG17, Ser15, SSPNW06, SBK22, SCSA+16, TS96, WSW15, WV11, YGP05, YZWZ13, ZSB+23, ZW23, ZZ14b, ZAG+18, Zör15, ZCK17, MM06]. **Application-aware** [NSRR23]. **Applications** [ARSW22, BNA+12, BDHK+04, Ben21, BCCHZU18, BS06, BBD+04, CSZ18, CSZ19, CSZ20, CSPZ21a, CSPZ21b, CSZ22, CSZ23b, CSZ23a, CGT12, CCT15, CD07, CL99, CP19, HJ05, Kon07, LKL21, LS05, MN08, MPZ+20, NP09, NR03, NW12, NM14, PAC02, PIM23, Pat24, Pat25, PPV20, RC07, SG12, VCY14, VAS+18, XZW15b, YHEP15, YB04, Yu24]. **Applied** [BMN+07, Cha01, JS03, LLWZ19, NFHM21, Pen20a, VT06]. **Applies** [LM11]. **Applying** [ARRW99, DKF09, GSH17, HLG18]. **Appraisal** [GSA14]. **Approach** [APVM11, AZ14, AR17, AKLM02, AHK08, AJV+16, Azi22, BGLY03, BKCP05, BCVL17, BDN19, BNN12, BCCHZU18, BBN24, BCG+18, BLQZ04, BBEM09, BV09, BMP+09, CKT+01, Che06, CC11, CY17, CB06, CJK+97, CYLY12, CRB18, CST20, DT12, DRT+25, DM20, DDK21, DP07, DC16b, DHV06, EAA+09, FdSdSR+15, FJK+99, FRD+17, Fom16a, Fom16b, Fom19, FA12, GMC+14, GQ09, GSH17, GPOP+17, GKS95, GBB15, HSH11, HSAEM13, HL16a, Ila20, JEMF06, JHA16, JS03, KKS+15, KS12, KIYM13, KS99, LLKX16, LRV98, LXYC09, LAL+09, LFJ11, LSL+16, LMP08, LDB+07, MMKH15, MPC+11, MNIK+09, MM06, MSN+20, MSB+10, MRS+18, NVW14, NVCW15, ODNW21, ODPB18, PK11, PBS+99, PdB13, PJB+15, PAS+13, PL06, QTRA24, RNH18, RKTS14, RAKL10, RMRT00, RRFS98, SVA+19, SLL08, SDFR16, ST02a, SSV19, SYYH02, SH17]. **Approach** [kSyPhC+22, SJ18, SB07, SCC+98, SRS02, SSB07, SZL+23, TBL18, TKSA24, UBTC06, UBGFD+19, VRS12, VND17, WYT12, WHL17, WxLW+23, WDF24, WVT23, WPS+25, Xu09, XSH+22, YLCC17, ZRZD11, ZKL+10, ZW03, ZPX+10, ZLP22, ZLM+17, ZZL00, ZZUPY06]. **Approaches** [BJEG98, CDS+16, FADH17, FCGD19, FDD21, GPRR12, KVM14, LST+17, cLcSwP+21, QGP10, SDC03, SI97, SLB+97, WQZ+19, ZXZ21]. **Appropriate** [Hua08]. **Approximability** [BSS13]. **Approximate** [DBHC24, DP07, EHFK24, Jah11, JDK+18, JS03, KMMF20, LSS01, MTH11, MT99, Mye96, Nic01, RDRF24, SC15, SSIP+19, SS01, WYKG05, YJ04]. **Approximates** [CMK23, JHLD20]. **Approximating** [BSMA06, GMS05, KMRG09b, SKW23]. **Approximation** [AHK08, AMRW96, CKdAHdF15, FHKR11, GK06, GPCP11, GWX18, HCC05, KV19, KSB98, KM08, LQ23, LJL+20, LS04, MT06, OSC11, PRSV08, PPV20, SFR+18, YY05, YT22]. **Approximation-Based** [YT22].

Approximations [GW94, JJGD16, RS98, RS01, ZRS+12, ZPG+24]. **Approximative** [MMKH15]. **AptaBlocks** [HWP20]. **Arabidopsis** [AJV+16, ZDZ+20]. **Arbitrary** [Dew01, IKL+03, LMSH03, MSR22]. **Arc** [HR08]. **Arc-Length** [HR08]. **Archaea** [TRS17]. **Architecture** [CJ22, CST20, SK17, SSD07]. **Architectures** [GFE+16, JSN09, PVFB06, ZB15]. **Archival** [MRY+23]. **Area** [DBM09]. **AREM** [NBC+11]. **ARG** [PMCB08]. **ARGLRR** [cWxLlS+23]. **Arithmetic** [HLY25]. **Aromatic** [TS96]. **Arrangement** [MYBK+11, ZZNM15]. **Arrangements** [XSS08]. **Array** [BVP+19, DMR+03, EZFP+19, FBJ04, KVDC06, KRD14, LL05a, Pic08, SLZH15, NHOV10]. **Array-CGH** [NHOV10]. **Arrayed** [BLEM08]. **Arrays** [Åst03, BDHK+04, CHK+02, FNC08, HG11, KMP+04, RD01, ST02a, WLF13, WI05]. **Arterial** [ZXZ21]. **Arthritis** [YBF19]. **Articles** [DMV17, HHC17, Sah18]. **Articulated** [CCYH18]. **Artificial** [DNZ17, DND+19, FdSdSR+15, LMT01]. **Asexual** [LLS11a]. **Aspects** [SY09]. **ASPP** [NZM+25]. **Assay** [LZHC15]. **Assays** [AAC+06, BLC+10a, KBZ+05, SGYBD05]. **Assembled** [DC16a]. **Assembler** [LYPC13, LYC15, SBP15]. **Assemblers** [MPC+11, WWH17]. **Assemblies** [DWS05, MSS10]. **Assembling** [GDHC95, Gui98, NBA+13, PVFB06]. **Assembly** [AI12, AM20, APC21, BNA+12, BLC10b, BVP+16, BDK+16, BVP+17, CN17, CDS+16, CRB18, Cos18, DKK20, GYD+15, IW95, KLZU06, KKC+22, KS99, LJK11, LFJ11, LH03, ML22, MB09, MP94, Mye95, NP09, PMP+15, PAS+13, RHY+04, RMC+23, SMM+04, SAM06, TM17, WHW+06]. **Assembly-to-Assembly** [SMM+04]. **Assess** [RS12]. **Assessing** [BMWG04, CWR24, FH18, KSG07, PDK+08, WWH17, WGW+01]. **Assessment** [APVM11, BMB24, CB06, DCSE11, MSMF09, NSA08, PGV16, SSH+10, SZTW12, Wen05]. **Assessments** [CZW+19]. **Assigning** [ODNW21]. **Assignment** [BKWK+00, BKCP05, CLR+05, CDH+06, FCV+07, JGL11, Ros05, WCC+06]. **Assignments** [CDH+16, LYL+04]. **Assimilation** [HMY+14]. **Assisting** [DCL18]. **Associated** [CCH+19, CKZL20, GLM16, JDSB04, KLS15, RS12, SlGW+23, SnGqC20, SZY+20, SVP19, SGCD19, WLFW03, YYJ19, YcXyW+21, ZLW+20, ZLSY20, ZXZ21]. **Associating** [LWLL19, LZL24, ZZUPY06]. **Association** [BT08, BDBB10, CTC21b, HWZ+21, KX14, KS05, KE13, LS17, Li08, LS23, LZX12, McP12, MDB11, OH03, PK19, RLK+09, SHE11, WYY+18, WLXW22, WAX22, WGS+23, Wu08, WES20, YRG+19, bYjHgZ+24, ZPC+18, ZPX+10, ZCZ+23, ZWD25]. **Associations** [BYGI12, CDQ+21, CJ21, GSV21, KE13, LWZ18, MWZ19, SJ12, SHZ+24, WxLW+23]. **Assumption** [HP96]. **Asthma** [SnGqC20]. **Asymmetric** [FLS94, WMG+24, YHT+17, ZGBK10]. **Asymmetry** [DS19]. **Asymptotics** [LPC08]. **Asynchronous** [ZH14]. **Asynchrony** [LYF+19]. **ATAC** [ZW23, XSH+22]. **ATAC-DEA** [ZW23]. **ATAC-Seq** [ZW23, XSH+22]. **Atherosclerosis** [YfZX+21]. **Atlas** [CWS+21, GE17, LLZ19, BR24]. **Atom** [BK08, HLMR11, KXL08, NFHM21, ZHY+20]. **Atomic** [WDA01, ZKWH17].

Atoms [Aku04]. **Atopic** [SnGqC20]. **Attachment** [LXYC09, WlLK+12]. **Attachments** [KKS+15]. **Attain** [DDC+20]. **attC** [PWKAF16]. **Attention** [Cha95, EZFP+19, NZM+25, Sef25, GZLY24, JAJ24]. **Attention-Based** [EZFP+19]. **Attention-Guided** [NZM+25]. **Attention-UNet** [JAJ24]. **Attentive** [DVS19]. **Attraction** [CSP+12]. **Attractor** [AMTY11, MA13]. **Attributes** [MRS+18]. **AUC** [LGC+09]. **Augmentation** [FFB20]. **Augmented** [ZM16]. **Autism** [GJL+21, YMxW21]. **Auto** [WYY+18]. **Auto-Learning** [WYY+18]. **Autocrine** [FL94]. **Autoencoder** [TMG+20, WYC+18, YYM+23, ZLL+22]. **Autoencoding** [MSMP19]. **Automata** [AAG14, AB00, SVD14]. **Automated** [BKWK+00, FCR+13, HRSC00, JGL11, LYL+04, LNW01, MZM18, RDRF24, RMC+23, XU97]. **Automatic** [ABF+04, AMS+22, AG23, AT05, BJEG98, FND+09, LZL+23, YQDW23]. **Automatically** [JGL11, TDV24]. **Automating** [WH20]. **Automation** [MPG+16, RGM+12]. **Automaton** [BNN12, CWC06]. **Autopoiesis** [SDFR16]. **Autoregressive** [UTD+20]. **Autosomal** [XSS08]. **Available** [EHC+13, KBČ19]. **Average** [TAA16, UBTC06, WW18, WW19]. **Averages** [AO08]. **Averaging** [SLL08]. **Avoiding** [SAM06]. **Award** [Prz24]. **Aware** [CPFP24, FBV15, GVMB24, JHLD20, LSBS18, MK16, YLZ+24, NSRR23]. **Axis** [ZKWH17]. **AXL** [GAWI19].

B [BZMM16, CCH+19, LZBK15, SVA+19, SSC23]. **B/RelA** [LZBK15]. **Bacillus** [MP16]. **Back** [GB08]. **Backbone** [Pen20a, WMD06, WCC+06]. **Backbones** [Pen20b]. **Backcross** [WMC04]. **Background** [Hav06, KFDT02, SZSW09, XWLJ08, ZS11]. **Backward** [YYZ23]. **Bacteria** [ASZ+16, BFP13, RKTS14, SDP+20, TRS17, ZAG+18]. **Bacterial** [AZ11, BCVL17, DCSE11, EAA+09, MLC10, NTMM06, PCS18, RPS02, SIK+05, TMC+18]. **Bacteriophage** [BHPS99]. **Bagging** [GWM+21a]. **bAIcis}** [ZRNA20]. **Balance** [BSP+25, BP06]. **Balanced** [SKO09]. **Balancing** [KWB+13]. **Ball** [HVPBK13]. **Ball-based** [HVPBK13]. **Ballast** [HVPBK13]. **Balls** [CGD09]. **Baltimore** [Ano00]. **Bands** [SSTM19]. **Barcoded** [TYSX19]. **Barcoding** [DLL+12]. **Barley** [LGS20]. **BARRA** [FDD21]. **Barrel** [NS18, ZWY+17]. **Barrett** [SZMZ19]. **Barrier** [FYJ18, SKW23]. **Base** [Fas94, FHS00, FLS94, Ham12, HPVS96, KS11, LFT+98, LJL+20, MN15]. **Base-Calling** [KS11]. **Base-Pairing** [Ham12]. **Based** [AL25, AS10, ACBM18, ALB+19, AMK00, AA18, ABTP23, ACL15, APC21, Ano21b, Ano22b, ASE20, AaHP+21, AS19, Azi22, BSP+25, BR24, BCVL17, BKT09, BB15, BDN19, BBN24, BSB+05, Bet10, BL02, BV09, BFL05, BSS13, CMK23, CDQ+21, CN17, CZS15, CDL+19, CLT+20, CKZL20, CWS+21, CJ21, CL21a, CMS+25, CZY19, CLLL20, DLL+12, DQS+11, DPHH05, DJK+00, DG02, DM20, DCP+08, DCD19, DBL+12, DWK+20, EZFP+19, EBK11, EMV98, FJAOB18, FA12, FCV+07, GMC+14, GZY+22, GZLY24, GCB15, GTA+04, GG04, HSG22, HZNF06a, HZNF06b, HTY22, Hav06,

HYY+10, HlAM20, HR22, HWP20, HLY25, HBW+05, HL13, HXY+23, HJ14, IJCL12, Jah11, JGL11, JWL24, JLY08, JZ10, JHA16, JHLD20, JRH+10, KV17, KS11, KMMF20, KS12, KSS09, KV23, KMZ+10, KFC+11, KGK14, KGÖ18, LWN+18, LS08a, LST+17, LLSH19, LHW+22, LBN94]. **Based** [LYC15, LSG04, LFJ11, LCG+22, LSAD05, LLT06, LDW+14, LLW18, LLZ19, LGS20, LS08b, LZX12, LP00, MSS+22, MWZ19, MK11, MZC+18, MH22, MRG+24, MM06, MS03, MKKK+17, MBRS11b, MEF24, MSN+20, MTF+12, MM21, NSRR23, NVCW15, NV12, NZM+25, NTWF11, OJFD18, OYY+12, OMS13, PRC+24, PBS+99, PD20a, PDZ+16, PJL20, PLZX25, PNIM17, PBMC17, PCS18, PIM23, QSY09, jQLsY+24, RC06, RWB+98, RMC+23, SSR21, SM20, SBD+00, Sef25, SRF16, SSV19, SBPS11, SlGW+23, kSyPhC+22, SM09, SCC+98, SWR08, SRZ+13, SSZG24, SLL+17, SDP+20, TMfTK23, TMH+21, TPH+09, TSTS12, TVNP15, UGS19, UBGFD+19, VRS12, VLZUBK07, VND17, VT06, VCY14, VY18, Vij22, WMG+24, WOG03, WWZ+16, WYC+18, WCL+18b, WWZY19, WPL+19, WWLC20, WZL+21, WHK21, WxLW+23, WFC25, WLM21, Wil99, WR23, WMPS11, WT07, Woo99, Wu96, WX08, WY11, WLA+18, WPS+25, XLZ+18a, XJL+22]. **Based** [XS07, XJZ+21, YWZ+19, YGP05, YLCC17, YLD+18, YHC19, bYjHgZ+24, YMxW21, YT22, YjDG+23, YZPC24, ZCY+20, ZZHL11, Zha16, ZHY+20, ZLW+20, ZZ20, ZlWL21, ZW23, ZLTZ25, ZS11, ZWK+20, ZYD+19, ZWD+04, ZAG+18, ZZL+23b, ZYD21, ZPD+23, ZS24, CGT12, CJP+22, DKA+17, HVPBK13, HWH+13, JJGD16, LSL+16, TH17a, ZZ14b, ZS14, AB16, BLC+10a, CDS+16, YCCL18, YWN11]. **Bases** [DDC+20, PO04, RL94]. **Basic** [AO08, Dei19b, NBB18]. **Basis** [AI12, GSSI14, LQPE+10, SVP19]. **Baum** [Jen09]. **Bayes** [ZCK17]. **Bayesian** [AS96, AV18, BF02, BB15, BV20, BDBB10, BRR02, CL99, DCD19, DMR+03, FLNP00, GE04, GBR17, GW06, HMY+19, HVAW04, HMF07, IFT14, JPB+15, JBBW10, LWN+18, Lar06, LAL+09, LYF+19, LMP08, MLOT17, MWZ19, MWP00, NSMV18, Neu14a, PP23, PS12, PKSB18, RMRT00, RMC+05, RBH+19, SLL08, SLB00, Ser15, SSIP+19, SDC+10, TBJF01, VND17, WDF24, WVT23, XLZ+24, XLZ+18b, XK05, XJS07, YDN02, ZRZD11, ZWSF05, ZRNA20, ZH07]. **BayesMD** [TKW08]. **BB** [Hor01]. **BBK*** [OJFD18]. **BCL** [KWM10]. **BCM** [CCDB21]. **BDEtools** [ADW23]. **BE** [PS11, BF98, CYF+20, NLC17]. **Beacon** [EAM+17]. **Beam** [CCG06, CCG06]. **Beating** [WPS+25]. **Behaved** [BSP+25]. **Behavior** [AFCK09]. **Behaviors** [RAKL10]. **Belief** [KXL08]. **Beltway** [EHFK24, Fom19]. **Benchmarking** [FCGD19, FDD21]. **Best** [VCY14]. **Beta** [CBM+02, JAG17, KAS09, MKBC05, NS18, PLL16, SOD+11]. **Beta-Barrel** [NS18]. **Beta-Binomial** [JAG17]. **Beta-Helix** [CBM+02]. **Beta-Sheet** [KAS09, SOD+11]. **Betamax** [GNI12]. **Better** [AOAAH17, BSWY98, CDS+16, HI97a]. **Between** [BSB+17, BYGI12, BH15, BG17, BSMA06, BLF14, CDL+19, CL21b, EMV98, FH18, HLCS10, JRS19, KK11, KNmS+22, KAC17, LYF+19, MWZ19, MTF+12, Par24, PNPC20, Sun18, TYS+20, WW19, WFL+20, YHW18,

YYL20, ZAG+18, Ami12, AFRV07, AFR+08, BMY01, Bet10, DLM10, GNME01, GB08, HMU06, JLMZ02, KYSE10, KVK08, MDB11, OK08, SH06]. **Between-Pathway** [HLCS10, KK11]. **Beyond** [Bay23, Let95, YWN11]. **Bi** [DBT11]. **Bi-Billboard** [DBT11]. **Bias** [BCPS04, DS19, Elh01, RCER21, SFA17, SKL+24, SG94]. **Biased** [Tay94]. **Biases** [KC96]. **Biclique** [BCCHZU18]. **Bicluster** [ASE20]. **Biclustering** [ACKK19, CK11, GHJ+12, SH17, vUMW08]. **Biclusters** [XWLJ08]. **Bidirectional** [WFC25, YL17]. **Bifurcations** [KG24]. **Big** [GBR17, SW11]. **BiGRU** [GZLY24]. **Biliary** [DYLK20]. **Billboard** [DBT11]. **Bin** [PMAP13]. **Binary** [AVS20, BSP+25, BR06, Bry96, CYY09, FBJ04, KMJ+20, KSSK09, MMA+21, SLA12, SMD+07, VA17, VSGD08, YWN11, vUMW08]. **Binders** [CGZD24]. **Binding** [BMB24, BZMM16, CRT+17, CWRF15, CY17, CGD09, GJZ06, HD16, KW21, LG22, LCY+05, OJFD18, OMS13, PZMM15, PQBB08, SKP+12, SMKS96, SSPNW06, SS04, WLF13, YJC18, ZRGHJ08, GMVC20]. **Binning** [APC21, DZS24, ML22, PKSB18, WLYC12, WY11]. **Binomial** [DLFS22, JAG17, KCG+19]. **Bio** [BMM+23, JMR+21, KFR04, MMN+21]. **Bio-Networks** [KFR04]. **Biochemical** [EAFM24, GW06, HLMR11, HXL+20, OBJO+03, SVP19, YY18]. **Bioinfomatic** [WQZ+19]. **Bioinformatic** [CYF+20, LLZ19, QbMyD+19, XXZ+21, YfZX+21, ZWQ19, ZLW+20, ZLB+20, ZDG+20]. **Bioinformatics** [AVS20, CSZ18, CSZ19, CSZ20, CSPZ21a, CSPZ21b, CSZ22, CSZ23b, CSZ23a, CCL+19, CCH+19, CKZL20, DNZ17, GFE+16, HA12, HSHC15, HHC17, HHZ+18, HASL18, KAD+19, LGD+19, LTL20, MXW+20, Pat24, Pat25, PS11, PVR+22, PMG+16, PSG+20, QQL+19, Rob96, AAoS+23, SSV19, SGCD19, Tan11, WXY+13, YSC15, YDG+20, ZCY+20, ZLSY20, ZXZ21, ZYD+19]. **Biol** [Ano20]. **Biological** [AMK00, AAC+06, ARSW22, AC17, BB15, CW09, CY17, CT07, CLDG03, DOB95, DGFMSS16, Elh11, ENS02, Fas94, FFM24, FP11, Fre11, GML20, GVTS04, GVTRS06, GBR17, HBD94, Ila20, JPR06, KW06, KNS14, KWBN19, KKS+06, LL05a, Ma11, MZS+17, MGW+07, MTH11, MC16, MBS+01, NB94, NSK09, PS12, PZZ20, QFLL22, RC14, RC15, RMK+18, RD09, SMS13, SM98, SG15, STRT96, SSTM19, SY09, TKW08, TA21, TBKR10, WLFW03, WHDN13, XL18, YS07, YDN12, YZ17, YY19, YjDG+23, Zha02, EN22]. **Biologically** [CIM+06, MMS95, NWN+10]. **Biology** [Ano94, Ano11b, Ano21a, AG98, Baf11, Ber11, Cal22, CKS12, CKS13, CKS14, CKS15, CGT12, DMV17, Dei19b, DND+19, DCL10, DFS95, EAM+17, GSSI14, JLmR+23, MR95, Mar95, PS11, PVR+22, Rob96, SG12, Sea01, Sun13, VRGC18, Woo99, Ano14, Prz24]. **Biomarker** [BR06, CYF+20, KWA11, LTL20]. **Biomarkers** [Ano20, CKZL20, FZF+20, FRD+17, KWB+13, LGD+19, LL05b, QLW20, SPSZ23, SKDR21, SVP19, TZZY20, VCY14, WWLC20, WQZ+19, WHLR20, XXZ+21, XWJZ20, YDG+20, YcXyW+21, ZLL+20, ZLSY20, ZDG+20]. **Biomedical** [EFM12, JJH+21, SKM05, SF03, VCY14, dGFMS16]. **Biomolecular** [CEKP+13, KC18, SNW98, YLC+20]. **Biomolecules** [AO08].

bioOTU [CDH+16]. **Biophysical** [SS04]. **Biopolymers** [WCC98]. **Bioremediation** [RPS02, SBRG20]. **Biosequence** [Buh03, HM14, SH04a, SM04]. **Biosequences** [BJEG98, ELP04]. **Biotic** [JJY+20]. **Bipartite** [ABR16]. **Bipartitions** [HLMS08]. **Birc5a}** [cLcSwP+21]. **BiRNN** [WFC25]. **BiRNN-DDI** [WFC25]. **Birth** [DAR23, JRH+09]. **Birthday** [Ano21a, IPSV22]. **BiRWDDA** [YWZ+19]. **Bistability** [CSP+12, VCS11]. **Bistable** [PCC+11]. **Bit** [CC11]. **Bitmap** [FDW20]. **Bivariate** [NHOV10]. **Blacklist** [WH20]. **Bladder** [LXL+20]. **BLAST** [AMOW10, CWC06, SBC+05]. **BLASTphylo** [ZMGN23]. **Blind** [CRT04, HSH11, IFT14]. **Block** [EVLZU19, GG04, KS05, LLCT05, SHB+03]. **Block-Free** [KS05]. **Block-Interchanges** [LLCT05]. **Blockers** [Tra19]. **Blocking** [YK19]. **Blocks** [BCCHZU18, JSN09, LZ10, MBR+94, MR08b, NMG+05, VST03, ZRHM94]. **Blood** [CUP19, FYJ18, YK19]. **Bloom** [PFK17, SK18, SHCM18]. **BLUP** [McP12]. **BNOmics** [GBR17]. **Bodies** [BDBB10]. **Body** [KC18, STV96]. **Boltzmann** [BHHR19, SSS20]. **Bonded** [MK06]. **Bone** [PM24, SRB+25, XLLS20]. **Boolean** [ADW23, AMK00, AMTY11, AFRV07, BCD+24, BS20, GQ09, GLM20, GSV+11b, GSV+11a, KR24, LL05a, LTSA15, MA13, SK13, VCS11, ZH14]. **Boost** [KWM10, GLM+09]. **Boosted** [yWCF06]. **Boosting** [DGW+13, WxLW+23]. **Bootstrap** [PABE+10]. **Bootstrapping** [FKZ09, GK18]. **Border** [KRD14]. **Borreliella** [RFH+25]. **Borreliella-Infected** [RFH+25]. **Both** [BJF+20, PRSV08]. **Bottlenecks** [MTYH09]. **Bottom** [PRC+13]. **Bottom-Up** [PRC+13]. **Bound** [AP10, CWRF15, CFH13, GP13, Hor01, MWD02, OJFD18, PU00, SMML24, TSTS12, YLC+17, ZZL22, ZWZ16]. **Boundary** [BLF14, RC06, SSS20]. **Bounded** [MP11, NR03, SD95, Sol09]. **Boundedness** [MDWZ24]. **Bounding** [FW12, IR22]. **Bounds** [BB06, KLM11, KKM+20, KS06, LTI10, MSS10, Sni19, WG08a, WZ24]. **BPscore** [ZW19]. **BPSO** [CYLY12]. **BPSO-CGA** [CYLY12]. **Brain** [AMS+22, BZB+22, FYJ18, YMxW21]. **Branch** [CWJ+21, CJK+97, Hor01, OJFD18, SMML24, YLC+17, ZWZ16]. **Branch-and-Bound** [SMML24, ZWZ16]. **Branch-and-Cut** [CJK+97]. **Branched** [HBK11]. **Branching** [GGM12, Sun95]. **Breadth** [JHA16]. **Breadth-First** [JHA16]. **Break** [Ale08]. **Breakage** [KB12, ZB15]. **Breakpoint** [AS10, Ale08, APA17, CBP21, EZFP+19, Kov14, SB98, ST05, SM16, SM17, kSyPhC+22, WZW15, XZS07]. **Breakpoints** [AFR+08, LS08a, SBD+00]. **Breaks** [TT12]. **Breast** [AS22, AF20, Ano22b, FRD+17, GCD20, HLK+13, JSZ+20, KTT20, LTZ18, LXS24, QLW20, SPSZ23, SGCD19, TMH+21, TXL+17, WFL+20, WZL19, ZZ20]. **Bridge** [KB12, ZB15]. **Bridges** [HWP20]. **Brief** [Tra19]. **Brownian** [FA12]. **Browser** [BP17, RGL94]. **Bruijn}** [WYT12, APF+20, BH14, CPFP24, CLJ+15, GTA22, HS23, MPC+11, OYB18, Ore20, RC24]. **Bubbles** [Sam09, WWZY19]. **Buffering** [LLJS19]. **Building**

[CJS12, MR08b, NHZ+15, PPL+23, SKSL97]. **Bulk** [LLG+20]. **Bundles** [CJD06]. **Buneman** [MBRS11a]. **Burden** [SWS+20]. **Burrows** [BVP+19, LMW05, Lip05]. **BWM*** [JJGD16].

C [CYZ+20, DLFS22, DZS24, MSRS24, RBH+19, ZLTS13]. **Cacti** [PER+18]. **Cactus** [PDE+11]. **Caenorhabditis** [LYF+19, YHT+17]. **CAGE** [SZVM10]. **CAIR** [RBKJ19]. **Calculated** [BGTSB98]. **Calculating** [DM17, HTZ+13, HMU06, LWZ21]. **Calculation** [BS98, LABD+06, NL09, SEV09, SD95, XLZ13]. **Calibration** [COL+18]. **California** [Cal22]. **Call** [Ano21a]. **Calling** [HMY+19, KS11, LHW+22, SFC11, TYSX19, WLA+18, XZ12]. **Can** [AWM+17, BF98, FHKR11, NLC17, VCS11]. **Canalyzing** [AMTY11, MA13]. **Cancer** [AS22, AF20, Ano20, Ano22b, Azi22, BP20, BR24, BSB+17, BLC+10a, BR06, CBP21, CW09, CWS+21, CNCK11, CZY19, CKB17, DCL18, DWK+20, FCGD19, FDD21, FSW+20, FRD+17, HHZ+18, HLK+13, HZL22, HFUH19, JMPR23, JZZ+19, JSZ+20, KTT20, Kha14, KCH04, KLC+11, LZHC15, LTZ18, LXS24, LL05b, LHC19, LLZ19, LXL+20, MXJ19, NCMS+21, OFS09, PNIM17, PSIM18, PIM23, Par24, QQL+19, QsYSxL23, QLW20, RM18, RV15, SPSZ23, SKDR21, SKL+24, SZY+20, SWS+20, SSZG24, SLT24, SGCD19, SSS+21, TMH+21, TA21, TXL+17, VUR11, VRU16, WXY+13, WPL+19, WZG+20a, WFL+20, WDZ20, WLC18, WZL19, WHLR20, YYJ19, ZCY+20, ZWQ19, ZZ20, ZDG+20, ZlWL21, ZYD+19]. **Cancer-Associated** [YYJ19]. **Cancer-Related** [CZY19]. **Cancers** [FLT+21, GAWI19]. **Candidate** [AJYJ18, EBK11, LL19a, WWLC20]. **Cannot** [BF98]. **Canonical** [AHK+02, BB15, MR08a, MHL22, NRW11]. **Cantor** [SF95]. **Capacity** [Elh11]. **Capillary** [MXW+20]. **Capsid** [CRB18]. **Capture** [FL94]. **Capturing** [EAM+17]. **Carbohydrate** [LKC21, WKC+95]. **Carbohydrate-Active** [LKC21]. **Carcinogenic** [DBBM09]. **Carcinoma** [BRC20, CCH+19, CWS+21, GCD20, GDL+15, LGD+19, LTL20, TYS+20, WSCL18, WWLC20, WWC+20, YDG+20, YcXyW+21]. **Cardiomyocytes** [WPS+25]. **Cardiomyopathy** [CKZL20]. **Careful** [DBT11]. **Carlo** [FDDK07, Hea97, JHN+23, KST96, LDW98, LLT06, LSHL04, NTMM06, XK05]. **Carrillo** [KS06]. **Carroll** [Sea01]. **Cartilage** [YBF19]. **Cas9** [ZDZ+20]. **Cascades** [BS09, LXL+20]. **Case** [BMR09, BZ08, CMLTZU14, EBS+22, Fom19, GJL+21, LBN94, LZBK15, LL23, McP12, MBS+01, OH03, PK19, PZZ20, Tra98]. **Case-Based** [LBN94]. **Case-Cohort** [LL23]. **Case-Control** [BZ08, McP12, OH03]. **Cassandra** [LCG18]. **CASTOR** [LC03a]. **Cat** [SW11]. **Catalytic** [SSB07]. **Catching** [WLF13]. **Categorical** [BFT04]. **Categorizing** [SLYC09]. **Causal** [BCPS04, KYSE10, Rot19, SMS13, WHJE19]. **Causality** [Ist19]. **Causation** [JCBX22]. **Causative** [FSD+14]. **Caused** [MRY+23]. **Causing** [KSS09]. **Cautionary** [BJ17]. **Cavity** [CRT+17]. **Cayley** [NFHM21]. **CCCTC** [KW21]. **CCCTC-Binding** [KW21]. **CD45** [CYZ+20]. **CDCA5** [BRC20].

cDNA [BCH+01, BLQZ04, CHK+02, GE04, WGW+01, YHC05]. **cDREM** [WBJ15]. **CE** [JDSB04]. **Cell** [BRC20, BZG+22, BNA+12, BGH+08, CWRF15, CWJ+21, CMS+25, CvS24, DSS+22b, DSS+22a, DSC+22, DLL+24, DCL18, FL94, FLT+21, GVA22, GWA+21, GSCG19, HD10, HAP12, HFUH19, JLSL24, KBZ+05, Kha14, LSBS18, LWN+18, LLG+20, LZHC15, LGD+19, LDBj22, LQ23, LTL20, MMA+21, MMKH15, MH22, MFJ+19, MSM20, MLS+23, MM19, MM21, MWL22, NZM+25, NBA+13, PLSL18, PLZX25, PM24, Par24, PD16, PD20b, QFLL22, jQLsY+24, RBH+19, RLA+06, SVA+19, SDFR16, SDK16, SCD+22, SH17, SZY+20, SZSA22, SSLL22, SZMS02, TINK98, TYS+20, TMG+20, WC16, WSCL18, WWZY19, WWLC20, WWC+20, cWxLlS+23, WVT23, XSH+22, YDG+20, ZCY+20, ZMppVN22, ZYB+04, ZLL+22, ZL22, ZTW05]. **Cell-Free** [LWN+18]. **Cell-Surface** [FL94]. **Cell-Type** [DSC+22]. **Cell-Type-Specific** [LQ23]. **Cells** [CMS+25, COL+18, KLC+11, LLS11b, LYF+19, LLL+20, TLP+14, WFL+20, WVT23, XLLS20]. **Cellular** [AAG14, BSK05, BS20, LBJM11, LBDVF10, MR08b, PLZX25, RRKT07, SVD14, SF12, TRB+09, XLZ+24, YLC+20, ZLU+22]. **Cellulases** [TRS17]. **Center** [SLL+17]. **Center-Star** [SLL+17]. **Central** [FYJ18, IPH18, KPW11, TA97, ZKWH17]. **Centroid** [WAM20]. **Centromeres** [OFS08]. **cerevisiae}** [SSW20]. **ceRNA** [JSZ+20, YcXyW+21]. **Certain** [BLR16, Kle99]. **Cervical** [LZHC15, LLZ19]. **CFINet** [LLT+25]. **CG** [Ano11b, Edi24]. **CGA** [CYLY12]. **CGH** [NHOV10]. **Chain** [ARSW22, BKWK+00, CH15, CL99, HI97a, Hea97, HJ14, KST96, LSAS03, LDW98, ML10, NTMM06, Pia02, RLH13, RBEB13, SPD95, Sun95, WZCS00, WV95, WF12, XK05, YSFW08, ZRZD11, ZF05]. **Chaining** [BCA15, CJ23, JGT22, UMR11, ZRHM94]. **Chains** [AKLM02, Bet10, CCJ09, GJM04, Nue04, PRKG16, RS98, RROF95, Sch00, ZS11]. **Challenge** [GI95]. **Challenges** [DOB95, GMC08, Ma11, Rot19]. **Change** [GP20, Lai12, PJB+15, WT07, XLZ+24, XLZ+18b]. **Change-Point** [Lai12]. **Change-Points** [PJB+15]. **Changes** [BRR02, CC03, CK09, CJD06, FSW+20, GLMW13, Ma11, NKR+01, TBJF01, YYY+09, ZWQ19]. **Channel** [JB10, SSS20, SF12, ZZC+24]. **Channels** [SF12, SkY12]. **Chaos** [Yin19]. **Character** [Bry96, CKT16, NR03]. **Characteristic** [PRC+24, PSIM18, VY18, YY05]. **Characteristic-Specific** [PSIM18]. **Characteristics** [JRH+10, XK05]. **Characterization** [Cha95, CSP+12, HJ05, JPR06, LHL16, SVA+19]. **Characterize** [Par24]. **Characterized** [AV18]. **Characterizing** [ABTP23, MR95, NME+15, TZHR14]. **Characters** [AA18, BKPW95, GBBS07, KNmS+22, OYB18, Prz07]. **Charge** [CEKP+13]. **Check** [vLKMR22]. **Checking** [LR05, PSB17]. **Chemical** [ABF+25, GZW+16, Sol09, Tra19, vLSV+24]. **Chemistry** [LLW03, NFHM21, TW05]. **Chemotaxis** [ZPG+24]. **Chemotherapy** [COL+18]. **Chen** [Ano20]. **Cherries** [ARC13]. **Cherry** [LTsL24]. **Cherry-Reduced** [LTsL24]. **ChExMix** [YKPM20]. **Child** [WZ24].

Childhood [SnGqC20]. **Chimeric** [NBA+13, ZFBK09]. **ChIP** [BR12, KVDC06, NBC+11, WH20, XZ12, ZCK17]. **ChIP-Seq** [WH20, XZ12, ZCK17, BR12]. **ChIP-Sequencing** [NBC+11]. **Choice** [DBT11]. **Cholangitis** [DYLK20]. **Cholesterol** [TGTG19]. **Cholesterol-Ester** [TGTG19]. **Chordal** [Gus10]. **Chromatin** [KW21, MSRS24, SKP+12, SDK16, SNQ+14]. **Chromatin-Modifying** [SKP+12]. **Chromatyping** [CCMS20]. **Chromosomal** [RBH+19, ST05, XJZ+21]. **Chromosome** [KWBS11, LVC+04, LRL+07, LJP20, LZC+23, SBNS21, ZW19, ZS17, ZLTS13]. **Chromosomes** [AKWZ95, BCC+09, CJK+97, HYJ+19, XJZ+21, YDN02, ZKT14]. **Chronic** [CKL+17, ES07, YLC+17, ZLM+17]. **Ciona** [Eri09]. **CIP** [CASP10]. **Circadian** [YHW18]. **Circuit** [STP18]. **Circuits** [BS20, FPSD22]. **Circular** [Ale08, BCC+09, Far97, ML00, VT06]. **Circulating** [LWN+18]. **Cis** [MYS+20, BR12, Ist19, MDB11, SS05a, CCG06, WT17, WX08]. **Cis-Regulatory** [MYS+20, BR12, Ist19, MDB11, SS05a, CCG06, WT17, WX08]. **Clark** [HATI11]. **Class** [BR06, CV11, HSH14, HJR12, JLSL24, LJ05a, MC10, MS03, QP09, RMS02, Vij22, WGL98, WJD14, WZC96, ZYB+04]. **Classes** [Mar94, NR03, NW12]. **ClassGraph** [CC23]. **Classification** [AVS20, ALB+19, AT05, Azi22, BDBF+00, BZB+22, BRR06, BFL05, BP16, CBS+20, CC23, CCF10, CWJ+21, CYLY12, DPSW20, DKF09, ENS03, FdSdSR+15, HA12, HVAW04, HY16a, HYJ+19, LDS12, LRD19, LCG+22, LZL+23, LFD03, MC10, MBLZ09, OAR+24, QP09, SRF16, TM22, URB+19, WRS+99, WTY19, YGP05, YTS12, YQDW23, ZZL23a, ZAG+18, ZM16]. **Classification-Based** [ALB+19]. **Classifications** [BL02, PWCN02]. **Classifier** [AaHP+21, KCH04, PIM23, RLK+09, SZTW12]. **Classifiers** [BGJ+04]. **Classify** [AB00, KBLS24]. **Classifying** [AS22, LGS20, MC08, MEF24, MTR+03, SF95, XYX+22, YKPM20]. **CLHGNNMDA** [ZWD25]. **Clinical** [Ano22b, BSB+05, KBJ07, MRY+23, TMH+21, YQDW23]. **Clique** [MTF+12]. **Clique-Based** [MTF+12]. **Cliques** [MSRS24, PWFZ17]. **Clock** [CKS06, HP96]. **Clocks** [RD09]. **Clonal** [FLT+21, SLS23, SHMS08]. **Clonality** [DMW+17]. **Clone** [DFS95, SBT00, Wen05]. **Clones** [JM95, Sch97a]. **Cloning** [CLM+16, SK23]. **Closed** [KFR04]. **Closed-Loop** [KFR04]. **Closely** [AWM+17, WYT12]. **Closely-Related** [WYT12]. **Closing** [PNPC20]. **Closure** [ML10]. **Cloud** [KAD+19, PDZ+16, TH17a]. **Cloud-Based** [PDZ+16, TH17a]. **Cluster** [AN18, GTA+04, HMN21, KBZ+05, KNS14, SZVM10, SDP+20, WMG+24]. **Cluster-Based** [WMG+24]. **Clustered** [CBW07, HSD05, MAN16]. **Clustering** [AO08, BF02, BDN19, BR06, BDSY99, BL02, BV09, CZNF19, CC11, CDH+16, DMDR17, DBB+02, DS03, ETLK19, FBJ04, FLT+21, GLM+09, GTA+04, HTY22, HSL07, HHC06, JHN+23, KBG18, KMZ+10, KABH15, LDBj22, LMP08, LC03a, MGW+07, MMK+21, MAN16, NVCW15,

OYY+12, PKSB18, QsYSxL23, jQLsY+24, SM20, SLL08, SPD18, TZB+23, TVNP15, WSW15, cWxLlS+23, XZW15b, YZ17, YL17, YJC18, ZZHL11, ZlWL21, ZWD+04, ZL22, ZCK17]. **Clustering-Hashing-Signal** [HHC06]. **Clusterings** [NWN+10]. **Clusters** [BJMS09, Boe18, CCT09, GPCP11, HG05, Jah11, KK22, LCXC05, LAF+14, LHXH08, MBC+18, NMG+05, Par07c, TZB+23, TWY02, VBSS10, WMPS11, YYZ+10, ZSV+09]. **Clusterwide** [ZWD+04]. **cmb.2019.0110** [Ano22b]. **cmb.2019.0224** [Ano20]. **cmb.2020.0112** [Ano21b]. **CNB** [JLmR+23]. **CNB-MAC** [JLmR+23]. **CNS** [DHY02]. **CNVeM** [WHY+13]. **Co** [BGL24, HM14, LZS09, TZZY20, TPSB19, TBKR10, WLM21, XJZ+21, ZHQS05]. **Co-Evolution** [HM14, TBKR10]. **Co-Expressed** [ZHQS05]. **Co-Expression** [BGL24, TPSB19, TZZY20, WLM21]. **Co-Occurrences** [XJZ+21]. **Co-Regulation** [LZS09]. **Coagulation** [LXL+20]. **Coalescence** [BW12, PMGE21]. **Coalescences** [TR11]. **Coalescent** [DLL+12, DR15, ME12, Ros07, TRW23, TRIN07]. **Coalescent-Based** [DLL+12]. **Coarse** [AJYJ18, CB07, DPS+20, PVFB06]. **Coarse-Grained** [AJYJ18, DPS+20]. **Coarse-Graining** [CB07]. **Code** [AMOW10, Ist19, LZL+23]. **Codes** [BDM+07, KKe23, NSZ99, PB18]. **Coding** [ADRS24, BWGM17, CC03, GT16, HLY25, JLY08, LZL+23, LWZ21, MM06, RM00, Sal95, Sel13, SlGW+23, SZTW12, SG94, SDP+20, SK19, TE96, TBB00, WH06, XMU96, YY05, YQDW23, YYJ19]. **Coding-Based** [HLY25, SlGW+23]. **Codon** [CHJ05, DS19, GYA+23, SG94, SLYC09, TVNP15]. **Codons** [WMK17]. **COE** [ZPX+10]. **Coefficient** [HL16a, SPD18]. **Coevolutionary** [DC16b]. **Coexpressed** [TML+02]. **Coexpression** [JJY+20, NXGL20, PdBdP+22, QLW20]. **Coffee** [LCG18]. **Cognitive** [Jos96]. **Cohort** [Ano20, LL23]. **Coil** [ODPB18, SLO07]. **Coiled** [ODPB18]. **Coincident** [Mar94]. **Coleochaete** [WC16]. **coli** [ALR18, Kha14]. **Colinear** [CJ23, JGT22]. **Collaboration** [WCZ+18]. **Collaborations** [YYL20]. **Collaborative** [CZY19]. **Collagen** [Yan09]. **Collapsed** [CP05]. **Collapsing** [GDHC95]. **Collecting** [TBP+13]. **Collections** [MNSV10, ZCK17]. **Collective** [HL16b, RAKL10]. **Colocalization** [GVMB24]. **Colombia** [EBS+22]. **Colon** [Kha14, MXJ19]. **Colonies** [ZZL22]. **Color** [APF+20, PTWB09, SFC11, TP11, YHC05]. **Colorectal** [BSB+17, DWK+20, QQL+19, WZG+20a, ZWQ19]. **Colored** [BP16, CPFP24, HS23]. **Colorful** [RRNB13]. **Comb** [CKS06, SFC11]. **Combination** [KVM14, ZZL23a]. **Combinations** [STRT96, VCY14]. **Combinatorial** [AA18, AKLM02, AHK+02, BDKSY00, Cha95, EAA+09, LLW03, MCC01, Neb02, NW12, OB10, PGBK11, Pev95, SVK10, ST02a, SZVM10, SZMS02, ST17, SLRM09, TW05, WJJ11, WBJ15, YJ06, ZFBK09]. **Combinatorics** [Clo06, HLR14, KB12, MN15, PV17]. **Combined** [FNC08, MG06, PL06, SKS+09, SG94, cWxLlS+23, WPS+25]. **Combines** [DRT+25]. **Combining** [AMR20, BG98, BMB24, BR23, EAA+09, KPS00, LN03, NCMS+21, PWFZ17, PGA+11, SH04a, XGD24, YRG+19, ZLL+22].

Comes [HPL+20]. **comets** [HD16]. **Command** [MA19]. **Common** [AL25, ATLS07, BFS10, BVP+19, CMvH15, CHKK99, DMHM97, EPSV98, GF16, HJ05, KLW96, LNW01, NW12, PYIM22, PSCP09, SSPNW06, SB07, TAA16, UBTC06, WWZ19, dMRR14]. **Commonalities** [MJS24]. **Communities** [BBP10, RHS+21]. **Community** [AZ11, Rob94, Sun18, WYT12]. **Commuting** [AT08]. **Compact** [OB16, Par07a, PQBB08]. **Comparative** [Ano11b, BBP10, BBEM09, BCA96, BGL24, BMR+19, CY10, DPSW20, DJK+99, Edi24, ES07, FW12, KV17, KPB+04, LSRR18, PTWB09, SMZ+12, SIK+05, WMG+24, WWZ+16, WH06, YYW14, NV09]. **Comparing** [ABR16, AS19, BG17, GNME01, GJL+21, HSG22, HBW+05, KRF+12, LVC+04, LMP08, MMS95, NK07, Neu14b, NV12, RYY22, WXY+24, ZKWH17, Zha97]. **Comparison** [AS10, AFCN13, BCH+07, BHRV00, BWS13, BR03, BS06, BPL02, Bet10, CH15, CWYB16, CT07, CGZ04, DLPH06, DHY02, EJT00, FP11, FS99, HBD94, HG18, KMUK22, KVZ24, KPW11, LST+17, LHXH08, LZF+05, ML00, MHS06, MP94, PD16, RCSW09, RND+23, RS01, SRF16, SSD07, SRZ+13, SJ12, SY09, TPH+09, VT06, WRSW10, WAM20, YYA11]. **Comparisons** [Lip05, Par07b, PDE+11, PWT18, SSTM19, VCY14, ZW19]. **Compatibility** [BKPW95, BSWY98, KAC17]. **Compatible** [BLR16, PMCB08]. **Compensating** [SS07]. **Compensation** [LTCH11]. **Competition** [SLT24]. **Complement** [LXL+20]. **Complementarity** [BMB24, CFR12, JPB+15, NLC17]. **Complementary** [CTC21b]. **Complete** [BL98, FJK+99, HP96, HPVS96, KMB+20, Sam09, TM17, GKM+10, OFCLH11]. **Completeness** [KKC+22]. **Completion** [KMCKS17, LLW+20, MSM20, ŽZ15]. **Complex** [BHL+18, CWYB16, FADH17, HMN21, JPR06, JCBX22, KLS15, KAD+19, KHK10, LCD11, LQPE+10, NLC17, OJOD+04, RBEB13, TMC+18, Vij22, VBSS10, yWCF06, WZCY21, WLS+11, Wu08, XSS08, ZSV+09, ZZNM15, ZZL+23b]. **Complexes** [FCS12, FKZ09, FR14, GMVC20, LZS09, LXYC09, LSSD18, MZS+17, SIK+05, WlLK+12]. **Complexity** [AWM+17, BK10, BDPSS01, BFK+11, CMLTZU14, CDKL09, CGP+98, GSSI14, Gus01, HLMS08, JZGA20, Jus01, KLZU06, Kov14, LHC09, MP11, MGSA06, NP09, OBDD19a, PG03, QGP10, RLVCVR17, SBC+05, VRU16, WJ94, WZZU07, YA11]. **Compomers** [Böc04]. **Component** [CWRF15, GSCG19, LSBS18, PD20a, PGAE04, RMC+23, SLYC09, TE96, ZZNM15]. **Composed** [AWM+17]. **Composition** [AC10, HZNF06a, HZNF06b, ML22, MLC10, RKTS14]. **Compositional** [CWH+22, FHZD17, YYA10]. **Compositions** [FLS94]. **Compound** [AJV+16, GPCP11, PRSV08, RS98, ZRS+12]. **Compounds** [Wil99]. **Comprehensive** [GWM+21a, HXL+20, KV17, KCH04, KLC+11, LHC19, PAS+13, WZH+18, WZG+20a, ZRNA20, ZF05]. **Compressed** [AZ11, RPR+15]. **Compressing** [KSK+11]. **Compression** [AOAAH17, CPFP24, GYZ19, HWSH18, KK11, MM06, RC24, VFOK18, WR23]. **Compression-Based** [MM06, WR23]. **Compressive** [YS23]. **Compressor** [AH20]. **Comput** [Ano20]. **Computation** [ARRW99, AT08, BGHY04,

BFT04, BCC+09, BJMS09, CIM+06, DSV12, ES06, Jah11, Kei05, KSSK09, OK08, PXLP23, PA03, RJS02, Ric06, RWB+98, RW99, SWS+20, SCC+98, SSIP+19, TCL+16, WWZ19, WX08, WHC09, ZW07]. **Computation-Based** [WX08]. **Computational** [AEB+04, Ano94, Ano00, Ano11b, Ano14, Ano21a, AP09, Baf11, BMM+23, BÖB+23, Ber11, BZMM16, BMP+09, CBH+12, CGOT10, CLSW02, DMV17, Dei19a, DDK21, DND+19, DKC15, DFS95, FA12, GSA14, GPOP+17, GSV21, HSHC15, HHC17, HASL18, HZL22, HTH+17, JLmR+23, JMR+21, JJGD16, Jus01, KV08, Kum22, LZHC15, LHC09, Ma11, MMN+21, MSN+20, OBJO+03, PDZ+16, PLSL18, PGV16, PS11, PVR+22, PG03, Prz24, QGP10, RBKJ19, SCB14, STHG+08, Sea01, SZL+23, SW11, Sun13, TS96, TBKR10, VRGC18, WJD14, WYC+18, WXY+24, Woo99, XXU98, XXCE00, ZLP22, ZLM+17, ZMK23, ZWZ16]. **Computational-Based** [WYC+18]. **Computationally** [SEV09]. **Computations** [CSA98, FG04]. **Compute** [BVP+16, Clo05, SLM15]. **Computed** [AG23]. **Computer** [Ist19, KMM17, LVC+04, SMKS96]. **Computers** [Elh11, FHS00]. **Computing** [AFRV07, AFR+08, BMY01, Bea95, Ben21, BCA96, BBDS21, BSSz+20b, BCA15, zCULW20, DLM10, DLD+14, FLL00, GKMS23, HKS08, HLMR11, JM97, KLM11, KW14, KR24, LJ05b, LFT+98, LTSA15, MTF+12, NBB18, PPL+23, PGM07, SVK10, SHRB11, SLA12, SM17, SVL+10, VRGC18, WC07, WW18, WW19, WY21, WZW10, WZ24]. **Concentrations** [Lie05]. **Concept** [BS09, GMF+08]. **Conceptual** [GCB20, KWB+94]. **Condition** [Kea97]. **Conditional** [FHZD17, LCWG06, LCGW09, LGS20, PZZ20, RM00]. **Conditioned** [BYGI12]. **Conditions** [BLF14, CD21, QFLL22, ZZUPY06]. **Conference** [Ano00, Ano10b, Ber11, DMV17, DNZ17, DND+19, Edi24]. **Conferring** [ZZZU20]. **Confidence** [KWM10, SFR+18]. **Configuration** [LJ05b]. **Configurations** [DR17, YE02]. **Confirmed** [MXW+20]. **Conflicting** [CEJM16, CHSY10, OR14]. **Conformational** [CJD06, FvdBB16, GLMW13, GC15, LBBV+18, ML10, NH08, NDMK17, SNW98, ZPD+10]. **Conformations** [AMK18, ZRZD11]. **Confounders** [SS07]. **Confounding** [TRIN07]. **Conjecture** [Zha97]. **Conjugate** [Lar06]. **Connected** [AC17]. **Connection** [Fic95, NZM+25]. **Connections** [DCD19, Yu24]. **Connectivity** [KSG07, LJCZ20, LBDVF10, XLZ+18b, ZLTZ25]. **Consecutive** [CHSY10, LH03, MP11]. **Consecutive-Ones** [MP11]. **Consensus** [APVM11, BTZ06, CY10, zCULW20, CJS12, EMD95, HSL07, MS00, QEk24, SPW22, SW11, WZG+20b]. **Consequences** [CMvH15]. **Conservation** [BBN11, CT07, HMK24, KSG07, RDH04]. **Conserved** [DKA+17, HG05, HS14, ISB12, KKS+06, Pen20b, SFN97, SS04, TRS17, dMRR14]. **Considering** [EBS+22, GPOP+17, LK24, SMS13]. **Consistency** [JLRS18, LCG18, RSEK24, TR11, WHD15, WMPS11]. **Consistent** [ARS17, MMS95, RRFS98, TRW23]. **Consistently** [JFLL20]. **Consisting** [KG24]. **Consolidated** [LDB+07]. **Constant** [BP14, BS98]. **constNJ** [Mat10]. **Constrained** [DZS24, EVLZU19, HD16, KPZU11, NK11, PYIM22,

PM24, SlGW+23, WDA01, YFBK07, XXCE00]. **Constraint** [QsYSxL23, SAM06, TMfTK23, VRS12]. **Constraint-Based** [TMfTK23, VRS12]. **Constraints** [AKG+13, DQS+11, FvdBB16, Ham12, HY16b, LW22, Mat10, MSZM96, NW05, WWZ19, ZZ14b, vLSV+24]. **Construct** [SFR+18]. **Constructed** [LGD+10]. **Constructing** [BDC97, BDCG+98, CY10, CCPT17, EZ98, GZW+16, JZL+20, KKe23, KS12, MBR+94, RROF95, SH05, WG98, Wu13, XvdL05]. **Construction** [BVP+17, CF14, CA12, DHM+05, DHWZ06, GLM16, HXL+20, KMB+20, LMW05, LLD+16, MS99, PMF+03, PCC+11, Prz07, VV97, YTS12, ZWK+20]. **Constructions** [CD07, CD08]. **Consuming** [MFJ+19]. **Consumption** [CCDB21]. **Contact** [AMW07, AMDY11, CCI+04, JAJ24, KWM10, LJK16, XS07, ZWY+17, KWM10]. **Contacts** [AP10, DLFS22, DZS24, GP13]. **Contagious** [BBN24]. **Contained** [Bro98]. **Containing** [HV07, JHA16, TGT08]. **Containment** [GYZ19]. **Content** [Hua10, LZX12, MLC10, SKGG17, Zha02, IP09]. **Content-Based** [LZX12]. **Context** [ARSW22, BF02, FB12, GVMB24, GTT06, HB11, IR22, KJmZ+22, ShHGC20]. **Context-Aware** [GVMB24]. **Context-Dependent** [IR22]. **Context-Sensitive** [HB11]. **Context-Specific** [BF02, KJmZ+22, ShHGC20]. **Contextual** [HPL+20]. **Contig** [DZS24, HSF+00, Lu15, PBMC17, RCSS12, TM17]. **Contigs** [CN17, ML22, Pre13]. **Contiguities** [OR14]. **Contiguous** [MRR+08]. **Contingency** [PK19]. **Continuous** [BJGG+03, CF14, DPR97, HJ14, KPS00, MV19, OC00, SLL+23, ZPD+10]. **Continuous-Time** [HJ14]. **Continuously** [HJD17]. **Contrast** [Åst03]. **Contrastive** [LZY+23, ZWD25]. **Contributing** [yWCF06]. **Contribution** [DCV+07]. **Contributions** [PVR+22, PIWR15]. **Contributors** [TEMM12]. **Control** [ADRS24, BZ08, Che06, CD21, JLmR+23, KFR04, McP12, OH03, PYIM19, PZZ20, QMMW11, RUGR18, ST02a, SSV19, SH04b, WZ23, WA10]. **Controllability** [Che06]. **Controlled** [LTTS12, ZHQS05]. **Controlling** [BHL+18, DT12]. **Convergence** [KFC+11, ZZL22]. **Converging** [HNW99]. **Conversion** [HZH+10, SDG+07]. **Convex** [HHX16, WTY19]. **Convexity** [CP19, TL23]. **Convolution** [Erd05, Ser15, ZCZ+23]. **Convolutional** [AMS+22, BLP+22, CLLL20, HYJ+19, MPZL23, MDL+18, PLSL18, TKSA24, XYX+22, Yu24]. **Cooperating** [HPY03]. **Cooperative** [Ami12, DQS+11]. **Coordinate** [LSL+16]. **Coordinated** [SnGqC20, ZTD+22]. **Coordinating** [FPSD22]. **Cophylogeny** [LHC09, OFCLH11]. **Copy** [ACBM18, CD18, CKZ+19, CQG10, FSW+20, HG11, Lai12, LLG+20, LABD+06, PNIM17, WCM+08, WHY+13, WV11, ZEKKR18, ZB15, ZZS17]. **Copy-Number** [ZEKKR18]. **Copying** [YHEP15]. **CORaL** [AFCN13]. **Core** [BHPS99, GKKS98, LXYC09, LHC19, RMWC16, SKG+00, WlLK+12]. **Core-Attachment** [LXYC09, WlLK+12]. **Coregulated** [BRC20, CC11]. **Coronary** [YHW18]. **Coronavirus** [DDK21, Pen20b, Tho21, YGP05]. **Correct** [RPW13]. **Correcting** [LGD+10, SKL+24, SBC+05, XMU96].

Correction [Ano02a, Ano02b, Ano05, Ano08, Ano09a, Ano11a, Ano14, BDK+16, ETLK19, KFDT02, SSLMW10, ZGRB10]. **Correlate** [CWRF15]. **Correlated** [CD18, KCG+19, WHD13, WHD15, WFH18]. **Correlation** [BB15, BL02, FVTH03, GVA22, HM14, KNmS+22, Kon07, KT01, MHL22, YHW18, ZPD+23, ZY23]. **Correlations** [AS23, DPHH05, KIYM13, MBVA07, SSLL22, TE96, VB09]. **Correspondence** [KPB+04]. **Corresponding** [ZKWH17]. **Corrigendum** [DFS96]. **cOSPREY** [PDZ+16]. **Cost** [ZZ14a]. **Costs** [HP97, JGT22]. **Cotranscriptional** [TKO21]. **Count** [BML+16, GLM16, JÖNK17, PFRD05, RS01, SSLL22]. **Counters** [RC24]. **Counting** [CGI+07, EZ98, FPS22, NS23, PGV16, Ros07, SRSD11, SF95]. **Counts** [Sch00, WVT23]. **Coupled** [BC94, Li09, LDLZ12, RLK+09]. **Coupling** [AWZ+17, LDLZ12]. **Course** [GK18, HMY+14, KK18]. **CoV** [ABTP23, Ano21b, BBH+21, MMK+21, NKG+21, SS23, TM22, ZSB+23]. **Covariance** [ÅMR07, LLD+16, ZH07]. **Covariation** [CCPT17]. **Covariations** [GJZ06]. **Covarion** [AR06, GJM04]. **Cover** [CCT15, Ore20]. **Cover-Free** [CCT15]. **Coverage** [CAB11, DDC+20, DMW+17, ML22, NM14, PV17, Pre13, Sch97a, Wen06]. **Covering** [ABR16, GHM+10, HNW99, OB16, OYB18, SMML24]. **Covers** [GKMS23]. **COVID** [BZB+22, LCG+23, MRG+24, MJCM22]. **COVID-19** [BZB+22, LCG+23, MRG+24, MJCM22]. **COX** [ALB+19, Ano22b, LL23, TMH+21, ZZ20]. **COX-2** [ALB+19]. **CpG** [FB12, JZZ+19, KLC+11, YCCL18]. **CpGCluster** [YCCL18]. **CpGCluster-Teaching** [YCCL18]. **CPH** [HTH+17]. **CPU** [WCZ+18]. **CPU/MIC** [WCZ+18]. **Craniopharyngioma** [fZbMqW+20]. **CRDet** [CWJ+21]. **Creating** [ZMK23]. **Creation** [WH20]. **CRISPR** [BBC16, ZDZ+20]. **CRISPR-Cas9** [ZDZ+20]. **Criteria** [GTA+04, LSG04, TNSS13]. **Criterion** [HSD05, LWLJ10, NM14, TP11, ZZL23a]. **Critical** [BHL+18, BSB+05, NXGL20, SnGqC20, WDZ20, ZW07]. **Critiquing** [CBS+20]. **CRMs** [Eri09]. **Cross** [BRD+05, BMN+07, BR23, CJC01, CXW16, DVS19, DBHC24, KMUK22, KAC17, LRNBJ10, LLT+25, MPZ+20, MDTD06, PMG+16, RV15, SSW20, YHW18, ZF07]. **Cross-Hybridization** [BMN+07]. **Cross-Immunoreactivity** [BR23]. **Cross-Kingdom** [PMG+16]. **Cross-Links** [CJC01]. **Cross-Membrane** [CXW16]. **Cross-Modal** [DVS19]. **Cross-Modality** [LLT+25]. **Cross-Organ** [KMUK22]. **Cross-Sectional** [BRD+05, RV15]. **Cross-Species** [DBHC24, ZF07]. **Cross-Validated** [MPZ+20]. **Cross-Validation** [KAC17, SSW20]. **Cross-Validatory** [MDTD06]. **Crossover** [AEB+04, SDG+07]. **Crosstalk** [SSW20]. **Crucial** [GPOP+17, PM24]. **Cryo** [HLG18, KAC17, LCG+22, NS18, YLZ+24, ZKWH17, BRZH15, HSH11]. **Cryo-Electron** [HLG18, KAC17, LCG+22, NS18, YLZ+24, ZKWH17]. **Cryo-EM** [BRZH15, HSH11]. **Cryoelectron** [ZLU+22]. **Crystal** [LLW+20]. **CSAM** [HHC06]. **CSAX** [NME+15]. **CsSNP** [WWZ+16]. **Cubic**

[YTMY17]. **Cuckoo** [Azi22]. **CUDA** [SSLMW10]. **CUDA-Enabled** [SSLMW10]. **CUDE** [DBM09]. **Cue** [JKG+04]. **Cue-Signal-Response** [JKG+04]. **CuMiDa** [FCGD19]. **Curated** [AEH17, DCL18, FCGD19, FDD21, SKDR21]. **Curcumin** [GAWI19]. **Curcumin-Synthetic** [GAWI19]. **CuRDa** [FDD21]. **Current** [CL21b, SLB+97]. **Curve** [CL21b, VY18]. **CUSA** [DBM09]. **Customizing** [IRCA21]. **Cut** [BMS10, BWS11, CJK+97, DHM97, LTCH11, Mar94, MJS23, SLM15, XLZ+18a]. **cutPrimers** [KBKF17]. **Cuts** [ZS17]. **Cutting** [KBKF17]. **Cycle** [AI12, AODD22, APA17, AT08, BRC20, OBJO+03, ZTW05]. **Cycles** [GQ09, XZS07]. **Cyclic** [KKe23, LSL+16]. **Cyclin** [CASP10]. **Cyclin-Dependent** [CASP10]. **Cysteine** [KMRG09b]. **Cytokine** [Con04]. **Cytometry** [PSG+20]. **Cytopede** [HD10].

d [HBD94, ABF+04, AT05, CFB+07, DSN14, EHK+02, GRM09, GWX18, GMS05, KMRG09a, KMRG09b, PSCP09, SVD14, Shi10a, ZLTS13]. **D-Electrophoresis** [EHK+02]. **D3GB** [BP17]. **DAG** [PVFB06]. **DAHNGC** [ZCZ+23]. **DahShu** [HTH+17]. **Damage** [LVC+04]. **Damage-Processing** [LVC+04]. **Data** [ÅMR07, ADP+08, AI12, ACKK19, Aku04, AGH+18, AB16, AR17, AS23, ACL15, AJV+16, AFCN13, ASE20, BB06, BKWK+00, BBN11, BJGG+03, BF02, BHGCS11, BB15, BDN19, BRD+05, BFT04, BDCKY03, BMR09, BBV+14, BCG+18, BFK+10, BGJ+04, BRZH15, BML+16, Boe18, BVP+16, Bro98, CR09, CCMS20, CCT09, CC11, CH15, CD18, CWH+22, CRT04, CQG10, CCPT17, CAC+23, CYY09, CYLY12, CS15, CBG+14, CF97, CHK+02, CBM+02, CvS24, DOB95, DMTV09, DZM+03, DJK+99, DLML10, DKC15, DMW+17, DLFS22, EZFP+19, EFM12, Ell20, EAA+09, EHC+13, FVTH03, FHZD17, FdSdSR+15, Fas94, FNC08, FBJ04, FSZ02, FRD+17, FPS22, FFSL22, FMH06, FLNP00, FLT+21, GZY+22, GHJ+12, GK18, GE04, GWA+21, GLM+09, GCB15, GSCG19, GBR17, GZW+16, GME01, GCD20, GZW+21, GLM16, Gus10, HTZ+13, HMY+14, Hav06, HMY+19]. **Data** [HHE13, HWH+13, HLK+13, HVAW04, HLCS10, HSL07, HM14, HZL22, HMF07, Hua10, HHJ+13, HTH+17, HWZ+21, ITSH00, IFT14, JKG+04, JLSL24, JZ10, JÖNK17, Jus06, KVM14, KS12, KP96, KCG+19, KV23, KVDC06, KMC00, Ker03, KMM17, KAC17, KK18, KAD+19, KK22, KGN09, KABH15, KBCBS11, KCH04, KT01, KPP+22, Lai12, LSBS18, LLSH19, LLG+20, LTCH11, LXYC09, LYPC13, LVC+04, LSG04, LJ05b, LL05a, LLS+19, LLWZ19, LLW+20, LKL21, LYH+19, LS23, LFD03, LRM11, LMW05, LABD+06, LL05b, LLD+16, LLZ19, LSHL04, LH03, LDB+07, LZX12, MLOT17, MSS+22, MMA+21, MPZL23, MGW+07, MS99, McP12, MH22, MRY+23, MEF24, MSM20, MLS+23, Mos03, MM19, MM21, MBS+01, MTR+03, NKR+01, NHOV10, NH08, NME+15, OMS13, OH03, PP23, PWCN02, PFK17, PLL16, Pic08, PSG+20, PC05, PSLP06, PX13, QFLL22, jQLsY+24, QP09, QLW20, RH19]. **Data**

[RUGR18, RLH13, RV15, RMC+05, RBK94, RHS+21, RBH+19, RG95, RL94, SIC+09, SK17, SM20, SG10, SG15, SKGG17, SS07, SHRB11, STHG+08, SDK16, SDC03, SS23, SRF16, SD95, SCD+22, SLL+23, SIK+05, SSLMW10, SH17, SnGqC20, SPBB15, SR10, SK23, SSZG24, SBRG20, SLZH15, SSLL22, TBL18, TA21, TXL+17, TAJZ23, TH17a, TH17b, TMG+20, UGS19, WMD06, WHDN13, WHD15, WZH+18, WDZ20, WZCY21, cWxLlS+23, WDF24, WV11, WVT23, WGW+01, WZW10, WlLK+12, XvdL05, XZ12, XZW15b, XSH+22, YS23, YHB+03, YL17, YS19, YA11, YLC+20, YMZ+12, ZRZD11, ZWSF05, ZLTS13, ZlWL21, ZW23, ZZL23a, ZL01, ZPB+10, ZZL+17, ZLL+22, ZL22, ZPD+23, ŽZ15, ZCK17, vUMW08, ARRW99].
Data-Based [GZY+22]. **Data-Driven** [CS15, ZZL23a]. **Data-Knowledge** [WHD15]. **Database** [AMOW10, BSB+17, BZW+00, FCGD19, GWL+19, GE17, HHJ+02, KV17, Kar95, KWB+94, KDL+94, KLC+11, LCG18, MXJ19, MR95, NCC+96, OAHA94, RGL94, RND+23, SKDR21, SM04, SZSW09, TINK98, TA21, VAS+18, bVRN+19, WHL17, WZC96, YLW+15, FDD21].
Databases [AaHP+21, CZW+19, EAFM24, Fas94, JDK+18, Mar95, MAN16, PBB+21, Rob94, SK18]. **Dataset** [DLL+24, MTR+03, XSH+22]. **Datasets** [BR12, CAB11, FDW20, LQ23]. **Dating** [CDFC00]. **Davidson** [Dei19b, Ist19]. **db** [bVRN+19]. **DBCAT** [KLC+11]. **dbHT** [DC16a].
dbHT-Trans [DC16a]. **DCGNN** [ZZC+24]. **DCJ** [BCC+09, BS10, KWBS11, YF09]. **DDI** [HXY+23, WFC25].
De-differentiation [KLV+13]. **DEA** [ZW23]. **Deactivation** [FDDK07].
Deaminase [MMHC98]. **Dec** [Ano20]. **Deciphering** [SCD+22]. **Decision** [CvS24, HZNF06a, HZNF06b, LL05b, Sal95, SDFH98]. **Decoding** [DLPH06, Yin19, ZHZ+16]. **Decomposable** [Far97]. **Decomposition** [Bar04, DWMT22, GBBS07, LRSG07, MEF24, SAM06, Xu09].
Decomposition-Based [MEF24]. **Decompositions** [KKC+22, NWN+10].
Deconvolution [DLL+24, GSS+20, Hav06, HSH11, LLG+20, RLA+06, SSH+20, SDK16].
Deconvolving [WSS03]. **Decoy** [YLW+15]. **Decycling** [MDK24]. **Deep** [AMS+22, BW12, DCH21, EZFP+19, FFB20, GWM+21a, HYJ+19, KW21, LCW16, MSS+22, MSM20, MJCM22, MHL22, MWL22, Nai18, NES22, PXLP23, PLSL18, PYG+19, jQLsY+24, SZSA22, TR11, WYC+18, XGD24, YMxW21, ZGRB10, ZGW22]. **Deep-Convolutional** [PLSL18]. **deepMc** [MSM20]. **DeepMinimizer** [HZK22]. **DeepPPThermo** [XGD24].
DeepSNP [EZFP+19]. **DeepVir** [MJCM22]. **Defense** [VND17]. **Deferred** [SV97]. **Define** [CNCK11]. **Defined** [JHA16]. **Defining** [NDMK17, ZZNM15]. **Definite** [ZLTS13]. **Definition** [KFC+11, UMR11].
Definitions [DAE+19, TBKR10]. **Defy** [HLK+13]. **Degeneracy** [BKKSD01]. **Degenerate** [LS05, PO04]. **Degeneration** [FZF+20].
Degradation [BFK+11, vLKMR22, YBF19]. **Degree** [MP11, RDR12].
Degrees [ML10, PFRD05]. **Deimmunization** [PCGBK13]. **Delaunay** [STV96]. **Delay** [ADW23, YMM+24]. **Delayed** [RSR+09]. **Delays** [GK06].
Deletion [DMP+06, TMfTK23]. **Deletions** [BP20, BWS11, HSH+09, YF09].

Delineating [KASM08]. **Denatured** [PGAE04]. **Dendritic** [URB+19]. **Dengue** [DM20]. **Denoising** [KABH15, LZL+23, YLZ+24, ZLL+22]. **Dense** [GPP+11, MZS+17]. **DenseNet** [JWL24]. **Density** [CKZ+19, CHK+02, FCS12, HSH11, HMK24, HLY25, KVDC06, NS18, SDP+20, ZKM21]. **Dentritic** [UTD+20]. **Dependence** [DPR97, FHZD17, HL16a, LTS20, SG15]. **Dependencies** [CKT16, DAL+08]. **Dependency** [BSKgG23, IR22]. **Dependent** [ABH03, CASP10, CHJ05, GTT06, HL16a, IR22, KK18, LFD03, NHOV10, RMK+18, SVP19, SLYC09, URB+19, VS98, DDK21]. **Depressive** [ZLTZ25]. **Deprivation** [RXH+20]. **Depth** [LHW+22, XLZ13]. **Deregulated** [LLZ19]. **Derivation** [SDG+07]. **Derivative** [HTM+22]. **Derived** [CASP10, LZ10, SVP19, WCL+18b, WZG+20a]. **Deriving** [HLMS08, ZMK22]. **DERNA** [GQEk24]. **Descendant** [QEk24]. **Descendants** [ZZS08]. **Descent** [Bro98, KLKH11, LSL+16, LLWZ19, SGP11, YCP16, ZL01, ZKT14]. **Descent-based** [LSL+16]. **Describing** [GSSI14]. **Description** [CT07, GRM09]. **Descriptive** [BGTSB98, HY16a]. **Descriptors** [CRT+17, Geo09]. **Design** [AMR20, AHK+02, BDKSY00, BBD+04, BZ08, CLM+16, CFR12, CDKL09, CS03, CM04, DHWZ06, GMC08, GQEk24, HD16, HJD17, HLH06, HWP20, JJGD16, JHLD20, KMP+04, Kle99, LG22, LS05, LL23, MSBR08, MPG+16, MT06, MCC01, MKKK+17, NSMV18, NW05, OJFD18, OB16, PDZ+16, PZZ+10, PA03, PQBB08, PCC+11, RDRF24, SSY+22, SVA+19, ST02a, TMfTK23, UBGFD+19, WDF24, WMC04, ZWZ16, dGFMS16]. **Designability** [LJK16]. **Designed** [BRS99, LZX12]. **Designer** [JR16]. **Designing** [BRS20, CGZD24, HMU06, SB05, Tak96, ZF07]. **Designs** [CCF10, CD08, DHM+05, FFSL22, HL03, Li08, LGD+10, PTWB09, TP11, YHC05]. **Desolvation** [DBM09]. **Despite** [MSS+22, RS13]. **Destabilization** [BB04]. **Detailed** [BP06, XMWZ20]. **Detect** [CLLL20, FFSL22, LS08a, NVW14, ODPB18, RPW13, Sch97b, TML+02]. **Detected** [NLC17]. **Detecting** [BBGS11, BMP+09, CTC21b, CKT16, CC12, DLFS22, GLMW13, HG11, HXL+17, HZH+10, JDH00, KYSE10, KKS+06, KPP+22, LAF+14, LN03, Mal98, MWP00, SIKS06, ST10, SDC+10, TH17a, TH17b, VUR11, WWZ+16, XYX+22, ZKL+10, ZWJ18]. **Detection** [AMS+22, ABLX00, BZG+22, BBC16, BK08, CWC06, CFE+13, CD18, CWJ+21, CL21a, CHKK99, CGD09, CV11, DCP+08, DP07, DHL00, EZFP+19, EAA+09, GP20, Gru98, GZW+21, Hav06, HLH04, HW01, JAG17, KMP08, LACB10, LPFT14, LLKX16, vLKMR22, LNW01, LTTS12, LYF+19, LZL24, MZS+17, MSNl23, NMH13, NS18, REKH97, RBOS15, SFA17, SPD18, SDDI+08, SSPNW06, SRS02, SK19, TKSA24, TRIN07, TBB00, VT06, WHY+13, WSS+15, WWH17, WH06, WLA+18, ZLU+22, ZPB+10, Zho10]. **Determinants** [KGLBK15, TGT08]. **Determination** [DEH10, Elh01, GKKS98, HKZ+04, KWM10, LLWZ19, MYBK+11, WMD06]. **Determine** [GSH17, JRHN09]. **Determining** [AMTY11, AKG+13, ALR18, BT08, GGM12, JLRS18, KKS+15, KNmS+22,

MA13, PIWR15, RDH04, YY18, ZRZD11]. **Deterministic** [CWC06, SDDI+08, YY18]. **Developed** [AS19]. **Development** [ACL+21, BRC20, BCD+24, Jos96, JBM15, KMM17, LZHC15, NXGL20, PC05, WH01, WFL+20]. **Developments** [CHM94]. **Deviation** [KFC+11, TSTS12, WFH18]. **Deviations** [Nue04]. **DFT** [TM22]. **DHFR** [SB21]. **Diabetes** [SVP19]. **Diabetic** [LL19c]. **Diacylglycerol** [BSB+05]. **Diagnosis** [HTM+22, KCH04, MDTD06, VA17, WWC+20, YMxW21]. **Diagnostic** [JZZ+19, KVM14, SZMZ19, WWLC20, fZbMqW+20]. **Diagnostics** [BLC+10a, KSB98]. **Diagrams** [Hua15, MR08b]. **Dialysis** [YLC+17]. **Diameter** [MWD02]. **Dictionary** [ASL06, PBS+99]. **Dictionary-Based** [PBS+99]. **Diet** [LLL+20]. **Difference** [ATLS07, EMV98, Par24, ZPG+24]. **Differences** [CMK23, Ker03, LQ23, MJS24, PIWR15, TYS+20]. **Different** [FCS12, LL19a, PD16, QFLL22, RKTS14, SPD95, YI17]. **Differentiable** [HZK22]. **Differential** [HTY22, HQ06, KCG+19, cLcSwP+21, MH22, NKR+01, PLL16, SK23, SDC+10, SBTV10, TBL18, WLM21, ZWSF05, ZW23, ZL22]. **Differentially** [ARHLK19, AJV+16, BCH+01, CCL+19, GP20, ITSH00, JÖNK17, KBČ19, LSRR18, MG06, QbMyD+19, WC04, WFL+20, WHK21, WZL19, ZLW+20, ZXZ21]. **Differentially-Expressed** [ITSH00]. **Differentiation** [TLP+14, XLZ+24, XLLS20, KLV+13]. **Diffusion** [EFM12, FA12, Sef25, ZS24]. **Diffusion-Based** [Sef25]. **Digest** [FJK+99, Mar94, fW23, Zha94]. **Digital** [BR06, GSS+20, SSH+20]. **DIME** [GYD+15]. **Dimension** [LQ23]. **Dimensional** [APF+20, ACL15, BGTSB98, CGZ04, EPSV98, GP13, GKG12, HD10, HZL22, KMZ+10, LKBT16, LLSH19, LZC+23, LL23, LCL+17, NDMK17, O'H15, PL06, RBH+19, RL94, SDMN19, Shi10b, SBNS21, TSTS12, YHC19, YE02, ZLU+22, ZZL+17]. **Dimensionality** [SPBB15, TPK03, ZLL+22]. **Dipeptidyl** [MCH+19]. **Diploid** [BDK+16, Gus01, SBP15]. **Diploids** [LLS11a]. **Diplotype** [OYY+12]. **dipSPAdes** [SBP15]. **Direct** [BGLY03, BBN24, GT16, Ham12, HPY03, TBS+07]. **Directed** [BHL+18, CLM+16, KTSS19, KLR23, KK23, LL05a, YFBK07, ZGBK10]. **Direction** [GZN16, MWL22]. **Direction-Guided** [GZN16]. **Direction-Selective** [MWL22]. **Directional** [DS19, PK19]. **Directly** [KJmZ+22]. **Dirichlet** [NBGA13, XJS07, YYA10, YYA11, YA11]. **Disambiguation** [SKM05]. **Disc** [FZF+20]. **Discerning** [DCD19]. **Discontinuous** [CYY23, MBK+03]. **Discordant** [HMN21]. **Discovered** [BSKgG23]. **Discovering** [BDCKY03, DDA+11, HVD17, MC10, Par07a, SPBB15, WLFW03, WAC08]. **Discovery** [AP04, BSK05, BR06, BGG07, BJEG98, CW20, EVLZU19, ELP04, GPRR12, HMN21, ISB12, KPB+04, KWA11, Li09, LW12, NTMM06, Par07b, QP09, SSKH+13, TKW08, WX08, WlLK+12, ZKC12, ZHQS05]. **Discrete** [Che06, HG18, Jus06, KPS00, SKGG17, YjDG+23, Zhu07]. **Discrete-Event** [Che06]. **Discretization** [DLML10, LZL24]. **Discriminant**

[LSG04, Mal98, MGW+07, ZZL+17]. **Discriminate** [BCVL17]. **Discriminating** [MP16]. **Discrimination** [EMD95, KLV+13, Mam96, TBS+07, WS04, ZHY+20]. **Discriminative** [JDH00, MD00, SS05a, Sin03]. **Disease** [AC17, BSKgG23, CDQ+21, CWR24, CD21, DCL18, EBK11, GSA14, GSV21, HTM+22, HWZ+21, KSS09, KV23, KS05, LFD03, LWZ18, MWZ19, NXGL20, PD16, PD20b, PE20, RS12, SCB14, SEV09, SlGW+23, VB09, yWCF06, WxLW+23, XAB+15, YHW18, YLC+20, ZPX+10, ZCZ+23, ZWD25, CJ21, bYjHgZ+24]. **Disease-Associated** [SlGW+23]. **Disease-Causing** [KSS09]. **Diseases** [BBN24, CZS15, FSD+14, JCBX22, KMCKS17, LZL+23, Wu08, YQDW23]. **Disequilibrium** [BG09, LWLJ10]. **Disjunct** [CD07]. **Disk** [HNW99]. **Disk-Covering** [HNW99]. **Disorder** [WXY+13, YDZ+25, YMxW21, ZLTZ25]. **Disordered** [GZW+16, HZNF06a, HZNF06b]. **Disorders** [JR16]. **Disparity** [SPSZ23]. **Dispersion** [WMC14]. **Displays** [WZ24]. **Disproportionate** [DSC+22]. **Disruption** [DLM10]. **Disruptions** [JRHN09, NLC17]. **Dissimilarity** [KVZ24, Wil99]. **Dissimilarity-Based** [Wil99]. **Distance** [AS96, AODD21, AODD22, AOJ+23, AZ14, AKG+13, BMY01, BHHR18, BG17, BBDS21, BSSZ+20a, BSSz+20b, CMK23, CCYH18, Che12, DJK+00, GMY10, HR12a, HJR12, HMU06, JR17, JRS19, JLMZ02, Jia11, KLM11, Kov14, KVK08, LS08a, LN01, LRV21, Lu15, MC16, MH22, MTF+12, PLZX25, QEk24, Ris16, SH06, SGBEM11, SLM15, SM16, kSyPhC+22, TCL+16, TM22, WW18, WW19, WAM20, WZW15, YzCW20, YJ04, ZHY+20, ZZ14a, ZAG+18, Zhu07]. **Distance-Based** [DJK+00, LS08a, PLZX25]. **Distance-Scaled** [ZHY+20]. **Distances** [AS10, AO15, AFRV07, BBH+07, BSMA06, BYL+20, Fom16a, Fom16b, Fom19, GM07, HPDLW09, LH24, NM14, SM17, WDA01]. **Distils** [CvS24]. **Distinct** [TYS+20, WPL+19]. **Distinctive** [JRH+10]. **Distinguish** [KWBN19, SDG+07]. **Distinguishable** [NS23]. **Distinguishing** [RPS02, STRT96]. **Distortion** [HlAM20]. **Distributed** [EN22, FDW20, PDZ+16, SIC+09, WZG+20b]. **Distribution** [AZ14, AJV+16, BS98, BLF14, LR05, LHW+22, LRSG07, LSG04, MD01, RS01, SH06, SBT00, Sch00, TZHR14, TS96, ZPD+23]. **Distributions** [BG97, ENS02, GW94, Kon09a, Kon09b, LBDVF10, NL09, SBK22, ŠV07]. **DIsulfide** [KLO18]. **Divergence** [Gu01, RKTS14]. **Diverse** [CTC21a, KWBN19, Wil99]. **Diversified** [MZS+17]. **Diversity** [AMK18, AV18, AFCK09, GNME01, KMP08, PMAP13, ZFBK09]. **Division** [LYF+19, WC16, YHT+17]. **DNA** [AOAAH17, AEB+04, AM97, ADRS24, ABH03, BLC+10a, Bea95, BNN12, BDKSY00, BB04, BG11, BDM+07, BMN+07, BFK+99, Böc04, CS00, CZC10, CCT09, CD18, CWS+21, CD07, Che04, CKZ+19, CQG10, CL99, CST20, DMP+06, DLL+12, DPHH05, DS12, Elh01, FVTH03, FLL00, FSW+20, FBJ04, Gel95, GPAR96, GGKS95, GM96, GMVC20, HBRW06, HSF97, HJ05, Hor01, HZL22, HLY25, HW01, IW95, IP09, JG11, JLY08, JRH+09, KMP+04, KKe23, KS12, KSSK09, KFDT02,

KV19, LWN+18, LG22, LMS96, LVC+04, LABD+06, LFT+98, LY99, MT06, MCC01, MK11, MWP00, MV19, MBVA07, MP94, Mil95, MGSA06, MTR+03, NCC+96, OBDV16, PWFZ17, PA03, Pev95, PQBB08, PO04, RMRT00, RPR+15, RYY22, RWB+98, RW99, RMC+23, SK17, Sal95, SDFH98, SPD95, Sch97b, Sel13, SNQ+14, SnGqC20, SRV98, SRM+98]. **DNA** [SCC+98, SH04b, Ste14, SZSW09, Sun99, SB05, TE96, TH17a, TH17b, TEMM12, Ves12, VS98, WGL98, WSW15, Wan94, WRS+99, WMC14, WWC+20, Wen05, Wen06, WSS03, XMU96, YKPM20, YYL20, YYW14, Yin19, ZPM97, ZSWM00, ZW03, ZCH+13, ZHS05, ZS11, ZWK+20]. **DNA-Based** [BLC+10a]. **DNA-Binding** [GMVC20]. **DNA-Mediated** [JRH+09]. **DNA-Microarray** [FVTH03]. **DNA-Sequencing** [CD18]. **DNASCANNER** [PRC+24]. **dNTP** [DCV+07]. **Do** [TaAF+22, ZFZL03]. **Docked** [ADPH15]. **Docking** [ALB+19, AKLM02, GAWI19, GZN16, HS15, PPV+14, SNW98]. **Does** [IP19]. **DOI** [Ano20, Ano21b, Ano22b]. **Domain** [DMHM97, GH16, JRH+10, LCL+17, MMHC98, Neu14a, Neu14b, RMWC16, SKM05, SSD07, ZZNM15]. **Domains** [CSP+12, GKKS98, LWLL19, LZL24, SKG+00]. **Dominance** [ST17]. **Dominant** [DS19]. **Dominating** [RPS02]. **donovani** [Vij22]. **Dosimeter** [SVCA17]. **Double** [BHHR19, BWS11, CQG10, KKe23, Mar94, MDTD06, MJS23, SGBEM11, SLM15, TT12, XLZ+18a, ZRGHJ08]. **Double-Cut-and-Join** [MJS23, SLM15, XLZ+18a]. **Double-Digest** [Mar94]. **Double-Layered** [CQG10]. **Double-Strand** [TT12]. **Down** [CC11, CŁM+18, PRC+13]. **Downregulations** [WHLR20]. **Draft** [TAJZ23]. **DREAM** [CKS12, CKS13, CKS15, CKS14]. **DRGAT** [Sef25]. **Drive** [PRC+13]. **Driven** [BLQZ04, CWS+21, CS15, DBW17, MFJ+19, MD03, PNIM17, ZZL23a]. **Driver** [PNIM17, SMC+15, SSZG24, ZlWL21]. **Drivers** [SH17]. **DrML** [GE14]. **Drosophila** [JBM15, KASM08, MYS+20, MSS21, POP23, SVCA17, YI17]. **Drug** [AL25, Ano21b, BÖB+23, BYL+20, CJP+22, DHY02, FYJ18, GSV21, HSBS10, HXY+23, HFUH19, ITdB09, KTT20, LJCZ20, NSA08, ÖBA+23, PXLP23, PYIM22, PIM23, Par24, PGA+11, SDDI+08, Sef25, SGK+12, WYC+18, WxLW+23, WFC25, WYLW21, YWZ+19, ZCZ+23]. **Drug-Drug** [WFC25]. **Drug-Like** [NSA08, SDDI+08]. **Drug-Target** [LJCZ20, PGA+11, WYC+18]. **Drugs** [Ano21b, AS11, GSV21, NXL+15]. **DSEP** [NXL+15]. **DTD** [SSH+20]. **Dual** [BHHR18, YMM+24, ZZC+24]. **Dual-Channel** [ZZC+24]. **Duchenne** [ZLB+20]. **Ductal** [CYF+20]. **Due** [KC96, ZMK22]. **DUPCAR** [MRR+08]. **Duplex** [BB04]. **Duplexes** [ABF+04]. **Duplicate** [AFR+08, DLM10, SLM15, SM17]. **Duplicated** [EHFK24]. **Duplicates** [AFRV07, JRHN09]. **Duplication** [ARC13, BAK13, Bay23, Ben97, BBWE09, CDEM08, CLDG03, EMV98, Gu01, JPB+15, JRH+09, JRHN09, LBEMG07, LMWR21, OSC11, PMGE21, TWY02, WT07, ZZS08, ZZ14a]. **Duplication-Based** [EMV98]. **Duplication-Loss** [ARC13]. **Duplication-Loss-Coalescence** [PMGE21].

Duplications [CDFC00, GE14, LM11, MRR+08, YF09, ZS17]. **During** [CEK+17, COL+18, KMUK22, LSAS03, TT12, UTD+20, WZCS00, XLZ+24, ZWQ19, JRH+09, LSHL04]. **DUSP1** [YBF19]. **DUST** [MGSA06]. **Dyads** [Li09]. **Dyes** [Tra19]. **Dynamic** [ADR24, BB15, Bet10, BRZH15, BS20, CKT+01, Che06, DCD19, EdCK+12, FNC08, Gui98, HlAM20, HWSH18, HD98, JKG+04, JJGD16, KW14, KAS09, KMZ+10, KLV+13, KK18, KT13, LLS+19, LSSD18, MTF+12, PLZX25, RMWC16, SS23, SB07, WZW15, WBJ15, Wu96, XLZ+24]. **Dynamical** [DCL10, GSV+11b, Jus06]. **Dynamics** [Ano21b, CB07, CKB17, DT13, FA12, GQ09, HCX09, KFC+11, MSS21, PGAE04, PLSL18, RAKL10, RZK06, SVA+19, SAM06, SVL+10, WH01, WPS+25, YK19]. **DynDom3D** [GH16]. **Dysregulated** [CNCK11, JFLL20]. **Dystrophy** [ZLB+20].

E-MAP [KK11, LTCH11]. **eALPS** [EHC+13]. **Early** [DCL18, JBM15, MSS21, NCMS+21, SBD+00]. **Early-Stage** [NCMS+21]. **Earth** [PLZX25]. **Easy** [Tra98, dMRR14]. **EasyQC** [RUGR18]. **EDAR** [ZPB+10]. **EDGA** [GZN16]. **Edge** [PFRD05]. **Edge-Count** [PFRD05]. **Edit** [AO15, BSSZ+20a, BSSz+20b, HMU06, JLMZ02, LJ05a, MC16, MTF+12, WAM20]. **Editing** [DCV+07, KMM17, WLA+18]. **Editor** [EAM+17]. **Editorial** [Ano94]. **EDoP** [ZAG+18]. **Education** [PS11, Tan11]. **Effect** [HSH+09, MXW+20, SBT00, ZKC12, ZLP22, Zho17]. **Effective** [GP13, HZH+10, PYIM19, PZC05, SRF16, TL23, WXY+24, ZW19, ZW07]. **Effectiveness** [CZW+19]. **Effects** [AS11, CHP94, CD21, DQS+11, FYJ18, FL17, KCG+19, MBVA07, NXL+15, PD20b, RND+23, SMKS96, ShHGC20, TRIN07, TBS+07, TTTL17, VCY14, WHC09]. **Efficacy** [Ila20]. **Efficiencies** [PTWB09]. **Efficiency** [GKS95, HJD17]. **Efficient** [Aku04, APF+20, AHK+07, AFR+08, ABG+03, ABLX00, BGHY04, BHHR18, BCVL17, BFT04, BMWG04, Bry96, CD07, CFH13, CAC+23, CGI+07, Clo05, DT12, DC16a, DWMT22, FDW20, GNME01, HD16, HTM+22, HMY+14, HS23, HBK11, JCZ08, Jah11, JRS19, JGB12, KZE10, KS11, Kle99, KT13, KMB+20, LLKX16, LNW01, LGD+10, LLCT05, LMW05, Lip05, LABD+06, LWLJ10, LHC02, LSHL04, Lu15, LMSH03, MMG14, MPZ+20, OK08, OJFD18, OB16, RC14, RJS02, RUGR18, RSM06, RDRF24, Ric06, RMK+18, RCSS12, SK17, Sch97b, SIKS06, Ser15, SYYH02, SOD+11, Shi07, TAA16, TDV24, VAS+18, WWZ19, Wu08, XWLJ08, XXU98, ZPX+10, ZPB+10]. **Efficiently** [BG09, BFS10, HH06, KE13, LHXH08, PGM07, SDMN19, SFR+18]. **EGFR** [OJOD+04]. **Eggs** [ZTW05]. **Ehrlich** [Tra19]. **Eigen** [PM24]. **Eigen-Single-Cell** [PM24]. **Eighths** [HI96]. **Elastic** [Guo15]. **Electrical** [CEK+17]. **Electroencephalogram** [EOD+18]. **Electron** [CŁM+18, HLG18, KAC17, LCG+22, NS18, WZG+20b, YLZ+24, ZKWH17]. **Electronic** [VA17]. **Electrophoresis** [EHK+02]. **Electrostatic** [NLC17]. **elegans** [LYF+19, YHT+17]. **Element** [DBT11, HKZ+04, KKS+15]. **Elementary** [BS09, OFS09]. **Elements**

[BH14, CCG06, ES06, HHJ+02, WHC09, ZPC+18, ZKC12]. **Elimination** [BMN+07]. **Ellipsoid** [YHC19]. **Ellipsoid-Fitting** [YHC19]. **Elucidating** [CXW16, MGVS14]. **Elucidation** [BDCG+98, PGA+11, SGK+12]. **Embedding** [AL25, AaHP+21, CAC+23, DAE+19, RYY22, SK21]. **Embeddings** [MV19]. **Embryo** [MSS21]. **Embryonic** [JBM15, YHC19]. **Embryos** [Bri19, LYF+19]. **Emergence** [MWL22]. **Emergent** [SVD14]. **EMINIM** [KZE10]. **EMP2** [QLW20]. **Empirical** [GE04, MBLZ09, TZHR14, WS04]. **Empirical-Map** [MBLZ09]. **Enabled** [APF+20, SSLMW10]. **Enables** [BKT09, GQEk24, TZB+23]. **Enabling** [IR22]. **Enacting** [MDTD06]. **Encoding** [AOAAH17, DC16a, HLY25, KGÖ18, LFT+98, WKC+95, Yin19]. **EnCPdock** [BMB24]. **Encryption** [ARRW99, BSP+24]. **End** [CJK+97, EZFP+19, GSN11, OBDV16]. **End-Probes** [CJK+97]. **End-to-End** [EZFP+19, OBDV16]. **Endhered** [BHKN25]. **Endometrial** [WHLR20]. **Energetics** [BMB24]. **Energies** [CWRF15, HD16]. **Energy** [BDM+07, CCDB21, CA15, CS15, Clo05, DPR97, GLJW09, GJL+22, HJD17, HR12b, HI97b, JHLD20, KXL08, LSHL04, LP00, MZC+18, MFJ+19, OC00, PK11, Pen20a, Pen20b, RC06, WC07, YE02, YSFW08, Zho10]. **Energy-Based** [LP00]. **Energy-Consuming** [MFJ+19]. **Energy-Filtered** [HR12b]. **Enforcing** [RSEK24]. **Engine** [RGL94, YjDG+23]. **Engineering** [CR09, GSH17, Jus06, MSMF09, SHG02]. **Enhanced** [KEL15, cLcSwP+21, LZY+23, QsYSxL23, RC24, TH17b, ZWD25]. **Enhancement** [HTM+22, HSL+24]. **Enhancers** [Ami12, LCW16, YYL20]. **Enhances** [DRT+25]. **Enhancing** [AMK18, GJZ06, GWM+21a, GWM+21b, Ste14]. **EnILs** [SZL+23]. **Enriched** [NVW14, ZKL+10]. **Enrichment** [IJCL12, IRCA21, MK16, WZCY21, fZbMqW+20]. **EnrichVisBox** [WZCY21]. **Ensemble** [AVS20, DCP+21, JJGD16, JHLD20, LXS24, LSAD05, LLW18, MSRS24, NSRR23, OJFD18, SDK16, SlGW+23, SOD+11, SSW20, SZL+23]. **Ensemble-Based** [JHLD20, LSAD05, OJFD18, JJGD16]. **Ensembled** [AG23]. **Ensembles** [FvdBB16, GZW+16]. **EnsMOD** [MSNl23]. **Enterocolitis** [ZYH20]. **Entity** [JJH+21]. **Entrez** [RGL94]. **Entropy** [BCVL17, CCDB21, KS12, Kei05, LLT06, LY99, NVCW15, YB04, ZLL+22]. **Entropy-Based** [KS12, LLT06, NVCW15]. **Entry** [RBK94]. **Enumerate** [Sie03]. **Enumeration** [AHK+07, Bry96, DR17, GSW16, JHA16, Rød06]. **Enumerative** [PV17]. **Environment** [GPOP+17, HL16b, RMC+23, YLC+17]. **Environmental** [CK09, ZZZU20]. **Enzymatic** [Aku04, FLL00, KM08]. **Enzyme** [BS09, Kru17, LSAD05, LKC21, RFH+25, SB21]. **Enzymes** [SBRG20]. **Epidemic** [HAM+22, MDWZ24, WZ23]. **Epidemiological** [SS23]. **Epidemiology** [OKKS21, RMC+05]. **Epidermal** [LLL+20]. **EpiGeNet** [BSB+17]. **Epigenetic** [BSB+17, LSY+05]. **Epigenetics** [HSH14]. **Epigenomic** [NVW14]. **Epistasis**

[CTC21a, CTC21b, MBC+18, ST17, ZPX+10]. **Epistatic** [ŽZ15]. **Epithelial** [WFL+20]. **Epitope** [HKL07, SZMS02, SS04, UBGFD+19]. **Epitope-Based** [UBGFD+19]. **Epitopes** [LZHC15, MBK+03, SVA+19, Vij22, ZYB+04]. **EPTool** [GWM+21b]. **epub** [Ano20]. **eQTL** [BCG+18]. **Equation** [ADW23, PD16, PD20b, SK23]. **Equations** [LLS11b]. **Equivalence** [DKF09, Mar94]. **Equivalences** [KT13]. **Equivalent** [GB08, ZZ14a]. **Equivalently** [JZ10]. **Era** [SF03]. **Eric** [Dei19b, Ist19]. **Error** [AO15, AOH16, BDK+16, ETLK19, GHM+10, HTZ+12, HL03, KMP08, KWBN19, LC09, LTTS12, LGD+10, PYIM19, RD01, SSLMW10, SP97, TRIN07, WG98, WZCS00, WCC+06, ZGRB10, ZPB+10, ZHZ+16]. **Error-Correcting** [LGD+10]. **Error-prone** [WZCS00]. **Error-Tolerance** [HTZ+12]. **Error-Tolerant** [HL03, SP97, WCC+06, ZHZ+16]. **Errors** [BFK+99, HHHS03, LK24, PdB13, RPW13, RW99, XMU96]. **Escape** [MJS23, YK19]. **Escherichia** [ALR18, Kha14]. **Esophagus** [SZMZ19]. **Essential** [DCP+21, Rob96, WZL+21]. **EST** [LMP08]. **Establishing** [AP09, SBAW97]. **Ester** [TGTG19]. **Estimate** [ENS02, LC09, TDV24]. **Estimated** [ZMK22]. **Estimates** [HTZ+13, KXL08, LY99, SVP19]. **Estimating** [BG02, BW12, DCV+07, DBM09, EHC+13, HH06, HPDLW09, JR12, JZ10, KIYM13, LST+17, LDW+14, MTR+03, PMCB08, RFH+25, TT12, WCM+08, WGC+21, WXY+24, WDF24, WTE25, WDA01]. **Estimation** [AO08, BKT09, Bun02, CŁM+18, COV+15, DMR+03, GCB20, HR22, KD13, KK18, LWN+18, LDW98, LLSH19, LMWR21, LLD+16, MPZ+20, NSRR23, PM24, PZH11, PMAP13, RCER21, RBH+19, SWK+07, SLO07, SR10, SK23, TBJF01, Tos05, WZCS00, WR23, YDN12, YDN02, ZGW22, ZH07, ZTW05]. **Estimations** [FB12]. **Estimator** [AT12, KT01, LRM11, NHOV10, Pen20a]. **Estimators** [ÅMR07, GF16]. **Estrogen** [QLW20]. **ESTs** [BMP+09]. **ET-Motif** [AOH16]. **Ethics** [Tan11]. **Etiology** [Kha14]. **Eugene** [GSLW94]. **Eukarya** [TRS17]. **Eukaryote** [SBD+00]. **Eukaryotes** [LM11]. **Eukaryotic** [CC12, DCW+17, Kei06, KDL+94, LJ05a, WOG03, ZWJ18]. **Euler** [RYZ23, YYZ23]. **Eulerian** [ZW03]. **Eutherian** [BDCG+98]. **Evaluate** [DLL+24, ZLM+17]. **Evaluating** [BG02, GST10, HLCS10, KGK14, Neu14b, SMM+04, WR23, ZGW22]. **Evaluation** [CASP10, CWL13, GKB00, GI95, GLJW09, HBD94, HSBS10, KV17, KNS14, PD20a, PTWB09, PC05, WCL+18b, YHC05, ZRNA20]. **Evaluations** [VCY14]. **Even** [BF98]. **Event** [Che06, WFC25]. **Event-Controllability** [Che06]. **Events** [BSB+17, BBWE09, HZH+10, HXY+23, KKK18, MWP00, Sam09]. **Everyone** [LBBV+18]. **Evidence** [ADD+07, AT12, GT16, LZS09, XXZ+21, ZLB+20, ZDG+20]. **EvOligo** [MKKK+17]. **Evolution** [ATLS07, AEB+04, ABH03, BBH+21, BV10, BNN12, BFP13, CKT16, CDEM08, CT07, COV+15, DCV+07, DG02, DSV12, DT13, FS99, GJM04, GZN16, HP96, HM14, HY16b, JRH+09, LBSB17, LTS20, LLCT05, MMA+21, MJS23, MAN16, NWLS05, POP23, PDSD06,

RS13, SBD+00, Sni19, SZVM10, SLS23, TBKR10, VS98, WT07, YAR21].
Evolutionary
[AS96, AFBS95, BRD+05, CS15, Csu02, DPS+20, Erw19, FB12, FT07, GT16, HP97, HLH06, Kle99, LM03, LN03, LM11, RPW13, TRS17, WP11, ZSV+09].
Evolvability [YS19]. **Evolve** [SSH94]. **Evolved** [SVD14]. **Evolves** [JC22].
Evolving [CGT12, KASM08]. **Exact**
[AOH16, APF+20, BFT04, BS98, CA15, DMB07, EHFK24, FG04, GP13, KVK08, LR00, MT06, MD01, NL09, OK08, RBH05, ROB+22, ROL+22, SSMT16, SLM15, SM16, XS07, Xu09, Xu10]. **Exactly** [KW14]. **Example** [Zha94]. **Examples** [TBKR10]. **Exceptional** [SPD95]. **Exceptionality** [PDK+08]. **Excerno** [MRY+23]. **Exclusive** [CKB17]. **Execution** [KAD+19].
Exemplar [Jia11, SM16, kSyPhC+22, WZW15]. **Exhaustive**
[DMDR17, TTTL17]. **Exome** [bVRN+19]. **Exon**
[AS23, KLZU06, LS98, WH06]. **Exons** [Gui98]. **Exopeptidase** [KGN09].
Expansion [HJD17, SHMS08]. **Expectation**
[GGM12, NBC+11, SRV98, YJC18, ZCH+13]. **Expectation-Maximization** [GGM12]. **Expected** [HA12, KK11, PFRD05, PV17]. **Experiment**
[Bri19, Mor19, PKZ11, SHG00]. **Experimental**
[ADD+07, AGH+18, BMY01, BG23, CWRF15, CAB+07, CF97, LZHC15, NSMV18, PMG+16, SLRM09, YHC05]. **Experimentally** [GE17].
Experiments [ARHLK19, BCH+01, BRR02, COL+18, CM04, Dei19a, DDC+20, FSD+14, GVTRS06, JAG17, KST96, MKKK+17, PZH11, PQBB08, SHMS08, SZSW09, WC04]. **Explain** [VCS11]. **Explainable** [FFB20].
Explaining [AAN+20, LQPE+10]. **exPlanations** [LQ23]. **Exploiting**
[AWZ+17, KX14, KJmZ+22, yWCF06]. **Exploration**
[CWS+21, JJH+21, QbMyD+19, RBKJ19, WP11, WQZ+19]. **Exploratory** [WV11]. **Explore** [BYGI12, BCVL17, HHC06, LL05a, NVW14]. **Explorer** [JJH+21]. **Exploring** [MYS+20, MMA+21, PK11, WXS14]. **Exponential** [AGH+18, Zha94, KKM+20]. **Exponentiation** [IM14]. **Expressed** [ARHLK19, AJV+16, BCH+01, CCL+19, ITSH00, JZ10, KBČ19, LSRR18, MG06, QbMyD+19, TVNP15, WC04, WFL+20, WZL19, ZLW+20, ZXZ21, ZHQS05]. **Expression** [ARHLK19, ACKK19, AGH+18, AFCN13, ASE20, AAN+20, BJGG+03, BF02, BDSY99, BDBF+00, BDCKY03, BSB+05, BLP+22, BGL24, BRR02, CK11, CK09, CW09, CC09, CQG10, DS04, DCH21, DBB+02, FZF+20, FSW+20, FFB20, FLNP00, GHJ+12, GK18, GLM+09, GMC08, GCD20, Hav06, HVAW04, HLCS10, HSL07, HWW+20, HQ06, HMF07, ITdB09, JC22, KBJ07, KYSE10, KS12, KCG+19, KMC00, KMZ+10, KCH04, LYMD03, LDS12, LFD03, LXL+20, LGS20, LLJS19, LCD11, LRNBJ10, LLL+20, MH22, NKR+01, NVCW15, NV12, POP23, PD20a, PNIM17, PZH11, PKZ11, PCC+11, PC05, RMS02, RD01, RFH+25, SD95, SKS+09, SnGqC20, SVCA17, SDC+10, SSLL22, SBTV10, TBL18, TBJF01, TXL+17, TYS+20, TPSB19, WXS14, WPL+19, WWC+20, WDZ20, WV11, WGW+01, WAC08, XvdL05, XLLS20, YL17, YYY+09, ZWSF05, ZWQ19, ZQZ20, ZMK22, ZL22, TZZY20, WLM21, NME+15]. **Expression-Based**

[MH22]. **Expression-Dependent** [LFD03]. **Expression-Detection** [Hav06]. **Expression-Interaction** [SKS+09]. **Expressions** [Mye96]. **Extant** [KNmS+22]. **Extended** [GSW16, GJL+22, HCS09]. **Extending** [YS19]. **Extensible** [KAD+19]. **Extension** [HMY+14, KMMF20, PSCP09]. **Extensions** [BSSZ+20a]. **Extensive** [RS13]. **Extensively** [FCGD19]. **External** [BVP+16, LW22]. **External-Memory** [BVP+16]. **Extracellular** [JRH+10]. **Extracting** [AC17, KK11, LLS+19, LZY+23, MS00, PdBdP+22]. **Extraction** [Aku04, BLQZ04, Bry96, GPP+11, LRD19, PD20a]. **Extractor** [AB16]. **Extremal** [TW05]. **Extreme** [JTSB10, LSG04]. **Extremely** [SY22].

F2 [KKe23]. **Facilitate** [XSH+22]. **Facilitates** [DZS24]. **Facilitating** [RAC+06]. **Factor** [BZMM16, GGU13, GJZ06, KW21, LZBK15, MYS+20, WV11, YYY+09, YJC18, ZQZ20, KS12]. **Factor-Mediated** [KW21]. **Factorial** [RNH18, RH19]. **Factories** [KK24]. **Factorization** [BMH21, LWZ18, MWZ19, MJCM22, NES22, WHDN13, ZEKKR18]. **Factors** [Ano22b, BSB+05, BZ08, KMUK22, MSMP19, SNQ+14, SKS+09, TMH+21, TRIN07, TLP+14, YJ06]. **Failure** [JFLL20, SVK10]. **Fair** [AS10]. **False** [MRY+23, SRV98, ZHQS05]. **Familial** [MRS+18]. **Families** [CCT15, DGH+01, GHM+10, GPCP11, HG05, HP96, MC08, MD00, PL06, TLK+06, WT07]. **Family** [BC94, BLEM08, CBS+20, CDEM08, CDFC00, ENS03, FJAOB18, FDDK07, Gru98, HHP+09, HXL+20, HBW+05, JJY+20, KWBN19, LBEMG07, NLH+23, WKC+95, YTS12]. **Family-Specific** [HBW+05]. **Fan** [JLRS18]. **Farthest** [Zör15]. **Fast** [APVM11, AMW07, AFBS95, AI12, AaHP+21, BBD+04, BVP+17, CBW07, CZNF19, CWL13, CHKK99, CGD09, Csu02, DG02, GVMB24, GGU13, GTA+04, GB08, HI96, HNW99, ISB12, JDK+18, KBS09, LRM11, LS04, MGSA06, NR03, NMH13, Nic01, OAR+24, OMS13, PPV20, PWKAF16, PKSB18, RJS02, RBOS15, Ris16, SC15, SEV09, Ser15, SM16, SY22, WHL17, WY21, fW23, Xu09, Xu10, YW21, YK05, MBC+18, LZL24]. **Fast-Converging** [HNW99]. **FaST-LMM** [MBC+18]. **fasta** [MA19]. **FastaHerder2** [MAN16]. **FastBill** [WT17]. **Faster** [ACL+21, CWC06, CKdAHdF15, FFM24, Kei05, KL98, Shi10b, ZUGVWS10]. **FastViromeExplorer** [TAJZ23]. **FastViromeExplorer-Novel** [TAJZ23]. **Fat** [LLL+20]. **Fate** [JRHN09, KBLS24]. **Fatigue** [ES07]. **Favors** [NMG+05]. **FDR** [ZHQS05]. **Feature** [BZB+22, CC09, CYY09, EOD+18, KDB+02, KCH04, LKBT16, LRD19, LTTS12, LCW16, LLW18, LLT+25, NTWF11, PD20a, PNIM17, QsYSxL23, Ric06, RND+23, SMC+15, SZTW12, XAB+15, YHB+03, ZLTZ25]. **Features** [CJ21, HHP+09, LJK16, LLS+19, LXS24, MBK+03, OAHA94, PPL+23, PLSL18, RPS02, WA10, XGD24]. **Features-Based** [CJ21]. **Federation** [Fas94]. **Feed** [EdCK+12]. **Feed-Forward** [EdCK+12]. **Feedback** [BHL+18, BBH+21, GQ09, QMMW11, YY19, ZFAS08]. **Feet** [BKPW95]. **Fetal** [LWN+18]. **Few** [KYSE10, LKC21]. **Few-Shot** [LKC21]. **FGF5}** [ZQZ20]. **Fickett** [SSTM19]. **Fidelity** [BDM+07, FLL00]. **Field**

[BV09, GK06, LGD+10, RRFS98]. **Fields** [LCWG06, LGS20, OAHA94]. **Fifth** [LJP20]. **Files** [AH20, MA19]. **Filling** [QBA+25, SSMT16]. **Filter** [HLG18, MRY+23, PFK17]. **Filtered** [HR12b, SS07]. **Filtering** [CJP+22, CZY19, DC16a]. **Filtering-based** [CJP+22]. **Filters** [COV+15, PFK17, PC05, RSM06, Yu24]. **Filtration** [BHHR18, BHHR19]. **Find** [NCMS+21]. **Finder** [LS98, LS08a]. **Finding** [AP10, BSP+24, BRZH15, BFS10, BT02, CCI+04, CP05, CZS15, DM20, FK06, HSF97, HZGD05, HL16a, HS14, JHS06, JMEB18, KLW96, LTsL24, LS98, LCY+05, LBXL11, LZF+05, LL05b, NWN+10, OMS13, PAC02, RSM06, RRNB13, RC06, ROB+22, ROL+22, SDFH98, SB07, Ste14, TP11, WXS14, WMC14, WYKG05, XWLJ08, ZHS05, ZS11]. **Finger** [TWY02]. **Fingerprint** [AMK00, FBJ04, Wen05]. **Fingerprinting** [HYY+10, RC14]. **Fingerprints** [MS99]. **Finite** [CWC06, DSV12, KKS+15, LGD+10, ZHY+20, ZPG+24]. **Firing** [CL21b]. **First** [JHA16, SLA12]. **FISH** [SHMS08, SBAW97]. **Fitness** [Kle99]. **fitter}** [AJYJ18]. **Fitting** [BFK+10, YHC19]. **Five** [CLT+20, JZZ+19, RPS02]. **Five-CpG** [JZZ+19]. **Fixed** [LTsL24]. **Fixed-Parameter** [LTsL24]. **fjoin** [Ric06]. **Flanking** [JRHN09]. **Flat** [HD10]. **Flexibility** [NH08, SNW98, TPK03]. **Flexible** [AKLM02, CL17, FL17, HJD17, SDDI+08, SNW04, SI97, TKW08, TS96, VLZUBK07, VT06]. **FlexProt** [SNW04]. **Flip** [DHM97]. **Flip-Cut** [DHM97]. **Floor** [Boh24]. **flopp** [SY22]. **Flow** [CF14, DWMT22, EAM+17, HSOE+18, KKC+22, SSS20, SY07, SkY12]. **Flowering** [XJZ+21]. **Fluorescence** [CL21a, FLT+21]. **Fluorescence-Based** [CL21a]. **Fluorouracil** [PIM23]. **Flux** [BSP+25, BS09, HJ14, LLS11b, NSH+23, PSP21, RBOS15, VB09]. **Fold** [CC06, Con04, CBM+02, GLJW09, KWM10, LCWG06, TBJF01, XLZ13]. **Fold-Changes** [TBJF01]. **Folding** [ABD+97, AS02, ADS03, BTZ06, BL98, CAB+07, CGP+98, DBW17, GPOP+17, GT16, Guo15, GWX18, GMS05, HI96, HI97a, HI97b, HCX09, HPR09, ISK99, JCZ08, KMRG09a, KMRG09b, NSZ99, PGAE04, SVD14, SC15, SOD+11, SHG00, TKT+05, TGT08, TKO21, TAY16, WOW+14, WZZU07, YTMY17, YLCC17, YLW+15, ZZ14b, ZUGVWS10]. **Folds** [BF98]. **Followed** [ALB+19]. **Footprinting** [BST02]. **Force** [CEK+17]. **Forecasting** [CWR24]. **Forest** [KPW11, TBP+13]. **Forests** [RLK+09, Voo14, WCL18a]. **Formal** [GMF+08, TBKR10]. **Formation** [Bri19, DLD+14, KW21, Li09, OJOD+04]. **Formatted** [FT07]. **Formed** [TT12]. **Forming** [YZPC24]. **Formulating** [Mye95]. **Formulation** [CCDB21, HV09, SLY06, YF09]. **Forth** [GB08]. **Forward** [EdCK+12, PL06]. **Forward-Inverse** [PL06]. **Foulds** [KVZ24, LRV21, PGM07, ZZ14a]. **Four** [GGKS95, LC09, MAN16, STV96]. **Four-Point** [LC09]. **Fourier** [CGD09, KL98, RJS02, WY21, YY05, YYW14, ZWJ18]. **Fourth** [Ano00]. **FOXM1}** [BRC20]. **fr** [XSH+22]. **Fraction** [LWN+18]. **Fractional** [HTM+22, HAM+22, WY21]. **Fractions** [KASM08]. **Fragment** [CL17, GDHC95, Mye95, PV17, SRV98, SRM+98, ZGBK10]. **Fragmentation**

[PV17, SHRB11]. **Fragments** [CFS+08, HHP+09, KSK+11, UMR11, WZG+20a]. **Frames** [EFM12]. **Framework** [AAC+06, AFRV07, AS11, BZMM16, BV09, CWR24, CJ22, Cos18, DMDR17, GCB20, GYD+15, HSG22, HXL+17, JDH00, KBLS24, KBG18, KNmS+22, MRM20, NSRR23, ÖBA+23, PP23, PXLP23, PLZX25, Par98, Par10, SS23, SZSA22, SLL+17, TPH+09, VY18, WCZ+18, WZG+20b, WES20, XGD24, YjDG+23]. **Franklin** [Prz24]. **Fréchet** [Zhu07]. **Fredman** [SSC23]. **Free** [ATLS07, AA18, BWS13, BDM+07, BHK+10, CCT15, DLPH06, GRM09, HWSH18, KXL08, KW06, KS05, KBČ19, KBCBS11, LWN+18, LRD19, vLKMR22, LLS+19, OKKS21, Pen20a, Pen20b, RCSW09, SRZ+13, TCL+16, WRSW10, ZPD+10, ZQZ20, Zho10]. **Freedom** [ML10]. **Frequencies** [HH06, WDF24]. **Frequency** [HG11, HXL+17, LCL+17, PRSV08, SR10, Sun18]. **Frequent** [LDLZ12, PPV20]. **Frog** [ZTW05]. **FRST** [Tos05]. **Fructo** [LKC21]. **Fructo-Oligosaccharides** [LKC21]. **FSG** [BVP+17]. **Full** [MD03]. **Full-Sensitivity** [MD03]. **Fully** [HRSC00, JGL11, XYX+22]. **Function** [AMK00, BP20, CL17, CFB+07, CWYB16, CFH13, DZM+03, Dew01, DPR97, FK06, FL17, GTT06, Gel95, GSS+20, GLJW09, GBB15, JDSB04, KNS14, MMG14, MAN16, OC00, RAC+06, Tos05, UGS19, WC07, WHD13, WHD15, YDZ+25]. **Function-Valued** [FL17]. **Functional** [BL02, CDQ+21, CXW16, DCS04, DCD19, GRM09, Gu01, KMZ+10, KBČ19, KGK14, LZBK15, MC08, MWRS16, MRS+18, PWCN02, PKK97, SSH+10, SBPS11, URB+19, VILR10, WZCY21, YMxW21, ZLTZ25, fZbMqW+20]. **Functionally** [DBHC24]. **Functions** [AMTY11, BG08, BRS99, CNCK11, FBV15, HJD17, KSSK09, Kon07, KLR23, MA13, RDH04, SKGG17, TRB+09, WLM21, YHT+17, YSFW08, YJ06]. **Fundamental** [PG03]. **Fungal** [LGS20]. **Funnels** [ISK99]. **Further** [SKW23]. **Fusion** [DB09, DWK+20, HWZ+21, HXY+23, KB12, MJS24, jQLsY+24, SMC+15, XJL+22, YWZ+19, ZB15]. **Fusions** [SK19]. **Future** [PMP+15]. **Future-Generation** [PMP+15]. **Fuzzy** [CMS+25, DAL+08, DKF09, Vij22, YJC18]. **Fuzzy-Based** [CMS+25].

G [BC94, GWL+19]. **G-Protein-Coupled** [BC94]. **G-Quadruplex** [GWL+19]. **G4** [YZPC24]. **G4-Forming** [YZPC24]. **GADEM** [Li09]. **Gain** [AJA+16]. **GAL** [CSP+12]. **Galled** [GKM+10, GMSZ12, JRS19]. **Galled-Tree** [GKM+10, GMSZ12]. **Galls** [GMSZ12]. **gambiae** [XSS08]. **Game** [Yin19]. **Gamete** [Bro98, ZL01]. **Ganglion** [XLLS20]. **Ganglion-Like** [XLLS20]. **Gap** [BDM+07, CJ23, DMP+06, Dew01, HSD05, JGT22, LHXH08, PNPC20, SSMT16, ZL09]. **Gap-Sensitive** [CJ23]. **Gapped** [BG02, CBH+12, CA12, JHS06, KMMF20, MP11, Met06, MT99, New08, Par07b]. **Gaps** [BCH+07, Bun02, CB06, DHL00, NR03]. **Gas** [ZHY+20]. **Gastric** [FSW+20, PIM23, Par24, ZYD+19]. **Gating** [HSL+24]. **Gaussian** [LZY+23]. **Gaussian-Enhanced** [LZY+23]. **GBA** [BK10]. **GC** [IP09, MLC10]. **GC-Content** [IP09]. **gCoda** [FHZD17]. **GD** [ZZL+17].

GD-RDA [ZZL+17]. **gDel_minRN** [TMfTK23]. **GDT** [LBXL11]. **Gels** [EHK+02, PL06]. **Gene** [ARHLK19, ACKK19, AGH+18, AEH17, AHK08, AK08, AFCN13, AaHP+21, AAN+20, AJA+16, AS19, BR24, BBGS11, BJGG+03, BF02, BKT09, BB15, BW12, Bay23, BR06, BDSY99, BDBF+00, BDCKY03, BCCHZU18, BSB+05, BLEM08, BLP+22, BV09, BGL24, BBH+07, BJMS09, BMP+09, BJF+20, BRR02, BBWE09, CLM+16, CP05, CDEM08, CK09, CDFC00, CW09, CC11, CZS15, CDH+16, CC09, CQG10, CCPT17, CYLY12, CZY19, CUP19, CLSW02, DMDR17, DS04, DPSW20, DR17, DCH21, DKA+17, DCL18, DBB+02, DCH09, DAE+19, DS03, DHV06, EVLZU19, EMV98, FPD13, FSW+20, GHJ+12, GK18, GMF+08, GLM+09, GCB15, GSA14, GTA+04, GMC08, GPRR12, GSV21, GE14, GSV+11b, GSV+11a, GB06, GPCP11, Gu01, GJL+21, HMY+14, HG05, HVAW04, HJR12, HSL07, HJ05, HHJ+02, HZH+10, HXL+20, HWW+20, IRCA21, ITdB09, Jah11, JR12, JC22, JBM15]. **Gene** [JRHN09, KBJ07, KS12, KR24, KCG+19, KPB+04, KMC00, KV08, KMZ+10, KWA11, KK18, KNS14, KGK14, KCH04, LPW05, LDS12, LSRR18, LST+17, LK24, LRSG07, LMWR21, LSG04, LJCZ20, LYH+19, LGC+09, LDW+14, LXL+20, LLJS19, LCD11, MPG+16, MSS+22, MPZL23, MSMF09, MK11, MSR22, MSN+20, MP16, NKR+01, NVCW15, NV12, NXGL20, Nou21, PBS+99, PAC02, POP23, PdBdP+22, Par07b, Par07c, PSIM18, PIM23, Par24, PWCN02, PGA+11, PZMM15, PCC+11, PC05, PE20, QsYSxL23, QGP10, RMS02, RAC+06, RPS02, RKTS14, RRKT07, RZK06, RND+23, RD01, RMC+05, Rot19, RXH+20, SBD+00, SZW+09, SCH09, SnGqC20, SM09, SVCA17, SZSA22, ST10, SK23, SDG+07, SZVM10, SDC+10, SSZC95, SSLL22, SP97, TMfTK23, TWY02, TBJF01, TPSB19, VBSS10, WSS+15, WPL+19, WWC+20, WDZ20, WHK21, WLC18, WV11, WBJ15, WMPS11, WT07, WGW+01, WAC08, WKC+95]. **Gene** [Wu96, XAB+15, XvdL05, XU97, XJZ+21, YYZ+10, YS10, YHT+17, YL17, YYY+09, YWN11, ZPC+18, ZWSF05, ZSV+09, ZL09, ZWQ19, ZZS08, ZWD+04, ZAG+18, ZHQS05, ZH14, ZPD+23, ZS24]. **Gene-Based** [WHK21]. **Gene-Cluster** [SZVM10]. **Gene-Conversion** [SDG+07]. **Gene-Expression** [DBB+02, KCG+19]. **Gene-Phenotype** [LJCZ20]. **Gene/Species** [DCH09]. **Genealogy** [LLS11a]. **GeNeDA** [MPG+16]. **GeneDMRs** [WHK21]. **GeNeo** [AAoS+23]. **General** [DEH10, DMR+03, Erw19, HJD17, HI97b, JLMZ02, LNW01, RZK06, SWK+07, SZL+23, Wen06, ZPX+10]. **Generalizability** [ÖBA+23]. **Generalization** [BG23, ZS14]. **Generalizations** [ADR13]. **Generalized** [ABD+97, APA17, AS19, BKPW95, CD11, GGU13, HVD17, HMK24, HL10, KXL08, Kei06, Kon07, LRV21, MBRS11a, MHL22, PAC02, SV97, XZ12, XJZ+21, YS10, dMRR14]. **GeneRank** [WZW10]. **Generate** [MP16]. **Generated** [LYPC13]. **Generates** [YY19]. **Generating** [GBB15, MSMF09, PKK97]. **Generation** [AB16, AR17, Boe18, BG15, BVP+16, CUP19, FSD+14, GCB15, HSL+24, JAG17, KBKF17, KMM17, KAD+19, LYPC13, LZX12, NP09, PMP+15, RUGR18, RGM+12, Rot19, RNI+06, SWS+20, SRZ+13, WCL+18b,

YYM+23, ZPB+10, ZZ14b]. **Generative** [CK11, DS04, FMH06, MRG+24, MD00, QBA+25, TMG+20, yWCF06]. **Generic** [SGYBD05]. **Genes** [ARHLK19, AC17, AFR+08, AJV+16, BCH+01, BLEM08, BL02, CCG06, CYF+20, CCL+19, CCH+19, CWS+21, CZY19, DMTV09, DLM10, DYLK20, EBK11, FSW+20, Fic95, GMF+08, GPAR96, GGM12, GCD20, GDL+15, Gui98, HSF97, HSD05, HHC06, ITSH00, JMPR23, JZ10, JÖNK17, JRH+09, KBLS24, KYSE10, KSS09, KBČ19, LBEMG07, LL19a, LL19b, LHC19, LL19c, LGS20, MG06, MDB11, PNIM17, PZH11, QQL+19, QbMyD+19, SDFH98, SEV09, SRF16, SLM15, SM17, SnGqC20, SZTW12, SSZG24, TML+02, TXL+17, TVNP15, WOG03, WC04, WSCL18, WFL+20, WDZ20, WZL19, YfZX+21, ZMGN23, ZLW+20, ZLB+20, ZLL+20, ZXZ21, ZYD+19]. **Genetic** [AK07, ALR18, BSB+17, BH15, BPL02, BBEM09, CMK23, CY10, CZS15, DCD19, FDW20, FG04, FL17, GBR17, GZN16, JBBW10, KSB98, LLKX16, LLSH19, Li09, LYH+19, LS23, LQPE+10, MRM20, MPZ+20, MJS24, NS18, PBB+21, PDdJFT08, RS13, RMC+05, RMC+23, SG10, SKGG17, SLL08, SH17, TPSB19, VB09, Wag04, WH01, WGC+21, WGS+23, WHC09, WHJE19, YMZ+12, ZLM+17, dJ02]. **Genetically** [ZGRB10]. **Genetics** [GKgUS21, SSIP+19, SJ12]. **GeNICE** [DMDR17]. **Genie** [REKH97]. **Genistein** [LJCZ20]. **Genome** [AS10, AODD21, BR24, BNA+12, BP17, BH11, BV20, BS06, BBD+04, BJF+20, BFP13, CBH+12, CTC21b, CHSY10, CGOT10, CWS+21, CC12, Cos18, CP19, DPHH05, DCW+17, DJK+99, DCSE11, DBBM09, DKA+17, Eri09, FZF+20, Fas94, FMH06, FCV+07, GVMB24, GMC+14, GZW+21, HSOE+18, HMY+19, HY16a, HSAEM13, HG18, ISB12, IP09, Ist19, IP19, JJY+20, JSN09, JCBX22, KMJ+20, KASM08, KPB+04, KX14, KSSK09, KE13, LYMD03, LPFT14, LLKX16, LZHC15, LZBK15, LRM11, LHXH08, Lip05, LLT06, LWLJ10, LLZ19, LZX12, MLC10, MHS06, MB09, MPC+11, MJS23, MZM18, NHZ+15, NSA08, NSH+23, OB10, OR14, PdB13, PJL20, PBMC17, PDE+11, PAS+13, PMAP13, RM18, RGM+12, Rob94, SB98, SB99, ST05, SGBEM11, SCH09, Sea01, SKSL97, Sni19, SBAW97, TZHR14, TPH+09, WCM+08, WAX22, WGS+23, WS11, WES20, YF09, YZWZ13, YCCL18]. **Genome** [Yu24, ZPC+18, ZPX+10, ZWT18, ZZS08, ZF07]. **Genome-Information** [LZX12]. **Genome-Scale** [GMC+14, MZM18, NSH+23, PdB13, RGM+12]. **Genome-Tiling** [FMH06]. **Genome-Wide** [CTC21b, FZF+20, ISB12, IP09, JJY+20, JCBX22, LYMD03, LZHC15, LZBK15, LLT06, LWLJ10, LZX12, TPH+09, WCM+08, WAX22, WGS+23, WES20, ZPC+18, ZPX+10, KE13, LLKX16]. **Genomes** [Ale08, AOJ+23, AFRV07, AFR+08, AJA+16, BCVL17, BBDS21, Boh24, BDK+16, CF14, DLM10, EVLZU19, HPDLW09, HZH+10, Kei06, LPW05, LMS96, LCXC05, MM06, MKB+20, NBA+13, OFS08, RHY+04, SBP15, SH06, Sel13, SLM15, SM17, TM22, TAJZ23, TTTL17, WYT12, XZS07, Xu10, YYZ+10, ZWJ18, ZDZ+20]. **Genomewide** [SS04]. **Genomic** [AZ14, BSP+24, BB04, BCCHZU18, BBEM09, BBH+07, BMR+19, Che04,

CGI+07, CM04, DRT+25, Dei19a, DCP+08, DP07, EZFP+19, ET07, FRD+17, FFSL22, GSN11, GCB20, GCD20, Ist19, KP96, KV23, KWB+94, KSK+11, LWLL19, LM11, LZF+05, LMW05, Ma11, MRM20, ODNW21, OKKS21, PBB+21, Par06, PK19, RLK+09, SGT15, SH06, SMZ+12, SF03, TRB+09, TBKR10, VAS+18, WDF24, WLF13, WYKG05, XU97, YS23, YGP05, Yua09, vUMW08]. **Genomics** [AMS97, Ano00, Ano11b, BBP10, CKS12, CKS13, CKS14, CKS15, Cos18, Edi24, FS99, KPB+04, KMB+20, KPP+22, MS03, NV09, Rot19, AAoS+23, ZMK23]. **Genomics-Guided** [AAoS+23]. **Genotype** [BZ08, GZY+22, HWH+13, KZE10, KMP08, LJ05b, McP12, WYY+18, YHEP15]. **Genotypes** [KS05, PBB+21]. **Genotypic** [RBK94]. **Genotyping** [EHC+13, HMY+19, SGYBD05]. **Genovo** [LJK11]. **GenRate** [FMH06]. **Genuine** [PRT08]. **Genus** [MP16, POP23, RPS02]. **Geodesic** [KVK08]. **Geographical** [ABTP23]. **Geometric** [APVM11, BWS13, CFB+07, CHKK99, EHK+02, Erd05, MYBK+11, SAM06, SY09, SKG+00, TBL18, XZW15b]. **Germline** [DRT+25, LHW+22]. **Getting** [HPL+20]. **GFFview** [DCW+17]. **Gibbs** [CP05, Kei06, Lar06, PWFZ17, Ste14, TML+02]. **Given** [JM95, PFRD05, RSM06]. **GLASS** [JR12]. **Glioblastoma** [LLT+25, ZWK+20]. **Glioma** [AMS+22, CLLL20, HWW+20, TKSA24]. **Global** [Lat99, LGC+09, LBDVF10, MH22, PM14, PX13, Rob96, SYYH02, WDA01, ZW03]. **Globally** [XXU98]. **Globular** [OC00]. **Glucose** [SLL+23]. **Glycation** [JWL24]. **Glycine** [ZDZ+20]. **Glycoprotein** [Pen20b]. **Glycoproteins** [Pen20a]. **GNN** [QTRA24]. **GO** [LACB10]. **Good** [YZ08]. **GoVec** [Nou21]. **Governing** [CUP19]. **GOWler** [HVD17]. **GPU** [And09, DBM09]. **GPU-Accelerated** [DBM09]. **GQ** [GWL+19]. **Grade** [WDZ20]. **Gradient** [WxLW+23]. **Gradients** [MSS21]. **Grading** [PLZX25]. **Grained** [AJYJ18, DPS+20]. **Graining** [CB07]. **Gram** [RSM06]. **Gramicidin** [LSAD05]. **Grammar** [SCSA+16]. **Grammatical** [CJS06, CJD06, KAS09, MBS+01]. **Grand** [AHK+02]. **Graph** [AODD22, APF+20, AMR20, BKCP05, BSB+17, BG06, BLP+22, BSS13, BP16, BVP+17, BSSZ+20a, BSSz+20b, CHS17, CJP+22, CY17, CP19, DM20, DSN14, Fre11, Gus10, HS23, HBW+05, JZGA20, KMJ+20, KV23, KK11, LTI10, LJK16, LWZ18, NK07, NSK09, Nou21, PMCB08, Par10, PDSD06, SSR21, Sef25, Ste14, TA21, WYT12, cWxLlS+23, WxLW+23, WPS+25, XZS07, Xu09, Xu10, YS07, ZZHL11, ZlWL21, ZZC+24, ZLTZ25, ZCZ+23]. **Graph-Based** [DM20, KV23, WPS+25]. **Graph2Seq** [WFC25]. **Graphical** [EAM+17, KV17, KGLBK15, LKL21, LCGW09, MJCM22, OAR+24, WG08a, YZ17]. **Graphics** [CFE+13, SSLMW10]. **Graphlet** [VILR10]. **Graphlets** [HS14]. **Graphs** [APA17, AAC+06, ABR16, BH14, BBP10, BBC16, BBV+14, BVP+16, CPFP24, CR09, CC23, CJ23, CLJ+15, GTA22, HSOE+18, KTSS19, KRF+12, KT13, KLR23, LAF+14, ML22, MPC+11, NFHM21, Par10, PDE+11, PAS+13, PFRD05, RM18, RC24, SDMN19, Sam09, SH05, Wu08, YCP16]. **GraphSlimmer** [TGA24]. **Greedy** [KMMF20, SM20, ZSWM00]. **Green**

[BMN+07]. **Gregor** [Dei19b]. **GRNUlar** [SZSA22]. **Grohar** [MZM18]. **Group** [BMN+07, CEKP+13, CFS13, CD11, HTZ+12, MKKK+17, PNMI15, PIWR15, SSY+22, YK19, ZHZ+16]. **Groups** [CCG06, DQS+11, DMTV09, HL10, RROF95, WZC96]. **Groupwise** [SHE11]. **Growing** [KLR23]. **Growth** [JB10, SRB+25]. **GS** [BR24]. **GS-TCGA** [BR24]. **GSEAplot** [IRCA21]. **GSMC** [PWFZ17]. **GTP** [OJOD+04]. **Guarantee** [MDK24]. **GUI** [OAR+24]. **Guide** [NDMK17]. **Guided** [GZN16, Li09, NZM+25, PCGBK13, AAoS+23, SHZ+24, ŻZ15]. **Guides** [CKL+17, ZZL23a]. **Gurtin** [CYY23]. **GWAS** [HATI11].

H [Ano20]. **H2A** [YI17]. **H2A.Z** [YI17]. **Haar** [YS23]. **Hairpin** [DLD+14]. **Hairpins** [CCJ09]. **Halving** [Boh24, SGBEM11]. **Hammerhead** [MRM+02]. **Hamming** [AO15, BHHR18, ETLK19, Ris16]. **Handling** [BAK13, HHHS03]. **Handprinting** [RC15]. **Hap** [HHE13]. **Hap-seq** [HHE13]. **HapCompass** [AI12]. **HAPLOFREQ** [HH06]. **Haplotype** [AI12, BB06, BDK+16, CFS+08, CDS+16, DEH10, GLMSO10, GG04, GKM+10, GMSZ12, HH06, HHE13, HCC05, KMP08, KHK10, LKW04, LJ05b, LL11, LS97, ME12, PMP+15, PMAP13, SHB+03, SY22, SR10, WDF24, XJS07, YHEP15, ZGRB10]. **Haplotypes** [ASL06, BGHY04, Gus01, SGP11, Ves12]. **Haplotyping** [BGLY03, DFG06, VM06]. **Happy** [DHM+05]. **Hard** [BRS20, QEk24]. **Hardness** [DHM97, GTA22, LJL+20, NSZ99, War95, HI97b]. **Hardware** [SSLMW10]. **Harmonic** [AT12]. **HarmonyDOCK** [PPV+14]. **Harnessing** [Vij22]. **Hashing** [HTY22, HHC06, KBG18, PNPC20, PKSB18]. **Hashing-Based** [HTY22]. **HattCI** [PWKAF16]. **Having** [BLR16, ZYB+04]. **Hazards** [LL23]. **HColonDB** [MXJ19]. **Head** [LTL20]. **Health** [CKL+17, GSH17, HTH+17, VA17]. **Healthy** [LLS11b]. **Heart** [JFLL20, YHW18]. **Heat** [LLS11b]. **Hedgehog** [DMHM97]. **Helical** [Con04, TS96]. **Helicity** [SLO07]. **Helicobacter** [UBGFD+19]. **Helix** [CJD06, CBM+02, SLO07, WY12, ZKWH17]. **Helix-Coil** [SLO07]. **Help** [BF98]. **Hepatitis** [CCH+19]. **Hepatocellular** [BRC20, CCH+19, GDL+15, YcXyW+21]. **Hepatocyte** [GSH17]. **Her-2-** [JSZ+20]. **Heritability** [SFR+18]. **Herpesvirus** [LMS96, LCXC05]. **Hes1** [ZML07]. **Heterogeneity** [FLT+21, KC96, RNH18, RH19, YYL20]. **Heterogeneous** [EOD+18, GFE+16, GVTS04, GBR17, LR05, MR95, Mar95, Nou21, ZGRB10, ZCZ+23, ZZL+23b]. **Heterozygosity** [HATI11]. **HetFHMM** [RNH18]. **Heuristic** [AHK08, Cha01, DMB07, RC14, SV97, TAY16]. **Heuristics** [KMP+04]. **Hexagonal** [GWX18, KMRG09a]. **HF** [HXY+23]. **HF-DDI** [HXY+23]. **HGT** [TRIN07]. **HHeterSW** [GFE+16]. **Hi** [DLFS22, DZS24, MSRS24, RBH+19, ZLTS13]. **Hi-C** [DLFS22, DZS24, MSRS24, RBH+19, ZLTS13]. **Hidden** [BC94, Bal95, BP14, CL99, EMD95, FDB18, GCB15, HSF97, HJ05, HW01, KMP08, Ker03, KS05, Mam96, PAC02, PWKAF16, QSY09, RNH18, RH19,

RLA+06, SPW22, SH04a, UTD+20, WS04, WTE07, WX08, YH01].
Hidden-State [RLA+06]. **Hierarchical** [BRR02, CK11, CSA98, CB07, JCZ08, KSSK09, LWN+18, NWN+10, PLSL18, ZL09, ZH07].
Hierarchical-Pooled [PLSL18]. **Hierarchies** [Neu14a, Neu14b]. **Hierarchy** [BET00]. **HIF** [MXW+20]. **HIF-1** [MXW+20]. **HIF2}** [cLcSwP+21]. **High** [APF+20, ACL15, BBN11, BLC10b, CLM+16, CKZ+19, CAC+23, CBG+14, CHK+02, DDC+20, FCR+13, FCV+07, GSN11, GLM+09, GDHC95, GNI12, HG11, HBD94, HZL22, HLY25, Hua10, KS11, KVDC06, KMZ+10, LKBT16, LLSH19, LBBV+18, LRM11, LL23, LLL+20, LDB+07, MBC+18, O'H15, OBDV16, OAR+24, Pen20b, RDR12, SSLMW10, SBRG20, TZB+23, TPH+09, WDZ20, WAC08, ZPG+24, ZQZ20, ZZL+17, ZHQS05, ZZUPY06, ZY23].
High-Accuracy [ZPG+24]. **High-Density** [CKZ+19, CHK+02, HLY25].
High-Dimensional
[APF+20, ACL15, HZL22, KMZ+10, LKBT16, LLSH19, O'H15, ZZL+17].
High-Grade [WDZ20]. **High-Order** [WAC08, ZY23]. **High-Performance** [HBD94, MBC+18]. **High-Quality** [GLM+09]. **High-Resolution** [GDHC95, LBBV+18, LRM11, TZB+23]. **High-Throughput** [BBN11, BLC10b, CLM+16, CAC+23, CBG+14, DDC+20, FCR+13, FCV+07, GSN11, GNI12, KS11, LDB+07, OBDV16, SSLMW10, SBRG20, TPH+09, ZZUPY06].
Higher [DM17, DBT11, SHZ+24, TRB+09]. **Higher-Order** [DM17, SHZ+24, TRB+09]. **Highly** [BSP+24, GFE+16, JMPR23, MNSV10, SBP15, TVNP15, TTTL17].
Highways [BBGS11]. **Hiking** [Cha01]. **Hinge** [SNW04]. **HiPPO** [PSG+20].
Hirschsprung [NXGL20]. **Histo** [YK19]. **Histo-Blood** [YK19].
Histocompatibility [Vij22]. **Histone** [Yua09]. **Histones** [BRR06].
Histopathological [MDL+18]. **Histopathology** [CLLL20]. **Histories** [DR15, KKM+20, Ros07, VBSS10]. **History** [LBEMG07, Ma11, MMA+21, RSEK24, SP11, Tra19, VA17, YDN02, ZSV+09].
Hit [CWC06]. **Hitch** [Cha01]. **Hitch-Hiking** [Cha01]. **Hits** [KWM10].
Hitting [ZKM21]. **HIV** [BYL+20, DCV+07, EBS+22, GT16, HAM+22, HPVS96, RYZ23, SS04].
HIV-1 [BYL+20, HPVS96, SS04]. **HIV/AIDS** [EBS+22, HAM+22, RYZ23].
HLA [HKL07, SGP11, ZYB+04]. **HLA-A*0201** [ZYB+04]. **HMM** [ZKL+10]. **HMMatch** [WTE07]. **Hoeffding** [AS19]. **Homo** [CYP+11, MYBK+11, YLD+18]. **Homo-Oligomers** [CYP+11, MYBK+11].
Homoclinic [KG24]. **Homogeneity** [LR05]. **Homologies** [JDH00].
Homologous [DC16a, Eri09, HJ05, PZH11, SYYH02]. **Homologs** [BF98].
Homology [AMOW10, BS98, BBD+04, CBW07, CV11, Gru98, HG05, Kon07, PZC05, SPD18, SSD07, SRS02, XBLM06]. **Homomorphic** [BSP+24].
Homoplasy [AA18, LTI10]. **Homoplasy-Free** [AA18]. **Homopolymer** [ETLK19]. **Homopolymer-Space** [ETLK19]. **Homotopy** [DOKT05].
Homozygous [TTTL17]. **Honor** [Ano21a]. **HOPE** [DOKT05]. **horikoshii** [RBKJ19]. **Horizontal** [BBGS11, ST10]. **Host** [HTY22, Kha14, SLYC09].
Host-Dependent [SLYC09]. **Hot** [DGW+13]. **Hotspots** [BB06]. **House**

[ZZL22, ZLP22]. **House-Hunting** [ZZL22, ZLP22]. **HP}** [BL98, ABD+97, GMS05, HCS09, SVD14, TAY16, YE02]. **HP-Model** [YE02]. **HPC** [KMRG09b, KMRG09a]. **HR** [JSZ+20]. **HSP70** [JJY+20]. **hT2R16** [CWRF15]. **HTFSMMA** [SHZ+24]. **HTLV** [CDC+11]. **HTLV-1** [CDC+11]. **HTML5** [AB16]. **HTML5-Based** [AB16]. **HTP** [CLM+16]. **HTP-OligoDesigner** [CLM+16]. **Hu** [Ano20]. **Hub** [CYF+20, YfZX+21, ZLB+20, ZYD+19]. **Hubs** [MTYH09, MSRS24]. **Huffman** [AOAAH17, AH20]. **Huge** [WLYC12]. **Hull** [WTY19]. **Hultman** [APA17]. **Human** [AF20, BR12, BCD+24, CBH+12, DBBM09, GPAR96, GSH17, GE17, HMY+19, HHC06, JSZ+20, LZHC15, LTZ18, LFD03, MXJ19, MDMC21, Nai18, PM24, Pen20b, PE20, Sal95, SCH09, SSV19, SKSL97, SCSA+16, SZTW12, TE96, YCCL18, YK19, ZWT18]. **Human-Specific** [SCH09]. **Humans** [DM20, Elh11, LDB+07, SGK+12, Yua09]. **Hunting** [Bry96, PWFZ17, ZZL22, ZLP22, ZTD+22]. **Hurdles** [SLRM09]. **Hybrid** [Azi22, BDC97, BZB+22, CXW16, CYLY12, CKL+17, DHV06, Hea97, HXY+23, LYC15, QTRA24, YK05]. **Hybridization** [AMRW96, BDPSS01, BMN+07, CLS11, DMP+06, DJK+99, DFS94, FH02, FLT+21, GI95, HHHS03, HPY03, Hub01, Kru98, Mil95, PU00, PO04, RRGC95, SLA12, ST02b, WHW+06, WI05, Wu13, YzCW20, DFS96]. **Hybrids** [SKSL97]. **Hydropathic** [CFR12]. **Hydrophilic** [AP10, BL98, HI96]. **Hydrophobic** [AP10, BL98, GP13, GWX18, HI96, KMRG09b, TGT08, TS96, YTMY17]. **Hydrophobic-Hydrophilic** [AP10]. **Hydrophobic-Polar** [GP13, GWX18, YTMY17]. **Hydrophobic-Polar-Cysteine** [KMRG09b]. **Hydrophobicity** [ABD+97]. **Hydroxyproline** [Yan09]. **Hypercholesterolemia** [MRS+18]. **Hyperdigraph** [OJOD+04]. **Hyperdigraph-Theoretic** [OJOD+04]. **Hypergraph** [AL25, YFBK07, ZWD25]. **Hypergraphs** [KK23]. **Hypermutability** [FB12]. **Hyperpaths** [KK23]. **Hyperplane** [BGJ+04]. **Hypertension** [TZZY20, ZXZ21]. **Hypotheses** [MDMC21]. **Hypothesis** [FDDK07, GML20, LSY+05, MSZW11, RNI+06, SFA17].

i.i.d [MD01]. **IBD** [LL11]. **ICCABS** [BMM+23, JMR+21, MMN+21]. **ICON** [WCZ+18]. **ICON-MIC** [WCZ+18]. **IDBA** [LYPC13, LYC15]. **IDBA-MT** [LYPC13]. **IDBA-MTP** [LYC15]. **idDock** [HS15]. **Ideal** [ZHY+20]. **Ideal-Gas** [ZHY+20]. **Ideals** [SS05b, SS05c]. **Identical** [AMOW10, SGP11]. **Identifiability** [AR06, AP09, DAR23, YAR21]. **Identifiable** [ŠV07]. **Identification** [ARHLK19, ALB+19, AF20, AJV+16, BSB+05, CDQ+21, CCG06, CCF10, CCH+19, CKZL20, CMS+25, CLSW02, CBG+14, DBBM09, DYLK20, EPSV98, FZF+20, FKZ09, GML20, GSV21, GDL+15, GBB15, HTY22, HRSC00, HV07, HYY+10, HBK11, HWW+20, HKZ+04, JPLD23, JZZ+19, JÖNK17, KTT20, KPB+04, KK22, KT13, LZHC15, LL19a, LGD+19, LGC+09, LCD11, MS00, MM06, MCH+19, MSB+10, MP16, NTWF11, OAR+24,

OBJO+03, OR14, PYIM22, PIM23, PWKAF16, PDT00, PDdJFT08, RXH+20, SFN97, SIK+05, SB21, SlGW+23, SnGqC20, SR10, Sni19, SMC+15, SSD07, SSZG24, SG94, TZB+23, TZZY20, TXL+17, TLK+06, VRU16, WSCL18, WAM20, WWLC20, WLC18, WKC+95, WTE07, WZL19, XXZ+21, XU97, YHT+17, YDG+20, YfZX+21, YJC18, YLC+20, ZWSF05, ZLW+20, ZLB+20, ZLL+20, ZDG+20, ZlWL21, ZXZ21, ZZL+23b, fZbMqW+20, dMRR14, Ano20].
Identifications [BG08]. **Identified** [XWJZ20]. **Identifies** [FSW+20, LTL20, OSK+15, TGT08]. **Identify** [LDLZ12, LCW16, MYS+20, YHW18]. **Identifying** [AMK00, BH14, BP20, BCH+01, BYL+20, BRR02, BBWE09, CJC01, CDL+19, CPR22, CZY19, CHK+02, DCP+21, DS04, FCS12, FRD+17, GMF+08, HG05, HSBS10, HXL+20, ITdB09, JWL24, KE13, KLC+11, LHXH08, MGW+07, MMK+21, PSIM18, SM98, SPSZ23, SS05a, SH17, SJ18, TEMM12, WC04, WVT23, YKPM20, YZ08, YYZ+10, YLD+18, ZZC+24, ZZZU20, ZY23].
Identity [Bro98, KLKH11, YCP16, ZL01, ZKT14]. **Identity-by-Descent** [YCP16]. **IDH1}** [CLLL20]. **Idiopathic** [ZXZ21]. **IDN** [JWL24]. **iGLASS** [JR12]. **iGly** [JWL24]. **iGly-IDN** [JWL24]. **II** [WRSW10, AMS97, CGOT10, SkY12, ZRGHJ08]. **II.** [Fom16b]. **III.** [Fom19]. **Illumina** [CWL13]. **ILP** [CDS+16]. **ILP-Based** [CDS+16]. **Image** [BLQZ04, DAL+08, FCR+13, PLSM+06, YHC19, ZKWH17]. **ImagePlane** [FCR+13]. **Images** [AG23, CSH+20, CLLL20, HTM+22, LTTS12, LCL+17, NZM+25]. **Imaging** [Hua10, HLG18, KKS+15, PLZX25]. **Imbalance** [DCV+07]. **Imbalanced** [HSH14, MEF24]. **IMFLer** [PSP21]. **Immersed** [SSS20]. **Immune** [JK96, LRNBJ10, LDB+07, SLT24]. **Immunity** [YMM+24, ZZN10]. **Immuno** [DLL+24]. **Immuno-Oncology** [DLL+24]. **Immunodeficiency** [BR23]. **Immunogene** [PM24]. **Immunoglobulin** [BP16, GKKS98, SKG+00, YK19]. **Immunoinformatics** [UBGFD+19]. **Immunoprecipitation** [BHGCS11]. **Immunoreactivity** [BR23]. **Impact** [BP20, DGFMSS16, JR16, SJ18, WWH17, ZPC+18]. **Imperfect** [LTI10]. **Implementation** [And09, MGSA06, NBB18, Vij22]. **Implementing** [NXL+15, PB18, WCZ+18]. **Implications** [BBWE09, FL94]. **Implicit** [BMR09, CYY23]. **Importance** [CZC10, RDR12]. **Important** [MTYH09]. **Impossibility** [Mos03]. **Improve** [GZY+22, GB06, HLG18, KVM14, TYSX19]. **Improved** [ÅMR07, AT12, BMH21, BS97, BG08, BK08, CL17, CLR+05, CDH+16, Fre11, GF16, JWL24, KFDT02, LS08a, MSBR08, MA13, MVP06, QTRA24, REKH97, SFA17, SSKH+13, SZW+09, SSH+10, SPW22, SK18, WC16, WT17, YzCW20, YLC+17, YLZ+24]. **Improvement** [AMS+22, JR12, YLW+15]. **Improvements** [HJR12, ZL22]. **Improves** [HKL07, JBM15, MSS+22, NTWF11, ZGEZu11]. **Improving** [AT08, BCG+18, CC23, CWJ+21, GKS95, HSH11, Ila20, KKC+22, LWN+18, LHW+22, NKR+01, ÖBA+23, PXLP23, PFK17, RK96, WHJE19, XLZ13, ZYD21]. **Imputation** [GVA22, HHE13, KZE10, MSS+22, McP12, MSM20,

MM19, WHJE19, YHEP15, ZL22, ŽZ15]. **Imputing** [DZS24, WES20]. **Inapproximability** [BJ17]. **Inaugural** [HTH+17]. **Inborn** [PdB13]. **InceptionV3** [AG23]. **Include** [YF09]. **Including** [AR06, TKO21]. **Inclusive** [WWZ19]. **Incompatible** [GBBS07]. **Incomplete** [BW12, BMR09, LJ05b, WR23, ZAG+18]. **Inconsistency** [HR22]. **Inconsistent** [EAFM24, KABH15, KWBN19]. **Incorporating** [GJZ06, KX06a, KX06b, LTS20, MPC+11, PS12, RH19]. **Incorporation** [Kon09b]. **Increase** [FA12]. **Increasing** [SHE11]. **Incremental** [AP04, KS06]. **IncRna** [JPLD23]. **Indel** [AODD22, DMB07, SSH+10, SP11]. **Indels** [AODD21, HB11, McC09, TRS17]. **Independent** [LYMD03, SJ12, ZQZ20]. **Index** [FDW20, JMPR23, KMB+20, MKB+20, ROB+22, ROL+22, YGP05, YHC19, bVRN+19]. **INDEX-db** [bVRN+19]. **Indexing** [Buh03, CGZ04, CM04, GHM+10, HS23]. **Indian** [bVRN+19]. **Indicators** [ADRS24]. **Indices** [LLW03, TW05]. **Indirect** [ADD+07, TBS+07]. **Individual** [BF98, PCS18]. **Individual-Based** [PCS18]. **Individuals** [LL11, McP12]. **Induced** [BB04, LDS12, YYL20, YLC+20, JKG+04]. **Inducing** [SZL+23]. **Induction** [BKT09]. **Inequalities** [RCSS12]. **Inequality** [AS19]. **Infants** [ZYH20]. **Infarction** [ZLSY20]. **Infected** [MDWZ24, RFH+25, WZ23, YYZ23]. **Infection** [DM20, LGS20, SCSA+16, STP18]. **Infer** [BB15, CMS+25, JSN09, RNH18]. **Inference** [ACBM18, ADD+07, ADR13, AEH17, ARSW22, ADR24, BB06, BBN11, BCPS04, BMR09, CYP+11, CGT12, CWH+22, CMvH15, CKB17, DMDR17, DCH21, DMW+17, DBB+02, FHZD17, FLJ11, FNPP02, GMC08, GW06, GLMSO10, GG04, GM96, GMSZ12, Gus01, HCC05, HMF07, IR22, JPB+15, JG11, JBM15, JBBW10, KHK10, KK23, LAL+09, LL11, LYH+19, LW22, ME12, MPZL23, NKR+01, O'H15, RV15, RSEK24, RBEB13, SSKH+13, SLL08, SHB+03, Ser15, SGP11, TS04, TR11, TNSS13, TZP+13, XLZ+18a, XJS07, YYA11, YT22, YWN11, ZZHL11, ZL01, ZKT14, ZS24, ZCK17]. **Inferential** [ARHLK19]. **Inferred** [MTYH09]. **Inferring** [AFBS95, Bay23, BG09, BLEM08, CDQ+21, DJK+99, GBR17, GM07, GKM+10, HJR12, KKM+20, LTCH11, LZBK15, MBRS11a, NSMV18, SKS+09, WBJ15, WHJE19, YYY+09]. **Infinitely** [ADR24]. **Inflated** [DLFS22, PLL16]. **Inflation** [WVT23]. **Influence** [BIPD17, GC15, Hua15, JÖNK17, Kru17]. **Influenced** [SRB+25]. **Influences** [RH19]. **Influential** [NLC17]. **Influenza** [AWM+17, LBSB17, MGVS14, ZZN10]. **INFO** [LS98]. **Informant** [DBT11]. **Informatics** [Rob94, TA21]. **Information** [AOJ+23, APF+20, AFCK09, AT08, BSKgG23, BG15, Bro98, CMK23, DCW+17, FS99, GSSI14, GKgUS21, GTA+04, GE17, HKL07, KX06a, KX06b, Let95, LYC15, LFT+98, LZX12, MPC+11, NWN+10, PdBdP+22, PU00, QGP10, RPW13, SFA17, SG15, SKGG17, SSB07, SY07, SkY12, SKT08, TXL+17, TEMM12, UGS19, YGP05, YLC+20, Zha02, ZZL23a, ZWD+04, ZZL+23b, ZY23, vLSV+24]. **Information-Based** [YGP05]. **Information-Theoretic** [ZZL23a].

Information-Theory [PU00]. **Information-Theory-Based** [CMK23]. **Informational** [OFE14]. **Informative** [AHK+07, Ros05]. **Inframe** [BP20]. **Infrared** [MGW+07]. **Infrastructure** [Rob96]. **Inheritance** [CK10, HWH+13]. **Inhibition** [GAWI19, MGVS14, MCH+19, MSN+20]. **Inhibitor** [CASP10, CCF10, CFS13, PZZ+10, ZHZ+16]. **Inhibitors** [ALB+19, AF20, CD11, DDK21, HTZ+12, HL03, MRG+24, RBKJ19, SB21, TGTG19]. **Initial** [AN18, OJOD+04, Ste14]. **Initiation** [CZNF19, HL16b, LJ05a, WOG03]. **Injury** [CYZ+20, LL19a, LL19b]. **Innate** [LRNBJ10]. **Innovation** [WT07]. **Input** [CBS+20, CL21b, Jus06]. **Inputs** [Fom19]. **Insertion** [DMP+06]. **Insertion-Deletion-Like** [DMP+06]. **Insertions** [BP20, BWS11, HSH+09, YF09]. **Insight** [LLJS19]. **Insights** [Elh11, MLC10, PV17, PDSD06]. **Inspired** [AMK18, MPG+16, WI05]. **Instance** [ASZ+16, CLLL20]. **Instant** [vLKMR22]. **Instantaneous** [BBN24]. **Insufficient** [LCY+05]. **Integer** [ADRS24, CCI+04, DWMT22, Gus10, HNTW09, LJ05b, PMGE21, kSyPhC+22, TMfTK23, Yin19, Zör15]. **Integer-Programming** [Gus10]. **Integers** [NL09]. **Integral** [TS96]. **Integrate** [WHC09]. **Integrated** [CWR24, CAB11, DCS04, FSW+20, JEMF06, JSZ+20, KP96, MRM20, WQZ+19, YcXyW+21, ZCY+20, ZWQ19, ZZ20, ZXZ21]. **Integrating** [AEH17, BLP+22, CW09, DOB95, GVTRS06, HS15, JM97, KS12, LLG+20, MLOT17, PZZ20, QFLL22, SCD+22, TXL+17, ZY23]. **Integration** [BCG+18, BR12, DSS+22b, FBV15, GZY+22, JBBW10, LZHC15, LYH+19, MHL22, PXLP23, TA21, VV97, WV11, YY19, YJC18]. **Integrative** [DZS24, FRD+17, GWL+19, JFLL20, LTL20, MNIK+09, PNMI15, ZLM+17]. **Inteins** [DMHM97]. **Intelligence** [DNZ17, DND+19, Kum22, DNZ17]. **Intensity** [LYS20]. **Intensive** [SEV09]. **Inter** [OYY+12, ZWY+17]. **Inter-Barrel** [ZWY+17]. **Inter-Diplotype** [OYY+12]. **Interacting** [FR14, LLKX16]. **Interaction** [ACKK19, AKN+06, AHPR12, BML+16, BSS13, BHK+10, CASP10, CDL+19, DZM+03, DGW+13, DBHC24, DSG+08, EBK11, FCS12, GZLY24, HHX16, HSH+09, HSBS10, HS14, HXY+23, JEMF06, KGLBK15, KKS+06, KKT+06, KSG07, LACB10, LAF+14, LWC+14, LJCZ20, LZL+23, LSSD18, LLT+25, MYS+20, MSRS24, NLH+23, NK07, PK11, PXLP23, PNIM17, PMG+16, PE20, PX13, QSY09, QR13, RDR12, SIKS06, SDK16, SB17, SIK+05, SKS+09, SY07, SkY12, TXL+17, WHD13, WFC25, YKPM20, Zho17]. **Interaction-Based** [PNIM17]. **Interactions** [Ami12, BLP+22, BMB24, BT08, BF09, CDL+19, CJ21, CJP+22, DM20, FH18, GLMW13, KS12, KK11, KMCKS17, LBJM11, LZY+23, LLJS19, SMD+07, SSW20, TBS+07, TTTL17, VB09, yWCF06, WHDN13, WSS+15, WYC+18, WYLW21, YLC+17, YFBK07, ZZC+24, ZYD21]. **Interactive** [BP17, HSG22, HAP12, MM21, PSP21, RUGR18, ZMGN23]. **Interactome** [FKZ09]. **Interactomes** [MTC11]. **Interactomic** [FRD+17]. **Interchanges** [LLCT05]. **Interdependencies** [BSB+17]. **Interesting** [MC10]. **Interface** [KV17, OAR+24, RUGR18]. **Interface-Based** [KV17]. **Interfaces** [CY17].

Interference [RPR+15]. **Intergenic** [AOJ+23, BJF+20]. **Interleukins** [SZL+23]. **Intermediate** [LS08b]. **International** [BMM+23, Ber11, CSZ18, CSZ19, CSZ20, CSPZ21a, CSPZ21b, CSZ22, CSZ23b, CSZ23a, DMV17, DNZ17, DND+19, JMR+21, LZL+23, MMN+21, Pat24, Pat25, YQDW23]. **Interoperation** [Kar95]. **Interplays** [Par24]. **Interpolation** [LCL+17]. **Interpretable** [Geo09]. **Interpretation** [BWS13, KST96, RAC+06]. **Interpreting** [LRL+07, Neu14b]. **INterruption** [LS98]. **Interspecies** [LM03]. **Interval** [CLR+05, LABD+06, ZZ10]. **Intervals** [ATLS07, BFS10, SFR+18, SDC+10, dMRR14]. **Intervention** [CKL+17, LTSA15, SVK10, VND17]. **Interventional** [DS04]. **Intervertebral** [FZF+20]. **Intestinal** [CYZ+20]. **IntOMICS** [PP23]. **Intra** [AS23]. **Intra-Exon** [AS23]. **Intracellular** [GPOP+17]. **Intractability** [Eli06]. **Intralocus** [HR22]. **Intrinsic** [HL16a]. **Intrinsically** [GZW+16]. **Introducing** [SBTV10]. **Intron** [LS98]. **Intron/Exon** [LS98]. **Intuitive** [KFC+11]. **Invariant** [SKG+00, ZRGHJ08]. **Invariants** [EZ98, FLS94, HP96, JPR06, SB99, SF95, SS05b, SS05c]. **Invasion** [ZPG+24]. **Invasive** [WFL+20]. **Inverse** [DS04, GMS05, KMRG09a, KMRG09b, LLW03, LLD+16, PL06]. **Inversion** [BMY01, LBEMG07, SR10, WW18, WW19]. **Inversions** [SLRM09, SRLM10, YDN02]. **Inverted** [BO07, Sel13]. **Investigate** [MRS+18]. **Investigated** [LL19c]. **Investigation** [SZY+20]. **Investigations** [PIWR15]. **Involved** [AC17, LL19b, LL19c, PMG+16, SBRG20, TXL+17, WDZ20, YHT+17]. **Involvement** [LXL+20]. **Involving** [CK10, LPFT14]. **Ion** [SSS20, SF12]. **IonHammer** [ETLK19]. **Ionizing** [ASZ+16]. **IonTorrent** [ETLK19]. **IPED** [HWH+13]. **iPhyloC** [HSG22]. **iRNA** [YLD+18]. **iRNA-2OM** [YLD+18]. **Irradiated** [SVCA17]. **Irredundant** [CV11]. **ISBRA** [CSZ18, CSZ19, CSZ20, CSPZ21a, CSPZ21b, CSZ23b, CSZ23a, Pat24, Pat25, CSZ22]. **ISCB** [CKS14, CKS15]. **Ischemia** [CYZ+20]. **ISFMDA** [CJ21]. **Islands** [BCCHZU18, KLC+11, YCCL18]. **IsoDA** [HWZ+21]. **Isoform** [BBV+14, HWZ+21]. **Isoforms** [Ami12, FLJ11]. **IsoLasso** [LFJ11]. **Isomers** [JHA16]. **Isomorphism** [HLMR11]. **IsoRank** [DBHC24]. **Isotopic** [AMR20, BKKSD01]. **Issue** [Ano09b, Ano21a, BMM+23, CSZ20, CSPZ21a, CSPZ21b, CSZ23b, CSZ23a, CKS12, CKS13, CKS14, CKS15, CMSZ12, Cow20, EN22, Gus05, HTH+17, Ist99, Ist20, IPSV22, JMR+21, Kum22, Len02, MS24, MMN+21, MV04, Miy06, Mye03, NV09, Pat24, Pat25, Pe'22a, Pe'22b, Pen22a, Pen22b, Sch21a, Sch21b, Sha00, Tan23, ZGW22, CSZ18, Dei19a, HASL18, JLmR+23, VRGC18]. **Issues** [Hua10, TBKR10, WIP97]. **itca** [ZZL23a]. **Itemset** [CCT09]. **Iterated** [PZZ20]. **Iterative** [And09, BYGI12, BS97, GTA+04, LZC+23, Mal98, PNPC20, XMU96, ZZL00].

J [Ano20]. **Jabberwocky}** [Sea01]. **Jacobson** [Clo05, GJL+22]. **Java** [NBB18]. **JCB}** [Ano21a]. **Jigsaw** [BKWK+00]. **Join**

[BWS11, MJS23, SLM15, XLZ+18a]. **Joined** [DNZ17]. **Joining** [GM07]. **Joins** [ZS17]. **Joint**
[ADRS24, CQG10, CBG+14, CKB17, DNZ17, DND+19, FLT+21, HHX16, KCH04, LL23, MLOT17, MSR22, YLC+17, ZFBK09, ZKT14]. **Joker** [OYB18, OYB18]. **Journal** [Ano14, Prz24]. **Juan** [EBS+22]. **Jukes** [SF95]. **Jump** [LDW98, NTMM06]. **Jumping** [SRS02]. **Junctions** [LS98].

K* [OJFD18]. **K-Boost** [GLM+09]. **K2P** [GMY10]. **Kappa** [BZMM16]. **Karyotypes** [OFS09]. **KEGG** [RND+23]. **Kernel** [WLXW22]. **Kernels** [LDS12, LJ05a, MBLZ09, NM14, VILR10]. **Key**
[CCH+19, FSW+20, LGD+19, LL19b, LL19c, MXW+20, QQL+19, QMMW11, XXZ+21, YDG+20, ZDG+20]. **Khachiyan** [SSC23]. **KIF4A** [BRC20]. **Kinase** [BSB+05, CASP10, CC03, GAWI19, VND17, WKC+95]. **Kinase-Encoding** [WKC+95]. **Kinases** [CDL+19, FDDK07]. **Kinetic** [BGH+08, GW06, TKO21]. **Kinetics**
[ADS03, CAB+07, Kru17, SC15, TKT+05]. **Kingdom** [PMG+16]. **Kinship** [Ell20]. **Kissing** [CCJ09]. **kit** [FDW20]. **kmer2vec** [RYY22]. **Knock** [HKS08]. **Knock-Out** [HKS08]. **Knockdown** [cLcSwP+21]. **Knot** [ES06, Erd05]. **Know** [HPL+20]. **Knowledge** [AEH17, Bet10, CW09, DRT+25, GVTRS06, PS12, PZZ20, SBTV10, WHD15, ZHY+20, ZS24, ZS14]. **Knowledge-Based** [ZHY+20, ZS14]. **Known** [ADS03, GLMW13]. **Krebs** [OBJO+03]. **Krylov** [WZW10]. **Kudu** [FDW20].

L [GSLW94, SHG02]. **L1** [RRKT07]. **Label** [YQDW23, WHD13]. **Labeled** [AODD22, EHFK24, HLMS08, JGL11, KVZ24, KK22]. **Labeling** [AMR20, BKKSD01, SK21]. **Labels** [BZG+22, ZZL23a]. **Lac** [ALR18, VCS11]. **Landscape** [AHK+02, Clo05, DPR97, JHLD20, PK11]. **Landscapes**
[ADS03, Cha95, CS15, Kle99, MZC+18, NVW14, WP11, ZYH20]. **Langevin** [HCX09]. **Language** [EAM+17, KPZU11, YDZ+25]. **Laplacian** [Fre11, NHOV10, WYLW21]. **Large** [ABL03, Ben21, BBWE09, CCT09, CP05, CB07, DGH+01, DLL+24, DCH21, HSH+09, JDK+18, LAF+14, LL11, Ma11, MNG+15, Nue04, OJFD18, PDZ+16, Par07c, PFRD05, Ris16, RHY+04, RLK+09, RLVCVR17, SSH+10, ST02b, SGK+12, SK18, TE96, TMC+18, TH17a, Wag04, WFH18, XU97, YZWZ13, ZH07, ZCK17]. **Large-Deviation** [WFH18]. **Large-Scale**
[ABL03, Ben21, BBWE09, DLL+24, DCH21, HSH+09, LAF+14, Ma11, PDZ+16, RLK+09, SSH+10, SGK+12, TE96, TMC+18, XU97, ZH07]. **Largest** [ZPC+18]. **Lasso** [PNMI15, LFJ11]. **Latent** [SDK16, TLK+06]. **Lateral** [RS13]. **Lattice** [ABD+97, GP13, GWX18, HI97a, ISK99, KMRG09a, RROF95, SSS20, YTMY17]. **Lattices** [HI97b, RRFS98]. **Lava** [Boh24]. **Law** [SBK22]. **Lawler** [GSLW94]. **Laws** [DHL00]. **Layered** [CQG10, LDLZ12]. **LB3D** [TSTS12]. **LC**
[KGN09, LTTS12, NTWF11, STHG+08]. **LC-MS**

[KGN09, NTWF11, STHG+08]. **LC/MS** [LTTS12]. **LCA** [GM07]. **LD** [Nue04, SB21]. **LD-SPatt** [Nue04]. **LDA}** [CSH+20]. **Leading** [OJOD+04]. **Leads** [MVP06]. **Leaf** [zCULW20]. **Leak** [MXW+20]. **Leapfrog** [Ben21]. **Leaping** [SAL09, Sol09]. **Learn** [AB00, FDB18]. **Learned** [HY16b, MBLZ09]. **Learning** [AVS20, AS22, ASZ+16, BRD+05, BCG+18, BML+16, BYL+20, CCDB21, CWR24, CJ21, CA15, CLLL20, DND+19, DCH21, DKF09, EFM12, FADH17, FCGD19, FDD21, FFB20, FND+09, GSS+20, GDL+15, GWM+21a, HPL+20, HSH14, HS15, HZK22, JK96, KGLBK15, KJmZ+22, KMCKS17, KFR04, KW21, KPP+22, LWC+14, LCG+22, LBJM11, LKC21, LZY+23, MSS+22, Mam96, MTC11, MDMC21, MBS+01, MWL22, NSMV18, Nou21, PWCN02, PYG+19, jQLsY+24, RND+23, SIC+09, SlGW+23, SZSA22, SSW20, SSS+21, WYY+18, WCL+18b, WPS+25, XGD24, YSFW08, bYjHgZ+24, YMxW21, ZRGHJ08, ZCH+13, ZRNA20, ZMppVN22, ZWD25, XSH+22, YCCL18]. **Learning-Based** [CLLL20, LCG+22, WCL+18b, YCCL18]. **Least** [JKG+04, KKA+15, LGS20, PD20b]. **Least-Squares** [KKA+15]. **Lecture** [Woo99]. **Legos** [MR08b]. **leguminosarum** [PdBdP+22]. **Leishmania** [Vij22]. **Length** [ARSW22, CL17, CHP94, CT07, HR08, KRD14, MK16, RSM06, SSMT16, SBT00, SSH+10, ZKM21, RBEB13]. **Length-Aware** [MK16]. **Lengths** [SkY12, ZL09]. **Lessons** [HY16b]. **Leucine** [ODPB18]. **Leukemia** [BDBB10, OSK+15, ZLM+17]. **Leukocyte** [HMY+19]. **Level** [FDDK07, LTsL24, LZS09, LBN94, LFT+98, LGS20, LYS20, OO24, PNIM17, RSR+09, SSW20, VFOK18, WTE25, XGD24]. **Level-1** [LTsL24, WTE25]. **Levels** [DMR+03, EHC+13, GSH17, PZH11, RMC+05, SLT24, WAC08]. **Levenshtein** [DP07]. **Leveraging** [BT08, FDW20, HKL07]. **Lewis** [Sea01]. **Libraries** [DFS95, LMP08, MKKK+17, OB16, SZMS02, ZFBK09]. **Library** [ALB+19, CD07, GE04, GAWI19, NBB18, PA03]. **Life** [KPW11, TaAF+22, YDZ+25]. **Lifting** [MWB10]. **Ligand** [BHRV00, CRT+17, CW20, FL94, GZN16, LLJS19, LW12, PK11, PPV+14]. **Ligand-Receptor** [BHRV00]. **Ligands** [HXL+20]. **Ligases** [MSN+20]. **Ligation** [FLL00]. **Light** [WxLW+23]. **Like** [DMP+06, HJD17, NSA08, SDDI+08, XLLS20, YZ08]. **Likelihood** [CKS06, CHJ05, DMB07, ET07, ITSH00, JS03, JGB12, MB09, NSRR23, ŠV07, SHE11]. **Limit** [GQ09, TA97]. **Limitations** [SLB+97]. **Limitless** [YYL19]. **Line** [Erd05, MA19]. **Lineage** [WR23]. **Lineages** [MSR22]. **Linear** [Ale08, AB00, ADRS24, BMY01, BCC+09, CHM94, CFS+08, CGSW14, DM17, DWMT22, DFG06, DEH10, GHJ+12, Gui98, GSW16, HI97a, HP96, Jen09, Ker03, LJ05b, LKL21, LJL+20, MPZ+20, PMGE21, PDdJFT08, RCSS12, SlGW+23, Shi10a, Shi10b, kSyPhC+22, SF95, SLL+17, TMfTK23, WAPM05, WW18, WW19, WAX22, Xu10, XZ12, ZZS17, Zör15]. **Linear-Space** [CHM94]. **Linear-Time** [BMY01, DFG06, ZZS17]. **Linearization** [BBH+07, HSOE+18]. **Linearized** [VRS12]. **Linearly** [CYY23]. **Lines** [HFUH19, IPH18, Par24]. **Linkage** [BG09, FG04, KL98, LWLJ10, RBEB13, WMC04]. **Linkages** [TZB+23].

Linked [GGM12]. **Links** [CJC01]. **Lipid** [RMC+05]. **Lipinski** [CLT+20]. **Lipman** [KS06]. **List** [MK06]. **Listing** [BSS11]. **Lists** [AFCN13, CZS15, LSRR18, LL05b, NV12, PFRD05]. **Literature** [MK11, SF03, dJ02]. **Live** [PLZX25, TAMW13]. **Live-Cell** [PLZX25]. **Liver** [PdB13]. **LMM** [MBC+18]. **LncRNA** [HHZ+18, JPLD23, JSZ+20, TYS+20, YcXyW+21]. **lncRNA-Associated** [YcXyW+21]. **lncRNAs** [NXGL20]. **Local** [ABD+97, BG02, BWS13, BDCKY03, Bun02, BR23, DK18, DLPH06, DWK+20, FND+09, HJD17, Han09, Hor01, HKZ+04, IP09, JHS06, Lat99, LTCH11, MD01, Met06, NBB18, QsYSxL23, RDH04, SM04, SS01, TBB00, YZWZ13, YLCC17, YK05, YH01, ZGRB10, Zhu07]. **Local-Alignment** [BG02]. **Local-to-Global** [Lat99]. **Locality** [BCH+07, HTY22, KBG18, MM19, SlGW+23]. **Locality-Constrained** [SlGW+23]. **Locality-Sensitive** [HTY22]. **Localization** [EZFP+19]. **Localized** [YYZ+10]. **Locally** [Clo05, EFM12, LACB10, SGdMT12]. **Locating** [BBWE09, Sal95]. **Location** [ABTP23]. **Loci** [CFE+13, LHC02, NMH13, WXS14]. **Locus** [JG11, SSV19, YWN11, ZPX+10]. **Lodgepole** [DR15]. **Log** [CCPT17, LKL21]. **Log-Linear** [LKL21]. **Log-Normal** [CCPT17]. **Logic** [HNTW09, Ist19, PSB17, SG10, SG12]. **Logical** [KS12]. **Logistic** [Ben21, BCG+18, CW20, HH14, LSG04, LXS24]. **Long** [AWM+17, BB04, BLP+22, CST20, FH18, GZW+21, HATI11, HHHS03, JDK+18, JFLL20, MRG+24, MBVA07, MDB11, QbMyD+19, RH19, SM20, SY22, YY19, YYJ19, YW21]. **Long-Range** [BLP+22, HATI11, MBVA07, MDB11, RH19]. **Long-Read** [GZW+21, SM20, SY22]. **Longest** [BVP+19, WWZ19]. **Longitudinal** [GZY+22, WYY+18]. **Loop** [CY09, HLL13, KFR04, KW21, LSL+16, YY19]. **Loops** [BBH+21, EdCK+12, GQ09, KV17, NRW11]. **LoopWeaver** [HLL13]. **LoopX** [KV17]. **Loss** [ARC13, AJA+16, BAK13, Bay23, CDEM08, GSS+20, HATI11, HQ06, LMWR21, PMGE21, WT07, YYM+23]. **Loss-Function** [GSS+20]. **Losses** [LM11, SGBEM11, SCH09]. **Lossless** [RDRF24]. **Low** [AV18, BK10, DMW+17, GWM+21a, HXL+17, HLK+13, KWM10, KIYM13, MGSA06, NDMK17, SBC+05, Sun18, WMC14, cWxLlS+23, ZBM98, ZY23]. **Low-Complexity** [BK10, MGSA06, SBC+05]. **Low-Coverage** [DMW+17]. **Low-Dimensional** [NDMK17]. **Low-Dispersion** [WMC14]. **Low-Frequency** [HXL+17, Sun18]. **Low-Order** [KIYM13, ZY23]. **Low-Quality** [GWM+21a]. **Low-Rank** [cWxLlS+23]. **Low-Scoring** [ZBM98]. **Lower** [BB06, KLM11, KKM+20, LY99, MSS10, MWD02, TSTS12, WG08a, ZZL22, ZKM21]. **LSG** [BVP+16]. **Lung** [BSB+05, DCL18, SZY+20, TYS+20, WSCL18, WPL+19, WWLC20, WWC+20, ZCY+20, ZLL+20, ZQZ20]. **LUTE** [HJD17]. **Lymph** [ZLW+20]. **Lymphocytic** [ZLM+17]. **Lysine** [AWZ+17, JWL24].

m [Lat99, SHMS08]. **M-FISH** [SHMS08]. **MAC** [JLmR+23]. **MacCamy**

[CYY23]. **Machine** [AS22, BCG+18, BRR06, CWR24, DND+19, DHY02, FADH17, FCGD19, FDD21, GDL+15, HPL+20, HS15, JLSL24, KPP+22, NM14, RND+23, SPSZ23, SSS+21, WCL+18b, WxLW+23, WPS+25, YM06]. **Machine-Learning** [KPP+22, SSS+21, WPS+25]. **Machines** [LN03, Yan09, Zho17]. **Macroevolutionary** [DHV06]. **Macromolecular** [CJS06]. **MAD** [ZCK17]. **MAD-Bayes** [ZCK17]. **MADMX** [GPP+11]. **Magnetic** [KKS+15, LLWZ19, LLW+20, WMD06]. **Main** [Ano10b, BKWK+00, MRG+24, TTTL17]. **Main-Chain** [BKWK+00]. **Maintained** [LJCZ20]. **Maintaining** [AMK18]. **Maintenance** [LSHL04]. **Major** [Cal22, TZB+23, Vij22, ZLTZ25]. **Mammal** [JC22]. **Mammalian** [JRH+09, JRHN09, PCC+11, ZSV+09, ZZNM15]. **MAMMLE** [NSRR23]. **Manage** [NCC+96]. **Manager** [BK10]. **Manifold** [LQ23, MTC11]. **Manipulation** [SNQ+14]. **Manipulations** [DT12]. **Manual** [BMB24]. **Manually** [SKDR21]. **Manufacturing** [ST02a]. **Many** [ADR24, KKM+20, MKB+20, PABE+10, ZFZL03]. **Manycore** [CST20]. **Map** [ADS03, AMDY11, BBEM09, CCI+04, MNIK+09, MBLZ09, PJL20, Par98, SGSN12, SBK22, XS07, KK11, LTCH11]. **Map-Based** [PJL20]. **Mappability** [TGA24]. **Mapper** [CWL13]. **Mapping** [Aku04, AKWZ95, AMS97, BG11, BK08, CJK+97, CS15, DHM97, DM17, FJK+99, GCB15, GGKS95, GI95, Hea97, HSF+00, IM14, JDK+18, KPS00, KS00, KSSK09, KLO18, LDW98, LHC02, LH03, MDB11, MBK+03, NCC+96, Pev95, Sch97a, SBT00, SMZ+12, SEV09, SMM+04, SRV98, SRM+98, SFC11, Tho21, WHY+13, Wen05, Wu08, YW21, Zha94, ZWT18]. **Mappings** [AKK11, HLMR11]. **Maps** [AMW07, AMS97, BDC97, BPL02, BCA96, BBH+07, CY10, GDHC95, HSH11, JM97, JAJ24, JBBW10, LJK16, LVS+07, MS99, NS18, SJ18, SKSL97, SBAW97, VLL+06, Wan94, ŻZ15]. **Margin** [KBCBS11]. **Marginal** [Ham12, LLKX16]. **Marker** [DYLK20, PIM23, Ros05]. **Markers** [HTY22, HWW+20, MRM20, SLL08, SZMZ19, WWC+20, WZL19, ZLM+17]. **Markov** [ARSW22, BC94, Bal95, BP14, BV09, BP06, CB07, CL99, EMD95, ENS03, FDB18, GJM04, GML20, GCB15, Hea97, HSF97, HJ05, HKZ+04, HJ14, HW01, JEMF06, KMP08, KS05, KST96, LDW98, Mam96, NTMM06, Nue04, PAC02, PWKAF16, PRKG16, QSY09, RNH18, RH19, RS98, RBEB13, RLA+06, SG10, SPD95, Sch00, SPW22, SH04a, UTD+20, WZ23, WS04, WTE07, WX08, XK05, YH01, YZPC24, ZHS05, ZS11, ZM16]. **Markov-Modulated** [GJM04]. **Markovian** [BLF14]. **Marrow** [PM24, XLLS20]. **Maruyama** [RYZ23]. **MAS** [ZHQS05]. **MASH** [CFB+07]. **Mask** [MGSA06]. **Masked** [HMK24]. **Masked-Minimizer** [HMK24]. **Masks** [HTM+22]. **Mass** [BKKSD01, BBN11, BG06, Böc04, CJC01, CKT+01, CŁM+18, DAC+99, DB09, DBL+12, FNC08, HYY+10, KVM14, LFD03, LL05b, LC03b, MDTD06, PDT00, PSG+20, SHRB11, WTE07]. **Mass-Spectrometry** [KVM14]. **Massive** [FDW20, SK17]. **Massively** [FHS00, NBB18]. **MASTtreedist** [HL13]. **MatBio** [AHIV23]. **Match** [BG98, KV19, NK07, RJS02]. **Match-and-Split** [NK07]. **Matches**

[AMOW10, BS98, BHKM22, BLF14, DS12, LM03, OK08, RSM06, ROB+22, ROL+22, SRV98, SDCF24]. **Matching** [AMW07, AO15, BG97, BG17, BG23, DR17, GGU13, JK96, KEL15, KS99, MKB+20, Mye96, NR03, NTWF11, RDRF24, Ris16, SD95, SHG00, WTE07, YS07]. **Matchings** [BHKN25]. **Mate** [DWS05, MPC+11]. **Mated** [CBH+12]. **Material** [KKS+15]. **Maternal** [LWN+18, MSS21]. **Mathematical** [BGH+08, CJ22, CKL+17, CD21, Dei19b, EBS+22, Gu01, HAM+22, Kru17, PZZ+10, RRKT07, SMKS96, Tak96, ZTW05]. **Mating** [CK10]. **MATLAB** [ADW23]. **Matrices** [Bal95, CCYH18, CD07, DGH+01, ENS02, FLS94, Kea97, KC96, LMT01, LZ10, MMA+21, MP11, WGC+21, WNMB99]. **Matrix** [ÅMR07, AMK00, AZ14, ASE20, BMH21, GGU13, GWM+21a, Ham12, HJR12, Hua08, IM14, JPR06, JRH+10, KMCKS17, LLW+20, LWZ18, LLW18, MWZ19, MSM20, MJCM22, NES22, PRSV08, SSY+22, TDV24, WHDN13, WGS+23, Zho10, ZH07, ŽZ15]. **Matrix-Based** [ASE20]. **Matroid** [RBOS15]. **Matters** [FFM24]. **Maturation** [KMUK22]. **Max** [LTCH11, LHXH08, Ser15, War95, ZDZ+20]. **Max-Convolution** [Ser15]. **Max-Gap** [LHXH08]. **Max-Product** [Ser15]. **Maximal** [AFCK09, GKMS23, GPP+11, KLW96, OK08, PWFZ17, ROB+22, ROL+22, Voo14, WZ10, ZZ10]. **Maximization** [FVTH03, GGM12, LGC+09, NBC+11, WHD15, YJC18, ZCH+13]. **Maximizing** [HA12, IKL+03]. **Maximum** [AMDY11, BCVL17, CCI+04, CMLTZU14, CFR12, CKS06, DMB07, EMD95, HSD05, HCC05, HV09, HL13, ITSH00, JS03, LJL+20, MP11, MB09, NSRR23, RRNB13, SPD18, ŠV07, WTM11, WS04, YB04]. **Maximum-Likelihood** [ITSH00]. **May** [CYF+20, LSRR18, YBF19]. **Maze** [Let95]. **MCAT** [YRG+19]. **MD** [Ano00]. **MDA** [NBA+13]. **MDC** [YWN11]. **MDC-Based** [YWN11]. **MDM2/MDMX** [CY09]. **MDMX** [CY09]. **MEA** [HA12]. **Mean** [AS23, AT12, GK06, KFC+11, TSTS12]. **Mean-Field** [GK06]. **Meaningful** [DBHC24, ZW19]. **Means** [RAC+06, TEMM12]. **Measure** [AS23, CC03, DAE+19, NV12, OYY+12, SKT08]. **Measurement** [DMR+03, LK24, LLW+20, LDW+14, PK19, RD01, SDFR16, ZPD+23]. **Measurements** [EHFK24, FL94, SSY+22, SMD+07, WPS+25]. **Measures** [ACL15, BSKgG23, CD21, DKA+17, EMV98, GKB00, GMY10, GJL+21, KVZ24, LS04, MSBR08, MHS06, PGA+11, SG15, SRF16, WMG+24]. **Measuring** [CN17, CKZ+19, HHP+09]. **Mechanical** [SLO07]. **Mechanism** [Ano21b, JRHN09, KB12, LZL+23, WXY+13, YS23, YK19]. **Mechanisms** [DS04, LTCH11, LTZ18, LGD+19, LHC19, PYIM22, SZY+20, WPL+19, XMWZ20, YDG+20]. **Mechanistic** [CKL+17]. **Median** [AT08, BJMS09, XLZ+18a, Xu09, Xu10]. **Medians** [PZZ20]. **Mediate** [TLP+14]. **Mediated** [JRH+09, KW21, PD20b, EdCK+12]. **Medical** [BMM+23, HTM+22, Hua15, JMR+21, JZL+20, LCL+17, MMN+21]. **Medicine** [PYG+19, SG12, SWS+20]. **mediterranea** [FCR+13]. **Medium** [NS18]. **Medulloblastoma** [MEF24]. **Meeting** [PS11]. **Meiosis** [TT12]. **melanogaster** [SVCA17]. **Melanoma** [XXZ+21, XMWZ20, XWJZ20].

MELC [Cos18]. **Mellitus** [SVP19]. **Members** [WKC+95]. **Membrane** [CXW16, CHK+02, TS96, YM06, ZWY+17]. **Membranes** [WWZY19]. **Memoriam** [GSLW94]. **Memory** [BP14, BVP+16, FPS22, GSV+11b, GSV+11a, Jen09, KZE10, MRG+24]. **Memory-Based** [MRG+24]. **Memory-Efficient** [KZE10]. **Mendel** [Dei19b]. **Mendelian** [KWBN19]. **Meniscal** [KKS+15]. **Mer** [FPS22, HTY22, NM14, RM21, RC24, SBK22, ARS17, Ben21, PFK17, PGV16, PNPC20]. **Merging** [MA19, PSLP06]. **Mers** [APC21, OYB18, PPV20, BHKM22, OB16, Ore20, TZHR14]. **Mesenchymal** [XLLS20]. **Meta** [Mal98, Nou21]. **Meta-Algorithm** [Mal98]. **Meta-Path** [Nou21]. **Metabolic** [AKK11, BBN11, BMH21, BK08, BF09, BFP13, CHS17, FS99, GMC+14, HKS08, HBK11, JTSB10, KTT20, KP96, KIYM13, KK24, LTSA15, MWRS16, MZM18, NSH+23, PSP21, QMMW11, RGM+12, RHS+21, RFH+25, SSC23, VB09, ZLL+20, ZS14]. **Metabolism** [HJ14, PdB13]. **Metabolisms** [FS99]. **Metabolite** [BSP+25, SHRB11, TMfTK23]. **Metabolites** [Lie05]. **MetaCluster** [WLYC12]. **Metagenome** [KMM17, SBRG20]. **Metagenomes** [LJK11, NBA+13, SBPS11]. **Metagenomic** [APC21, AaHP+21, BML+16, CC23, DLFS22, DZS24, FPRV18, GYD+15, GLM16, JÖNK17, ML22, PWT18, PKSB18, TAJZ23, WWH17, WY11, ZM16]. **Metagenomics** [MV19, PPV20, PLL16, RPR+15]. **Metaheuristic** [RLCVVR18]. **MetaMLP** [AaHP+21]. **Metaphase** [HYJ+19]. **MetaProb** [APC21]. **Metastasis** [TXL+17, WFL+20, WDZ20]. **Metastatic** [XMWZ20]. **Metatranscriptomic** [LYPC13, LYC15, RHS+21]. **MethCP** [GP20]. **Method** [ARHLK19, AV18, AJYJ18, ADD+07, ADR13, AS19, BV20, BS97, BRS99, CDH+16, CXW16, CW20, CJ21, CC09, CZY19, CGZ04, CV11, DCP+21, DMTV09, DCD19, DOKT05, FS99, FH18, HMY+19, HLH06, HZH+10, HLY25, HHJ+13, HG18, HHC06, HNW99, JR12, JLY08, JLSL24, JHA16, KSS09, KST96, KM08, LC09, LRD19, LS08a, LHW+22, LK24, LNW01, LVS+07, LLW+20, LLT06, LSSD18, LYS20, LW12, Mam96, MRM+02, MSN+20, MTF+12, MBK+03, NSA08, NXL+15, OSK+15, PD20a, PMF+03, PIWR15, RS12, RLH13, RC06, RYY22, SSR21, SNW98, Ser15, SD95, Ste14, SLL+17, SLZH15, SDP+20, SK19, TRW23, TZB+23, TCL+16, TML+02, TVNP15, TTTL17, VLZUBK07, WXY+13, WYC+18, WCL+18b, WTY19, cWxLlS+23, WZ23, XLZ+18b, XvdL05, XXU98, XXCE00, YKPM20, YWZ+19, YDN12, YHT+17, YHC19, YYZ23, YYW14, ZWY+17, ZGBK10, ZPD+23]. **Methodology** [GVTRS06, HVAW04]. **Methods** [AMK18, ARS17, BG98, BPL02, BSWY98, BZ08, CCI+04, CHM94, CHP94, CGOT10, CH15, CWH+22, CYY23, CB07, DBM09, EAA+09, Hea97, HJR12, HAP12, JGB12, KPS00, KVDC06, KPB+04, LWLL19, MSMF09, MDK24, MD00, MS03, Pev95, RAC+06, RPR+15, SG12, SSS20, SB21, ST17, WJD14, WXY+24, XK05, YHB+03, ZWQ19]. **Methylated** [CCL+19, GP20, WHK21]. **Methylation**

[CWS+21, CKZ+19, HZL22, KLC+11, LSY+05, MEF24, SnGqC20, WSCL18, WWLC20, WWC+20, WZL19, YLD+18, YYL20, ZWK+20].
Methylation-Based [ZWK+20]. **Methylation-Driven** [CWS+21].
MetReS [VAS+18]. **Metric**
[CN17, DP07, GMY10, PGM07, SK21, SM04, ZW19]. **Metrics**
[BG23, DMP+06, Far97, MZS+00, TM22]. **MFE** [CCJ09]. **MHC**
[SS04, ZRGHJ08, ZYB+04]. **MIC** [WCZ+18]. **Mice** [LLL+20, RFH+25].
Michael [Ano21a, IPSV22, PVR+22]. **MiCId** [OAR+24]. **miCloud}**
[KAD+19]. **Micro** [DHV06]. **Microarray**
[ÅMR07, ADP+08, BCH+01, BHGCS11, BR06, BBD+04, BRR02, CR09, CCT09, CC11, CRT04, CYY09, CYLY12, CKB+06, CHK+02, DMTV09, DGFMSS16, FdSdSR+15, FCGD19, FSZ02, FMH06, GLM+09, GME01, Hav06, HLK+13, ITSH00, JZ10, KMC00, Ker03, LRSG07, LSG04, LSY+05, LL19c, MLOT17, MTR+03, NKR+01, OMS13, OH03, PQBB08, PC05, QP09, RAC+06, SS07, SDC03, SRF16, SDC+10, SZSW09, TP11, WC04, WFL+20, WHW+06, WGW+01, WZW10, YHB+03, YLC+20, ZLW+20, FVTH03].
Microarrays [BLQZ04, CKZ+19, DBB+02, KFDT02, LDB+07, PTWB09, PQBB08, RPR+15, SH04b, SZSW09, YHC05, ZFZL03]. **Microbe** [LWZ18].
Microbial [BML+16, HTY22, RND+23, WYT12, YT22]. **Microbiome**
[CWH+22]. **Microbiomic** [PIWR15]. **Microelectronics** [MPG+16].
Microenvironment [DLL+24]. **Microenvironments** [CSH+20].
Micrographs [YLZ+24]. **Microorganism** [OAR+24]. **MicroRNA**
[CK11, CDQ+21, CJ21, HMF07, MWZ19, MDMC21, SHZ+24, XWJZ20, bYjHgZ+24, ZYH20, ZZ20]. **MicroRNA-Disease**
[CJ21, bYjHgZ+24, CDQ+21]. **MicroRNAs**
[AAN+20, KV08, LLZ19, PMG+16, SlGW+23, ZZUPY06]. **Microsatellite**
[PSLP06]. **Microsatellites** [LSAS03]. **Microscopy**
[HLG18, KAC17, LCG+22, NS18, NZM+25, YLZ+24, ZKWH17].
Microspectroscopy [MGW+07]. **Migration** [RSEK24]. **MIMD** [BCA96].
Mimotopes [HLH06]. **Min** [SBK22]. **Mingle** [MA19]. **Mini** [NBA+13].
Mini-Metagenomes [NBA+13]. **Minimal**
[CHSY10, DS19, KR24, SH05, WNMB99]. **Minimal-Risk** [WNMB99].
Minimization [JHLD20, KRD14, WYLW21]. **Minimization-Aware**
[JHLD20]. **Minimize** [SLT24]. **Minimizer**
[FPS22, HZK22, HMK24, ZMK23]. **Minimizers** [APC21, Yu24].
Minimizing [TR11, YSFW08]. **Minimum** [BDK+16, CW13, DG02, DWMT22, LJ05b, MDK24, OSC11, TMfTK23, TGA24, YE02, ZHQS05].
Minimum-Evolution [DG02]. **Mining** [CCT09, CY17, DSN14, EAA+09, HHJ+02, HAP12, HBW+05, JSN09, MZS+17, NBG+02, QLW20, RAKL10, RMC+05, SDMN19, SF03, SCSA+16, WZW10]. **Minisatellites** [BR03].
Minor [TZB+23]. **miR** [WHLR20, YBF19, XWJZ20]. **miR-101** [YBF19].
miR-1201 [XWJZ20]. **miR-142-5p** [XWJZ20]. **miR-145-5p** [WHLR20].
miR-1826 [XWJZ20]. **miR-449a** [WHLR20]. **miR-550a** [XWJZ20].
Mirkin [Zha97]. **miRNA**

[JSZ+20, EdCK+12, HHZ+18, LXS24, PD20a, ZWD25]. **miRNA-mediated** [EdCK+12]. **miRNAs** [CCL+19]. **Mismatch** [TAA16]. **Missense** [SMC+15]. **Missing** [BV09, EHFK24, FBJ04, Gus10, LLW+20, MSS+22, McP12, UGS19]. **MIST** [BSKgG23]. **Mitochondrial** [GE17, MFJ+19, SBD+00, Sel13]. **Mitogen** [VND17]. **Mitogen-Activated** [VND17]. **Mitogenome** [AM20]. **Mitosis** [LXL+20]. **Mix** [BLC10b]. **Mixed** [MPZ+20, PTWB09, TMfTK23, WLXW22, WAX22, WSS03, WGW+01, WMC04]. **Mixed-Integer** [TMfTK23]. **Mixing** [SDK16]. **MixProTool** [WZH+18]. **Mixture** [AR06, AL07, CQG10, HYY+10, KK22, RCER21, ŠV07, TBB00, TDV24, UTD+20, WCM+08, WVT23, YYA10, YYA11, YAR21]. **Mixtures** [NBGA13, TEMM12]. **MMG4** [YZPC24]. **Mobile** [CKL+17]. **MoCha** [LHL16]. **Modal** [DVS19]. **Modality** [LLT+25]. **Mode** [ITdB09]. **Model** [ATLS07, APVM11, ABD+97, AP10, ARSW22, AL07, Ano22b, ADRS24, ASZ+16, AT12, AG23, AHK+02, AP09, Aug12, ASL06, BH11, BCG+18, BL98, BV09, BDBB10, BRR02, CFS13, CYY23, CQG10, CCPT17, CKB+06, CKL+17, Clo05, CEK+17, CD21, COL+18, CLLL20, DBW17, DCS04, DSV12, DAR23, DMR+03, DT13, EBS+22, Fas94, FS08, FMH06, GZLY24, GCB15, GP13, GRM09, GSV+11b, GSV+11a, GG04, GWX18, GJL+22, GMS05, HI96, HAM+22, HSF97, HB11, HCS09, HL16b, JMPR23, JAG17, JG11, JD05, JK96, KBJ07, KKS+15, KS11, KMMF20, KCG+19, KWB+94, KG24, KMRG09a, KMRG09b, KLV+13, KS05, KDL+94, KWBS11, Kru17, LLS11b, LKL21, LCG+22, LMT01, LM11, LL23, LTSA15, MLOT17, MDWZ24, ME12, MWZ19, MWP00, MRG+24, MFJ+19, MMS95, Mor19, OBJO+03, OYY+12, PZZ+10, PCS18, PMGE21, PD16, PD20b, PV17, QsYSxL23]. **Model** [jQLsY+24, QMMW11, RH19, RRKT07, RYZ23, RCER21, RSR+09, RD01, RWB+98, RLA+06, SWK+07, SLL08, SVD14, SS05a, SZMZ19, SPW22, SMD+07, SKS+09, SMC+15, SHG00, SF95, SLT24, TMH+21, TBB00, Tos05, TAY16, URB+19, VST03, WC07, WXS14, WSS+15, WC16, WYY+18, WMP+20, WLXW22, WZ23, WFC25, WTM11, WMC04, WX08, XJL+22, XLZ+24, XLZ+18b, XZ12, YTMY17, YHEP15, YY19, YYZ23, YMM+24, YFBK07, YS19, YT22, YAR21, YA11, YLC+20, YQDW23, YZPC24, ZKWH17, ZZ20, ZPG+24, ZLTZ25, ZPD+10, ZWK+20, ZCZ+23, ZH07, ZM16, ZS24, ZWD25, ZTW05, YE02]. **Model-Based** [BV09, GG04, KS11, ZS24]. **Model-Free** [ATLS07, GRM09]. **Model-Testing** [Aug12]. **Modeled** [SVD14]. **Modeling** [ADW23, BS09, BBV+14, BGH+08, BZMM16, CY09, CSH+20, DMP+06, DMHM97, Dei19a, DS04, EdCK+12, FPD13, FA12, FL17, GVTS04, GE14, Gu01, HD10, HLL13, JB10, JLmR+23, JLSL24, KAS09, KV08, KGN09, LSL+16, MMKH15, MV00, NW05, PdB13, POP23, PCS18, PD20b, PRC+13, RZK06, RMK+18, Rot19, SGT15, SMKS96, SKL+24, SS23, SB17, SAM06, STP18, SHMS08, Sun99, TS04, TKW08, Tra19, VRS12, WH01, yWCF06, WWZY19, WV95, WLF13, WVT23, YY19, YJ06, YB04, ZML07, ZLTS13, ZPD+10, ZLP22, dJ02]. **Modelling** [Ben98, MMHC98]. **Models** [AJYJ18, AGH+18, AR06, BC94,

Bal95, BH15, BÖB+23, BP14, BMS10, BCD+24, BS20, BP06, BFP13, CBS+20, CKT16, CWR24, CCF10, CHJ05, CLDG03, CP19, Dei19b, DPS+20, DJK+99, DJK+00, DCH09, EMD95, FDB18, GGU13, GW06, GP20, GLM20, HVD17, Han09, HI97a, HNTW09, HP96, HLCS10, HHL06, HJ05, HW01, IR22, JPB+15, JAJ24, JGB12, KGLBK15, KS12, KR24, KK11, KMP08, Ker03, KK22, LWN+18, LTS20, Lar06, LCGW09, LLW18, LQPE+10, LP00, Mam96, MZC+18, MPZ+20, MZM18, MWL22, OC00, ÖBA+23, PAC02, PPL+23, PTWB09, PS12, PD16, PWKAF16, PDdJFT08, QSY09, QBA+25, RNH18, RROF95, RGM+12, RM00, RBEB13, SPD95, SLO07, SSC23, SK13, SOD+11, SH04a, SK23, ŠV07, ShHGC20, SSS+21, TMfTK23, TDV24, UTD+20, VCS11, WAPM05, WCM+08, WJD14, WAX22, WJJ11, Wen05]. **Models** [WG08a, WS04, WGW+01, WI05, WTE07, Wu08, XK05, YY18, YIJ04, YjDG+23, YH01, YJEP08, ZHS05, Zho10, ZH14, ZS14, Zör15]. **Modes** [BS09, CZNF19, SVK10, PZZ20]. **Modes/Medians** [PZZ20]. **ModHMM** [BV20]. **Modification** [BG08]. **Modification-Site** [BG08]. **Modifications** [Yua09]. **Modified** [Guo15, HLG18, SLZH15]. **Modifier** [BSKgG23]. **Modify** [LSAD05]. **Modifying** [SKP+12]. **Modular** [BV20, FS08, PVFB06, SCD+22]. **Modulated** [GJM04]. **Modulatory** [LZBK15]. **Module** [CDQ+21, GKD22, RBOS15]. **Modules** [LDLZ12, MYS+20, NSK09, SS05a, WT17, WX08, ZlWL21]. **Modulo** [YjDG+23]. **Molecular** [ARRW99, AMW07, ALB+19, Ano11b, Ano21b, ABG+03, AG98, Baf11, Ber11, Bet10, BGJ+04, CR09, CSA98, CKS06, DSV12, DWK+20, EAFM24, GJM04, GRM09, HP96, KLV+13, KFC+11, LGD+19, Lie05, LHL16, MJR+24, MR95, Mar95, MK06, MRG+24, MMS95, OSK+15, PYIM22, Par24, PA03, PS11, QTRA24, RAKL10, RMWC16, SVA+19, SZMZ19, SMML24, Sun13, SGCD19, TYSX19, WPL+19, WDA01, XMWZ20, YDG+20, YK19, Zha97, ZYB+04]. **Molecule** [AWM+17, CL21a, SSPNW06, SHZ+24, YYM+23]. **Molecules** [CFR12, DHY02, GKKS98, QMMW11, SDDI+08, SKG+00, Sun18, WGL98]. **Moments** [DM17, GRM09]. **MONI** [ROL+22]. **Monitoring** [SLL+23]. **Monophyly** [MSR22]. **Monotony** [ABL03]. **Monte** [FDDK07, Hea97, JHN+23, KST96, LDW98, LLT06, LSHL04, NTMM06, XK05]. **Morphine** [QbMyD+19]. **Morphogenesis** [MMPS18, WMP+20]. **Morphologies** [MFJ+19]. **Morphology** [UTD+20]. **Mosaic** [BBP10]. **Most** [MBRS11a, SP11]. **Motif** [AOH16, AP04, BG98, Ber95, BS97, BFL05, GPP+11, KEL15, KPB+04, KV19, LR05, Li09, LCGW09, MC10, MTH11, MKBC05, MVP06, Nic01, OMS13, PWFZ17, RBH05, Ste14, TKW08, Tay94, TH17a, TH17b, YRG+19, ZCH+13, ZS11, Zho10, AOH16, AS23, AL07, SSV19]. **Motif-Based** [BFL05, SSV19]. **Motif-Biased** [Tay94]. **Motif-Sets** [MC10]. **Motifs** [AL07, BG97, BG15, BT02, CFB+07, CA12, DSN14, FK06, GGU13, HVPBK13, HLH04, HZGD05, HBW+05, ISB12, JHS06, KJmZ+22, LNW01, LCY+05, LBJM11, Mal98, MS00, MPVZ05, NBG+02, NTMM06, ODPB18, Par07a, PDK+08, PSCP09, RDR+02, RL94, SPD95, Sin03, TML+02,

VLZUBK07, WMC14, WZZU07, XK05, YB04, ZHS05]. **MOTIFSIM** [TH17a, TH17b]. **Motility** [Ben98, HD10]. **Motion** [AS02, ADS03, ABG+03, GRM09, TKT+05]. **Motions** [Sun18, TTTA07]. **Motivation** [BFK+11]. **Movement** [LLS11b]. **Movements** [GH16]. **Mover** [PLZX25]. **MRI** [LLT+25]. **mRNA** [ALR18, CS03, HHZ+18, JSZ+20, KCG+19, MRM+02, SSW20, TYS+20, ZZ20, ZF07]. **mRNA-to-Genome** [ZF07]. **mRNAs** [LJ05a, NXGL20]. **MS** [BKKSD01, KGN09, LTTS12, NTWF11, STHG+08]. **MSOAR** [FCV+07]. **MT** [LYPC13]. **MTP** [LYC15]. **Muchnik** [Zha97]. **MuffinInfo** [AB16]. **MUL** [CJS12]. **MUL-Tree** [CJS12]. **Multi** [Ale08, AAC+06, AM97, BMR+19, DCP+21, DSS+22a, Gus10, HLMS08, JBM15, JGB12, KIYM13, Li08, LLS+19, LS23, MC10, MA19, MBRS11a, MDMC21, MHL22, PP23, PNMI15, QsYSxL23, TDV24, WHD13, XYX+22, YFBK07, YWN11]. **Multi-Alignments** [AM97]. **Multi-Allele** [JGB12]. **Multi-Break** [Ale08]. **Multi-Class** [MC10]. **Multi-Ensemble** [DCP+21]. **Multi-fasta** [MA19]. **Multi-Hypotheses** [MDMC21]. **Multi-label** [WHD13]. **Multi-Labeled** [HLMS08]. **Multi-Locus** [YWN11]. **Multi-Matrix** [TDV24]. **Multi-Node** [AAC+06]. **Multi-Omics** [DSS+22a, LLS+19, MHL22, PP23, PNMI15, KIYM13]. **Multi-Phenotype** [LS23]. **Multi-Residue** [YFBK07]. **Multi-Scale** [XYX+22]. **Multi-Species** [JBM15]. **Multi-Stage** [Li08]. **Multi-State** [Gus10, MBRS11a]. **Multi-Trait** [BMR+19]. **Multi-View** [QsYSxL23]. **Multibasin** [CS15]. **Multicellular** [SDFR16]. **Multicenter** [SSS+21]. **Multichromosomal** [XZS07, Xu10]. **Multiclass** [ZZL23a]. **Multidimensional** [BFK+10, MVP06]. **Multidomain** [PDSD06, SSD07]. **Multifasta** [AH20]. **Multifeature** [XJL+22]. **Multigene** [GPCP11]. **Multigenomic** [CP19]. **Multigenomics** [SSZG24]. **Multigranularity** [YQDW23]. **Multigroup** [MDWZ24, WZH+18]. **Multilabel** [BYL+20]. **Multilayer** [SPD18, bYjHgZ+24]. **Multilevel** [TS04]. **Multilocus** [DLL+12]. **Multiloop** [DLD+14]. **Multimapping** [CEJM16]. **Multimeric** [GH16]. **Multimodal** [GZY+22, HXY+23, WHDN13, ZMppVN22]. **Multinomial** [MEF24]. **Multiobjective** [EOD+18, HLH06, NSRR23, RLCVVR18]. **Multiomic** [DSC+22]. **Multiomics** [DSS+22b, DWK+20, HWZ+21, TA21, ZlWL21]. **Multiomics-Based** [DWK+20]. **Multiparametric** [KBZ+05]. **Multiparty** [PXLP23]. **Multipath** [LDW+14]. **Multiphenotype** [Ell20]. **Multiple** [ASZ+16, BG97, BAK13, BB15, BRD+05, BZMM16, CP05, CHS17, CD18, CLLL20, DB09, Eli06, EPSV98, FJK+99, FND+09, GKB00, GB06, GWM+21a, GKS95, HHX16, Hor01, HW01, Jus01, KBS09, KD13, KVDC06, KX06a, KX06b, KS06, Kon07, LNW01, LR00, LYH+19, LH24, LS08b, LTSA15, LMSH03, MWP00, MNG+15, MSZM96, NSRR23, NMH13, OK08, PWCN02, PZMM15, PX13, RC15, RH19, RS98, RK96, RLCVVR18, SB98, SHRB11, SDDI+08, SSPNW06, SPW22, SI97, SSTM19, SLL+17, SZL+23, SB05, SLY06, TRIN07, TH17b, TBP+13, VV97, WJ94, WWZ19, WZG+20b, War95, WSHB98, Wu13, XBLM06, YHW18, YYZ+10, YJ04, YJ06, YA11,

ZEKKR18, ZRHM94, ZW03, ZHZ+16, ZKT14, ZL22]. **Multiple-Alignment** [ZRHM94]. **Multiple-Instance** [CLLL20]. **Multiple-Tilt** [WZG+20b]. **Multiplex** [Hub01, MLY+11]. **Multiplexed** [AAC+06, BDHK+04, CSH+20]. **Multiplexing** [SGYBD05]. **Multiplication** [AMK00]. **Multipoint** [KL98]. **Multiresolution** [PL06, XZW15a, YZ17]. **Multiscale** [BBH+21, SB17]. **Multiset** [Fom16a, Fom16b, Fom19]. **Multisimilarity** [YWZ+19]. **Multistage** [Kru98]. **Multistate** [HD16]. **Multistring** [BVP+19]. **Multitask** [DCH21, KMCKS17]. **Multithread** [BVP+19]. **Multitype** [DAR23]. **Multivalent** [SB17]. **Multivariable** [GSSI14, SG15]. **Multivariate** [ARHLK19, BFK+10, CC09, DMDR17, JKG+04, KCG+19, Pic08, UGS19]. **MuScL** [PX13]. **Muscle** [CEK+17, LL19a, LL19b]. **Muscular** [FSD+14, ZLB+20]. **MUSTA** [LNW01]. **Mutagenesis** [CLM+16, PGBK11]. **Mutant** [AWM+17, CWRF15, LYF+19, LZY+23, RMWC16, PMAP13]. **Mutant-Affected** [LZY+23]. **Mutant-Bin** [PMAP13]. **Mutants** [CWRF15, NFJ13]. **Mutase** [RBKJ19]. **Mutated** [VUR11]. **Mutation** [ABH03, BHKM22, CBG+14, CLLL20, HPDLW09, HMY+19, IR22, JPB+15, LSAS03, LTZ18, PDT00, Pia02, RV15, SSKH+13, SWS+20, SJ18, SMC+15, SDCF24, WZCS00, YK19]. **Mutation-Tolerant** [PDT00]. **Mutational** [BWGM17, FFSL22, GT16, MRY+23, NES22, RH19, WP11]. **Mutations** [DT12, DRT+25, FSD+14, GKD22, JAG17, NLC17, NKG+21, OSK+15, ZZZU20]. **Mutual** [ZZ14b, ZWD+04]. **Mutually** [CKB17]. **Mycobacterium** [MSN+20, YM06]. **Myeloid** [OSK+15]. **Myocardial** [ZLSY20].

n [KAD+19, JGL11, Lat99]. **N-Labeled** [JGL11]. **N5** [RBKJ19]. **N5-CAIR** [RBKJ19]. **naiveBayesCall** [KS11]. **Narratives** [HAP12]. **Native** [ADS03, FvdBB16, PGAE04]. **Natural** [ALB+19, BBDS21, Boh24, CS03, GGM12, LY99, ML10, WTY19, YS10]. **ncRNA** [ZZC+24]. **ncRNA-Protein** [ZZC+24]. **Near** [AMOW10, DEH10, NB94]. **Near-Linear** [DEH10]. **Near-Optimal** [NB94]. **Nearest** [KBG18, LTS20, STV96]. **Nearest-Neighbor** [LTS20, STV96]. **Nearly** [BBN24, LBXL11]. **Necessary** [PABE+10]. **Neck** [LTL20]. **Necrotizing** [ZYH20]. **Need** [ZFZL03]. **Negative** [BMH21, BFK+99, CC11, DLFS22, GQ09, JSZ+20, KCG+19, LWZ18, NES22, QLW20, SPSZ23, SSW20, WA10, YY19]. **Negative-Binomial** [KCG+19]. **Negative-Coregulated** [CC11]. **Neighbor** [ABH03, CHJ05, GM07, HPL+20, KBG18, LTS20, STV96]. **Neighbor-Dependent** [ABH03, CHJ05]. **Neighborhood** [BSP+25, DGW+13, FCS12, WLM21]. **Neighborhood-Based** [BSP+25]. **Neighbors** [BIPD17]. **NEK2** [LTL20]. **Neoepitope** [AAoS+23]. **Neogenin** [BSB+05]. **Nephropathy** [LL19c]. **Nervous** [FYJ18]. **Nested** [AMTY11, BFS10, DMTV09, MTH11, MA13, RRGC95, SMKS96, SSW20, ShHGC20, dMRR14]. **Net** [Guo15, NZM+25, AG23]. **NetMix** [RCER21]. **NetMix2** [CPR22]. **Network** [ACKK19, AMTY11, ADD+07, AEH17, AC17,

BB15, BDBB10, BCD+24, CDL+19, CWH+22, CPR22, CCPT17, CSP+12, CLLL20, DMDR17, DCH21, DCD19, DHY02, DWK+20, DT13, EZFP+19, FHZD17, FPD13, FP11, FRD+17, FND+09, FJAOB18, FBV15, Fre11, GQ09, GW06, GYA+23, GSV+11b, GSV+11a, GDL+15, GLM16, HHZ+18, HVAW04, HHL06, HSBS10, HAP12, HSL+24, HYJ+19, IFT14, ITdB09, JEMF06, JPB+15, JLmR+23, JSZ+20, JK96, Jos96, JBM15, KTT20, KSS09, KLV+13, KDL+94, LDS12, LLSH19, LDLZ12, LZBK15, LLS+19, LL19b, LJCZ20, LJP20, LZL+23, LYH+19, LMT01, LLD+16, LKC21, LLT+25, MYS+20, ML04, MPZL23, MGVS14, MC16, MNIK+09, MRG+24, MA13, MDL+18, MR08b, Mye96, NXGL20, OJOD+04, OSK+15, PXLP23, PYIM22, PIM23, PM24, PS12, PDK+08, PRC+13, PCC+11, PE20, RCER21, RND+23, Rot19, SIC+09, SSR21, SSC23, Sef25, SM09, SCSA+16, SSZC95]. **Network** [Sun18, Tak96, TKSA24, TMfTK23, TZB+23, TNSS13, TPSB19, TBS+07, VND17, WJD14, WYC+18, WFC25, WZ24, XAB+15, XYX+22, XL18, YcXyW+21, YIJ04, YT22, ZRNA20, ZZC+24, ZLTZ25, ZCZ+23, ZZL+23b, ZH14, ZWD25, ŽZ15]. **Network-Based** [FJAOB18, KSS09, PIM23, VND17, ZLTZ25]. **Network-Classifier** [PIM23]. **Network-Constrained** [PYIM22, PM24]. **Network-Guided** [ŽZ15]. **Network-Induced** [LDS12]. **Network-Structured** [RCER21]. **NetworkProfiler** [PSIM18]. **Networks** [AMK00, AA18, AMS+22, ABF+25, AHK08, AK08, AFCK09, BBN11, BHL+18, BB15, BCPS04, BLP+22, BML+16, BFL05, BSS13, BK08, BG15, BF09, BHK+10, BR23, CR09, CGT12, CCYH18, CW13, CJP+22, CT07, CLDG03, CUP19, DPSW20, DBHC24, DCD19, DSG+08, EBK11, FCS12, FdSdSR+15, FT07, FLNP00, GMC+14, GK18, GVTS04, GVTRS06, GMF+08, GBR17, GLM20, GYZ19, GKM+10, GMSZ12, GBBS07, GBB15, HMY+14, HHX16, HKS08, HNTW09, HSH+09, HAP12, HS14, JTSB10, KBS09, KW14, KS12, KR24, KIYM13, KV23, KW06, KK18, KKS+06, KKT+06, KSG07, KFR04, KKS22, LTsL24, LACB10, LST+17, LL05a, LSSD18, LCD11, LBDVF10, LTSA15, MZS+17, MPG+16, MPZL23, MSMF09, MWRS16, MTYH09, MSRS24, Nai18, NLH+23, NK07, NSMV18, PP23, PdBdP+22, PMCB08, PSIM18, Par24, PS12, PZMM15, PSB17, PDdJFT08, PFRD05]. **Networks** [PX13, QSY09, QGP10, RC14, RC15, RZK06, RK96, RDR12, RMC+05, RNI+06, SMS13, SG10, SVK10, SLA12, SIKS06, SS23, Ser15, SZSA22, SES11, Sol09, SK23, SVL+10, SY07, SkY12, SPC19, TINK98, TMC+18, VRS12, Wag04, WZZ01, WHD13, WZG+20a, WLF+23, WTE25, Wu13, XvdL05, YS07, YDN12, YE02, YMxW21, ZGW22, Zha16, ZH14, ZS24]. **Neural** [AMS+22, BFL05, CJP+22, CLLL20, DPSW20, DCD19, DHY02, EZFP+19, FdSdSR+15, GYA+23, HYJ+19, KKS22, LMT01, LKC21, MPZL23, MRG+24, MDL+18, Nai18, NLH+23, PXLP23, RK96, SVD14, STP18, SSZC95, TKSA24, TLP+14, WH01, WYC+18, WLF+23, WFC25, ZGW22, ZZC+24, ZLTZ25, ZS24, ZWD25]. **Neuron** [CL21b]. **Neuronal** [URB+19]. **Neutral** [DT13, JGB12]. **Next** [AB16, AR17, Boe18, BVP+16, FSD+14, GCB15, JAG17, KBKF17, KMM17, KAD+19, LYPC13, LZX12,

NP09, RUGR18, SWS+20, SRZ+13, WCL+18b, ZPB+10, ZZ14b].
Next-Generation [AB16, AR17, Boe18, BVP+16, FSD+14, GCB15, JAG17, KAD+19, LYPC13, LZX12, RUGR18, SWS+20, SRZ+13, WCL+18b, ZZ14b].
NF [LZBK15]. **NF-** [LZBK15]. **NGS** [KBCBS11, WLYC12, ZRS+12]. **NIAS** [BIPD17]. **NIAS-Server** [BIPD17]. **NMR** [ABF+04, BKWK+00, BKCP05, CYP+11, CLR+05, JGL11, LYL+04, WCC+06, XXCE00].
NMR-Constrained [XXCE00]. **Node** [AAC+06, RC14, RC15, ZLW+20].
node2vec [WZL+21]. **Nodes** [BG17, Csu02]. **NOE** [ABF+04, ZRZD11].
NOEs [MYBK+11]. **NOESY** [AKG+13, BKWK+00]. **Noise** [Aug12, DMR+03, Fom19, GSCG19, GMY10, HLK+13, LLJS19, LYS20, ZS24].
Noisy [AGH+18, AEH17, LL05a, LH03, NH08, ZB15]. **NOMe** [CCMS20].
Nomogram [HXL+20]. **Non** [BMH21, BL02, CN17, CK10, Eri09, JGB12, LAF+14, LWZ18, MK06, NES22, SZY+20, ŠV07, TKSA24, TE96, VSGD08, YYJ19, YY05]. **Non-Binary** [VSGD08]. **Non-Bonded-List** [MK06]. **Non-Coding** [TE96, YYJ19].
Non-Fourier [YY05]. **Non-Homologous** [Eri09]. **Non-Identifiable** [ŠV07].
Non-Negative [BMH21, LWZ18, NES22]. **Non-Neutral** [JGB12].
Non-Overlapping [CN17]. **Non-Random** [CK10]. **Non-Sequence** [BL02].
Non-small [SZY+20]. **Non-Subsampled** [TKSA24]. **Non-Uniform** [LAF+14]. **Nonadaptive** [HTZ+12]. **Nonadditive** [MRM20].
Noncanonical [CGZD24]. **Noncoding** [JFLL20, QbMyD+19, RPW13].
Noncompacted [Guo15]. **Nonconfoundable** [SMS13]. **Nonconserved** [ZS11]. **Noncooperative** [BZMM16]. **Noncrossing** [HPR09]. **Nongreedy** [AH20]. **Nonhomogeneous** [GCB15, SBT00]. **Nonidentifiability** [ZMK22].
Nonlinear [BBN24, CYY23, DCL10, FVTH03, JLSL24, LLKX16, LLS11b, LXS24, LJL+20, PRKG16]. **Nonnegative** [WHDN13]. **Nonoverlapping** [WW18, WW19]. **Nonparametric** [ADR24, CEK+17, GLM16, LMP08, WJJ11]. **Nonpathogenic** [SCB14].
Nonrandom [LCXC05]. **Nonredundant** [CZW+19]. **NonSmall** [ZCY+20].
Nonstructural [Tho21]. **Nonsynonymous** [SCB14]. **Nonuniform** [WC16].
Nonuniformity [PV17]. **Norm** [QsYSxL23, WYLW21]. **Normal** [CCPT17, COL+18, HMY+19, ZRS+12]. **Normalization** [Åst03, FVTH03, HMN21, KBCBS11, WA10, ZWSF05].
Normalization-Free [KBCBS11]. **Normalized** [PM14]. **Normalizing** [DLFS22]. **Noroviruses** [YK19]. **Notation** [EAM+17, Par07a]. **Notch** [TLP+14]. **Note** [BGHY04, BH15, JM95, Jen09, LZL+23, ZW07].
Note-Code [LZL+23]. **Notion** [PSCP09]. **NOTUNG** [CDFC00]. **Novel** [ACKK19, ADD+07, CMK23, CSH+20, DCP+21, DMDR17, DP07, FMH06, FH18, GYD+15, HG18, HHC06, Ila20, JCZ08, JJGD16, JHLD20, KEL15, LSAD05, LRM11, LKC21, LLJS19, LZX12, MK06, MPC+11, MKKK+17, ML10, MCH+19, NV12, NXL+15, PAS+13, RNH18, RBKJ19, RYY22, SSR21, ST10, SRS02, TZB+23, TAJZ23, TVNP15, TLP+14, UMR11, UBGFD+19, WLYC12, WLF+23, WQZ+19, WY11, XWJZ20, YWZ+19, YYW14, ZRNA20, ZWK+20, TAJZ23]. **Novelty** [Erw19]. **November** [Ano00]. **Novo**

[BDN19, Böc04, BG06, CGZD24, CBG+14, DAC+99, DCP+08, GYD+15, KWM10, LJK11, LYPC13, LC03b, WMD06, BVP+17, CKT+01, Cos18, DB09, MLY+11, SM20, WWH17, WYLW21]. **NP** [BL98, GKM+10, HI97b, OFCLH11, PX13, QEk24, War95]. **NP-** [War95]. **NP-Complete** [GKM+10, OFCLH11, BL98]. **NP-Hard** [QEk24]. **NP-Hardness** [HI97b]. **NP-MuScL** [PX13]. **NPI** [ZZC+24]. **NPI-DCGNN** [ZZC+24]. **nt** [Böc04, HMY+19]. **Nuclear** [BZMM16, BDBB10, LYL+04, LLWZ19, LLW+20, QsYSxL23, WMD06]. **Nuclei** [XYX+22]. **Nucleic** [CCJ09, CFH13, JMEB18, MKKK+17, RC07]. **Nucleolar** [BT08]. **Nucleosome** [CCMS20, YI17]. **Nucleotide** [ACBM18, BLR16, Boe18, CZNF19, CTC21b, EZFP+19, FSD+14, GJZ06, HXL+17, Kon09b, LWN+18, MNG+15, PRC+24, RS12, RKTS14, RSR+09, SCB14, SFC11, SLL+17, WCL+18b, WLF13]. **Nucleus** [Kha14]. **Null** [MG06, SFA17]. **Nullomers** [TZHR14]. **Number** [AP10, ACBM18, AFR+08, BBN24, CHP94, CD18, CKZ+19, CQG10, DLM10, DDC+20, FSW+20, GP13, GJL+22, HG11, IKL+03, Lai12, LLG+20, LCY+05, LABD+06, PRSV08, PNIM17, TGA24, TL23, TT12, WCM+08, WLYC12, WHY+13, WXY+24, WV11, WZ24, YzCW20, YDN02, ZEKKR18, ZZS17]. **Number-Driven** [PNIM17]. **Numbers** [APA17, ZB15]. **Numerical** [AO08, CWYB16, CYY23, CF97, Geo09, MDWZ24, RS01, Ser15, SS01, WZ23, YY18, YYZ23]. **Nussinov** [Clo05, GJL+22].

O [Lat99, YLD+18]. **Obesity** [WCL+18b]. **Observation** [BV09, HMY+14, SKL+24, TT12]. **Observations** [GLM20]. **Observed** [Ell20, LDW98, RPS02]. **Obtain** [FDB18]. **Occupancy** [YYY+09]. **Occurrence** [BG15, RDR+02, WSCL18, WLC18]. **Occurrences** [Han09, Jah11, PRSV08, RS98, XJZ+21, ZRS+12]. **Occurring** [WHC09]. **Off** [HI97a]. **Off-Lattice** [HI97a]. **offs** [WAX22]. **Oligo** [ST02a]. **OligoDesigner** [CLM+16]. **Oligomers** [CYP+11, MYBK+11, Mil95]. **Oligonucleotide** [Åst03, HWP20, KVDC06, MS99, WLF13, WI05]. **Oligonucleotides** [Elh01, MKKK+17]. **Oligosaccharides** [LKC21]. **o}m** [XSH+22]. **OMGS** [PJL20]. **Omics** [DSS+22a, LLS+19, LLD+16, MSNl23, MHL22, PP23, PNMI15, WZCY21, KIYM13]. **Omnitigs** [TM17]. **OMPcontact** [ZWY+17]. **On-Premises** [KAD+19]. **Oncogenesis** [DJK+99, DJK+00, HHL06]. **Oncology** [DRT+25, DLL+24]. **One** [AAN+20, CCYH18, CD08, GKG12, JLSL24, MD01, PTWB09]. **One-** [CD08, PTWB09]. **One-Articulated** [CCYH18]. **One-Class** [JLSL24]. **One-Dimensional** [GKG12]. **Ones** [CHSY10, LH03, MP11]. **Online** [BK10, CLM+16, HWP20, RAKL10]. **Ontology** [DAE+19, KGK14, LWC+14, LDW+14, Nou21]. **Open** [FJAOB18, JB10, MPG+16, ZRNA20]. **Open-Channel** [JB10]. **Open-Source** [MPG+16, ZRNA20]. **Opera** [GSN11]. **Operating** [VY18]. **Operational** [CDH+16]. **Operations** [BMS10, OFS09]. **Operator** [LGS20]. **Operon** [VCS11]. **Optical** [AMS97, DHM97, KPS00, KS00, LDW98,

LVS+07, PJL20, SGSN12, VLL+06, WPS+25]. **Optima** [BAK13, LH24]. **Optimal** [AB00, BW12, Bay23, BBD+04, BRZH15, CCI+04, CD11, Clo05, DSS+22a, FPU99, FH02, GSN11, GPRR12, GNI12, GQEk24, GJL+22, HI96, HI97a, HAM+22, HHE13, HSL07, KS06, Kon07, KK24, LG22, LBXL11, NB94, NFJ13, PTWB09, PU00, SGdMT12, SLT24, TP11, TNSS13, VM06, XXU98, ZMK22]. **Optimality** [TP11]. **Optimally** [BDHK+04, SES11]. **Optimization** [AMOW10, Azi22, BSP+25, BHGCS11, BZB+22, BRS99, BWGM17, Bry96, CGT12, Cha95, CC09, CYY09, DOKT05, EHFK24, GKG12, GPRR12, GYA+23, HD16, HHX16, HYY+10, HMK24, KLR23, KCH04, Lat99, LLS+19, ML10, MBRS11b, Neu14a, OBDV16, PGBK11, RRFS98, SRM+98, WDA01, YLCC17, YCCL18, YFBK07, ZFBK09, ZZL00]. **Optimization-Based** [HYY+10, MBRS11b, YLCC17, CGT12]. **Optimize** [ADRS24, HD16, OJFD18, TPSB19]. **Optimized** [CL21a, HTM+22, MWL22, XLZ+18b]. **Optimizing** [BSP+25, BLC+10a, CDFC00, FG04, GLJW09, JPLD23, XBLM06]. **Oral** [UBGFD+19, YDG+20]. **Orbits** [KG24]. **Orchard** [LTsL24]. **Order** [BDCKY03, BJF+20, DM17, FPS22, KIYM13, Par07b, SBD+00, SZW+09, SHZ+24, TRB+09, Ves12, WAC08, ZZS08, ZAG+18, ZY23]. **Order-Preserving** [BDCKY03]. **Ordered** [AMS97, FNC08, Par98, SMML24]. **Ordering** [DFS95, JM95, Lu15]. **Orders** [BLEM08, ML00, XJZ+21]. **Ordinal** [Kea97]. **Ordinary** [SK23]. **ORFs** [Fic95]. **Organ** [KMUK22]. **Organelles** [WLA+18]. **Organism** [CP05]. **Organization** [CSA98, CXW16, HSAEM13, LC03a, TRB+09]. **Organizational** [SDFR16]. **Organized** [WZC96]. **Organizer** [LS98]. **Organizing** [Jos96, YE02]. **Organs** [AG23]. **Organs-at-Risk** [AG23]. **Orientations** [BSS13]. **Oriented** [SSIP+19]. **Orienting** [SES11]. **Origin** [ODNW21]. **Origins** [YY05]. **Ortholog** [FCV+07]. **Orthologous** [LWZ21]. **Orthology** [OO24]. **Oryza** [ZDZ+20]. **Oscillations** [YY19]. **Oscillator** [ZML07]. **Oscillatory** [BZMM16, Kru17]. **OSIRIS** [BGTSB98]. **OSPREY** [CGZD24, GKD22]. **Osteosarcoma** [MDL+18]. **OT3** [RBKJ19]. **Our** [Elh11]. **Outcome** [BSB+05, ZZL23a]. **Outcrossing** [WMC04]. **Outer** [ZWY+17]. **Outlier** [MSNl23]. **Output** [CN17]. **Ovarian** [WDZ20]. **Over-** [LMS96, Sch97b]. **Over-Representation** [cLcSwP+21]. **Over-Represented** [LACB10]. **Over/Underexpression** [GPRR12]. **Overall** [ZPC+18, ZQZ20]. **Overestimate** [LSRR18]. **Overexpression** [BRC20, YBF19]. **Overlap** [AMDY11, BBC16, CCI+04, CC23, LSRR18, SRF16, XS07]. **Overlapping** [AS95, BSK05, CN17, DDA+11, PNMI15]. **Overlaps** [CZS15, JGT22, Ric06, UMR11, Wen05]. **Overrepresented** [TML+02]. **Overview** [RSW00, Sch00, SMZ+12, SKM05, SF03, YMZ+12].

p25 [CASP10]. **p25-Derived** [CASP10]. **p53** [GQ09, RMWC16, CY09]. **p53-MDM2** [CY09]. **p53-MDM2/MDMX** [CY09]. **Pacemakers** [Sni19]. **Pack** [MKBC05]. **Package**

[AVS20, ADW23, ADR24, BSKgG23, FPD13, IRCA21, JPLD23, NCC+96, PBMC17, QFLL22, SSH+20, SLL+23, WHK21, XL18, ZZL23a]. **Packet** [NHOV10]. **Packing** [DQS+11, HBW+05]. **Pain** [CKL+17]. **Painting** [LVC+04]. **Pair** [MPC+11, PAC02, PRT08, SFA17]. **Pair-Wise** [PRT08]. **Paired** [GSN11, Lai12, MPC+11, PAS+13]. **Paired-End** [GSN11]. **Pairing** [BHRV00, FHS00, Ham12, HPVS96, WMK17]. **Pairs** [BHHR19, BMN+07, CL17, CTC21b, DWS05, GKS95, IKL+03, KNmS+22, KS06, LJL+20, TGT08, YJ04, ZHQS05]. **Pairwise** [EPSV98, Fom16a, Fom16b, Fom19, Gru98, KKT+06, LN03, LH24, LHXH08, Mat10, NMG+05, PWT18, SYYH02, WG08b]. **Palindromes** [LCXC05]. **Palmitoylation** [KKK18]. **Pan** [KMB+20, SWS+20, NHZ+15]. **Pan-Cancer** [SWS+20]. **Pan-Genome** [NHZ+15]. **Pan-Genomics** [KMB+20]. **Pancreatic** [CYF+20, WXY+13, ZDG+20]. **PANDA** [PSG+20]. **Pandemic** [LCG+23]. **Panel** [JMPR23]. **Panels** [FFSL22, Ros05, SWS+20]. **Pangenome** [CJ23]. **Pangenomic** [ROL+22]. **Papers** [Ano17, Ano21a, DNZ17, DND+19, HTH+17]. **Papillary** [CWS+21]. **Papilloma** [DBBM09]. **Papillomavirus** [LZHC15]. **Paradigm** [BR06, MJR+24, MKBC05, MDTD06, RMS02, ZZZU20]. **Paradigms** [AP04]. **Parallel** [And09, BCA96, CZNF19, Cha01, CF14, CST20, EOD+18, FHS00, NBB18, PB18, PWFZ17, PWT18, RLCVVR18, SSLMW10, SLL+17, VRGC18, WCZ+18, YMM+24]. **Parallelism** [BCA96]. **Paralogous** [KBLS24]. **Paralogy** [OO24, PMF+03]. **Parameter** [AP09, DKK20, DCL10, DAR23, FND+09, KD13, LTsL24, O'H15, YS10, YDN12, YAR21, ZZL00, ZTW05]. **Parameterization** [KC18, ZGEZu11]. **Parameterized** [CDKL09, XJB07]. **Parameters** [CA15, GKG12, SWK+07, SVP19]. **Parametric** [GLJW09, NP09]. **Parametrically** [AS96]. **Parametrized** [SDCF24]. **Paratope** [DVS19]. **Pareto** [GQEk24]. **Parkinson** [PD16, PD20b, PE20, YLC+20]. **Parotid** [KLV+13]. **Parsimonious** [BSS11, DCH09, MBRS11a, SP11, Wu13]. **Parsimony** [BSWY98, CMLTZU14, GLMSO10, HM14, HCC05, KW14, KNmS+22, MJS23, WTM11]. **Parsing** [DCW+17, RC07]. **Part** [CSZ23b, CSZ23a, IPSV22, Pat24, Pat25, Pe'22a, Pe'22b]. **Partial** [BBC16, BFK+11, GZY+22, JKG+04, KIYM13, PD20b, TT12, fW23, Zha94, ZZN10]. **Partially** [EHFK24, Ell20]. **Particle** [BSP+25, CYY09, COV+15, LLS+19, LCG+22, YLCC17]. **Partite** [CHS17, JTL+10]. **Partition** [Che12, CMvH15, CFH13, WC07]. **Partition-Distance** [Che12]. **Partitioning** [BG06, CEKP+13, SY22, YFBK07, ZPD+23]. **Partitions** [BG17]. **Passage** [KM08]. **Past** [MWP00]. **PASTA** [MNG+15]. **Pasto** [EBS+22]. **Path** [ABR16, BSS13, HWH+13, HP97, Nou21, PYG+19, SSMT16, SV97, SkY12, YF09, YS07, ZW03, ZKM21]. **Path-Based** [BSS13, HWH+13]. **Pathogenic** [DS04]. **Paths** [Ben21, GKS95, XZS07]. **Pathset** [PAS+13]. **pathTiMEx** [CKB17]. **Pathway** [ADP+08, AF20, ABF+25, BMH21, ES07, HLCS10, IJCL12, KK11, KLR23, KK23, LXL+20, MXW+20, QMMW11, RND+23,

RFH+25, SSR21, SBPS11, VND17, WV11]. **Pathway-Based** [SBPS11]. **Pathways** [ABF+04, AS02, AKK11, BRD+05, BMR09, CHS17, CKB17, DGFMSS16, DM20, DYLK20, EAM+17, FS99, GQ09, HBK11, JTSB10, LVC+04, LL05a, LBJM11, LHL16, MGVS14, MZM18, OBJO+03, PD16, QQL+19, QSY09, RV15, RHS+21, SIKS06, SOD+11, SGK+12, SAM06, TBP+13, VUR11, VRU16, Wag04]. **Patient** [DCL18, KBJ07, PdB13]. **Patient-Gene** [KBJ07]. **Patient-Specific** [DCL18]. **Patients** [Ano20, DYLK20, ZZ20]. **PaTre** [PMF+03]. **Pattern** [BR06, Bri19, CC11, Che04, ELP04, KBZ+05, KS99, NR03, Par07b, RDRF24, Ris16, SSPNW06, WLC18, ZRS+12]. **Patterns** [AGH+18, BDSY99, BHKN25, BJEG98, CPFP24, CZC10, CY17, EJT00, GHJ+12, HRSC00, HKZ+04, KMZ+10, KKS+06, KW21, LYMD03, MP16, Nue04, PMCB08, PKZ11, PV17, SCD+22, SB07, SCSA+16, TA97, TYS+20, WAC08, YZ08, YI17, ZKL+10]. **Paul** [Tra19]. **Pauses** [YY19]. **Pausing** [SKP+12]. **PBX1** [QLW20]. **PCA** [And09]. **PCR** [BLC+10a, SSY+22, SWK+07, SMKS96]. **PDB** [CCI+04]. **PDFll** [YDZ+25]. **Peak** [CLR+05, XZ12, ZW23, AEH17]. **PeakPass** [WH20]. **Peaks** [JGL11]. **Pedigree** [ABR16, HWH+13, KLKH11, KRF+12, KT13, LJ05b, PG03]. **Pedigrees** [CBG+14, DEH10, KHK10, LL11]. **PEM** [AJYJ18]. **PEM-fitter}** [AJYJ18]. **Penalized** [LST+17, LGC+09, MEF24]. **Penalty** [Dew01, LLD+16, YL17]. **Peptidase** [MCH+19]. **Peptidase-4** [MCH+19]. **Peptide** [BG06, CKT+01, CGZD24, DAC+99, DB09, GBB15, HYY+10, LZHC15, LC03b, MLY+11, Ore20, PZZ+10, SLO07, SZMS02, Vij22, WTE07, ZRGHJ08]. **Peptides** [DBL+12, STHG+08, SZL+23, SS04, ZYB+04]. **Peptidic** [HLH06]. **Per-Tile** [AS23]. **Perfect** [BGLY03, BGHY04, BCC+09, DFG06, Gus10, VM06, WZZ01]. **Perfection** [OBS11]. **Performance** [BRS99, CHP94, DGW+13, EOD+18, HBD94, KVM14, KWB+13, MSMF09, MBC+18, PFK17, PGV16, WXY+24, ZRNA20]. **Performed** [HQ06]. **Period** [WY21]. **Periodic** [BLF14, SM98]. **Periodicities** [ZWJ18]. **Periodicity** [TLK+06]. **Permeability** [DHY02, FYJ18]. **Permutation** [ELP04, GB08, HL10, Par07b, VT06]. **Permutations** [BMY01, BS06, SS07, Sie03, SKO09, SRLM10, ZAG+18]. **Permuted** [ZHS05]. **Perspective** [EOD+18, MG06, Par10]. **Perspectives** [BSS11]. **Perturbation** [LYH+19]. **Perturbations** [Wag04]. **Perturbed** [AC17, PD16]. **Pfeature** [PPL+23]. **PFM** [PRSV08]. **PFOLD** [TBJF01]. **PFstats** [FJAOB18]. **PGI** [CM04]. **PgtE** [SVA+19]. **Phage** [BBP10, ZY23]. **Phages** [TAJZ23]. **Pharmacoinformatic** [SB21]. **Pharmacophore** [SDDI+08]. **Phase** [CL21b, HR12b, LYMD03, SLZH15, bVRN+19]. **Phase-Independent** [LYMD03]. **Phaseable** [HATI11]. **Phasing** [HATI11, HHE13, SY22]. **Phenome** [MNIK+09]. **Phenotype** [GZY+22, GLM16, HTY22, LJCZ20, LS23, WYY+18, YHT+17, dGFMS16]. **Phenotype-Associated** [GLM16]. **Phenotypic** [CMK23]. **Phenylalanine**

[LSAD05]. **Phi** [CAB+07]. **Phi-Values** [CAB+07]. **Philosophy** [Dei19a]. **Phosphatase** [CYZ+20]. **Phosphoglycerate** [CC03]. **Phosphorylation** [SVL+10]. **Phylogenetic** [AA18, AR06, ARS17, AT12, BST02, BG17, BG23, CHP94, CC12, DMHM97, DM17, EZ98, FLS94, FNPP02, GMC+14, GYZ19, GBBS07, HSG22, HY16a, HV09, HNW99, IM14, JS03, KW14, KPW11, KVK08, LC09, Lar06, LRM11, LRV21, LMSH03, ML04, Mat10, MMHC98, MBRS11b, MLS+23, PJB+15, Prz07, SB99, SLA12, SH04a, SF95, SS05b, SS05c, SZUP06, VV97, WZZ01, WTE25, WTM11, Wu13, XLZ+18a, ZMGN23, ZEKKR18, ZSB+23, Zha16, vLSV+24]. **Phylogenetically** [AHK+07, McC09]. **Phylogenetics** [WMG+24]. **Phylogenies** [BDCG+98, BSMA06, GM07, MMS95, Mos03, SSKH+13, SW11, WGC+21, Zha97]. **Phylogenomic** [CMvH15, MSS+22, UBTC06]. **Phylogenomics** [ATLS07]. **Phylogeny** [ACL+21, ARC13, BGLY03, BGHY04, Cha95, Cha01, zCULW20, CA12, DPHH05, DG02, DFG06, Gus10, MBRS11a, NSRR23, NKG+21, Par06, SB98, SZW+09, SWR08, ŠV07, TAMW13, VM06, VBSS10, WR23, YWN11, ZGW22, ZZHL11, ZZS08]. **Phylogeographic** [ME12]. **Physical** [AKWZ95, AK07, BPL02, BCA96, CJK+97, GGKS95, GI95, HSF+00, JM97, LH03, MS99, NCC+96, Sch97a, SES11, SBAW97, YIJ04]. **Physicochemical** [CLT+20]. **Physiological** [Lie05, PRC+13]. **Picked** [JGL11]. **Picking** [LAP03]. **Piecewise** [PDdJFT08, PLSM+06]. **Piecewise-Linear** [PDdJFT08]. **Piers** [Boh24]. **Pipeline** [CFB+07, FCR+13, PBMC17, RHS+21, SSW20, WWH17]. **Pipelines** [ACL+21, KAD+19]. **PIR** [WZC96]. **Placement** [BRZH15]. **Planarian** [FCR+13]. **Planktonic** [RHS+21]. **PLanner** [KLO18]. **Planning** [AS02, ADS03, SLS23, TKT+05, ZFBK09]. **Plans** [SSS+21]. **Plant** [GWL+19, HV07, VND17, WLA+18, XJZ+21, YSC15, GWL+19]. **Plant-GQ** [GWL+19]. **Planted** [AOH16, RBH05]. **Plants** [BBWE09]. **Plasma** [LWN+18, RMC+05]. **Platform** [JZL+20, SSIP+19, TH17b]. **Platforms** [EOD+18, SFC11]. **Play** [KAD+19]. **Plenary** [Woo99]. **Plug** [KAD+19]. **Plug-n-Play** [KAD+19]. **PML** [BDBB10]. **Pockets** [CRT+17, NSA08]. **Point** [CWRF15, GP20, Kea97, LC09, Lai12, NFJ13, PV17, SSPNW06, VRGC18, VY18, XLZ+24, XLZ+18b]. **Points** [Fom16a, Fom16b, Fom19, PJB+15, RC06, VND17]. **Poisson** [AMRW96, CCPT17, GPCP11, KV19, KBCBS11, LKL21, LWZ21, PRSV08, RS98, ZRS+12]. **Polar** [GP13, GWX18, KMRG09b, YTMY17]. **Policy** [CWR24]. **Poliovirus** [TZB+23]. **Polyadenylation** [HV07]. **Polygenic** [MPZ+20]. **Polyhedral** [LRV98]. **Polymer** [JD05]. **Polymerase** [CH15, DDK21, LSAS03, Pia02, RLH13, Sun95, WZCS00, WV95, ZF05]. **Polymorphic** [SBP15]. **Polymorphism** [Boe18, CTC21b, EZFP+19, LWN+18, WLF13]. **Polymorphism-Based** [LWN+18]. **Polymorphisms** [ACBM18, HG11, RS12, SCB14, SR10, yWCF06, WCL+18b]. **Polynomial** [CJS12, KLM11, LYL+04, LMWR21, LXS24, SLY06, TRW23, WMD06]. **Polynomial-Time** [CJS12, KLM11, LYL+04, LMWR21, TRW23, WMD06].

Polynomials [ES06]. **Polypeptides** [AC10]. **Polyploid** [BDK+16, SY22, WMC04]. **Polyploidy** [BBWE09]. **Pombe** [WHW+06]. **Pontoons** [Boh24]. **Pool** [DCV+07, DCL18]. **Pooled** [BG11, CM04, EHC+13, FSD+14, JAG17, PLSL18, WDF24]. **Pooling** [CCF10, CD08, CDKL09, DHM+05, HL03, KST96, LGD+10, SBAW97]. **Poor** [ZQZ20]. **PopInf** [ODNW21]. **POPSTR** [ACBM18]. **Population** [ACBM18, BG11, DSV12, FFM24, GZN16, KKM+20, KPP+22, MRS+18, NHZ+15, ODNW21, OYY+12, PMAP13, Ros05, RLA+06, SLL08, SSIP+19, YMZ+12, ZW07, ZLP22, ZKT14]. **Populations** [AV18, ADR24, BGTSB98, BG09, GNME01, Gus01, KG24, LWLJ10, SDG+07, TMC+18, WSS03]. **Portable** [RGL94]. **Poses** [PPV+14]. **Position** [GGU13, GWM+21a, LLW18, PRSV08, RJS02, ZCH+13]. **Position-Specific** [GWM+21a, RJS02]. **Positional** [BDPSS01, YS99]. **Positioning** [YI17]. **Positions** [GKKS98, WMK17, ZS11]. **Positive** [BFK+99, DQS+11]. **Positivity** [MDWZ24, RYZ23, WZ23, ZPG+24]. **Positivity-Preserving** [WZ23, ZPG+24]. **Possibilities** [CGOT10]. **Possible** [KFC+11, LXL+20, WHC09]. **Post** [KV08]. **Post-Transcriptional** [KV08]. **Postduplication** [KBLS24]. **Potency** [HH14]. **Potential** [ALB+19, AF20, Ano21b, CCH+19, CJ21, CYZ+20, FZF+20, GLJW09, HSBS10, LGD+19, LHC19, LTL20, MWZ19, OC00, RRGC95, RC06, RXH+20, SZY+20, SK19, TGTG19, YDG+20, YcXyW+21, bYjHgZ+24, YYL19, YfZX+21, ZHY+20, ZLL+20, ZYH20, fZbMqW+20]. **Potentials** [Bet10, HI97b, SkY12]. **Potpourri** [CTC21a]. **Power** [EOD+18, HQ06, RCSW09, SBK22, SHE11, WRSW10, ZKL+10, ZLP22]. **Power-Law** [SBK22]. **Powerful** [WZH+18, WZCY21]. **PPH** [DFG06]. **PPI** [LXYC09]. **PQ** [LPW05, Par06]. **Practicable** [LYS20]. **Practical** [BMB24, BG23, CB06, GKS95, JR17, LR00, MSBR08, PZC05, SMZ+12, TCL+16, YzCW20]. **Practice** [NWLS05, OBS11, RRNB13]. **Pre** [BHGCS11]. **Pre-Processing** [BHGCS11]. **Precedence** [RG95, Ves12]. **Precise** [PWT18]. **Precision** [BMH21, DRT+25, HTH+17, PYG+19, SWS+20]. **Predator** [KG24]. **Predefinition** [SNW04]. **Predict** [BF98, BLP+22, CZNF19, CAB+07, GKD22, JAJ24, LJ05a, NCMS+21, NXL+15, TVNP15, XJL+22, Yan09, ZWK+20]. **Predicted** [BF98, Gui98, KKW10, SS04, YYY+09, Yua09]. **Predicting** [AWZ+17, AS22, AS11, CJ21, CJP+22, CBM+02, DDC+20, DHY02, FADH17, HZNF06a, HZNF06b, HXY+23, IKL+03, KSS09, LJK16, LXYC09, Lie05, LSSD18, LKC21, PKK97, Sef25, SSB07, SZL+23, WHDN13, WYC+18, WWC+20, WxLW+23, WLM21, Wu96, XGD24, YLCC17]. **Prediction** [AP10, ADPH15, AKN+06, ASZ+16, BÖB+23, BMH21, BL02, CWR24, CBP21, CFB+07, CCJ09, CW09, CAB11, DMHM97, DQS+11, DVS19, DZM+03, DCS04, DGW+13, DBT11, DCL18, DOKT05, FYJ18, FHS00, FSD+14, FK06, FBV15, GZY+22, GZLY24, Gel95, GB06, GJZ06, GWM+21a, GWM+21b, HPL+20, HI97a, HKL07, HHP+09, HCS09, HH14, HWZ+21, HFUH19, JCZ08, JLY08, JRH+10, KWM10, KAS09, Kha14, KNS14,

KJmZ+22, KKK18, LKBT16, LBN94, LGC+09, LWZ18, LQPE+10, LLT+25, LP00, MJR+24, MMG14, MWZ19, MK11, MRM+02, MS03, MDMC21, MWB10, MVP06, Nai18, NLH+23, NSH+23, ÖBA+23, PPL+23, PMG+16, PX13, QTRA24, RMS02, RK96, SLO07, AAoS+23, SK21, SBRG20, SHZ+24, SZMS02, SKT08, VILR10, VA17, WAPM05, WHD13, WHD15, WZL+21, WFC25, WT17, WYLW21, YTMY17, YCCL18, YSFW08, bYjHgZ+24, YM06, YQDW23, ZGEZu11, ZWY+17, ZYB+04, ZCZ+23]. **Prediction** [Zho17, ZYD21, ZWD25, dGFMS16, vLSV+24]. **Predictions** [CEJM16, MPZ+20, PXLP23]. **Predictive** [FPD13, KVM14, KWB+13, SKP+12, SVP19, WYY+18]. **Predictor** [JR16, YLD+18]. **Predictors** [YDZ+25]. **Predicts** [NVCW15]. **Preface** [AHIV23, Ano10a, Ano11b, Ano17, Apo07a, Apo07b, Baf11, Ber11, CSZ18, CSZ19, CSZ20, CKS12, CKS13, CKS15, CMSZ12, Cho13, Cow20, DMV17, DNZ17, Gus05, HHC17, HASL18, Ist20, JPW15, KCBJ11, Len02, MVVR19, Miy06, Pev98, PS11, Prz16, Sah18, Sha00, Sha15, Spe08, Sun13, Tan23, TD08, VRGC18, WIP97]. **Preferences** [EBS+22, LBBV+18, SLYC09, ZCH+13]. **Prefix** [BVP+19]. **Preimplantation** [BCD+24]. **Preliminary** [Ano21b]. **Premises** [KAD+19]. **Preprocessing** [AR17, DGFMSS16]. **Preprocessor** [RHY+04]. **Presence** [AJA+16, Bay23, GCB20, HG05, KYSE10, TZHR14, WR23]. **Present** [SCH09]. **Preserve** [BP06]. **Preserved** [SSLL22]. **Preserving** [BDCKY03, MDWZ24, RM21, RYZ23, SSZG24, TGA24, WZ23, YS23, ZPG+24]. **Pressure** [BWGM17, SSW20, WP11]. **Pretraining** [YLZ+24]. **Prevalence** [Rød06]. **Prevention** [LL19a]. **Prey** [KG24]. **Primary** [BGTSB98, DYLK20, GCD20, KX06a, KX06b, XMWZ20, XWJZ20]. **Prime** [CWYB16]. **Primer** [CLM+16, LS05, SMKS96]. **Primers** [KBKF17]. **Principal** [CWRF15, GSCG19, LSBS18, PD20a, PGAE04, SLYC09, TE96]. **Principal-Component** [PD20a]. **Principle** [DG02]. **Principled** [CPR22]. **Principles** [Dei19b, Ist19]. **print** [Ano20]. **Prior** [AEH17, BB15, PS12]. **Priori** [Wen05]. **Prioritization** [CTC21a, GSA14, PE20, XAB+15]. **Prioritizations** [GJL+21]. **Prioritize** [Li08, LS23]. **Prioritizing** [EBK11]. **Priors** [WS04, YYA10, YYA11]. **Prism** [GWX18, KMRG09a]. **Privacy** [SSZG24, YS23]. **Privacy-Preserving** [SSZG24, YS23]. **Private** [PBB+21]. **Privatedriver** [SSZG24]. **Prize** [TBP+13]. **Prize-Collecting** [TBP+13]. **ProALIGN** [KJmZ+22]. **Probabilistic** [AAG14, AB00, BSK05, BG15, CFS+08, DCS04, DT13, GVTRS06, GE14, HS15, HB11, HHL06, JK96, KKS+15, Kon09b, LFD03, MWZ19, PK11, PSB17, RSW00, RS13, SWK+07, SG12, SBK22, STP18, TZP+13, URB+19, Wen05, WG08a, YH01, ZPD+10, ZS24]. **Probabilities** [FHS00, HPVS96, PFRD05, YZ08]. **Probability** [DLD+14, DFS94, ENS02, FL94, Ham12, LC09, LS17, LS23, LWZ21, MSR22, RDR+02, SD95, VST03, WTM11, DFS96]. **Probe** [FdSdSR+15, JM95, KMP+04, MSBR08]. **Probed** [SNQ+14]. **Probes** [AKWZ95, CJK+97, FPU99, JM97]. **Probing** [FvdBB16, ZZ14b, vLSV+24].

Problem [AOH16, ARC13, BV10, BDCKY03, BDKSS03, BWGM17, BFK+11, BDK+16, Cha95, Cha01, CFS+08, Che12, CHS17, CDH+06, DMB07, DFG06, Fom16a, Fom16b, Fom19, GYZ19, GMS05, Gus10, HATI11, Jia11, KSB98, KRD14, LTI10, LAL+09, LHC09, LH24, LS05, Lu15, MP11, Mar94, MTH11, OSC11, OFCLH11, PSCP09, QBA+25, SG15, SSMT16, SV97, SSPNW06, SMML24, SZUP06, Tak96, TAA16, TBP+13, Wan94, fW23, WCC+06, XS07, Xu09, ZZS17, Zör15]. **Problems** [AVS20, CCF10, Cha95, CP19, DHM97, EHFK24, GPOP+17, KSSK09, KWBS11, Kov14, LLW03, LHC02, MS03, NSZ99, OBDD19a, PAC02, Par98, PG03, RBH05, TW05, Xu10, Zör15, dGFMS16]. **ProCanBio** [SKDR21]. **Procedure** [HSOE+18, RBK94]. **Process** [AMRW96, BHKM22, CL21a, GJM04, HVD17, KM08, LSAS03, LWZ21, MJS23, NBGA13, RS98, SWK+07, SRB+25, SDCF24, TDV24, UTD+20, XJS07, YYZ23]. **Processed** [MSB+10]. **Processes** [AC17, BSK05, GGM12, JPLD23, PRKG16, PRC+13, Sch97a, Sun95]. **Processing** [BHGCS11, CFE+13, LVC+04]. **Product** [ALB+19, Ser15]. **Production** [ALR18, BSP+25, CCDB21, CEK+17, KM08, TMfTK23]. **Production-Passage-Time** [KM08]. **Products** [LDW+14, NBA+13]. **PROFALIGN** [TGT08]. **Professor** [Ano21a, IPSV22]. **Profile** [AaHP+21, FDB18, GKG12, GW94, HWW+20, LDS12, LS08b, PM24, PV17, WDZ20, XLLS20, YAR21]. **Profile-to-Profile** [GKG12]. **Profiles** [BDBF+00, BSB+05, CCMS20, CW09, CD18, DS04, FFB20, KBJ07, KLC+11, PD20a, RMS02, SKP+12, SS04, TGT08, WPL+19, WWC+20]. **Profiling** [BGJ+04, ITdB09, LDB+07, MLC10, ZYH20]. **Prognosis** [Ano20, Ano22b, GCD20, HLK+13, HZL22, TMH+21, WWC+20, WDZ20]. **Prognosis-Related** [GCD20]. **Prognostic** [CYF+20, HWW+20, QLW20, WZL19, WHLR20, ZWK+20, ZQZ20]. **Program** [AM97, CDFC00, KDL+94, MSNl23, TSTS12, TDV24, TS96]. **Programming** [AKG+13, ADRS24, BRZH15, CCI+04, CKT+01, DWMT22, Gui98, Gus10, HNTW09, HD98, JJGD16, KW14, KAS09, LJ05b, LJL+20, MTF+12, PMGE21, kSyPhC+22, SB07, TMfTK23, WZW15, Wu96, ZLTS13, Zör15]. **Programming-Rounding** [LJL+20]. **Programs** [MP94, PKK97]. **Progress** [SBT00]. **Progression** [CKB17, RV15, SKL+24, ZWQ19]. **Progressive** [MSZM96]. **Project** [SBT00]. **Projection** [LQ23]. **Projections** [BT02, NDMK17]. **Prokaryotes** [LM11]. **Prokaryotic** [EVLZU19, MM06, PBMC17, TZHR14, YS19, ZMGN23]. **Proliferation** [COL+18]. **Promote** [YBF19]. **Promoted** [BRC20]. **Promoter** [BV10, HZGD05, HHJ+02, HKZ+04, MS00, NTMM06, SKP+12, YYY+09]. **Promoter-Proximal** [SKP+12]. **Promoters** [EAA+09, LCW16, LLW18]. **Promyelocytic** [BDBB10]. **prone** [WZCS00]. **Proof** [Ist19, War95]. **Proofs** [HI97b]. **Propagation** [CPR22, IR22, KXL08]. **Propensities** [STV96]. **Propensity** [JMPR23]. **Properties** [AWZ+17, CLT+20, DGW+13, FDDK07, GSV+11b, GJZ06, HL16b, JTSB10, KKS+15, Neb02, NW12, OSK+15,

PRC+24, POP23, PSB17, RSW00, SNQ+14, SKO09, SS04, TR11, WFH18].
Property [CHSY10, CGD09, GWM+21a, LH03, MP11, QTRA24].
Proportion [JZ10]. **Proportional** [Ano22b, LL23, TMH+21, UMR11].
PROSES [KGÖ18]. **ProSite** [WZC96]. **Prospects** [Erw19, KPP+22].
Prostate [HHZ+18, HXL+20, JMPR23, SKDR21, SGCD19, SSS+21, YYJ19].
Prostatic [Ano20]. **Protagonist** [LBBV+18]. **ProtBert** [GZLY24].
ProtBert-BiGRU-Attention [GZLY24]. **Protease** [MRG+24]. **Protective** [KLS15, ZCY+20]. **Protein**
[AMK18, APVM11, ABD+97, AP10, ACKK19, ADPH15, AJYJ18, AKG+13, AKLM02, AS02, ADS03, Ami12, AHK+02, AT05, BF98, BP20, BKWK+00, BC94, BET00, Ber95, BS97, BL98, BG08, Bet10, BMB24, BWGM17, BFL05, BSS13, BGG07, BT08, BDBB10, BHK+10, CWC06, CL17, CBS+20, CZC10, CJC01, CLR+05, CFB+07, CWYB16, CDL+19, CB07, CAB+07, CS15, CV11, CYZ+20, CBM+02, CGP+98, DBW17, DMHM97, DK18, DZM+03, DGW+13, DC16a, DGH+01, DBHC24, DM20, DSN14, DAL+08, DPR97, DKF09, DSG+08, DBL+12, DOKT05, DT13, Erd05, ENS03, FCS12, FADH17, FK06, FJAOB18, FBV15, FT07, FKZ09, GZLY24, GE17, GKMS23, GPOP+17, GST10, GLJW09, GZN16, GLMW13, GWX18, GWM+21a, GWM+21b, GMS05, GMVC20, HD16, HJD17, HPL+20, HI96, HI97a, HI97b, HRSC00, HHX16, HS15, HYY+10, HHP+09, HCS09, HSH+09, HSBS10].
Protein [Hor01, HS14, HBW+05, ISK99, JDH00, JEMF06, JJY+20, JAJ24, JR16, JJGD16, JHLD20, KV17, KBS09, KXL08, KGLBK15, KWM10, KAS09, KKW10, KD13, KMRG09a, KMRG09b, KX06a, KX06b, Kle99, KLW96, KJmZ+22, KGK14, KGÖ18, KKT+06, KSG07, KMCKS17, LTS20, Lat99, LACB10, LZS09, LBN94, LXYC09, LYC15, LAL+09, LSL+16, LLWZ19, LJP20, LN03, LBBV+18, LSAD05, LBJM11, LCWG06, LCGW09, LZ10, LSSD18, LWZ21, LZY+23, LLJS19, LYS20, LS04, LW12, LDB+07, MC08, MC10, MMG14, MN08, MTC11, MYBK+11, MZC+18, MD00, MAN16, MBLZ09, MVP06, NLH+23, NBG+02, NK07, NR03, Neu14a, Neu14b, NBGA13, NH08, NW05, NFJ13, NDMK17, NTWF11, OJFD18, OMS13, ODPB18, PK11, PDZ+16, PPL+23, PDT00, PQBB08, PSCP09, PPV+14, PVFB06, PLSM+06, PFRD05, PE20, QSY09, QBA+25, RROF95, RRFS98, RK96, RDR12]. **Protein** [RM00, RL94, SDMN19, Sal95, SVD14, SLB00, SIKS06, SK21, Sel13, SB17, SIK+05, SNW04, SOD+11, SMD+07, Shi10a, Shi10b, SJ18, SLB+97, SHG00, SHG02, SLZH15, Sun18, SK19, SKT08, TGTG19, Tay94, TPK03, TSTS12, TBB00, TTTA07, TXL+17, TAY16, TLK+06, VILR10, VND17, VT06, WOW+14, WMD06, WHD13, WHDN13, WHD15, WTY19, WZL+21, WLM21, WS04, WG08b, WZC96, WSHB98, WlLK+12, XGD24, XK05, XXCE00, XJB07, XLZ13, XLLS20, YTMY17, YLCC17, YJ04, YFBK07, YYA11, YLW+15, YTS12, YK05, YAR21, YJEP08, ZRZD11, ZPM97, ZWY+17, ZFAS08, ZPD+10, ZGBK10, ZZNM15, ZWZ16, Zho17, ZZL+23b, Zhu07, YKPM20, ZZC+24].
Protein-Binding [OMS13]. **Protein-Coding** [BWGM17, LWZ21, SK19].
Protein-Encoding [DC16a]. **Protein-Level** [XGD24]. **Protein-Ligand**

[LLJS19, PK11, PPV+14]. **Protein-Protein** [Ami12, BT08, DAL+08, HSH+09, HSBS10, LACB10, RDR12, SMD+07]. **Protein-specific** [LW12]. **Proteins** [AWZ+17, AB00, BK10, BGTSB98, BIPD17, CHKK99, CGZ04, DCP+21, DMHM97, DCS04, DC16a, ES06, EBK11, EPSV98, FW12, GH16, GZW+16, Guo15, HZNF06a, HZNF06b, HLL13, JGL11, JMEB18, JWL24, JRH+10, KEL15, Kha14, KDL+94, KKK18, LJK16, LNW01, LSHL04, MBK+03, OC00, PGAE04, PCGBK13, PDSD06, SKP+12, SF12, STV96, TGT08, Tho21, TS96, WAPM05, WF12, YDZ+25, YE02, YFBK07, YM06, ZFBK09, ZY23]. **Proteome** [CAB11, GE17, Vij22]. **Proteomic** [KVM14, LFD03, MDTD06]. **Proteomics** [CAB11, LAL+09, WZH+18]. **Protocol** [CGZD24]. **Protocols** [FDB18]. **Proudly** [Prz24]. **PROuST** [CGZ04]. **Provable** [HD16, JJGD16, JHLD20, OJFD18]. **Provably** [Buh03, JHLD20, TAA16]. **Provides** [PV17]. **Proximal** [SKP+12]. **Proximity** [LPW05]. **Proxy** [AS23]. **Prune** [KLM11, YzCW20]. **Pruning** [LCG+22, MBRS11a]. **PseRat** [AWZ+17]. **Pseudo** [AFRV07, BZG+22, CHJ05, LGD+10, WMC04]. **Pseudo-Boolean** [AFRV07]. **Pseudo-Labels** [BZG+22]. **Pseudo-Likelihood** [CHJ05]. **Pseudo-Symplectic** [LGD+10]. **Pseudo-Test** [WMC04]. **Pseudogenes** [MSB+10, SCH09]. **Pseudoknot** [HR08, HPR09, LP00, MR08a, NRW11, NW12, RW10, WLS+11]. **Pseudoknots** [IKL+03, MWB10, Rød06, TKO21]. **Pseudoknotted** [HDBZ08, RC07, SRSD11, WAM20]. **Pseudoprogression** [LLT+25]. **Pseudorabies** [STP18]. **PSI** [AMOW10]. **PSI-BLAST** [AMOW10]. **PSSM** [GWM+21b]. **pSuc** [AWZ+17]. **pSuc-PseRat** [AWZ+17]. **PTEN** [JR16]. **PTEN-related** [JR16]. **PTENpred** [JR16]. **Public** [YLC+20]. **Pulmonary** [TZZY20, ZXZ21]. **Pulsed** [DCD19]. **Pure** [DAR23, GLMSO10]. **Pure-Birth** [DAR23]. **Purification** [WlLK+12]. **Putative** [HHJ+02, ST10]. **Puzzling** [SWR08]. **PY-SUMMA** [AVS20]. **pyBrick** [RMC+23]. **pyBrick-DNA** [RMC+23]. **pydebiaseddta** [BÖB+23]. **PyGTED** [BSSz+20b]. **pylori** [UBGFD+19]. **PyPathway** [XL18]. **Pyrococcus** [RBKJ19]. **Pyrophosphate** [YSC15]. **Pyrosequencing** [Kon09a, RPW13]. **Python** [AVS20, BP17, BSSz+20b, RMC+23, XL18, ZZL23a]. **Python-Based** [RMC+23].

QGB [OAHA94, SG94]. **QMix** [TDV24]. **QNet** [DSG+08]. **qp** [CR09]. **qp-Graphs** [CR09]. **QR** [TRW23]. **QR-STAR** [TRW23]. **QSAR** [ALB+19, ZYB+04]. **Quadratic** [WW18]. **Quadruplex** [GWL+19]. **Quality** [APVM11, AS23, GLM+09, GWM+21a, HlAM20, vLKMR22, MFJ+19, RUGR18, SM20, ST02a, SH04b, SKT08, Tos05, VFOK18]. **Quantification** [DBL+12, HHJ+13, IPH18, STHG+08, WYT12]. **Quantified** [CRB18]. **Quantify** [LWLL19]. **Quantifying** [CLS11, CHK+02, LQ23]. **Quantile** [LVS+07, WA10]. **Quantitative** [Cal22, CFE+13, CC03, CH15, GKgUS21, GAWI19, JLSL24, LHC02, LQPE+10, Mal98, MP94, MSS21, NMH13, RLH13, SMD+07, TEMM12, WXS14, ZF05, ZYB+04]. **Quantities**

[CAB+07]. **Quantum** [BSP+25]. **Quantum-Behaved** [BSP+25]. **Quartet** [AS19, HR22, MSS+22, SWR08]. **Quartet-Based** [AS19, HR22, SWR08]. **Quartets** [BDCG+98, GMY10, LC09]. **Quasispecies** [TZP+13]. **Query** [Shi07]. **Querying** [BK10, BHK+10, DSG+08, FP11, OAHA94, QSY09, ZCK17]. **Quest** [ABL03]. **Questions** [Ma11]. **Quick** [PZC05]. **Quorum** [MMKH15].

R [AVS20, ADR24, BP17, IRCA21, JPLD23, SSH+20, WHK21]. **R/PY** [AVS20]. **R/PY-SUMMA** [AVS20]. **R/Python** [AVS20]. **R2KS** [NV12]. **Raceway** [JB10]. **Racial** [SPSZ23]. **radiata** [JJY+20]. **Radiation** [ASZ+16, BDC97, Hea97, SKSL97]. **Radiology** [HSL+24]. **Radius** [TVNP15]. **Ramanujan** [YYW14, ZWJ18]. **Ramanujan-Fourier** [YYW14]. **Random** [AZ14, AFCK09, BKCP05, BV09, BG15, BT02, CK10, DAL+08, DZS24, JD05, Jus06, KCG+19, LCWG06, LGS20, MD01, MBLZ09, Par10, PFRD05, RS01, RDR+02, RLK+09, SH06, Sch97a, SD95, WG08b, XWLJ08, XZS07, bYjHgZ+24]. **Random-Graphs** [Par10]. **Random-Walk** [MBLZ09]. **Randomized** [DC16b]. **Randomness** [CBP21, Ila20]. **Range** [BLP+22, DPHH05, HATI11, MBVA07, MDB11, PPL+23, RH19, YY18]. **Ranges** [ZMK22]. **Rank** [GJL+21, KSSK09, cWxLlS+23, ZCH+13]. **Rank-Similarity** [GJL+21]. **Ranked** [AFCN13, CZS15, NV12, SRF16]. **Ranking** [BKT09, BG08, FdSdSR+15, TPH+09]. **Ranking-Based** [TPH+09]. **RAP** [OMS13]. **Rapamycin** [ZZNM15]. **Rapid** [Bun02, SBRG20]. **Rapidly** [KASM08, YCP16]. **Rare** [AWM+17, FSD+14, JAG17, KLS15, KKK18, LS17, LS23, OK08]. **RareVar** [HXL+17]. **Ras** [OJOD+04]. **RASCAL** [DC16b]. **Rate** [CL21b, DT12, DGH+01, GF16, KC96, LM03, WZCS00, ZHQS05]. **Rates** [ALR18, CAB+07, CHJ05, CŁM+18, LTTS12, SSH94]. **Ratio** [HLK+13, SHE11]. **Ratios** [AWZ+17, BLR16, NKR+01]. **Raw** [CAC+23, RBK94]. **Ray** [NS18, KAC17, BLC10b]. **RB** [LS08a]. **RB-Finder** [LS08a]. **RDA** [ZZL+17]. **RDCs** [MYBK+11]. **rDNA** [RPS02]. **RDscan** [LHW+22]. **Re** [Ale08, GST10, ZGW22]. **Re-Evaluating** [GST10, ZGW22]. **Re-Uses** [Ale08]. **Reaction** [Aku04, CH15, FA12, KK23, Kru17, LSAS03, PSB17, RLH13, Sol09, Sun95, TMfTK23, WZCS00, WV95, YY19, ZF05]. **Reaction-Diffusion** [FA12]. **Reactions** [CŁM+18, HLMR11, KM08, Pia02, YY18]. **Read** [CC23, ETLK19, GZW+21, HWSH18, KSSK09, KMB+20, LHW+22, SFA17, SM20, SY22, SSLMW10, TGA24, WHY+13, WHL17, ZGRB10]. **Reading** [WGL98]. **Reads** [APC21, AWM+17, BBC16, BLC10b, CEJM16, CBH+12, CWL13, CAC+23, FLJ11, GHM+10, GCB20, HS23, JDK+18, KBKF17, MV19, MKB+20, NBC+11, PMP+15, PAS+13, SMZ+12, SRZ+13, TYSX19, WLYC12, YW21, ZRS+12, ZWT18]. **Reads2Vec** [CAC+23]. **Real** [CH15, GMC08, HG18, RLH13, SSY+22, YS19, ZF05]. **Real-Time** [CH15, GMC08, HG18, RLH13, ZF05]. **Real-Valued** [SSY+22]. **ReAligner** [AM97]. **Realignment** [DK18]. **Realistic** [CLS11, MSMF09]. **Realizability**

[ABF+25]. **Really** [SPBB15]. **Reanalyses** [DRT+25]. **Rearrangement** [AS10, AODD21, AFRV07, BCC+09, BMS10, BBH+07, BBDS21, FCV+07, KWBS11, Kov14, Lu15, MHS06, Par06, SB98, ST05]. **Rearrangements** [Ale08, BJF+20, CMvH15, CP19, LM11, MZC+18, OB10, SB99]. **Reasonable** [YY18]. **Reasoning** [Hua15, LBN94, MD00, YjDG+23]. **Rebalanced** [YYM+23]. **Recalibration** [HSL+24]. **Recall** [OAR+24]. **Receiver** [VY18]. **Receptor** [BHRV00, BC94, CYZ+20, QLW20, ZYD21]. **Receptor-Negative** [QLW20]. **Receptors** [FL94]. **Recipient** [Prz24]. **Reciprocal** [OFS07]. **Recognition** [Ber95, BS97, BRR06, CC06, Che04, Con04, GPAR96, GLJW09, KWM10, LCWG06, LCGW09, LLW18, MKBC05, Mil95, SNW98, SP97, WOG03, WSCL18, WLC18, XLZ13, YZPC24]. **Recognizing** [Far97, MKBC05, SZTW12]. **RECOMB** [Ano11b, Baf11, Ber11, PS11, Sun13, Ano09b, Ano10b, Ano17, CKS12, CKS13, CKS14, CKS15, Cho13, Cow20, Edi24, Gus05, Ist20, Len02, MS24, MV04, Miy06, Mye03, NV09, Pe'22a, Pe'22b, Pen22a, Pen22b, Sah18, Sch21a, Sch21b, Sha00, Tan23, Woo99]. **RECOMB-CG** [Ano11b, Edi24]. **RECOMB/ISCB** [CKS14, CKS15]. **RECOMB'97** [WIP97]. **RECOMB'99** [Ist99]. **Recombinant** [LJ05b]. **Recombination** [BB06, GF16, GM96, HR22, HW01, LTI10, LS08a, MWP00, PRKG16, SH05, SDG+07, TZP+13, WZZ01, Wu08, YCP16, YFBK07, ZSB+23, ZGBK10]. **Recombinations** [PMCB08, Par10]. **Recommendation** [FYJ18]. **Reconciled** [BBWE09]. **Reconciliation** [BAK13, EAFM24, VSGD08, ZSB+23, ZZZU20]. **Reconciliation-Scenario** [ZZZU20]. **Reconciliations** [DCH09]. **Reconciling** [BAK13]. **Reconfigurable** [FPSD22]. **Reconstruct** [Mat10]. **Reconstructability** [Par10]. **Reconstructed** [RND+23]. **Reconstructing** [ASL06, CCMS20, CCYH18, FLT+21, GSN11, MRR+08, Ma11, Mos03, NWLS05, PP23, PBB+21, QGP10, SK13, SS95, SSH94, TBKR10, VBSS10, Wag04, XSS08, ZB15, ZLU+22]. **Reconstruction** [AV18, ARS17, AZ11, AK08, AJA+16, BV09, CHSY10, CFS+08, DJK+00, DG02, DHV06, ET07, Fom16a, Fom16b, Fom19, Fre11, FPU99, HWH+13, HP97, HV09, HNW99, JBM15, JHN+23, KV23, KLKH11, KLR23, LC09, LTI10, LKW04, LL11, LZC+23, LHC09, LRM11, MGVS14, NKG+21, OSK+15, OR14, OFCLH11, PS12, PRT08, RG95, SMS13, SZW+09, SWR08, SZUP06, TBP+13, UBTC06, WZG+20b, ZGRB10, ZSV+09]. **Reconstructions** [AS10, CGOT10]. **Records** [VA17]. **Recovering** [LLW+20, MDWZ24, RM18, RS13, SZSA22, SJ12, TAJZ23]. **Recovery** [Csu02, GMC+14, WZ10, WMK17]. **Recruitment** [Yua09]. **Rectal** [LHC19]. **Recurrence** [HXL+20]. **Recurrent** [CCL+19, GYA+23, LLZ19, MRG+24, NKG+21, RL94, SDMN19, WFC25]. **Recursion** [BP14]. **Recursive** [JHLD20]. **Redesign** [FPD13, LSAD05]. **REDO** [WLA+18]. **Reduced** [HZNF06a, HZNF06b, LTsL24, RCER21, Zör15]. **Reduced-Bias** [RCER21]. **Reduced-Size** [Zör15]. **Reduces** [FPS22, SFA17]. **Reducing**

[BKKSD01, QGP10, RLVCVR17]. **Reduction** [GSCG19, LQ23, RW99, SPBB15, TPK03, XS07, ZLL+22]. **Reduction-Based** [XS07]. **Redundant** [BHL+18]. **Reference** [BCCHZU18, HlAM20, HWSH18, Jah11, JDK+18, Kha14, LPFT14, NHZ+15, PMAP13, bVRN+19, WHL17, ZHY+20, XSH+22]. **Reference-Anchored** [BCCHZU18]. **Reference-Based** [HlAM20]. **Reference-Free** [HWSH18]. **Refinement** [BBEM09, CFB+07]. **Refining** [AM97]. **Reflects** [MH22]. **Regaining** [Elh11]. **Regeneration** [CUP19]. **Regimes** [RKTS14]. **Region** [GP20, JLY08, SG94]. **Regional** [NCC+96, RDH04]. **Regions** [BK10, BCVL17, BSP+24, BET00, BGG07, BR12, CD18, DBBM09, GT16, HZNF06a, HZNF06b, HZGD05, HHJ+02, JRHN09, LPFT14, LLW+20, MRR+08, MDB11, NVW14, Sal95, SSV19, SNW04, TGT08, TML+02, WLFW03, WHK21, XMU96, YYZ+10, ZBM98]. **Registering** [YCP16]. **Registration** [YHC19]. **Regraft** [KLM11, YzCW20]. **Regression** [ADP+08, BYGI12, Ben21, BBN24, CW20, DLFS22, GLM16, HH14, JKG+04, LKBT16, LLKX16, LST+17, LLSH19, LSG04, LFJ11, LXS24, MEF24, PLL16, SDC03, WAPM05, WSHB98, ZKC12]. **Regression-Based** [LLSH19]. **Regular** [CGSW14, GSW16, GJL+22, KPZU11, SD95, SCSA+16]. **Regularities** [CIM+06]. **Regularization** [Ben21, Fre11, TaAF+22, cWxLlS+23]. **Regularized** [DMTV09, GLM16, LKL21, LXS24, LWZ18, WYLW21, ZZL+17]. **Regulating** [KDL+94]. **Regulation** [BSK05, Dei19a, FS08, GVTS04, JFLL20, KV08, LZS09, cLcSwP+21, OFE14, QMMW11, TS04, WBJ15, ZPC+18]. **Regulations** [MJS24]. **Regulatory** [AEH17, AHK08, BH14, BB15, BCPS04, BLP+22, BR12, CKS12, CKS13, CKS14, CKS15, CCG06, CR09, CUP19, CSP+12, DDA+11, DBT11, FPD13, GMF+08, GK06, GLM20, GSV+11b, GSV+11a, HMY+14, HHZ+18, HHJ+02, Ist19, IP19, JBM15, KS12, KR24, KPB+04, KK18, LL19b, MPG+16, MYS+20, MPZL23, MS00, MXW+20, MDB11, PP23, PSIM18, PIM23, PM24, Par24, PZMM15, PDdJFT08, QGP10, RZK06, Rot19, SS05a, SNQ+14, SM09, SZSA22, SK23, TBS+07, WH01, WZG+20a, WT17, WX08, WHC09, XvdL05, ZPC+18, ZS24, dJ02]. **Reincorporation** [KWBS11]. **Reinforcement** [PYG+19]. **Reinforcing** [CWJ+21]. **RelA** [LZBK15]. **Relapse** [ZQZ20]. **Relapse-Free** [ZQZ20]. **Related** [AMK00, Ano22b, AWM+17, CZY19, GCD20, GDL+15, HTY22, McP12, RXH+20, TZZY20, TMH+21, TGT08, WYT12, YH01, JR16]. **Relation** [KMJ+20, LWC+14]. **Relational** [JEMF06, PSCP09]. **Relations** [BH15, SMS13]. **Relationship** [Bro98, GAWI19, Sun18, YZ17, ZL01]. **Relationships** [BDCG+98, JFLL20, KYSE10, LN03, LC03a, MH22, OO24, TRS17]. **Relative** [CT07, DQS+11, DCV+07, Elh01, RMWC16, TVNP15, YY18]. **Relaxation** [WCC98]. **Relaxed** [WZ23]. **Relevance** [BKT09, GK18]. **Relevance-Based** [BKT09]. **Relevant** [BK08, DMTV09]. **Reliability** [GRM09, UGS19]. **Reliable** [BZG+22, CLR+05, HV07]. **Remaining**

[ZKM21]. **RemeDB** [SBRG20]. **Remodeling** [SRB+25]. **Remote** [CV11, JDH00, LN03, SRS02]. **Remotely** [TGT08]. **Removable** [Gus10]. **Removal** [zCULW20, WHL17, ZPB+10]. **Remove** [AMOW10]. **Renal** [LGD+19]. **Renewal** [TA97]. **Repeat** [DCP+08, SZUP06]. **Repeat-Annotated** [SZUP06]. **Repeated** [CvS24, LBEMG07]. **Repeats** [AMRW96, DP07, JMEB18, LSS01, MTH11, WYKG05, AM20]. **Reperfusion** [CYZ+20]. **Repertoire** [Jos96, WZG+20a]. **Repetition** [CPFP24]. **Repetition-Aware** [CPFP24]. **Repetitions** [CIM+06, SM98]. **Repetitive** [HHJ+02, LPFT14, MNSV10]. **Repetitiveness** [Zho17]. **Replacement** [KC96, LYL+04, MV00]. **Replicates** [PABE+10]. **Replication** [Pia02]. **Replications** [YHB+03]. **Replicative** [YYL19]. **Report** [HSL+24]. **Reported** [MRS+18]. **Reporting** [CGI+07]. **Repositioning** [MJCM22, YWZ+19]. **Representation** [APF+20, ABG+03, CBW07, CWYB16, CLJ+15, DSC+22, JLY08, cLcSwP+21, LZY+23, MMG14, Nou21, RM21, Rød06, SS23, Ste14, VA17, cWxLlS+23, WxLW+23, WFC25, Xu10, YZ17, Yin19, ZL09]. **Representations** [BJGG+03, BWGM17, CJS06, HBW+05, KMJ+20, MBS+01]. **Representative** [YSC15]. **Represented** [LACB10, Sch97b]. **Representing** [MD00]. **Reproducibility** [SMKS96]. **Reproducibly** [ODNW21]. **Reproduction** [BBN24, TL23, WXY+24]. **Repurpose** [GSV21]. **Repurposing** [AL25]. **Requirements** [MTR+03, OFE14]. **Resampling** [ACL15]. **Resampling-Based** [ACL15]. **Research** [Ano11b, Ano21b, Ber11, CSZ18, CSZ19, CSZ20, CSPZ21a, CSPZ21b, CSZ22, CSZ23b, CSZ23a, FCGD19, FDD21, KWB+94, MXJ19, MAN16, Pat24, Pat25, PS11, WSCL18, Baf11, Sun13]. **Resequencing** [CBH+12]. **Residual** [NZM+25]. **Residue** [HCX09, HBW+05, LBBV+18, LZ10, SJ18, Sun18, TS96, YFBK07, ZWY+17]. **Residue-Based** [HBW+05]. **Residues** [STV96, SSB07, VILR10]. **Resistance** [ASZ+16, BYL+20, GKD22, PCS18, PYIM22, Par24]. **RESISTOR** [GKD22]. **Resolution** [GDHC95, HSH11, LBBV+18, LRM11, NS18, TZB+23]. **Resolve** [AWM+17]. **Resolved** [JLRS18, MFJ+19]. **Resolving** [CEJM16, GMY10]. **Resonance** [JGL11, KKS+15, LYL+04, LLWZ19, LLW+20, WMD06]. **Resource** [NW05]. **Respect** [BET00, Clo05, HD16, WC07]. **Respiratory** [DDK21, Tho21]. **Response** [BZMM16, CWRF15, JKG+04, LRNBJ10, LDB+07, SGK+12, SLT24, VND17]. **Responses** [CK09, Sef25]. **Responsible** [MGW+07]. **Restart** [DZS24]. **Restoration** [CL99, HMY+14]. **Restricted** [KWBS11]. **Restriction** [AMS97, BDKSS03, CDH+06, GDHC95, LDW98, Par98, SRV98, SRM+98, Wan94]. **Restructuring** [Fas94]. **Results** [CF97, DBT11, RAC+06, SLRM09, WZCY21, WLA+18, YS19, Zho17]. **Reticulate** [CW13, LHC09, NWLS05]. **Reticulated** [ML04]. **Reticulations** [WZ24]. **Retinal** [MWL22, XLLS20]. **Retraction** [Ano20, Ano21b, Ano22b].

Retrieval [KDL+94, MNSV10]. **Retrotransposition** [RRKT07]. **Retrotransposons** [FDB18]. **Retrovirus** [CDC+11]. **Reuse** [ST05]. **Reveal** [LL19b, MBK+03, YI17]. **Revealing** [NSK09]. **Reveals** [BR12, CSH+20, FMH06, GC15, JFLL20, KMUK22, NXGL20, QMMW11, SDK16, SLT24, TLP+14, WMK17, YcXyW+21, ZYH20]. **Reversal** [AOJ+23, AT08, BSS11, MWD02]. **Reversals** [AODD21, AT08, BO07, HL10, OBDD19a, OBDD19b, OFS07, Sie03, Tra98]. **Reverse** [CR09, HPY03, Jus06, MSMF09, Ore20, SLZH15]. **Reverse-Phase** [SLZH15]. **Reversible** [LDW98, NTMM06]. **Reversible-Jump** [LDW98]. **Review** [LWLL19, MK11, dJ02]. **Reviewers** [Ano22a, Ano23, Ano24, Ano25]. **Revision** [GLM20]. **Revisited** [AMDY11, BTZ06, BAK13, KPZU11, WS11]. **Rewards** [ZTD+22]. **Rheumatoid** [YBF19]. **Rhizobium** [PdBdP+22]. **RHOJ** [ZCY+20]. **Rhythm** [YHW18]. **Rhythmic** [LYMD03]. **Ribosomal** [DPSW20, WHL17]. **Ribosome** [WMK17]. **Riboswitch** [YSC15]. **Ribozymes** [MRM+02]. **RIBRA** [WCC+06]. **Rich** [ZGEZu11]. **Rictor** [ZZNM15]. **Ridge** [BYGI12]. **Rigid** [CA12, HJD17, KC18]. **Rigidity** [SJ18, TTTA07]. **Rigorous** [KBLS24]. **Ring** [CWJ+21]. **Rings** [DS19]. **Risk** [Ano22b, AG23, BZ08, GSH17, KLS15, MPZ+20, NCMS+21, PBB+21, TMH+21, WCL+18b, WNMB99]. **Risks** [SVP19]. **RMS** [YK05]. **RMSD** [Shi07]. **RN** [ACKK19]. **RNA** [FDD21, ABF+04, AKN+06, AS23, AHPR12, AJV+16, BCH+07, BTZ06, Bar04, BHGCS11, BLR16, BBV+14, BHKN25, BFK+11, BRS20, BCA15, CA15, CCPT17, Clo05, Clo06, DDA+11, DS19, DC16a, DDK21, DLD+14, FHS00, FFB20, FvdBB16, FR14, FH18, GVA22, GWA+21, GSCG19, GQEk24, Ham12, HR08, HDBZ08, HR12a, HR12b, Han09, HTZ+13, HPR09, HHJ+13, HPVS96, IKL+03, JCZ08, JHS06, JLMZ02, JTL+10, JLSL24, JRH+09, KKC+22, LSBS18, vLKMR22, LRV98, LFJ11, LKL21, LPC08, LP00, MR08a, MLOT17, MH22, MWB10, MSM20, MLS+23, MZS+00, MM19, MM21, MN15, NS23, Neb02, NRW11, NW12, OB16, PZH11, PV17, QFLL22, jQLsY+24, QR13, RPR+15, RW10, Rød06, SGdMT12, SGT15, SRSD11, Sel13, SC15, SH17, SPBB15, SLYC09, SPC19, TBL18, TKT+05, TKO21, VLZUBK07, WC07, WP11, WHL17, WAM20, WZG+20a, cWxLlS+23]. **RNA** [WZZU07, WLS+11, WY12, WLA+18, YYJ19, YB04, ZGEZu11, ZHY+20, ZZ14b, ZLL+22, ZL22, ZUGVWS10, vLSV+24]. **RNA-** [JRH+09]. **RNA-Degradation** [vLKMR22]. **RNA-Dependent** [DDK21]. **RNA-Derived** [WZG+20a]. **RNA-RNA** [AHPR12, FH18]. **RNA-Seq** [FDD21, AS23, BBV+14, DC16a, HHJ+13, LFJ11, MLS+23, MM19, MM21, QFLL22, SH17, SPBB15, ZL22, AJV+16, CCPT17, GVA22, GWA+21, LSBS18, MSM20, PZH11, TBL18]. **RNA-Sequencing** [cWxLlS+23]. **RNAs** [FH18, JFLL20, QbMyD+19, RPW13, SB07]. **RNN** [PVFB06]. **Roadmap** [ABG+03, CAB+07]. **Robinson** [KVZ24, LRV21, PGM07, ZZ14a]. **Robotics** [AMK18]. **Robotics-Inspired** [AMK18]. **Robots** [dGFMS16]. **Robust** [BÖB+23, BDN19, BGJ+04, BYL+20, GSCG19, HI97b, HHJ+13, KK24,

MJR+24, Met06, PYIM19, Sol09, SDC+10]. **Robustness** [BS20, DLL+12, DCSE11, GT16, GSV+11a, KWB+13, LRM11, SDFR16, SHB+03, ŠV07]. **Role** [AEB+04, BET00, CYZ+20, GPOP+17, Kha14, LLZ19, SCB14, SDG+07, YYJ19, ZCY+20]. **Roles** [CXW16]. **Room** [Tan11]. **Root** [CJ22, KFC+11, TSTS12]. **Rooted** [Bay23, HMU06, JR17, JRS19, KLM11, Prz98, SLA12, YzCW20, YWN11]. **Rooted-Unordered** [HMU06]. **Rooting** [TRW23]. **Rosalind** [Prz24]. **Rotamer** [HJD17, ZRZD11]. **Rotamer-Like** [HJD17]. **Rotenone** [YLC+20]. **Rotenone-Induced** [YLC+20]. **Rough** [Hua15]. **Rough-Set** [Hua15]. **Rounding** [LJL+20]. **Rounds** [FH02]. **Route** [Elh11, YYL19]. **Routes** [BK08]. **rRNA** [CDH+16, MP16, RKTS14]. **rRNAFilter** [WHL17]. **rSPR** [YzCW20]. **Rule** [CLT+20, MS03, Vij22]. **Rule-Based** [MS03]. **Rules** [ABD+97, Aku04, BK08, CvS24, GST10, KVM14, WCL18a]. **Run** [FHKR11, YZ08]. **Runs** [Che04].

S. [WHW+06]. **Saccharomyces** [SSW20]. **Saddle** [RC06]. **Safe** [TM17]. **Safety** [KKC+22]. **SAGE** [CLSW02]. **SAL** [SAL09]. **Salmonella** [MTYH09, SVA+19]. **Sample** [BFT04, BYL+20, HATI11, HTZ+13, MSNl23, MGW+07, MZC+18, PYIM19, RH19, SDC+10, VRU16, WC04, ZGRB10]. **Sample-Based** [MZC+18]. **Sample-Specific** [PYIM19]. **Sampled** [AMK18]. **Sampler** [BHHR19, Kei06, Neu14a]. **Samples** [AaHP+21, DMW+17, FPRV18, GM96, Gus01, JG11, KYSE10, KDB+02, MSR22, ODNW21, ZEKKR18, ZKT14]. **Sampling** [AL07, BHHR18, CZC10, CP05, GNI12, GC15, Lar06, MBRS11b, NK11, NDMK17, PWFZ17, Ste14, TML+02, WC07, WP11, ZGW22]. **San** [EBS+22]. **sapiens** [YLD+18]. **SAR** [BKKSD01]. **Sarbecoviruses** [ZSB+23]. **SARS** [Ano21b, ABTP23, BBH+21, MMK+21, NKG+21, SS23, TM22, YGP05, ZSB+23]. **SARS-CoV-2** [Ano21b, ABTP23, BBH+21, MMK+21, NKG+21, SS23, TM22, ZSB+23]. **Satellite** [AEB+04, Edi24, PS11, Ano11b]. **Satellites** [SM98]. **Satisfiability** [MA13, YjDG+23]. **Satisfying** [Mat10]. **sativa** [ZDZ+20]. **SATrans** [KBČ19]. **Saturated** [Clo06, GJL+22, WC07]. **Saudi** [MRS+18]. **SAXS** [DKC15]. **SC1** [MM21]. **Scaffold** [BDKSS03, CDH+06, MCH+19, QBA+25]. **Scaffolding** [BHPS99, PJL20, RCSS12, kSyPhC+22]. **Scaffolds** [GSN11]. **Scalable** [APF+20, DBHC24, GLM+09, KMP+04, LW22, LCG18, NKG+21, OSK+15, RC15]. **Scale** [ABL03, Ben21, BBWE09, DLL+24, DCH21, GMC+14, HSH+09, HQ06, KW06, LAF+14, LLS+19, Ma11, MZM18, NSH+23, OKKS21, PdB13, PDZ+16, RGM+12, RLK+09, SSH+10, ST02b, SGK+12, TE96, TMC+18, XYX+22, XU97, ZH07]. **Scale-Free** [KW06, LLS+19, OKKS21]. **Scaled** [LLWZ19, ZHY+20]. **Scales** [FA12]. **Scaling** [DHL00, DWK+20, GLMW13, HLL13]. **ScalpelSig** [FFSL22]. **Scan** [TTTL17]. **Scanning** [NFJ13]. **Scattering** [KAC17]. **scDesign2** [SSLL22]. **Scenario** [ZZZU20]. **Scenarios** [BCC+09, OB10]. **Schatten** [WYLW21]. **Scheduling** [CLR+05]. **Schema** [HMY+14]. **Scheme**

[BDKSY00, HMK24, MDWZ24, MBRS11b, RYZ23, TPH+09, VFOK18]. **Schemes** [HZK22, RDRF24, SGYBD05, WLFW03, ZKM21]. **Schizophrenia** [PD20a]. **Schmidtea** [FCR+13]. **Science** [HTH+17, Ist19, TaAF+22]. **Sciences** [BMM+23, JMR+21, MMN+21]. **scINSIGHT** [QFLL22]. **Sclerosis** [TZZY20]. **Score** [BG97, BMWG04, GW94, HlAM20, IJCL12, Kei05, MD01, MBVA07, RDH04, VFOK18, Jus01]. **Scores** [BG98, BG02, KW14, KC96, LBXL11, LABD+06, MPZ+20, MLS+12, PBB+21, RJS02]. **Scoring** [AA18, BRS99, GTT06, GWM+21a, JM95, JDSB04, LSAD05, LW12, RAC+06, TGT08, WLFW03, WNMB99, ZBM98]. **SCOT** [DSS+22b, DSS+22a]. **SCOTv2** [DSC+22]. **Screening** [ALB+19, Ano21b, CD07, CC09, DDK21, GAWI19, GCD20, JMPR23, LXS24, LL23, SSY+22, TMH+21, Vij22, WDZ20, XXZ+21, ZLSY20, ZDG+20, ZYD+19, ZHQS05, Ano22b]. **Screens** [FCR+13, GNI12, SSH+10]. **SCRFs** [LCWG06]. **scRNA** [MPZL23]. **scRNA-seq** [MPZL23]. **SDGCCA** [MHL22]. **SE** [NZM+25]. **Seamless** [KAD+19]. **Search** [AKN+06, APF+20, AMOW10, Azi22, Bar04, BZW+00, BBD+04, BWGM17, Buh03, CBW07, CCG06, Cha01, CZW+19, CYY09, DMDR17, DC16a, DCD19, FFM24, FDB18, Gru98, HD16, HS15, HSL07, IP09, JHA16, Kon07, KPW11, LTCH11, LSAD05, MPVZ05, MD03, NBB18, PZC05, RDRF24, RGL94, SCSA+16, SK18, SM04, SB05, TSTS12, VLZUBK07, XBLM06, YLCC17, ZWZ16]. **Search-Based** [Azi22]. **Searching** [BZ08, FNC08, NR03, PSCP09, RL94, Shi10a, Shi10b]. **Second** [Rot19, DMV17]. **Second-Generation** [Rot19]. **Secondary** [BKWK+00, Bar04, BLR16, BRZH15, BRS20, BIPD17, Clo05, Clo06, ES06, FK06, GWM+21b, HR12a, HR12b, IKL+03, JCZ08, JTL+10, KKW10, KX06a, KX06b, LBN94, MVP06, MZS+00, MN15, NS23, Neb02, RC07, RK96, Rød06, SGdMT12, SLB00, SPC19, SKT08, TKO21, VT06, WC07, WAM20, XK05, vLSV+24]. **Secretion** [FL94]. **Section** [AHIV23]. **Sectional** [BRD+05, RV15]. **Secure** [PXLP23, ZWT18]. **Seed** [PNPC20, YZ08]. **Seed-Like** [YZ08]. **Seeds** [BCA15, Kon07, NM14, PZC05, SB05, XBLM06, YZ08, ZF07]. **Segment** [SFN97, Wu96]. **Segment-Based** [Wu96]. **Segmentation** [AG23, BV20, BLQZ04, LCWG06, NZM+25, Pic08, RMRT00, SLB00, TKSA24, YHC19]. **Segmentations** [DCSE11, ZW19]. **Segmenting** [Kei06]. **Segments** [IP09, SBC+05, WWZ+16]. **Segregating** [CGI+07]. **Select** [KSSK09, Li08]. **Selected** [Ano17, CJ21, DMV17, DNZ17, DND+19, HHC17, HTH+17, Sah18]. **Selecting** [DMTV09, GTA+04, MG06, RS12, Ros05, Wil99]. **Selection** [BZB+22, BMR+19, CTC21a, CYY09, CYLY12, CS03, COL+18, EOD+18, FdSdSR+15, GGM12, GT16, GLM16, HSF+00, KLS15, Kon07, KPP+22, LKBT16, LS17, LK24, LSG04, LCW16, LS23, LWLJ10, LGS20, MRM20, MRM+02, PNIM17, PYIM19, PZC05, QsYSxL23, RS12, RND+23, RLK+09, SMC+15, SZTW12, VND17, XJL+22, YT22, ZKM21, Zör15]. **Selective** [DT13, MWL22, SB21, ZGBK10]. **Self**

[Jos96, MJR+24, MSS10, PLZX25, RRFS98, SAM06, YE02].
Self-Assemblies [MSS10]. **Self-Assembly** [SAM06]. **Self-Consistent** [RRFS98]. **Self-Organizing** [Jos96, YE02]. **Self-Supervised** [PLZX25]. **Self-Training** [MJR+24]. **Semantic** [DAE+19]. **Semantics** [JSN09]. **SEME** [CWL13]. **Semi** [BZG+22, FNC08, GML20, PO04, ZLTS13, ZMppVN22]. **Semi-Definite** [ZLTS13]. **Semi-Degenerate** [PO04]. **Semi-Markov** [GML20]. **Semi-Ordered** [FNC08]. **Semi-Supervised** [BZG+22, ZMppVN22]. **Semidefinite** [AKG+13]. **Semigroups** [AMR20, NFHM21]. **Semimetric** [SK21]. **Semisupervised** [TMG+20]. **Sense** [SKM05]. **Sensing** [AZ11, MMKH15, RPR+15]. **Sensitive** [Buh03, CJ23, HTY22, HB11, ISB12, KBG18, MM19, Par24, YK05, ZF07]. **Sensitivity** [CDC+11, FDDK07, HFUH19, MD03, NSH+23, SJ18]. **Sentence** [DAE+19]. **Sentinel** [LCG+23]. **Separating** [DS12]. **Separation** [CRT04, GMY10, IFT14]. **Septic** [CKZL20]. **Seq** [FDD21, HHE13, AS23, BBV+14, DC16a, HHJ+13, LFJ11, MLS+23, MM19, MM21, QFLL22, SH17, SPBB15, WH20, XZ12, XSH+22, ZW23, ZL22, ZCK17, AJV+16, BR12, CCPT17, GVA22, GWA+21, LSBS18, MPZL23, MSM20, PZH11, TBL18]. **Sequence** [AI12, AWZ+17, AS23, ARSW22, AL07, AM97, AG98, ABH03, AMRW96, AMOW10, AHK+02, BLR16, BDN19, BWS13, Ben97, BS98, BET00, BL02, BHKM22, BFL05, BT08, BMWG04, BCA15, Bun02, CBW07, CHP94, CZW+19, CBM+02, Dew01, DPR97, DMW+17, DHL00, EMD95, FLJ11, FT07, FPU99, Gel95, GTA22, GNME01, GKB00, GYD+15, GWM+21a, GKS95, HD16, HRSC00, HSOE+18, HMY+19, HLH04, HP96, HB11, HBD94, HZK22, HHP+09, HHJ+02, HY16b, HMF07, Hua08, IW95, JZGA20, JLY08, JRH+10, Jus01, KGLBK15, KTSS19, KD13, KS99, Kle99, KS06, KGÖ18, KABH15, KSK+11, KW21, KPZU11, LRV98, LR00, LN03, LBJM11, LZF+05, LC03a, LWZ21, LH03, LS08b, MC10, MSBR08, MNSV10, Mal98, Mam96, MSZW11, MRM+02, MD01, MBVA07, MBR+94, MP94, Mil95, MBLZ09, MNG+15, MBS+01, NP09, NSRR23, New08, NL09].
Sequence [NBB18, OJFD18, OAHA94, PFK17, PRT08, RCSW09, RK96, RLCVVR18, ST05, SMZ+12, SF12, SPW22, SI97, SSTM19, ST10, SK18, SRZ+13, SG94, SSH94, SY09, SS01, SLL+17, SHCM18, SDP+20, SLY06, Tay94, TBB00, WGL98, WSW15, WRSW10, WJ94, WRS+99, WTY19, War95, WJJ11, WLF13, WFH18, WHW+06, WSS03, WMPS11, WNMB99, XvdL05, YYM+23, YI17, YLD+18, YYA11, YB04, YS99, YH01, ZPM97, ZCH+13, Zho10].
Sequence-Based [KGÖ18, WMPS11, YLD+18]. **Sequence-Specific** [HZK22]. **Sequence-to-Graph** [JZGA20]. **Sequence/Structure** [BCA15].
Sequences [AS96, AOAAH17, ABTP23, ADRS24, BSS11, BF98, BTZ06, BSP+24, BV10, BGTSB98, BB04, BZW+00, BWGM17, BLF14, CZNF19, CZC10, CC03, CDH+16, Che04, CIM+06, CGI+07, CC12, CV11, CST20, DK18, DPHH05, DGH+01, DS12, DAL+08, DLPH06, DCP+08, Elh01, ET07, ENS02, FDB18, GSN11, GML20, GPAR96, GKMS23, GM96, HV07, HJ05, Hor01, HKZ+04,

JG11, KKW10, KSSK09, KDL+94, LRD19, LR05, LG22, LY99, LS08b, MC08, MTH11, MHS06, MM06, MNG+15, MGSA06, NB94, NBG+02, OK08, ODPB18, PRC+24, PB18, RYY22, RS01, RDR+02, RM00, RLVCVR17, SGT15, SM98, STRT96, SPD95, Sch97b, SYYH02, SDG+07, SZTW12, Ste14, SSZC95, SK19, TE96, TBB00, TBKR10, VS98, WOW+14, WLFW03, WMC14, WFH18, WYKG05, WH06, WY11, XU97, YI17, YZ17, YY05, YYW14, Yin19]. **Sequences** [YZPC24, Yua09, ZSWM00, Zha02, ZW03, ZS11]. **Sequencing** [AB16, AR17, AMRW96, BNA+12, BDPSS01, BFK+99, Böc04, Boe18, BLC10b, BVP+16, CS00, CCMS20, CKT+01, CWL13, CAC+23, CL99, CBG+14, DAC+99, DB09, DDC+20, DFS94, DFS96, EHC+13, FSD+14, Fom16a, Fom16b, Fom19, FH02, FLT+21, GCB15, GSCG19, GCB20, GZW+21, HHHS03, HTZ+13, HHE13, HPY03, Hub01, JAG17, JLSL24, KS11, KCG+19, KBKF17, KMM17, KAD+19, Kon09b, KWBN19, Kru98, LLG+20, LYPC13, LKL21, LC03b, LZX12, MLOT17, MMA+21, MH22, MV19, MRY+23, MLY+11, NP09, OBDV16, PMP+15, Pev95, PV17, PU00, PO04, jQLsY+24, RUGR18, RRGC95, SK17, ST02b, SWS+20, SK18, SRZ+13, TYSX19, WCL+18b, Wen06, XMU96, ZGRB10, ZPB+10, ZZ14b, ZLL+22, CD18, NBC+11, cWxLlS+23]. **Sequencing-based** [ZZ14b]. **Sequencing-by-Hybridization** [PU00]. **Sequential** [BKCP05, GW06, YJC18]. **Sequentially** [YFBK07]. **Sequentially-Constrained** [YFBK07]. **Series** [BJGG+03, DLML10, FSZ02, KT01, LDLZ12, LLL+20, SLL+23, SDC+10, ZLU+22]. **Serous** [WDZ20]. **Serum** [LFD03]. **Server** [DCW+17, JJH+21, KGÖ18, PBMC17, ZFAS08, BIPD17]. **Service** [SSIP+19]. **Service-Oriented** [SSIP+19]. **Set** [BR24, FPS22, Fom16a, Fom16b, Fom19, GSSI14, Hua15, IRCA21, KLW96, LS23, LLW18, LWZ21, MT06, OH03, SSPNW06, SBK22, WZ24]. **Set-Adaptive** [FPS22]. **Set-Based** [BR24]. **Set-Min** [SBK22]. **Set-Valued** [LLW18]. **Sets** [AS19, BHL+18, BKT09, BS06, Bry96, CHSY10, DAL+08, Jus06, KDB+02, KWA11, KKA+15, MC10, MDK24, Mat10, RM21, RC24, RLVCVR17, SM09, SBRG20, TH17a, TH17b, UGS19, Wil99, ZHZ+16, ZKM21, ZAG+18, ZCK17]. **Settling** [Eli06]. **Several** [RS01, TA97]. **Severe** [DDK21, Tho21]. **Sex** [GGM12, POP23]. **Sex-Specific** [POP23]. **Sexual** [EBS+22]. **sFFT** [Kei05]. **SGA** [LTCH11]. **SGFNNs** [CJP+22]. **Shadows** [SG15]. **Shape** [AMW07, CRT+17, NTWF11, SBNS21, YHC19]. **Shape-Based** [NTWF11]. **Shapes** [FR14, LPC08, RW10]. **Shapley** [LQ23]. **Shared** [DBL+12, KBG18, MH22]. **Sharing** [JZL+20, ZTD+22]. **Sharp** [LC09]. **Shearlet** [TKSA24]. **Sheet** [KAS09, SOD+11]. **Shewanella** [McC09]. **Shift** [CL21b, GZW+16, ZRGHJ08]. **Shift-Invariant** [ZRGHJ08]. **Shiny** [PBMC17]. **Short** [AS95, BBC16, DPHH05, FLJ11, GHM+10, GCB20, HV03, KSSK09, LMS96, MRG+24, Mil95, NBC+11, SSLMW10, SWR08, SZTW12, WI05, YY19, YB04, ZHS05, ZWT18, ZKM21]. **Short-Range** [DPHH05]. **Short-Read** [KSSK09, SSLMW10]. **Short-Term** [MRG+24].

Shortening [YYL19]. **Shortest** [BSS13, GKS95, KK23]. **Shortest-Paths** [GKS95]. **Shot** [LKC21]. **Shotgun** [KS99, LAL+09, RHY+04, Wen06]. **ShRangeSim** [Boe18]. **ShRec3D** [LZC+23]. **Shrinkage** [HLG18, LGS20, NHOV10]. **Shuffling** [Sun99]. **Side** [AKLM02, AS11, Bet10, FYJ18, HSG22, HI97a, NXL+15, RROF95, YSFW08, ZRZD11]. **Side-Chain** [YSFW08, ZRZD11]. **Signal** [ADD+07, BS09, BMR09, BLQZ04, CXW16, EAM+17, Hav06, HLK+13, HHC06, JKG+04, MLS+23]. **Signal-to-Noise** [HLK+13]. **Signaling** [AF20, HNTW09, HAP12, LXL+20, MXW+20, NSMV18, OJOD+04, RNI+06, SIC+09, SVK10, SIKS06, SK13, TINK98, TBP+13, TLP+14, VRS12]. **Signals** [CKB+06, CC12, YB04]. **Signature** [JZZ+19, MP16, NES22, TRS17, WSCL18, WLC18, ZZ20]. **Signatures** [BF09, FFSL22, KWBN19, KPP+22, MRY+23, NCMS+21, RXH+20, SGCD19, ZYH20]. **Signed** [BMY01, CJP+22, GB08, Sie03, SRLM10]. **Signet** [CWJ+21]. **Significance** [Bun02, CB06, FH18, GE04, HKZ+04, JDSB04, JD05, KMMF20, KGK14, KBCBS11, KSG07, KT01, LM03, MLS+12, New08, Par07c, PM14, SGSN12, WGW+01, YS99, YH01]. **Significant** [DS12, JMEB18, KNmS+22, KWA11, KE13, MG06]. **Significantly** [LLZ19, LY99, VUR11]. **Silencing** [MSN+20]. **Silico** [AF20, HWP20, MJCM22, MRS+18, PdB13, SVA+19, SJ18, GPRR12, Kha14, MSMF09, RKTS14]. **SIMD** [BCA96]. **Similar** [BSP+24, BGG07]. **Similarities** [DSN14, Ker03, ZYD21]. **Similarity** [ADPH15, ACL15, BS06, BCA15, Buh03, CZY19, DKA+17, DHL00, DAE+19, Erd05, EBK11, FADH17, GJL+21, HV09, KGK14, LWLL19, LN03, LDW+14, LS04, MSBR08, MD03, OYY+12, PGA+11, SSH+10, SRF16, SG94, SB05, TH17a, TH17b, WGC+21, WGS+23, YGP05, YZ17]. **Similarity-Based** [CZY19]. **Simple** [BHKM22, CJD06, CvS24, FS08, Fom16a, Fom16b, Fom19, GB08, GJL+22, GMSZ12, LSRR18, NR03, Ric06, Ris16, RCSS12, SDCF24, TS96, WLFW03, WW18, ZZL00]. **Simpler** [ACL+21]. **Simplification** [XZW15a]. **Simplified** [RBK94, SHG00, fW23, War95]. **Simplifying** [Mye95]. **Simulating** [MN08, SHG00, SSLL22, TTTA07, YY18]. **Simulation** [Ano21b, ABG+03, Ben98, Boe18, Bri19, CY09, CEKP+13, CXW16, CAB+07, JGB12, KM08, LSHL04, PCS18, PJB+15, PYG+19, PZMM15, RS12, RMK+18, SVA+19, SMKS96, SAL09, SHG00, SHG02, TLP+14, YLZ+24, YMZ+12, dJ02]. **Simulation-Aware** [YLZ+24]. **Simulations** [HCX09, ISK99, KFC+11, MK06, RAKL10, TMC+18, YS19]. **Simulator** [SLS23, WLF+23]. **Simultaneous** [BG97, BLC10b, CDH+16, COL+18, HMY+19, QP09, RV15, SB05, TBP+13, WOW+14, ZZ14b, ZUGVWS10]. **Simultaneously** [ZCH+13]. **Single** [ACBM18, AH20, AWM+17, BNA+12, BMS10, Boe18, BMR+19, CTC21b, CWRF15, CL21a, CMS+25, CvS24, DSS+22b, DSS+22a, DSC+22, DMW+17, EZFP+19, FSD+14, FLT+21, GVA22, GWA+21, GSCG19, GMVC20, HXL+17, JLSL24, LSBS18, LWN+18, LLG+20, LDBj22, LQ23, LFT+98, MMA+21, MMKH15, MH22, MSM20, MLS+23, MM19, MM21, NFJ13,

NBA+13, PM24, QFLL22, jQLsY+24, RS12, RSR+09, RBH+19, SCB14, SCD+22, SH17, SZSA22, SDG+07, SSLL22, TMG+20, WCL+18b, cWxLlS+23, WLF13, WVT23, XSH+22, YWN11, ZMppVN22, ZLL+22, ZL22]. **Single-Cell** [BNA+12, CMS+25, CvS24, DSS+22b, DSS+22a, DSC+22, FLT+21, GVA22, GWA+21, JLSL24, LSBS18, LLG+20, LDBj22, LQ23, MMA+21, MH22, MSM20, MLS+23, MM21, NBA+13, QFLL22, jQLsY+24, RBH+19, SCD+22, SH17, SZSA22, SSLL22, TMG+20, cWxLlS+23, WVT23, XSH+22, ZMppVN22, ZLL+22, ZL22]. **Single-Crossover** [SDG+07]. **Single-Cut** [BMS10]. **Single-Molecule** [AWM+17]. **Single-Nucleotide** [ACBM18, EZFP+19, FSD+14, HXL+17, LWN+18, SCB14, WCL+18b, WLF13]. **Single-Point** [CWRF15, NFJ13]. **Single-Stranded** [GMVC20]. **Single-Trait** [BMR+19]. **Singleton** [AMTY11, MA13]. **Singular** [CFS+08, MEF24]. **Sinusoidal** [CL21b]. **siRNA** [HH14, MSN+20]. **siRNA-Based** [MSN+20]. **Sister** [LYF+19]. **Site** [BG08, CLM+16, HV07, LTS20, MS00, Nai18, REKH97, XLZ+24, YFBK07, YJC18, ZGBK10, PWKAF16]. **Site-Directed** [CLM+16, YFBK07, ZGBK10]. **Sites** [CZNF19, CGI+07, CGD09, GJZ06, JWL24, LDW98, LG22, LCY+05, LJ05a, Mar94, MFJ+19, MRM+02, Pen20b, PZMM15, PKK97, SMKS96, SSH94, VS98, WOG03, XJL+22, Yan09, YLD+18]. **Situ** [FLT+21]. **Six** [Kea97, ZLL+20]. **Six-Point** [Kea97]. **Size** [COV+15, FFM24, HATI11, HTZ+13, MTR+03, SLT24, WC04, Zör15]. **Sizes** [BJF+20, ZW07]. **Sizing** [LVS+07]. **Skeletal** [LL19a, LL19b]. **Sketch** [SBK22]. **Sketches** [ZMK23]. **Sketching** [HMK24, MDK24]. **Skewed** [FLS94]. **Skipping** [ZS11]. **Sleep** [RXH+20]. **Sliding** [LS08a]. **SlimGene** [KSK+11]. **SLIQ** [RCSS12]. **Slow** [MZC+18, WMK17]. **Slowly** [KASM08]. **SMAD4** [NLC17]. **Small** [ARC13, BFT04, DCL18, FFB20, KNmS+22, KDB+02, KAC17, LJK16, MDK24, SHZ+24, SPC19, WG98, ZKM21, SZY+20]. **Small-World** [SPC19]. **Smallest** [LTSA15]. **Smith** [GFE+16, PB18, Zha97]. **Smith-Waterman** [GFE+16]. **Smooth** [CEK+17]. **Smoothing** [DSN14, NHOV10]. **snoRNA** [SSW20]. **snoRNA-mRNA** [SSW20]. **SNP** [CTC21a, CFS+08, HG11, LKW04, OH03, PMCB08, SGYBD05, SDG+07, SFC11, TTTL17, War95, YLC+17]. **SNP-Environment** [YLC+17]. **SNP-Hardness** [War95]. **SNPs** [Li08, LLT06, WWZ+16, WTE25]. **Social** [CK10]. **Society** [Prz24]. **Socioeconomic** [CD21]. **Soft** [vLSV+24]. **Software** [BSKgG23, BÖB+23, FPD13, GBR17, GI95, HHZ+18, KLO18, KBČ19, MSNl23, MKKK+17, TH17b, ZRNA20]. **Solely** [KFC+11]. **Solution** [BCG+18, BS10, HAM+22, SSS20, Tak96]. **Solutions** [CZW+19, CKS06, DFS94, DFS96, Ell20, Gus10, TRIN07, Xu10]. **Solvable** [SLY06]. **Solve** [MTH11]. **Solvent** [DBM09, WAPM05]. **Solver** [XLZ+18a]. **Solving** [AOH16, BSWY98]. **Somatic** [DRT+25, LHW+22, SSKH+13, SLS23]. **Some** [DHM+05, HP96, LLW03, SG12, YSC15]. **Sorting** [BO07, BMS06, BS10, BJF+20, CKdAHdF15, FHKR11, HV03, HL10,

LLCT05, LBJM11, OBDD19a, OBDD19b, OFS07, OFS08, OFS09, Sie03, SKW23, SLRM09, SRLM10, Tra98, WR23, XLZ+18a, ZS17]. **Source** [CRT04, IFT14, MPG+16, ZRNA20]. **Sources** [CHK+02, DOB95, LYH+19, PX13, WHDN13]. **Southern** [Cal22]. **Soybean** [LS23]. **SP** [Jus01]. **SP-Score** [Jus01]. **SPA** [SYYH02]. **Space** [AB00, BS10, CHM94, DCH09, ETLK19, FT07, Geo09, GKS95, HSL07, HL13, Lat99, LMW05, Lip05, MMA+21, MVP06, NBGA13, O'H15, OK08, RMK+18, ST10, SFC11, WXS14, WW18, ZPD+10, ZCK17]. **Space-Dependent** [RMK+18]. **Space-Efficient** [LMW05, Lip05]. **Spaced** [Kon07, Li09, NM14, PNPC20, XBLM06, ZF07]. **Spacers** [Mye96]. **Spaces** [BWGM17, LGD+10, OJFD18]. **SPAdes** [BNA+12]. **Spanners** [TS96]. **Spanning** [OKKS21]. **Spark** [SLL+17, HFUH19, LCG18]. **Sparse** [AHK08, AK08, BKWK+00, BFT04, BGJ+04, ENS03, HLH04, HH14, JJGD16, KGLBK15, KMJ+20, KLZU06, LLD+16, PNMI15, WXS14, cWxLlS+23, bYjHgZ+24, vUMW08]. **Sparsely** [SIC+09]. **Sparsity** [CC09, TNSS13]. **Spatial** [BET00, CXW16, CSH+20, DAL+08, DLL+24, MMKH15, NSZ99, SS05a, SCD+22, YHEP15, ZPD+23]. **Spatial-Temporal** [DAL+08]. **SpatialCTD** [DLL+24]. **Spatially** [HSD05, MFJ+19]. **Spatio** [BH15]. **Spatio-Genetic** [BH15]. **Spatiotemporal** [SB17]. **SPatt** [Nue04]. **Special** [AHIV23, Ano09b, Ano21a, BMM+23, CSZ18, CSZ20, CSPZ21a, CSPZ21b, CSZ23b, CSZ23a, CKS12, CKS13, CKS14, CKS15, Cha95, CMSZ12, Cow20, Dei19a, EN22, Gus05, HASL18, HTH+17, Ist99, Ist20, IPSV22, JLmR+23, JMR+21, Kha14, Kum22, Len02, MS24, MMN+21, MV04, Miy06, Mye03, NV09, Pat24, Pat25, Pe'22a, Pe'22b, Pen22a, Pen22b, Sch21a, Sch21b, Sha00, Tan23, VRGC18, WIP97]. **Speciation** [CDEM08, DAR23, OSC11]. **Species** [ADR13, BW12, Bay23, BF09, DBHC24, DR15, DR17, DBT11, DCH09, EMV98, HJR12, HR22, JR12, JC22, JBM15, LMWR21, LLCT05, LW22, LRNBJ10, MSR22, NWLS05, RDH04, TRW23, TR11, VSGD08, WLYC12, YSC15, ZF07]. **Specific** [BF02, BYL+20, CN17, DBBM09, DCL18, GWM+21a, HZK22, HBW+05, KJmZ+22, Lai12, LQ23, POP23, PSIM18, PYIM19, PKZ11, RJS02, SCH09, SZMZ19, SSZG24, ShHGC20, TRS17, WCM+08, WWLC20, ZF07, LW12, RM18]. **Specificity** [GC15, HD16, JC22, KGLBK15, LSAD05, ZDZ+20]. **Spectra** [ABF+04, BG06, DB09, HPY03, LRL+07, WTE07]. **Spectral** [Bar04, BG06, GBB15, MK11, QP09, WTE07, ZZHL11]. **Spectrometry** [BBN11, Böc04, CJC01, CKT+01, CŁM+18, DAC+99, DBL+12, FNC08, KVM14, LFD03, LL05b, LC03b, MDTD06, PDT00, SHRB11]. **Spectrum** [DB09, DCP+08, RM21, WY21, YMxW21]. **Spectrum-Based** [DCP+08]. **Spectrum-Preserving** [RM21]. **Speeding** [GFE+16, SSC23]. **Speeding-up** [GFE+16]. **SPEM** [YDN12]. **Spherical** [CGD09]. **Spike** [ABTP23, Pen20b]. **Spiking** [KKS22, WLF+23]. **Spines** [URB+19, UTD+20]. **Splice** [LS98, Nai18, REKH97]. **Splice-Site** [Nai18]. **Spliced** [BMP+09, SP97]. **Splicing** [BH14, BBV+14, DMHM97, LDLZ12, Sam09, YB04, ZKC12]. **Spline** [BPL02]. **Split** [NK07, SK18, YYZ23]. **Split-Step** [YYZ23].

Splitting [GDHC95, WCL18a]. **Spontaneous** [CCL+19]. **Spots** [DGW+13]. **Spotted** [KFDT02]. **Spurious** [BHKM22, DS12, DLFS22, SDCF24]. **Squamous** [LTL20, TYS+20, WSCL18, WWLC20, WWC+20, YDG+20]. **Square** [KFC+11, KRD14, TSTS12]. **Squared** [WCL18a]. **Squares** [JKG+04, KKA+15, PD20b]. **Src** [FDDK07]. **Stability** [MHS06, OJFD18, PYIM19, Prz07, RC06, RMWC16, ZFBK09]. **Stable** [BKKSD01, DBW17, GLM20, KMRG09b]. **Stacked** [WYC+18]. **Stacking** [IKL+03, LJL+20]. **Stacks** [CGSW14, GSW16, GJL+22]. **Stage** [CD08, LST+17, Li08, NCMS+21, WSS+15]. **Stand** [TaAF+22]. **Standard** [ARRW99]. **Star** [SLL+17, ADR13, TRW23]. **Start** [XLZ+24]. **Starting** [PV17]. **Starting-Point** [PV17]. **State** [ALR18, BR06, CNCK11, GLM20, Gus10, MBRS11a, OC00, PGAE04, PSB17, RLA+06, ZHY+20, ZCK17]. **State-Space** [ZCK17]. **States** [DBW17]. **Stationary** [NHOV10, NVCW15, YY19]. **Statistic** [LZX12, Sch97b, SEV09]. **Statistical** [AM20, AO08, AS19, BDM+07, CWL13, CWH+22, CKL+17, DMHM97, FH18, GMC08, Han09, HSD05, HKZ+04, Hua10, JDSB04, JD05, KMMF20, KLS15, Kon09a, Kon09b, LMWR21, LBDVF10, LMSH03, MMHC98, MLS+12, NKR+01, Par07c, PM14, PC05, RSW00, SGSN12, SPD95, SLO07, SLRM09, TPH+09, TRIN07, XvdL05, YS23, YHB+03, YS99, YH01]. **Statistically** [AS10, ARS17, BLQZ04, JMEB18, KWA11, TRW23]. **Statistics** [AB16, APC21, BG98, BG02, BHKM22, Che04, HY16a, JZ10, KKA+15, KV19, MBVA07, MT99, Nic01, Nue04, OAR+24, Pia02, RCSW09, SDCF24, WRSW10, WG08b, WES20]. **Status** [CK10]. **Steady** [ALR18, PSB17]. **Steady-State** [ALR18, PSB17]. **Steepest** [LLWZ19]. **Steiner** [LAP03, TBP+13]. **Stem** [LLL+20, MSBR08, TLP+14, XLLS20]. **Stemness** [JLSL24]. **Step** [SLA12, SAL09, XJL+22, YYZ23]. **Steps** [Fom16a, Fom16b, Fom19, OJOD+04]. **Stepwise** [HL16a, Mal98]. **Steric** [GC15]. **Sticker** [RWB+98]. **Sticker-Based** [RWB+98]. **Sticky** [HWP20]. **Stimulation** [CEK+17]. **Stochastic** [ABG+03, CY09, CCDB21, CKT16, CAB+07, DM17, EAA+09, GQ09, GW06, GK06, GMY10, HP96, IM14, MDWZ24, ML10, POP23, PZMM15, RYZ23, RZK06, RSR+09, SFR+18, SAL09, Sol09, SVL+10, TLP+14, WZ23, WI05, YYZ23, YMM+24, YYL19, ZH14]. **Stomach** [NCMS+21]. **Storage** [HLY25, MNSV10]. **Storing** [FNC08]. **Storm** [BZB+22]. **STR** [TEMM12]. **Strand** [RRGC95, TT12]. **Stranded** [GMVC20]. **Strands** [IPH18, PRSV08]. **Strategies** [Buh03, GI95, GNI12, HKS08, LTSA15, SVK10, SBAW97]. **Strategy** [Cha01, GPP+11, Kar95, KLS15, RZK06, SLL+17]. **Strength** [ZHQS05]. **Strengths** [RND+23]. **Streptophyte** [ATLS07]. **Stress** [BB04, JJY+20]. **Stress-Induced** [BB04]. **Strikes** [GGKS95]. **String** [BVP+16, BVP+17, KSSK09, NSZ99, NM14, RM21, RG95, SD95, Zör15]. **Strings** [AS95, SS95, WW19]. **Strip** [WZ10]. **Stromal** [SGCD19, WFL+20]. **Strong** [FB12, Fic95, GT16, KDB+02, LCY+05, LLW18]. **Strong/Weak** [LLW18]. **Structural** [AT05, Ber95, BS97, CYP+11, CSP+12, DPS+20, DGW+13, FvdBB16, FNPP02, GRM09, GZW+21, GJZ06, HDBZ08,

HVPBK13, HSHC15, HHC17, HASL18, JHS06, JHA16, KEL15, LPFT14, LN03, LCGW09, MZC+18, MKBC05, MVP06, MRS+18, MBK+03, NSA08, PD16, PPV+14, PDdJFT08, RPW13, RL94, SFA17, SNW98, SSC23, URB+19, WLS+11, WY12, XZW15b, ZW19, ZRNA20]. **Structurally** [Wil99]. **Structure** [AP10, ACBM18, ADPH15, AO15, AOH16, AS95, AT05, BKWK+00, Bar04, BDCKY03, BET00, BHPS99, BRZH15, BCA15, CL17, CCI+04, CSA98, CD18, CJS06, CA15, DMHM97, DQS+11, DSN14, DPR97, DCD19, DOKT05, EJT00, ES06, FK06, FS08, GAWI19, GTA+04, GZW+16, GRM09, GWM+21a, GWM+21b, GMS05, HPL+20, HI97a, HCS09, HBW+05, IFT14, JCZ08, JGL11, JDSB04, JD05, KWM10, KKW10, KMRG09b, KX06a, KX06b, KX14, KJmZ+22, LSBS18, LNW01, LBN94, LRV98, LSL+16, LLWZ19, LZC+23, LN01, Lie05, LS04, MDWZ24, MMG14, MYBK+11, MVP06, NBGA13, OB10, PYIM22, PCGBK13, PD20b, RC07, RRFS98, RK96, RBH+19, SDMN19, SLL08, SLB00, SHB+03, SJ18, Sun18, SKT08, VLZUBK07, VT06, WMD06, WYY+18, WDF24, WDA01, WLS+11, WY12, WG08b, Wu96, XJB07, YJ04, YK05, ZGEZu11, ZKWH17, ZLU+22, ZHY+20, ZFAS08]. **Structure** [ZZ14b, Zhu07, vLSV+24]. **Structure-Approximating** [GMS05, KMRG09b]. **Structure-Aware** [LSBS18]. **Structure-Based** [JGL11, VLZUBK07]. **Structure-Guided** [PCGBK13]. **Structured** [Eri09, KS99, MS00, MPVZ05, RYZ23, RCER21, RK96, RDR+02]. **Structures** [APA17, AKG+13, ADS03, AHPR12, BLR16, BGTSB98, BMP+09, BRS20, BIPD17, Clo05, Clo06, CGZ04, EAFM24, GLMW13, HR08, HR12a, HR12b, HLR14, Han09, HM14, HPR09, IKL+03, JLMZ02, JTL+10, JHA16, KV17, KXL08, KC18, KLW96, KT13, LLW+20, LBBV+18, LMP08, LSHL04, MR08a, MZS+00, MN15, NS23, Neb02, NRW11, Par06, PVFB06, QR13, RW10, Rød06, RL94, SIC+09, SGdMT12, SGT15, SRSD11, SDK16, SNW04, Shi10a, Shi10b, SPC19, TKO21, VILR10, WC07, WAM20, WSHB98, WlLK+12, ZZ14b]. **STS** [GI95, SBT00]. **Studies** [BR06, BZ08, CTC21b, GAWI19, JCBX22, KBJ07, KE13, LS17, Li08, LS23, RLK+09, SMKS96, SLS23, SS01, TPH+09, TaAF+22, VCY14, WAX22, WHJE19, WES20, YL17, YK19, ZYB+04]. **Study** [AS02, Ano21b, BMY01, BCA96, BGL24, BMR+19, DPSW20, DBBM09, EBS+22, FW12, GJL+21, GWM+21a, HSH+09, LDLZ12, LZBK15, MBS+01, PdB13, RS12, RKTS14, RBKJ19, RMWC16, SCB14, SSH+10, SHG02, TKT+05, WYY+18, WLXW22, WZZU07, WS04, YSC15, ZPX+10]. **Studying** [BV10, GPOP+17, MMA+21]. **Stumping** [CvS24]. **Subforest** [JHS06]. **Subgraph** [HLMR11, MZS+17, Wan94, ZZ10]. **Subgroups** [MEF24]. **Subject** [TZP+13]. **SubMAP** [AKK11]. **Submatrix** [BDCKY03]. **Subnetwork** [AKK11, CNCK11]. **Subnetworks** [CPR22, CNCK11, LTsL24, RCER21]. **Suboptimal** [LC03b, SP97]. **Subpopulation** [Hua10, SLT24]. **Subpopulations** [KKM+20, SDK16, SH17, WVT23]. **Subroutine** [AMOW10]. **Subsampled** [TKSA24]. **Subsequence** [AC10]. **Subsequences** [WWZ19]. **Subset**

[WA10]. **Subsets** [CBS+20]. **Subspace** [CCT09, WSW15, WZW10]. **Substitution** [Bal95, CHJ05, ENS02, Hua08, LMT01, LZ10, TDV24, WTM11]. **Substitutions** [SJ18, VST03]. **Substrate** [LSAD05]. **Substrates** [CDL+19]. **Substring** [RG95, TAA16, UBTC06, WWZ19]. **Substrings** [AHK+07, SS95]. **Substructure** [CHKK99, Shi07, TSTS12]. **Substructures** [EPSV98, PSCP09, SDMN19]. **Subtopologies** [KLW96]. **Subtree** [BSMA06, HL13, KLM11, YzCW20]. **Subtrees** [RRNB13]. **Subtype** [SSZG24]. **Subtype-Specific** [SSZG24]. **Subtypes** [FRD+17, MMK+21, WPL+19, YKPM20]. **Subtyping** [DWK+20]. **Subunit** [SVA+19]. **Succinylation** [AWZ+17, XJL+22]. **SuccSPred2.0** [XJL+22]. **Sudoku** [HY16b]. **Sufficient** [CBS+20, DDC+20, KKA+15]. **Suffix** [CF14, MS00, SLL+17]. **Suggests** [CYF+20, SSW20, ZPC+18]. **Sum** [GKS95, KS06, YJ04]. **Sum-of-Pairs** [GKS95, KS06, YJ04]. **SUMMA** [AVS20]. **Summaries** [DM17]. **Summarization** [NSK09]. **Summary** [Woo99, WES20]. **Summed** [DLM10]. **Super** [JSN09, SYYH02]. **Super-Blocks** [JSN09]. **Superbubbles** [PER+18]. **Supercomputer** [WCZ+18]. **SuperCurve** [SLZH15]. **Superfamilies** [WZC96]. **Superordinal** [BDCG+98]. **Superposition** [KKA+15]. **Superpositions** [WG08b]. **Superstrings** [AS95]. **SuperTAD** [LZL24]. **SuperTAD-Fast** [LZL24]. **Supertypes** [HKL07]. **Supervised** [BZG+22, GWA+21, MHL22, PLZX25, YTS12, ZMppVN22]. **Support** [BRR06, DHY02, JLSL24, LN03, NM14, PSG+20, SPSZ23, Yan09, YM06, YJEP08, Zho17]. **Supra** [BV20]. **Supra-Bayesian** [BV20]. **Sure** [LL23]. **Surface** [DBM09, FL94, HD10, SCC+98]. **Surface-Based** [SCC+98]. **Surfaces** [BGG07, LFT+98, RC06]. **Surprise** [ABL03, Elh11]. **Surprises** [DHM+05]. **Surprising** [BFT04]. **Survey** [CHM94, CWH+22, GLMSO10]. **Survival** [BSB+05, CW09, LKBT16, LGC+09, WCL18a, ZZ20, ZWK+20, ZQZ20, ZYD+19]. **Susceptible** [LS23, MDWZ24, WZ23, YYZ23]. **Susceptible-Infected-Recovering** [MDWZ24]. **Susceptible-Infected-Susceptible** [YYZ23]. **Sustained** [YY19]. **SVLR** [GZW+21]. **SVMs** [LJ05a]. **Swapping** [ZGBK10]. **Swaps** [HV03]. **Swarm** [BSP+25, CYY09, LLS+19, YLCC17]. **Switch** [AK07, ALR18]. **Switches** [DPS+20]. **Switching** [WZ23]. **SWsnn** [WLF+23]. **SYBR** [BMN+07]. **Symbolic** [HLK+13]. **Symmetric** [ATLS07, CYP+11, MK16, MYBK+11, MGSA06]. **Symmetrical** [KC18]. **Symmetrization** [DBT11]. **Symplectic** [LGD+10]. **Symposium** [CSZ18, CSZ19, CSZ20, CSPZ21a, CSPZ21b, CSZ22, CSZ23b, CSZ23a, HTH+17, Pat24, Pat25]. **Synchronize** [RD09]. **Synchronized** [GQ09]. **Syncmers** [SDCF24]. **Syndrome** [DDK21, ES07, MXW+20, Tho21]. **Synonymous** [DT12, TVNP15]. **Syntenic** [LN01]. **Synteny** [MDB11]. **Synthesis** [CL21a, DCL10, Kon09b, LCD11, Ore20]. **Synthetase** [LSAD05]. **Synthetic** [Ami12, GAWI19, LG22, PCC+11]. **System** [FYJ18, FCV+07, LSY+05, LLS11b, OAHA94, SK17, SDFH98, SDFR16,

TA21, Vij22, YDN12, ZDZ+20]. **Systematic** [HRSC00, NME+15, QMMW11, SSV19]. **Systemic** [MXW+20, TZZY20]. **Systems** [BDKSY00, Ben98, CKS12, CKS13, CKS14, CKS15, DCL10, EAM+17, FDDK07, GSSI14, GSH17, GK06, Ila20, JPR06, Jus06, KLV+13, KK18, LZS09, MR95, PM24, PCC+11, RRKT07, RMK+18, dJ02]. **Systems-Level** [FDDK07, LZS09].

T [BGH+08, HVD17, LZHC15, LCG18, SVA+19, SZMS02, ZYB+04]. **T-Cell** [BGH+08, LZHC15, SZMS02, ZYB+04]. **T-Coffee** [LCG18]. **T-GOWler** [HVD17]. **T4** [BHPS99]. **Table** [MD03]. **Table-Driven** [MD03]. **Tables** [PK19]. **Tabu** [CYY09]. **Tag** [BDKSY00, MT06]. **Tagging** [LLT06]. **TagSNP** [LWLJ10]. **Tailored** [Ila20]. **Taking** [BG15]. **Tales** [BJ17]. **Talk** [YHW18]. **Taming** [PMGE21]. **TAMPA** [DWS05]. **Tandem** [Ben97, BG06, CJC01, CKT+01, DAC+99, DP07, FNC08, LSS01, LC03b, MTH11, NTWF11, TWY02, WYKG05, WTE07, WlLK+12]. **Tandemly** [BLEM08, LBEMG07]. **TAP** [WlLK+12]. **Target** [AKN+06, AaHP+21, BÖB+23, CN17, DCL18, HFUH19, LJCZ20, MLC10, MRM+02, MDMC21, MDB11, ÖBA+23, PGA+11, WYC+18, WYLW21, YBF19, ZZNM15, ZDZ+20]. **Target-Specific** [CN17]. **Targeted** [FFSL22, KBKF17, Yua09]. **Targeting** [Kha14]. **Targets** [AL25, GPRR12, GCB20, HHHS03, HSBS10, HMF07, KTT20, OSK+15, YYY+09, fZbMqW+20]. **Task** [MWL22]. **Task-Optimized** [MWL22]. **Tasks** [MJR+24, NLH+23]. **Tau** [Sol09]. **Tau-Leaping** [Sol09]. **Taxa** [CHP94, GLM16, TRS17]. **Taxa-Specific** [TRS17]. **Taxon** [ZGW22]. **Taxonomic** [CDH+16, FPRV18, ZMGN23]. **Taxonomical** [LC03a, PIWR15]. **Taxonomy** [CF97, URB+19]. **TCGA** [Ano20, BR24]. **Teaching** [YCCL18]. **Team** [ZL09]. **Teams** [ZL09]. **Technical** [CKB+06]. **Technique** [ST10]. **Techniques** [CBH+12, CCT09, CGZ04, DGFMSS16, FSZ02, FP11, SFR+18, WRS+99]. **Technological** [VRGC18]. **Technologies** [BLC10b, DKF09]. **Technology** [LYPC13]. **Teeth** [BKPW95]. **Tells** [SPBB15]. **Telomere** [YYL19]. **Temnothorax** [ZZL22, ZLP22]. **Temperature** [MSS10, RKTS14]. **Template** [DQS+11, GHM+10, ZPD+10]. **Template-Based** [DQS+11]. **Template-Free** [ZPD+10]. **Temporal** [BCPS04, CC03, DAL+08, KBJ07, RSEK24, SKS+09, WYY+18]. **Temporally** [CGT12]. **Ten** [JMPR23]. **Tensor** [QsYSxL23]. **Term** [MRG+24]. **Terms** [DAE+19, LACB10]. **Tessellation** [STV96]. **Test** [CTC21a, GE04, GNME01, HQ06, JZ10, KBCBS11, LH03, MK16, SDC+10, SHE11, VY18, WMC04, ZPX+10]. **Testing** [Aug12, BMN+07, CTC21b, CFS13, CD11, FCGD19, FDD21, FDDK07, GPCP11, HTZ+12, ITSH00, KVDC06, LCG+23, McP12, MSZW11, MLS+23, SSY+22, ZHZ+16]. **Tests** [BG23, DS03, LSY+05, MBC+18]. **TetR** [Ami12]. **Tetraploids** [WMC04]. **Text** [YQDW23]. **Texts** [HVD17]. **Texture** [HTM+22]. **thaliana** [AJV+16, ZDZ+20]. **Their**

[Ano21b, BSK05, BKPW95, BET00, CKB17, DAE+19, JFLL20, Kha14, Kon07, Lie05, MDB11, MZM18, OKKS21, PTWB09, SKGG17, SH17, SCSA+16, SLYC09, WZG+20a, WHC09, ZZUPY06]. **Theorem** [TA97]. **Theoretic** [GTA+04, OJOD+04, QGP10, SSB07, ZZL23a]. **Theoretical** [BH11, DS19, PDSD06, WRSW10, Yu24]. **Theories** [YjDG+23]. **Theories-Based** [YjDG+23]. **Theory** [BSKgG23, Bri19, CMK23, CJD06, DSV12, Erd05, Erw19, GKgUS21, GBBS07, Gus10, LCW16, LS05, MMPS18, NP09, NWLS05, OBS11, OFS07, PU00, RBOS15, SSR21, SG15, SLO07, TA97, UGS19, Wen06, WI05, Fom16a]. **Theory-Based** [UGS19]. **Therapeutic** [AL25, PCGBK13, fZbMqW+20]. **Therapy** [EBS+22]. **there** [Tan11]. **Thermodynamic** [BDM+07, DMP+06]. **Thermostability** [XGD24]. **Thiamine** [YSC15]. **Thinking** [SW11]. **Thoracic** [AG23]. **Though** [BF98]. **Thousands** [Csu02]. **Threading** [BRS99, GKG12, Lat99, MLS+12, SLB+97, XXCE00, ZRGHJ08]. **Threading1** [XXU98]. **Three** [BGTSB98, CYF+20, CGZ04, EPSV98, HI96, HD10, LZC+23, LCL+17, PB18, RBH+19, RL94, SDMN19, Shi10b, SBNS21, TSTS12, WPL+19, WXY+24, Xu09, YHC19, ZLU+22]. **Three-Dimensional** [BGTSB98, CGZ04, EPSV98, HD10, LZC+23, LCL+17, RBH+19, RL94, SDMN19, Shi10b, SBNS21, TSTS12, YHC19, ZLU+22]. **Three-Eighths** [HI96]. **Threshold** [AFCK09, CFS13, CD11, HTZ+12, HlAM20]. **Thresholding** [BGL24]. **Thriving** [RKTS14]. **Throughput** [BBN11, BLC10b, CLM+16, CAC+23, CBG+14, DDC+20, FCR+13, FCV+07, GSN11, GNI12, KS11, LDB+07, OBDV16, SSLMW10, SBRG20, TPH+09, ZHQS05, ZZUPY06]. **ThurGood** [SMM+04]. **Thyroid** [CWS+21, JZZ+19]. **Tianhe** [WCZ+18]. **Tianhe-2** [WCZ+18]. **TIGR** [Ano00]. **Tile** [AS23]. **Tiled** [PB18]. **Tiling** [BBD+04, FMH06, Pic08]. **Tilt** [WZG+20b, ZLU+22]. **Time** [AB00, BMY01, BJGG+03, BV10, BS98, BBN24, CFS+08, CH15, CDH+06, CLS11, CJS12, DM17, DLML10, DFG06, DEH10, FSZ02, FHKR11, FA12, GK18, GMC08, GK06, Gui98, GKS95, HI97a, HMY+14, HG18, HJ14, KLM11, KK18, KT01, KM08, LYL+04, LMWR21, LLL+20, LCL+17, MFJ+19, Mor19, RLH13, RLVCVR17, SLL+23, Shi10a, Shi10b, SVP19, SDC+10, SRLM10, SLY06, TRW23, URB+19, WMD06, WW18, WW19, ZZS17, ZZL22, ZF05]. **Time-Course** [GK18, HMY+14, KK18]. **Time-Dependent** [SVP19, URB+19]. **Time-Frequency** [LCL+17]. **Time-Resolved** [MFJ+19]. **Time-Series** [BJGG+03, FSZ02, LLL+20]. **Time-Varying** [BBN24]. **Times** [BNN12, FB12]. **Timing** [CK09]. **Tissue** [BDBF+00, CSH+20, GSS+20, JC22, POP23, SSH+20]. **Tissue-** [POP23]. **Tissues** [CLLL20, SCD+22]. **TNF** [JKG+04]. **TNF-Induced** [JKG+04]. **Toggle** [AK07]. **Tolerance** [HTZ+12, QbMyD+19, YY18]. **Tolerant** [GHM+10, HL03, PDT00, SP97, WCC+06, ZHZ+16]. **Tomato** [CJ22]. **Tomograms** [ZLU+22]. **Tomography** [AG23, WZG+20b]. **Too** [KKM+20]. **Tool** [AMOW10, AP09, BK10, BVP+16, CLM+16, CTC21b, CW13, CF14, DC16a, DWS05, DSG+08, FDW20, FJAOB18, GWM+21b, HD10, KBKF17,

KLO18, LDBj22, MM21, NXL+15, NBB18, PRC+24, PPL+23, RUGR18, SBRG20, WWZ+16, WZH+18, WT17, YRG+19, ZMGN23, ZZC+24].
Toolbox [AHK+02, AAoS+23, WZCY21]. **Toolkit** [HWP20]. **Tools** [AFR+08, DAE+19, GSH17, KLC+11, PSG+20]. **Top** [CŁM+18, PRC+13]. **Top-Down** [CŁM+18, PRC+13]. **Topographic** [MSMP19]. **Topological** [BF09, CMvH15, EBK11, LLW03, LWLL19, Mat10, Par07a, QR13, SHZ+24, TW05, WAM20, XZW15a]. **Topologically** [DBW17, LZL24]. **Topology** [AR06, AHPR12, BRZH15, BHK+10, CHP94, GST10, IJCL12, RND+23]. **Topology-Based** [IJCL12]. **Topology-Free** [BHK+10]. **Toric** [SS05b, SS05c]. **Torsional** [WCC98]. **Toxicogenomics** [GSH17]. **TPX2** [BRC20]. **Traces** [MN08]. **Tracing** [NS18, SP11]. **Tracking** [NFHM21, SS23]. **Tractability** [WZ10]. **Tractable** [LTsL24]. **Trade** [WAX22]. **Trade-offs** [WAX22]. **Training** [BÖB+23, MJR+24, YJEP08]. **Trait** [BMR+19, CFE+13, LHC02, NMH13, WXS14]. **Traits** [FL17, KLS15, LQPE+10, yWCF06]. **Trajectory** [CMS+25]. **Trans** [DC16a]. **Transactivation** [CDC+11]. **Transcript** [ADRS24, DKK20, DMR+03, HHJ+13, OO24, YYJ19, ZMK22]. **Transcription** [ALR18, BZMM16, Che06, GGU13, GJZ06, HL16b, KS12, KDL+94, LDLZ12, LZBK15, MYS+20, Pic08, RRKT07, RSR+09, SNQ+14, SKS+09, TS04, XLZ+24, YJ06, YYY+09, YJC18]. **Transcriptional** [FS08, GK06, JFLL20, KV08, LZS09, LL19b, MSRS24, OFE14, SKP+12, XvdL05]. **Transcriptome** [JFLL20, KBČ19, LFJ11, MNIK+09, SM20, WLXW22, ZPD+23]. **Transcriptomic** [DLL+24, FRD+17, KMUK22, MLOT17, SCD+22, SK18, WVT23]. **Transcriptomics** [CMS+25]. **Transcripts** [DDA+11, DC16a, FMH06]. **Transducers** [ENS03]. **Transduction** [ADD+07, BS09, BMR09, CXW16, EAM+17]. **TRANSFAC** [KDL+94]. **Transfer** [AFCK09, BBGS11, BAK13, BG17, CŁM+18, LCG+22, RS13, ST10, TGTG19, WZG+20a, XSH+22]. **Transform** [BVP+19, CGD09, HG18, LMW05, LCL+17, NHOV10, RJS02, TKSA24, YS23, YYW14, ZWJ18]. **Transformation** [PL06, ZZS17]. **Transformations** [AMR20, BP06, KC18, PLSM+06, YF09]. **Transformed** [JZ10]. **Transformer** [NLH+23]. **Transforming** [GB08, Prz98]. **Transforms** [KL98, Lip05]. **Transition** [CL17, CMS+25, FLS94, HR12b, VST03, WS04, YZ08]. **Transitions** [DPS+20]. **Translation** [CZNF19, DT12, LJ05a, RM00, WOG03, WMK17, ZMppVN22]. **Translator** [XSH+22]. **Translocations** [BMS06, HL10, OFS07, OFS08]. **Transmembrane** [Tho21, TS96]. **Transmission** [KV23, SK17, YMM+24]. **Transport** [DSS+22a, TS96]. **Transposable** [ZPC+18]. **Transposition** [AODD22, AOJ+23, MWD02, WW18]. **Transpositions** [AODD21, BO07, FHKR11, HL10, OBDD19a, OBDD19b, SKW23]. **Transpositions*** [CKdAHdF15]. **Transposons** [CS00]. **Transversal**

[DHWZ06]. **Traversal** [BSSZ+20a, BSSz+20b, SOD+11]. **Treatment** [DCL18, SCB14, SSS+21, VCY14]. **Tree** [AO15, AOH16, AR06, ADR13, ARS17, AH20, ARSW22, AL07, BHRV00, BCG+18, CHP94, CC06, CF14, DJK+99, DJK+00, DHV06, GMC+14, GYZ19, GKM+10, GMSZ12, HD16, HR22, HP97, HL13, HNW99, JK96, LW22, MSS+22, ML04, MS00, MSR22, NWN+10, QEk24, Sal95, SDFH98, SV97, SY22, SCSA+16, SLL+17, SZUP06, TR11, VV97, WAM20, War95, WZ24, ZL09, ZZ10, Zha16, CJS12]. **Tree-Based** [Zha16]. **Treelike** [RS13]. **Trees** [AFBS95, AA18, ARC13, AS19, BW12, Bay23, BSB+05, BG17, Bry96, BBWE09, CDFC00, CMvH15, Csu02, DR15, DR17, DCH09, EMV98, HSG22, HZNF06a, HZNF06b, HJR12, HMU06, HLMS08, JRS19, JR12, JS03, KVZ24, KPW11, KVK08, LAP03, LPW05, LMWR21, LRV21, LMSH03, ML00, ME12, Mat10, MBRS11b, MTF+12, OKKS21, PJB+15, PMF+03, Prz07, SHRB11, SLA12, SK18, SSH94, SW11, SHCM18, TRW23, VSGD08, WG98, WTM11, WF12, Wu13, WZ24, YWN11]. **Trefoils** [MKBC05]. **Trend** [KPW11, RS13]. **Trends** [Woo99]. **Tri** [WHDN13]. **Tri-Factorization** [WHDN13]. **Triangular** [ABD+97]. **Triggered** [CŁM+18]. **Trimer** [NLC17]. **Trios** [KWBN19]. **Triple** [JSZ+20, LSY+05, SPSZ23, WY12]. **Triple-Negative** [SPSZ23]. **Triples** [MN15]. **Triplet** [HR22, JR17, JRS19]. **Triplet-Based** [HR22]. **Triplets** [JLRS18, LZ10]. **Triplex** [Sel13]. **tRNA** [MSN+20, SSZC95]. **tRNA-Ligases** [MSN+20]. **trpzip2** [HCX09]. **True** [DQS+11, SRV98]. **Truncated** [GSCG19, RYZ23, YYZ23]. **Tsukuba** [Hor01]. **Tuberculosis** [ZLW+20, MSN+20, YM06]. **Tumor** [ACL+21, AMS+22, COV+15, COL+18, DRT+25, DLL+24, DMW+17, HMY+19, LLG+20, LLS11b, MMA+21, RNH18, RH19, RV15, SSKH+13, SRB+25, SWS+20, SLT24, ZEKKR18, ZPG+24]. **Tumors** [TKSA24]. **Tuning** [LYS20]. **Tuple** [HJD17, BS98]. **tuples** [WY11]. **Turner** [WC07]. **Turnover** [SDFR16]. **Turnpike** [EHFK24]. **Twenty** [AAN+20]. **Twenty-One** [AAN+20]. **Twist** [IPH18]. **Two** [AGH+18, AFR+08, CD08, DLM10, FH18, GP13, GNME01, GGM12, JG11, LST+17, LBN94, LDLZ12, LL19a, MSS10, MBC+18, MJS24, PB18, PTWB09, PD16, PSG+20, PL06, RDH04, SLA12, SWS+20, SDC+10, TP11, VFOK18, WSS+15, WW19, XJL+22, YHC05, YDN02, ZLU+22, ZPX+10]. **Two-Color** [PTWB09, TP11, YHC05]. **Two-Dimensional** [GP13, PL06, ZLU+22]. **Two-Exponential** [AGH+18]. **Two-Layered** [LDLZ12]. **Two-Level** [LBN94, VFOK18]. **Two-Locus** [JG11, ZPX+10]. **Two-Sample** [SDC+10]. **Two-Sex** [GGM12]. **Two-Species** [RDH04]. **Two-Stage** [CD08, LST+17, WSS+15]. **Two-Step** [XJL+22]. **Two-Way** [MBC+18, MJS24]. **Type** [CYZ+20, DSC+22, DLL+24, LQ23, MH22, RMWC16, SGP11, SVP19, WFC25]. **Types** [ADR24, BB15, FCS12, LL19a, MWL22, PWCN02]. **typhi** [SVA+19]. **typhimurium** [MTYH09]. **Typing** [TEMM12]. **Tyrosine** [CYZ+20, GAWI19].

U [AG23, CN17, NZM+25]. **U-Net** [AG23, NZM+25]. **uF2** [KKe23]. **Ultra** [MNG+15, OBS11, RLVCVR17]. **Ultra-Large** [MNG+15, RLVCVR17]. **Ultra-Perfection** [OBS11]. **Ultrabubbles** [PER+18]. **Ultrafast** [CW13]. **Unaligned** [BTZ06, HPDLW09, MC08, YZWZ13]. **Unambiguous** [McC09]. **Unassigned** [BKWK+00, ZRZD11]. **Unbalance** [FBV15]. **Unbalance-Aware** [FBV15]. **Unbalanced** [AOJ+23, AH20]. **Unbiased** [FPRV18, LKBT16, WP11]. **Uncertain** [BGJ+04, EHFK24, ODNW21]. **Uncertainty** [CRB18, WHY+13, WGS+23]. **Uncovering** [PNIM17, PYIM22, PM24]. **Uncovers** [POP23]. **Under-represented** [Sch97b]. **Underexpression** [GPRR12]. **Undergoing** [BHKM22]. **Undergraduate** [Cal22]. **Underlying** [SM09]. **Undermines** [ZTD+22]. **Underrepresentation** [LMS96]. **Understand** [SPSZ23, WPS+25]. **Understanding** [Bri19, TPK03]. **Unequal** [AEB+04]. **UNet** [JAJ24, TKSA24]. **Unexplained** [CCL+19]. **Unfolding** [GME01, NES22]. **UNIFAN** [LDBj22]. **Uniform** [LAF+14, LQ23, Par98, SY22]. **Unifying** [WES20]. **Uninfected** [RFH+25]. **UNIPred** [FBV15]. **Unique** [AKWZ95, CJK+97, DFS94, DFS96, JM97, STRT96, WWC+20]. **Unit** [CFE+13]. **United** [HCX09]. **United-Residue** [HCX09]. **Units** [CDH+16]. **Universal** [BDKSY00, BDHK+04, JLY08, KMUK22, PQBB08, ZKM21]. **University** [Cal22]. **Unknown** [LHL16, SMS13, SS07, WDF24]. **Unknowns** [SMS13]. **Unlabeled** [ABR16]. **Unordered** [HMU06, MTF+12]. **Unpruned** [HJD17]. **Unraveling** [DGFMSS16]. **UNRES** [HCX09]. **Unrooted** [Prz98, WTE25]. **Unstructured** [OB16]. **Unsupervised** [AVS20, FKZ09, LDBj22, PD20a, PMAP13, PX13]. **Untyped** [LL11]. **Unusual** [ABLX00, ABL03]. **Unveiling** [MJS24, Par24]. **Unwanted** [LG22]. **Up-Down** [CC11]. **Updating** [Ham12, MK06]. **Upon** [YK19]. **Upper** [AP10, CFH13, GP13, KLM11, LTI10, WG08a, ZZL22]. **UPSEC** [MC08]. **Upstream** [TML+02]. **URMS** [YK05]. **URMS-RMS** [YK05]. **Urokinase** [CRT+17]. **Usage** [FPS22, SLYC09, TVNP15, XLZ+24]. **Use** [Che04, FK06, LR00, RLK+09, SG94, TM22, XLZ13]. **Useful** [MBS+01]. **User** [JHA16, KV17, OAR+24, RUGR18]. **User-Defined** [JHA16]. **Uses** [Ale08]. **Using** [AL25, AMW07, ACKK19, AOH16, AOAAH17, AOJ+23, AKWZ95, AS22, APF+20, AMS+22, AS02, ADS03, AZ11, APC21, ASZ+16, AT08, AG23, AAN+20, Aug12, AS19, BHL+18, BYGI12, BMH21, BBC16, BMR09, BG11, BCG+18, BBEM09, BRR06, BRS99, BLP+22, BMN+07, BFL05, BBH+07, BK08, Böc04, BG17, BP16, BFP13, BT02, CL17, CBH+12, CBS+20, CCT09, CD18, CAB+07, CKZ+19, CCPT17, CYY09, CZY19, CGZ04, CGD09, CHK+02, COV+15, DB09, DZM+03, DGW+13, DPSW20, DM20, DDK21, DAL+08, DPR97, DMW+17, DMR+03, DLFS22, DWK+20, EFM12, ET07, EAM+17, ENS02, ENS03, EHC+13, FZF+20, FRD+17, FCR+13, FS99, Fre11, FLNP00, FDDK07, GMF+08, GGU13, GYA+23, GLM20, GB06, GCD20, GZW+21, GWM+21a, HG11, HMY+14, HMN21, HHE13, HWH+13, HH14, HYJ+19, HL10, HG18, HHC06, HFUH19, JCZ08, JM97, JMPR23].

Using [JG11, JAJ24, JBBW10, KXL08, KKS+15, KW14, KIYM13, KV23, KK11, KMP08, KWA11, KK22, KLKH11, KST96, KS06, KSK+11, KCH04, KL98, KPP+22, LWN+18, LS98, LDW98, LRSG07, LTCH11, LBN94, LSG04, LLS11b, LLW+20, LXS24, LYH+19, LQ23, LBJM11, LCWG06, LWZ21, MSS+22, ML00, ML22, ME12, MPZL23, MDK24, MS00, MRG+24, MD00, MRY+23, MEF24, MSN+20, MDB11, MTF+12, NWN+10, NS18, Nou21, NBB18, OYB18, PK11, PP23, PD20a, Par06, Par07a, Par10, PCS18, PTWB09, PFK17, PWKAF16, PE20, PO04, QP09, RMS02, RNH18, RM21, RBOS15, RPW13, RRFS98, RK96, RHS+21, ROB+22, SM20, SPSZ23, Sal95, SLL08, SPD18, SVD14, SSS20, SS07, SFR+18, SSC23, SB21, SOD+11, SH17, SSTM19, SAM06, SMC+15, SK18, SZSW09, SBAW97, TBL18, TKT+05, TZZY20, TBB00, VA17, WCM+08]. **Using** [WHY+13, WMC14, WSS+15, WYC+18, WCL+18b, WTY19, WGC+21, WMC04, WH06, WTE07, WA10, WY11, WYLW21, XAB+15, XYX+22, XvdL05, YS23, YGP05, Yan09, YJ04, YM06, ZB15, ZRZD11, ZZC+24, ZL01, ZHS05, ZMK23, ZCZ+23, ZWZ16, Zho17, ZM16]. **Utility** [MA19]. **Utilization** [PAS+13]. **Utilizing** [Ore20, TKSA24].

v2 [PRC+24]. **Vaccinated** [WZ23]. **Vaccination** [LBSB17, ZZN10]. **Vaccine** [LZHC15, SVA+19, UBGFD+19]. **Validate** [AJYJ18]. **Validated** [MPZ+20]. **Validation** [BZ08, KAC17, PMG+16, RRKT07, SWK+07, SSW20, WHW+06]. **Validatory** [MDTD06]. **Value** [BFT04, JZZ+19, Kei05, LSG04, MEF24, SM20, TSTS12, WZL19]. **Value-Based** [SM20]. **Valued** [FL17, LLW18, SSY+22]. **Values** [CAB+07, FBJ04, Met06, SBC+05, SS01, UGS19, VY18, WG08b, YS10, YY18]. **Variability** [JÖNK17, NKR+01]. **Variable** [ARSW22, CL17, MLC10, RS12, RLK+09, RBEB13, SSH94]. **Variable-Length** [CL17, RBEB13]. **Variables** [BYGI12, HL16a, MGW+07]. **Variance** [BS98, KMC00, SRV98]. **Variant** [CBG+14, FDW20, GZW+21, HMN21, LS17, LHW+22, TYSX19, WLA+18]. **Variant-Kudu** [FDW20]. **Variants** [AWM+17, BBV+14, HXL+17, JHN+23, KLS15, LPFT14, LS23, MMK+21, MRY+23, MRS+18, SS23, TGA24, WHJE19]. **Variation** [CCT15, CD18, CKZ+19, CKB+06, CHK+02, FDW20, GG04, KWBN19, Lai12, NWN+10, RMC+05, SFA17, TZB+23, WHY+13, WSS03]. **Variational** [WG08a, YYM+23, YT22]. **Variations** [ACBM18, LLKX16, WHC09]. **Varies** [LM03]. **Varying** [BBN24, HL16b, ZKC12]. **Vasculitis** [WQZ+19]. **Vavien** [EBK11]. **Vector** [BRR06, DHY02, JLSL24, KKA+15, LYL+04, LN03, NM14, SPSZ23, VA17, WTY19, Yan09, YM06, YJEP08, Zho17]. **Vectors** [FBJ04, Jus06]. **Vegas** [SP97]. **Vegetation** [KG24]. **VEGFA}** [MXW+20]. **Verified** [GE17, HLL13]. **Versatile** [PCC+11, WZCY21]. **VERSE** [ZKC12]. **Versions** [GF16]. **Versus** [CRT+17, GMY10, TS96]. **Vertex** [BHL+18]. **Vertices** [BHL+18]. **Very** [HLH04, KYSE10]. **Via**

[BHRV00, MMK+21, Sef25, SlGW+23, SJ18, ADP+08, ABR16, AMS97, BGHY04, CTC21a, CJC01, CKT+01, CLR+05, CC06, zCULW20, CT07, DAC+99, DKK20, DPS+20, DWMT22, DBL+12, FPSD22, GM07, Gru98, GLMW13, GKM+10, GMSZ12, Gus10, HHX16, HSL07, HL16a, JHN+23, KKC+22, KJmZ+22, LPW05, LZL+23, LWLJ10, LZY+23, LC03b, MGVS14, MJS24, MDMC21, NK07, NSK09, NTWF11, OFS07, PYIM22, PKSB18, PLSM+06, QbMyD+19, QLW20, RBEB13, RC24, SDDI+08, SAL09, SGP11, TBP+13, WHDN13, WHD15, Wen05, WGW+01, XJS07, ZKM21]. **Viability** [SDFR16]. **Viaducts** [Boh24]. **Vibrio** [LLCT05]. **Victor** [Tos05]. **Victor/FRST** [Tos05]. **Videos** [PLSL18]. **ViDis** [JZL+20]. **View** [QsYSxL23, VRGC18, VY18]. **Viewpoint** [HA12]. **Vigna** [JJY+20]. **Viral** [AV18, BBH+21, CRB18, JHN+23, KV23, LRD19, Pen20a, PMAP13, SF12, TZP+13, ZSB+23, SCSA+16]. **virDTL** [ZSB+23]. **VirE2** [GMVC20]. **Virion** [ZY23]. **Virtual** [ALB+19, MN08]. **Virulence** [MTYH09]. **Virus** [AWM+17, CCH+19, LBSB17, SAM06, STP18, WWH17, YMM+24, ZYD21]. **Virus-Associated** [CCH+19]. **Viruses** [DBBM09, HY16a, SLYC09, TAJZ23]. **VisBicluster** [ASE20]. **Visual** [HSL+24]. **Visualization** [ASE20, HL13, MZM18, PSP21, TPH+09, XL18]. **Visualizing** [DCW+17, GBR17, ODNW21, WZH+18, WZCY21]. **Vital** [CYF+20]. **Vitro** [COL+18]. **Vivo}** [DCV+07, KKS+15]. **Volumes** [FW12]. **Voting** [XWLJ08].

Waiting [BV10, BNN12]. **Walk** [DZS24, MBLZ09]. **Walks** [HBRW06, bYjHgZ+24]. **Waterborne** [CD21]. **Waterman** [Ano21a, GFE+16, IPSV22, PB18, PVR+22]. **Watershed** [NZM+25]. **Watershed-Based** [NZM+25]. **Wave** [WLF13]. **Wavelet** [HBRW06, HLG18, HG18, KMZ+10, NHOV10, NVW14, NVCW15, YS23]. **Wavelet-Based** [KMZ+10]. **Way** [LLJS19, MBC+18, MJS24]. **Ways** [MAN16]. **Weak** [LLW18]. **Weaknesses** [RND+23]. **Weavings** [Erd05]. **Web** [DCW+17, HSG22, HWP20, JJH+21, KGÖ18, MM21, PRC+24, PBMC17, PSP21, WWZ+16, WZH+18, WZCY21, ZMGN23, ZW23, ZFAS08]. **Web-Based** [HSG22, HWP20, MM21, PRC+24, WWZ+16, ZW23]. **Web-Server** [ZFAS08]. **Webserver** [GH16]. **Weight** [GGU13, LLW18, Zho10]. **Weighted** [ÅMR07, BO07, BK08, CHS17, CIM+06, HLL13, JK96, LS23, LDW+14, LSSD18, NXGL20, Nou21, OBDD19b, PMP+15, SPW22, TPSB19, WWZY19]. **Welch** [Jen09]. **Were** [XWJZ20]. **Whale** [BKPW95]. **WhatsHap** [PMP+15]. **Wheeler** [BVP+19, LMW05, Lip05]. **Where** [CPFP24, TaAF+22]. **Which** [NMG+05, YF09]. **While** [GDHC95]. **Whither** [Ano94]. **Whole** [BH11, BFP13, CC12, CF14, DCSE11, DBBM09, HMY+19, HZH+10, LPW05, LRM11, Lip05, Vij22, ZS17, ZZS08]. **Whole-Genome** [BFP13, HMY+19, LRM11]. **Wide** [CTC21b, FZF+20, ISB12, IP09, JJY+20, JCBX22, LYMD03, LZHC15, LZBK15, LLT06, LWLJ10, LZX12, PPL+23, TPH+09, WCM+08, WAX22,

WGS+23, WES20, ZPC+18, ZPX+10, KE13, LLKX16]. **Wiener** [YYZ23]. **Wild** [CJ22, RMWC16]. **Wild-Type** [RMWC16]. **Wildcards** [AO15]. **Window** [LS08a, MDK24]. **Winnowing** [BZW+00]. **Wiring** [MR08b]. **Wirings** [HSH+09]. **Wise** [PRT08]. **WITCH** [SPW22]. **Within** [GT16, HVD17, MSRS24, HI96, Tan11, TLK+06, WHC09, YYZ+10, ZZS08]. **Without** [BHKM22, IM14, KV19, LG22, PMAP13, SNW04, SDCF24, TZZY20, WHL17, ZBM98, AT05, HLMR11, HP96]. **Wnt** [AF20, HXL+20]. **Wobble** [WMK17]. **Wobble-Pairing** [WMK17]. **Word** [AaHP+21, BLF14, CZC10, DAE+19, MCC01, RS01, Sch00, SKM05]. **word2vec** [RYY22]. **WordPress** [BP17]. **Words** [ABLX00, ABL03, GML20, LMS96, RS98, RSW00, Sch97b]. **Work** [IP19]. **Workbench** [NCC+96]. **Workflow** [MPG+16, OAR+24, TYSX19]. **Workplace** [LCG+23]. **Workshop** [Ano11b, HSHC15, JLmR+23, DNZ17, DND+19, HHC17, HASL18]. **World** [SPC19, YS19]. **Worst** [CMLTZU14]. **Wrap** [MKBC05]. **Wrap-and-Pack** [MKBC05]. **Wrapper** [RLK+09]. **Wrong** [HQ06].

X [KAC17]. **X-ray** [KAC17]. **XGBoost** [WZL+21].

Y-DNA [Ves12]. **Y-Linked** [GGM12]. **Years** [Ano21a]. **Yeast** [BL02, CGOT10, FS08, FKZ09, KYSE10, LZS09, SIK+05, TRB+09, WMK17]. **Yggdrasil** [AL07]. **Yielding** [ALR18].

Z [Ano20]. **Zebrafish** [LJP20]. **Zernike** [GRM09]. **Zero** [DLFS22, Jia11, PLL16, WVT23]. **Zero-Inflated** [DLFS22, PLL16]. **Zeta** [MMK+21]. **Zigzag** [CGSW14]. **Zinc** [TWY02]. **Zipper** [ODPB18]. **Zseq** [AR17].

References

Alexeev:2018:CSP

[AA18] Nikita Alexeev and Max A. Alekseyev. Combinatorial scoring of phylogenetic trees and networks based on homoplasy-free characters. *Journal of Computational Biology*, 25(11): 1203–1219, November 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0082; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0082`.

Alon:2006:MNG

[AAC+06] Noga Alon, Vera Asodi, Charles Cantor, Simon Kasif, and John Rachlin. Multi-node graphs: a framework for multiplexed biological assays. *Journal of Computational Biol-*

ogy, 13(10):1659–1672, December 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1659; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1659.

Agapie:2014:PCA

[AAG14] Alexandru Agapie, Anca Andreica, and Marius Giuclea. Probabilistic cellular automata. *Journal of Computational Biology*, 21(9):699–708, September 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0074; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0074.

Arango-argoty:2021:MFW

[AaHP+21] Gustavo A. Arango-argoty, Lenwood S. Heath, Amy Pruden, Peter J. Vikesland, and Liqing Zhang. MetaMLP: a fast word embedding based classifier to profile target gene databases in metagenomic samples. *Journal of Computational Biology*, 28(11):1063–1074, November 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0273; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0273.

Asiaee:2020:EGE

[AAN+20] Amir Asiaee, Zachary B. Abrams, Samantha Nakayiza, Deepa Sampath, and Kevin R. Coombes. Explaining gene expression using twenty-one MicroRNAs. *Journal of Computational Biology*, 27(7):1157–1170, July 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0321; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0321.

Seesi:2023:GBT

[AAoS+23] Sahar Al Seesi, Anas Al-okaily, Tatiana V. Shcheglova, Elham Sherafat, Fahad H. Alqahtani, Adam T. Hagymasi, Anupinder Kaur, Pramod K. Srivastava, and Ion I. Măndoiu. GeNeo: a bioinformatics toolbox for genomics-guided neoepitope prediction. *Journal of Computational Biology*, 30(4):538–551, April 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/

abs/10.1089/cmb.2022.0491; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0491.

Apostolico:2000:OAP

[AB00] Alberto Apostolico and Gill Bejerano. Optimal amnesic probabilistic automata or how to learn and classify proteins in linear time and space. *Journal of Computational Biology*, 7(3–4):381–393, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Alic:2016:MHB

[AB16] Andy S. Alic and Ignacio Blanquer. MuffinInfo: HTML5-Based statistics extractor from next-generation sequencing data. *Journal of Computational Biology*, 23(9):750–755, September 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0031; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0031.

Agarwala:1997:LRP

[ABD+97] Richa Agarwala, Serafim Batzoglou, Vlado Dančík, Scott E. Decatur, Sridhar Hannenhalli, Martin Farach, S. Muthukrishnan, and Steven Skiena. Local rules for protein folding on a triangular lattice and generalized hydrophobicity in the HP model. *Journal of Computational Biology*, 4(3):275–296, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.275; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.275.

Adamiak:2004:AAN

[ABF+04] R. W. Adamiak, J. Blazewicz, P. Formanowicz, Z. Gdaniec, M. Kasprzak, M. Popenda, and M. Szachniuk. An algorithm for an automatic NOE pathways analysis of 2D NMR spectra of RNA duplexes. *Journal of Computational Biology*, 11(1):163–179, January 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652704773416948; https://www.liebertpub.com/doi/pdf/10.1089/106652704773416948.

Andersen:2025:PRC

[ABF+25] Jakob L. Andersen, Sissel Banke, Rolf Fagerberg, Christoph Flamm, Daniel Merkle, and Peter F. Stadler. Pathway re-

alizability in chemical networks. *Journal of Computational Biology*, 32(2):164–187, February 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0521; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0521`.

Apaydin:2003:SRS

[ABG+03] Mehmet Serkan Apaydin, Douglas L. Brutlag, Carlos Guestrin, David Hsu, Jean-Claude Latombe, and Chris Varma. Stochastic roadmap simulation: an efficient representation and algorithm for analyzing molecular motion. *Journal of Computational Biology*, 10(3–4):257–281, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Arndt:2003:DSE

[ABH03] Peter F. Arndt, Christopher B. Burge, and Terence Hwa. DNA sequence evolution with neighbor-dependent mutation. *Journal of Computational Biology*, 10(3–4):313–322, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Apostolico:2003:MSL

[ABL03] Alberto Apostolico, Mary Ellen Bock, and Stefano Lonardi. Monotony of surprise and large-scale quest for unusual words. *Journal of Computational Biology*, 10(3–4):283–311, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Apostolico:2000:EDU

[ABLX00] Alberto Apostolico, Mary Ellen Bock, Stefano Lonardi, and Xuyan Xu. Efficient detection of unusual words. *Journal of Computational Biology*, 7(1–2):71–94, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Amar:2016:CUP

[ABR16] Lamiaa A. Amar, Nahla A. Belal, and Shaheera Rashwan. Comparing unlabeled pedigree graphs via covering with bipartite and path. *Journal of Computational Biology*, 23 (11):912–922, November 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0040; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0040`.

Ali:2023:CSC

[ABTP23] Sarwan Ali, Babatunde Bello, Zahra Tayebi, and Murray Patterson. Characterizing SARS-CoV-2 spike sequences based on geographical location. *Journal of Computational Biology*, 30(4):432–445, April 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0391; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0391`.

Apostolico:2010:SCP

[AC10] Alberto Apostolico and Fabio Cunial. The subsequence composition of polypeptides. *Journal of Computational Biology*, 17(8):1011–1049, August 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0073; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0073`.

Anand:2017:EGI

[AC17] Rajat Anand and Samrat Chatterjee. Extracting genes involved in disease from a connected network of perturbed biological processes. *Journal of Computational Biology*, 24(5):460–469, May 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0090; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0090`.

Ahn:2018:PIA

[ACBM18] Jaeil Ahn, Brian Conkright, Simina M. Boca, and Subha Madhavan. POPSTR: Inference of admixed population structure based on single-nucleotide polymorphisms and copy number variations. *Journal of Computational Biology*, 25(4):417–429, April 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0127; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0127`.

Ahn:2019:RNB

[ACKK19] Jaegyoon Ahn, Junhyeok Choi, Harrim Kim, and Jibum Kim. RN^+: a novel biclustering algorithm for analysis of gene expression data using protein–protein interaction network. *Journal of Computational Biology*, 26(5):432–441, May

2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0003; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0003.

Amaratunga:2015:RBS

[ACL15] Dhammika Amaratunga, Javier Cabrera, and Yung-Seop Lee. Resampling-based similarity measures for high-dimensional data. *Journal of Computational Biology*, 22(1):54–62, January 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0195; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0195.

Ali:2021:SFD

[ACL+21] Sarwan Ali, Simone Ciccolella, Lorenzo Lucarella, Gianluca Della Vedova, and Murray Patterson. Simpler and faster development of tumor phylogeny pipelines. *Journal of Computational Biology*, 28(11):1142–1155, November 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0271; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0271.

Albert:2007:NMS

[ADD+07] Réka Albert, Bhaskar DasGupta, Riccardo Dondi, Sema Kachalo, Eduardo Sontag, Alexander Zelikovsky, and Kelly Westbrooks. A novel method for signal transduction network inference from indirect experimental evidence. *Journal of Computational Biology*, 14(7):927–949, September 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0015; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0015.

Adewale:2008:PAM

[ADP+08] A. J. Adewale, I. Dinu, J. D. Potter, Q. Liu, and Y. Yasui. Pathway analysis of microarray data via regression. *Journal of Computational Biology*, 15(3):269–277, April 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0002; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0002.

Akbal-Delibas:2015:APD

[ADPH15] Bahar Akbal-Delibas, Marc Pomplun, and Nurit Haspel. Accurate prediction of docked protein structure similarity. *Journal of Computational Biology*, 22(9):892–904, September 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0114; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0114`.

Allman:2013:STI

[ADR13] Elizabeth S. Allman, James H. Degnan, and John A. Rhodes. Species tree inference by the STAR method and its generalizations. *Journal of Computational Biology*, 20(1):50–61, January 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0101; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0101`.

Ascolani:2024:RPN

[ADR24] Filippo Ascolani, Stefano Damato, and Matteo Ruggiero. An R package for nonparametric inference on dynamic populations with infinitely many types. *Journal of Computational Biology*, 31(12):1305–1311, December 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0600; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0600`.

Arbib:2024:ILP

[ADRS24] Claudio Arbib, Andrea D'ascenzo, Fabrizio Rossi, and Daniele Santoni. An integer linear programming model to optimize coding DNA sequences by joint control of transcript indicators. *Journal of Computational Biology*, 31(5):416–428, May 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0166; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0166`.

Amato:2003:UMP

[ADS03] Nancy M. Amato, Ken A. Dill, and Guang Song. Using motion planning to map protein folding landscapes and analyze folding kinetics of known native structures. *Journal of Computational*

Biology, 10(3–4):239–255, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Akman:2023:BMP

[ADW23] Ozgur E. Akman, Kevin Doherty, and Benjamin J. Wareham. BDEtools: a MATLAB package for Boolean delay equation modeling. *Journal of Computational Biology*, 30(1):52–69, January 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0658; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0658`.

Alkan:2004:RUC

[AEB+04] Can Alkan, Evan E. Eichler, Jeffrey A. Bailey, S. Cenk Şahinalp, and Eray Tüzün. The role of unequal crossover in alpha-satellite DNA evolution: a computational analysis. *Journal of Computational Biology*, 11(5):933–944, October 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.933; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.933`.

Altarawy:2017:PIC

[AEH17] Doaa Altarawy, Fatma-Elzahraa Eid, and Lenwood S. Heath. PEAK: Integrating curated and noisy prior knowledge in gene regulatory network inference. *Journal of Computational Biology*, 24(9):863–873, September 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0199; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0199`.

AlvesPinto:2020:SIP

[AF20] Icaro Alves Pinto and Nelson José Freitas Da Silveira. In silico identification of potential inhibitors of the Wnt signaling pathway in human breast cancer. *Journal of Computational Biology*, 27(7):999–1010, July 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0311; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0311`.

Agarwala:1995:FAI

[AFBS95] Richa Agarwala, David Fernández-Baca, and Giora Slutzki. Fast algorithms for inferring evolutionary trees. *Journal of Computational Biology*, 2(3):397–407, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.397; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.397`.

Andrecut:2009:MIT

[AFCK09] M. Andrecut, D. Foster, H. Carteret, and S. A. Kauffman. Maximal information transfer and behavior diversity in random threshold networks. *Journal of Computational Biology*, 16(7):909–916, July 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0007; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0007`.

Antosh:2013:CCR

[AFCN13] Michael Antosh, David Fox, Leon N. Cooper, and Nicola Neretti. CORaL: Comparison of ranked lists for analysis of gene expression data. *Journal of Computational Biology*, 20(6):433–443, June 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0017; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0017`.

Angibaud:2008:ETC

[AFR+08] Sébastien Angibaud, Guillaume Fertin, Irena Rusu, Annelyse Thévenin, and Stéphane Vialette. Efficient tools for computing the number of breakpoints and the number of adjacencies between two genomes with duplicate genes. *Journal of Computational Biology*, 15(8):1093–1115, October 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0061; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0061`.

Angibaud:2007:PBF

[AFRV07] Sébastien Angibaud, Guillaume Fertin, Irena Rusu, and Stéphane Vialette. A pseudo-Boolean framework for computing rearrangement distances between genomes with dupli-

cates. *Journal of Computational Biology*, 14(4):379–393, May 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.A001; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.A001`.

Apostolico:1998:SAM

[AG98] Alberto Apostolico and Raffaele Giancarlo. Sequence alignment in molecular biology. *Journal of Computational Biology*, 5(2):173–196, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.173; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.173`.

Ashok:2023:ASO

[AG23] Malvika Ashok and Abhishek Gupta. Automatic segmentation of organs-at-risk in thoracic computed tomography images using ensembled U-Net InceptionV3 model. *Journal of Computational Biology*, 30(3):346–362, March 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0248; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0248`.

Alexandrov:2018:TEM

[AGH+18] Theodore Alexandrov, Nina Golyandina, David Holloway, Alex Shlemov, and Alexander Spirov. Two-exponential models of gene expression patterns for noisy experimental data. *Journal of Computational Biology*, 25(11):1220–1230, November 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0063; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0063`.

Alyami:2020:NUH

[AH20] Sultan Alyami and Chun-Hsi Huang. Nongreedy unbalanced Huffman tree compressor for single and multifasta files. *Journal of Computational Biology*, 27(6):868–876, June 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0249; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0249`.

Alzamel:2023:PMS

[AHIV23] Mai Alzamel, Christopher Hampson, Costas Iliopoulos, and Fatima Vayani. Preface: MatBio 2021 special section. *Journal of Computational Biology*, 30(2):117, February 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.29080.pre`.

Aspnes:2002:CTP

[AHK+02] James Aspnes, Julia Hartling, Ming-Yang Kao, Junhyong Kim, and Gauri Shah. A combinatorial toolbox for protein sequence design and landscape analysis in the grand canonical model. *Journal of Computational Biology*, 9(5): 721–741, October 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652702761034154; https://www.liebertpub.com/doi/pdf/10.1089/106652702761034154`.

Angelov:2007:EEP

[AHK+07] Stanislav Angelov, Boulos Harb, Sampath Kannan, Sanjeev Khanna, and Junhyong Kim. Efficient enumeration of phylogenetically informative substrings. *Journal of Computational Biology*, 14(6):701–723, July 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R011; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R011`.

Andrecut:2008:HAS

[AHK08] M. Andrecut, S. Huang, and S. A. Kauffman. Heuristic approach to sparse approximation of gene regulatory networks. *Journal of Computational Biology*, 15(9):1173–1186, November 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0087; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0087`.

Andersen:2012:TRR

[AHPR12] Jørgen E. Andersen, Fenix W. D. Huang, Robert C. Penner, and Christian M. Reidys. Topology of RNA-RNA interaction structures. *Journal of Computational Biology*, 19(7):928–943, July 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-

8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0308; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0308.

Aguiar:2012:HFC

[AI12] Derek Aguiar and Sorin Istrail. HapCompass: a fast cycle basis algorithm for accurate haplotype assembly of sequence data. *Journal of Computational Biology*, 19(6):577–590, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0084; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0084.

Avdeyev:2016:RAG

[AJA+16] Pavel Avdeyev, Shuai Jiang, Sergey Aganezov, Fei Hu, and Max A. Alekseyev. Reconstruction of ancestral genomes in presence of gene gain and loss. *Journal of Computational Biology*, 23(3):150–164, March 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0160; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0160.

Anjum:2016:IDE

[AJV+16] Arfa Anjum, Seema Jaggi, Eldho Varghese, Shwetank Lall, Arpan Bhowmik, and Anil Rai. Identification of differentially expressed genes in RNA-seq data of *Arabidopsis thaliana*: a compound distribution approach. *Journal of Computational Biology*, 23(4):239–247, April 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0205; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0205.

AlNasr:2018:PFC

[AJYJ18] Kamal Al Nasr, Christopher Jones, Feras Yousef, and Ruba Jebril. *PEM-fitter*: a coarse-grained method to validate protein candidate models. *Journal of Computational Biology*, 25(1):21–32, January 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0191; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0191.

Andrecut:2007:PAG

[AK07] M. Andrecut and S. A. Kauffman. A physical analogy of the genetic toggle switch. *Journal of Computational Biology*, 14(7):973–983, September 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0038; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0038`.

Andrecut:2008:SRG

[AK08] M. Andrecut and S. A. Kauffman. On the sparse reconstruction of gene networks. *Journal of Computational Biology*, 15(1):21–30, January 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0185; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0185`.

Alipanahi:2013:DPS

[AKG+13] Babak Alipanahi, Nathan Krislock, Ali Ghodsi, Henry Wolkowicz, Logan Donaldson, and Ming Li. Determining protein structures from NOESY distance constraints by semidefinite programming. *Journal of Computational Biology*, 20(4):296–310, April 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0089; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0089`.

Ay:2011:SAM

[AKK11] Ferhat Ay, Manolis Kellis, and Tamer Kahveci. SubMAP: Aligning metabolic pathways with subnetwork mappings. *Journal of Computational Biology*, 18(3):219–235, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0280; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0280`.

Althaus:2002:CAP

[AKLM02] Ernst Althaus, Oliver Kohlbacher, Hans-Peter Lenhof, and Peter Müller. A combinatorial approach to protein docking with flexible side chains. *Journal of Computational Biology*, 9(4):597–612, August 2002. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652702760277336; https://www.liebertpub.com/doi/pdf/10.1089/106652702760277336.

Alkan:2006:RRI

[AKN+06] Can Alkan, Emre Karakoç, Joseph H. Nadeau, S. Cenk Sahinalp, and Kaizhong Zhang. RNA–RNA interaction prediction and antisense RNA target search. *Journal of Computational Biology*, 13(2):267–282, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.267; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.267.

Akutsu:2004:EEM

[Aku04] Tatsuya Akutsu. Efficient extraction of mapping rules of atoms from enzymatic reaction data. *Journal of Computational Biology*, 11(2–3):449–462, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Alizadeh:1995:PMC

[AKWZ95] Farid Alizadeh, Richard M. Karp, Deborah K. Weisser, and Geoffrey Zweig. Physical mapping of chromosomes using unique probes. *Journal of Computational Biology*, 2 (2):159–184, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.159; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.159.

Andersson:2007:MYS

[AL07] Samuel A. Andersson and Jens Lagergren. Motif Yggdrasil: Sampling sequence motifs from a tree mixture model. *Journal of Computational Biology*, 14(5):682–697, June 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R010; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R010.

Abbasi:2025:DRU

[AL25] Hanieh Abbasi and Amir Lakizadeh. Drug repurposing using hypergraph embedding based on common therapeutic targets of a drug. *Journal of Computational Biology*, 32(3):316–329,

March 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0427; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0427.

Ai:2019:QCB

[ALB+19] Shangjie Ai, Guanfei Lin, Yong Bai, Xiande Liu, and Linghua Piao. QSAR classification-based virtual screening followed by molecular docking identification of potential COX-2 inhibitors in a natural product library. *Journal of Computational Biology*, 26(11):1296–1315, November 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0142; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0142.

Alekseyev:2008:MBR

[Ale08] Max A. Alekseyev. Multi-break rearrangements and breakpoint re-uses: From circular to linear genomes. *Journal of Computational Biology*, 15(8):1117–1131, October 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0080; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0080.

Atitey:2018:DTR

[ALR18] Komlan Atitey, Pavel Loskot, and Paul Rees. Determining the transcription rates yielding steady-state production of mRNA in the *Lac* genetic switch of *Escherichia coli*. *Journal of Computational Biology*, 25(9):1023–1039, September 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0055; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0055.

Anson:1997:RPR

[AM97] Eric L. Anson and Eugene W. Myers. ReAligner: a program for refining DNA sequence multi-alignments. *Journal of Computational Biology*, 4(3):369–383, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.369; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.369.

Alqahtani:2020:SMA

[AM20] Fahad Alqahtani and Ion I. Măndoiu. Statistical mitogenome assembly with RepeaTs. *Journal of Computational Biology*, 27(9):1407–1421, September 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0505; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0505`.

Andonov:2011:MCM

[AMDY11] Rumen Andonov, Noël Malod-Dognin, and Nicola Yanev. Maximum contact map overlap revisited. *Journal of Computational Biology*, 18(1):27–41, January 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0196; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0196`.

Amit:2012:ACC

[Ami12] Roee Amit. Anti-cooperative and cooperative protein-protein interactions between TetR isoforms on synthetic enhancers. *Journal of Computational Biology*, 19(2):115–125, February 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0257; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0257`.

Akutsu:2000:AIB

[AMK00] Tatsuya Akutsu, Satoru Miyano, and Satoru Kuhara. Algorithms for identifying Boolean networks and related biological networks based on matrix multiplication and fingerprint function. *Journal of Computational Biology*, 7(3–4):331–343, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Abella:2018:MED

[AMK18] Jayvee R. Abella, Mark Moll, and Lydia E. Kavraki. Maintaining and enhancing diversity of sampled protein conformations in robotics-inspired methods. *Journal of Computational Biology*, 25(1):3–20, January 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0164;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0164.

Aspnas:2010:COS

[AMOW10] Mats Aspnäs, Kimmo Mattila, Kristoffer Osowski, and Jan Westerholm. Code optimization of the subroutine to remove near identical matches in the sequence database homology search tool PSI-BLAST. *Journal of Computational Biology*, 17(6):819–823, June 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0053; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0053.

Aastrand:2007:ICM

[ÅMR07] Magnus Åstrand, Petter Mostad, and Mats Rudemo. Improved covariance matrix estimators for weighted analysis of microarray data. *Journal of Computational Biology*, 14(10):1353–1367, December 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0078; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0078.

Andersen:2020:CGT

[AMR20] Jakob L. Andersen, Daniel Merkle, and Peter S. Rasmussen. Combining graph transformations and semigroups for isotopic labeling design. *Journal of Computational Biology*, 27(2):269–287, February 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0291; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0291.

Arratia:1996:PPA

[AMRW96] Richard Arratia, Daniela Martin, Gesine Reinert, and Michael S. Waterman. Poisson process approximation for sequence repeats, and sequencing by hybridization. *Journal of Computational Biology*, 3(3):425–463, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.425; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.425.

Anantharaman:1997:GOM

[AMS97] Thomas S. Anantharaman, Bud Mishra, and David C. Schwartz. Genomics via optical mapping II: Ordered restriction maps. *Journal of Computational Biology*, 4(2):91–118, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.91; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.91`.

Altameem:2022:IAG

[AMS+22] Ayman Altameem, Basetty Mallikarjuna, Abdul Khader Jilani Saudagar, Meenakshi Sharma, and Ramesh Chandra Poonia. Improvement of automatic glioma brain tumor detection using deep convolutional neural networks. *Journal of Computational Biology*, 29(6):530–544, June 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0280; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0280`.

Akutsu:2011:DSA

[AMTY11] Tatsuya Akutsu, Avraham A. Melkman, Takeyuki Tamura, and Masaki Yamamoto. Determining a singleton attractor of a Boolean network with nested canalyzing functions. *Journal of Computational Biology*, 18(10):1275–1290, October 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0281; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0281`.

Agarwal:2007:FMS

[AMW07] Pankaj K. Agarwal, Nabil H. Mustafa, and Yusu Wang. Fast molecular shape matching using contact maps. *Journal of Computational Biology*, 14(2):131–143, March 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0004; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0004`.

Altschul:2018:ICA

[AN18] Stephen F. Altschul and Andrew F. Neuwald. Initial cluster analysis. *Journal of Computational Biology*, 25

(2):121–129, February 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0050; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0050`.

Andrecut:2009:PGI

[And09] M. Andrecut. Parallel GPU implementation of iterative PCA algorithms. *Journal of Computational Biology*, 16(11): 1593–1599, November 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0221; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0221`.

Anonymous:1994:EWC

[Ano94] Anonymous. Editorial: Whither computational biology. *Journal of Computational Biology*, 1(1):1–2, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.1`.

Anonymous:2000:ATF

[Ano00] Anonymous. Abstracts from TIGR's Fourth Annual Conference on Computational Genomics November 16–19, 2000 Baltimore, MD. *Journal of Computational Biology*, 7(3–4):631–651, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Anonymous:2002:Ca

[Ano02a] Anonymous. Correction. *Journal of Computational Biology*, 9(3):594–595, June 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/106652702760138646`.

Anonymous:2002:Cb

[Ano02b] Anonymous. Correction. *Journal of Computational Biology*, 9(4):685, August 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/106652702760277390`.

Anonymous:2005:C

[Ano05] Anonymous. Correction. *Journal of Computational Biology*, 12 (6):907, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print),

1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.907.

Anonymous:2008:C

[Ano08] Anonymous. Correction. *Journal of Computational Biology*, 15(8):1132, October 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.C002.

Anonymous:2009:C

[Ano09a] Anonymous. Correction. *Journal of Computational Biology*, 16 (6):886, June 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.00C1.

Anonymous:2009:SRI

[Ano09b] Anonymous. Special RECOMB 2008 issue. *Journal of Computational Biology*, 16(8):969, August 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.001P.

Anonymous:2010:P

[Ano10a] Anonymous. Preface. *Journal of Computational Biology*, 17 (9):1095–1096, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.004p.

Anonymous:2010:RMC

[Ano10b] Anonymous. RECOMB Main Conference 2009. *Journal of Computational Biology*, 17(3):201, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.Pr01.

Anonymous:2011:C

[Ano11a] Anonymous. Correction. *Journal of Computational Biology*, 18(1):129, January 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.cor1.

Anonymous:2011:PSW

[Ano11b] Anonymous. Preface: Satellite Workshop on Comparative Genomics, Research in Computational Molecular Biol-

ogy (RECOMB-CG 2010). *Journal of Computational Biology*, 18(9):1019–1021, September 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.008p; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.008p.

Anonymous:2014:CJC

[Ano14] Anonymous. Correction: *Journal of Computational Biology*: 2014; **21**/4:303–319. *Journal of Computational Biology*, 21(6): 476, June 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.Cor1. See [KW14].

Anonymous:2017:PSP

[Ano17] Anonymous. Preface: Selected papers from RECOMB 2016. *Journal of Computational Biology*, 24(6):471, June 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.29006.ms.

Anonymous:2020:RIP

[Ano20] Anonymous. *Retraction of*: Identification of Prognosis Biomarkers of Prostatic Cancer in a Cohort of 498 Patients from TCGA, by Chen Z, Hu H. (J Comput Biol Dec 2019: epub ahead of print; DOI: 10.1089/cmb.2019.0224). *Journal of Computational Biology*, 27(4):673, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0224.retract.

Anonymous:2021:JCP

[Ano21a] Anonymous. *JCB* call for papers for the special issue on "40 Years of Computational Biology: In Honor of Professor Michael Waterman's 80th Birthday". *Journal of Computational Biology*, 28(7):633–635, July 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/fpi/10.1089/cmb.2021.29043.cfp; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.29043.cfp.

Anonymous:2021:RSP

[Ano21b] Anonymous. *Retraction of:* A Study of Potential SARS-CoV-2 Antiviral Drugs and Preliminary Research of Their Molecu-

lar Mechanism, Based on Anti-SARS-CoV Drug Screening and Molecular Dynamics Simulation (doi: 10.1089/cmb.2020.0112). *Journal of Computational Biology*, 28(7):744, July 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0112.retract`.

Anonymous:2022:AR

[Ano22a] Anonymous. Acknowledgment of reviewers 2021. *Journal of Computational Biology*, 29(1):1, January 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.29053.ack`.

Anonymous:2022:RSC

[Ano22b] Anonymous. *Retraction of:* Screening of clinical factors related to prognosis of breast cancer based on the Cox proportional risk model (doi: `10.1089/cmb.2019.0110`). *Journal of Computational Biology*, 29(6):597, June 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2019.0110.retract`. See [TMH+21].

Anonymous:2023:AR

[Ano23] Anonymous. Acknowledgment of reviewers 2022. *Journal of Computational Biology*, 30(1):1–2, January 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.29078.ack`.

Anonymous:2024:AR

[Ano24] Anonymous. Acknowledgment of reviewers 2023. *Journal of Computational Biology*, 31(1):1, January 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.29108.ack`.

Anonymous:2025:AR

[Ano25] Anonymous. Acknowledgment of reviewers 2024. *Journal of Computational Biology*, 32(1):1–2, January 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.10852.revack`.

Anandakrishnan:2008:ABC

[AO08] Ramu Anandakrishnan and Alexey Onufriev. Analysis of basic clustering algorithms for numerical estimation of statistical averages in biomolecules. *Journal of Computational Biology*, 15(2):165–184, March 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0144; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0144`.

Al-Okaily:2015:ETT

[AO15] Anas Al-Okaily. Error tree: a tree structure for Hamming and edit distances and wildcards matching. *Journal of Computational Biology*, 22(12):1118–1128, December 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0132; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0132`.

Al-Okaily:2017:TBC

[AOAAH17] Anas Al-Okaily, Badar Almarri, Sultan Al Yami, and Chun-Hsi Huang. Toward a better compression for DNA sequences using Huffman encoding. *Journal of Computational Biology*, 24(4):280–288, April 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0151; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0151`.

Alexandrino:2021:GRD

[AODD21] Alexsandro Oliveira Alexandrino, Andre Rodrigues Oliveira, Ulisses Dias, and Zanoni Dias. Genome rearrangement distance with reversals, transpositions, and indels. *Journal of Computational Biology*, 28(3):235–247, March 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0121; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0121`.

Alexandrino:2022:LCG

[AODD22] Alexsandro Oliveira Alexandrino, Andre Rodrigues Oliveira, Ulisses Dias, and Zanoni Dias. Labeled cycle graph for transposition and indel distance. *Journal of Computational Biol-*

ogy, 29(3):243–256, March 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0279; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0279.

Al-Okaily:2016:MSE

[AOH16] Anas Al-Okaily and Chun-Hsi Huang. ET-Motif: Solving the exact (l, d)-planted motif problem using error tree structure. *Journal of Computational Biology*, 23(7):615–623, July 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0238; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0238.

Alexandrino:2023:RTD

[AOJ+23] Alexsandro Oliveira Alexandrino, Andre Rodrigues Oliveira, Géraldine Jean, Guillaume Fertin, Ulisses Dias, and Zanoni Dias. Reversal and transposition distance on unbalanced genomes using intergenic information. *Journal of Computational Biology*, 30(8):861–876, August 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0087; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0087.

Apostolico:2004:IPM

[AP04] Alberto Apostolico and Laxmi Parida. Incremental paradigms of motif discovery. *Journal of Computational Biology*, 11 (1):15–25, January 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652704773416867; https://www.liebertpub.com/doi/pdf/10.1089/106652704773416867.

August:2009:NCT

[AP09] Elias August and Antonis Papachristodoulou. A new computational tool for establishing model parameter identifiability. *Journal of Computational Biology*, 16(6):875–885, June 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0211; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0211.

Ahn:2010:FUB

[AP10] Namsu Ahn and Sungsoo Park. Finding an upper bound for the number of contacts in hydrophobic-hydrophilic protein structure prediction model. *Journal of Computational Biology*, 17(4):647–656, April 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0009; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0009`.

Alexeev:2017:GHN

[APA17] Nikita Alexeev, Anna Pologova, and Max A. Alekseyev. Generalized Hultman numbers and cycle structures of breakpoint graphs. *Journal of Computational Biology*, 24(2):93–105, February 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0190; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0190`.

Andreace:2021:MMR

[APC21] Francesco Andreace, Cinzia Pizzi, and Matteo Comin. MetaProb 2: Metagenomic reads binning based on assembly using minimizers and K-mers statistics. *Journal of Computational Biology*, 28(11):1052–1062, November 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0270; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0270`.

Almodaresi:2020:ESE

[APF+20] Fatemeh Almodaresi, Prashant Pandey, Michael Ferdman, Rob Johnson, and Rob Patro. An efficient, scalable, and exact representation of high-dimensional color information enabled using de Bruijn graph search. *Journal of Computational Biology*, 27(4):485–499, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0322; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0322`.

Apostolico:2007:Pa

[Apo07a] Alberto Apostolico. Preface. *Journal of Computational Biology*, 14(5):537–538, June 2007. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.00P1.

Apostolico:2007:Pb

[Apo07b] Alberto Apostolico. Preface. *Journal of Computational Biology*, 14(6):699–700, July 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.00P2.

Adamczak:2011:FGC

[APVM11] Rafał Adamczak, Jaroslaw Pillardy, Brinda K. Vallat, and Jaroslaw Meller. Fast geometric consensus approach for protein model quality assessment. *Journal of Computational Biology*, 18(12):1807–1818, December 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0170; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0170.

Allman:2006:ITT

[AR06] Elizabeth S. Allman and John A. Rhodes. The identifiability of tree topology for phylogenetic models, including covarion and mixture models. *Journal of Computational Biology*, 13(5):1101–1113, June 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1101; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1101.

Alkhateeb:2017:ZAP

[AR17] Abedalrhman Alkhateeb and Luis Rueda. Zseq: an approach for preprocessing next-generation sequencing data. *Journal of Computational Biology*, 24(8):746–755, August 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0021; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0021.

Andreotti:2013:DLS

[ARC13] Sandro Andreotti, Knut Reinert, and Stefan Canzar. The duplication-loss small phylogeny problem: From cherries to trees. *Journal of Computational Biology*, 20(9):643–659, September 2013. CODEN JCOBEM. ISSN 1066-5277 (print),

1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0057; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0057.

Acosta:2019:MMI

[ARHLK19] Juan Pablo Acosta, Silvia Restrepo, Juan David Henao, and Liliana López-Kleine. Multivariate method for inferential identification of differentially expressed genes in gene expression experiments. *Journal of Computational Biology*, 26(8):866–874, August 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0013; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0013.

Adleman:1999:AMC

[ARRW99] Leonard M. Adleman, Paul W. K. Rothemund, Sam Roweis, and Erik Winfree. On applying molecular computation to the Data Encryption Standard. *Journal of Computational Biology*, 6(1):53–63, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.53; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.53.

Allman:2017:SCM

[ARS17] Elizabeth S. Allman, John A. Rhodes, and Seth Sullivant. Statistically consistent k-mer methods for phylogenetic tree reconstruction. *Journal of Computational Biology*, 24(2):153–171, February 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0216; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0216.

An:2022:NCT

[ARSW22] Shaokun An, Jie Ren, Fengzhu Sun, and Lin Wan. A new context tree inference algorithm for variable length Markov chain model with applications to biological sequence analyses. *Journal of Computational Biology*, 29(8):839–856, August 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0604; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0604.

Armen:1995:SSS

[AS95] Chris Armen and Clifford Stein. Short superstrings and the structure of overlapping strings. *Journal of Computational Biology*, 2(2):307–332, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.307; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.307`.

Agarwal:1996:BED

[AS96] Pankaj Agarwal and David J. States. A Bayesian evolutionary distance for parametrically aligned sequences. *Journal of Computational Biology*, 3(1):1–17, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.1; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.1`.

Amato:2002:UMP

[AS02] Nancy M. Amato and Guang Song. Using motion planning to study protein folding pathways. *Journal of Computational Biology*, 9(2):149–168, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270252935395; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935395`.

Adam:2010:SFC

[AS10] Zaky Adam and David Sankoff. A statistically fair comparison of ancestral genome reconstructions, based on breakpoint and rearrangement distances. *Journal of Computational Biology*, 17(9):1299–1314, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0121; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0121`.

Atias:2011:AFP

[AS11] Nir Atias and Roded Sharan. An algorithmic framework for predicting side effects of drugs. *Journal of Computational Biology*, 18(3):207–218, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0255;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0255.

Avni:2019:NQB

[AS19] Eliran Avni and Sagi Snir. A new quartet-based statistical method for comparing sets of gene trees is developed using a generalized Hoeffding inequality. *Journal of Computational Biology*, 26(1):27–37, January 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0129; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0129.

Alkhathlan:2022:PCB

[AS22] Lina Alkhathlan and Abdul Khader Jilani Saudagar. Predicting and classifying breast cancer using machine learning. *Journal of Computational Biology*, 29(6):497–514, June 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0236; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0236.

Alnasir:2023:IEM

[AS23] Jamie J. Alnasir and Hugh P. Shanahan. Intra-exon Motif correlations as a proxy measure for mean per-tile sequence quality data in RNA-Seq. *Journal of Computational Biology*, 30(2):131–148, February 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0476; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0476.

Aouabed:2020:VMB

[ASE20] Haithem Aouabed, Rodrigo SantamaríA, and Mourad Elloumi. VisBicluster: a matrix-based bicluster visualization of expression data. *Journal of Computational Biology*, 27(9):1384–1396, September 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0385; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0385.

Ayers:2006:RAH

[ASL06] Kristin L. Ayers, Chiara Sabatti, and Kenneth Lange. Reconstructing ancestral haplotypes with a dictionary model. *Journal of Computational Biology*, 13(3):767–785, April 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.767; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.767`.

Aastrand:2003:CNO

[Åst03] Magnus Åstrand. Contrast normalization of oligonucleotide arrays. *Journal of Computational Biology*, 10(1):95–102, February 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652703763255697; https://www.liebertpub.com/doi/pdf/10.1089/106652703763255697`.

Aridhi:2016:PIR

[ASZ+16] Sabeur Aridhi, Haïtham Sghaier, Manel Zoghlami, Mondher Maddouri, and Engelbert Mephu Nguifo. Prediction of ionizing radiation resistance in bacteria using a multiple instance learning model. *Journal of Computational Biology*, 23(1):10–20, January 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0134; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0134`.

Aung:2005:APS

[AT05] Zeyar Aung and Kian-Lee Tan. Automatic 3D protein structure classification without structural alignment. *Journal of Computational Biology*, 12(9):1221–1241, November 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1221; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1221`.

Arndt:2008:IRM

[AT08] William Arndt and Jijun Tang. Improving reversal median computation using commuting reversals and cycle information. *Journal of Computational Biology*, 15(8):1079–1092, October 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0116; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0116.

Arima:2012:IHM

[AT12] Serena Arima and Luca Tardella. Improved harmonic mean estimator for phylogenetic model evidence. *Journal of Computational Biology*, 19(4):418–438, April 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0139; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0139.

Adam:2007:CIS

[ATLS07] Zaky Adam, Monique Turmel, Claude Lemieux, and David Sankoff. Common intervals and symmetric difference in a model-free phylogenomics, with an application to streptophyte evolution. *Journal of Computational Biology*, 14(4):436–445, May 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.A005; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.A005.

August:2012:UNM

[Aug12] Elias August. Using noise for model-testing. *Journal of Computational Biology*, 19(8):968–977, August 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0134; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0134.

Ahn:2018:ABM

[AV18] Soyeon Ahn and Haris Vikalo. aBayesQR: a Bayesian method for reconstruction of viral populations characterized by low diversity. *Journal of Computational Biology*, 25(7):637–648, July 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0249; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0249.

Ahsen:2020:RPS

[AVS20] Mehmet Eren Ahsen, Robert Vogel, and Gustavo A. Stolovitzky. R/PY-SUMMA: an R/Python package for unsupervised ensemble

learning for binary classification problems in bioinformatics. *Journal of Computational Biology*, 27(9):1337–1340, September 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0348; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0348`.

Artyomenko:2017:LSM

[AWM+17] Alexander Artyomenko, Nicholas C. Wu, Serghei Mangul, Eleazar Eskin, Ren Sun, and Alex Zelikovsky. Long single-molecule reads can resolve the complexity of the influenza virus composed of rare, closely related mutant variants. *Journal of Computational Biology*, 24(6):558–570, June 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0146; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0146`.

Ai:2017:PPP

[AWZ+17] Haixin Ai, Runlin Wu, Li Zhang, Xuewei Wu, Junchao Ma, Huan Hu, Liangchao Huang, Wen Chen, Jian Zhao, and Hongsheng Liu. pSuc-PseRat: Predicting Lysine succinylation in proteins by exploiting the ratios of sequence coupling and properties. *Journal of Computational Biology*, 24(10):1050–1059, October 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0206; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0206`.

Amir:2011:BCR

[AZ11] Amnon Amir and Or Zuk. Bacterial community reconstruction using compressed sensing. *Journal of Computational Biology*, 18(11):1723–1741, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0189; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0189`.

Alexeev:2014:RMA

[AZ14] Nikita Alexeev and Peter Zograf. Random matrix approach to the distribution of genomic distance. *Journal of Computational Biology*, 21(8):622–631, August 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0066;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0066.

Aziz:2022:CSB

[Azi22] Rabia Musheer Aziz. Cuckoo search-based optimization for cancer classification: a new hybrid approach. *Journal of Computational Biology*, 29(6):565–584, June 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0410; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0410.

Bafna:2011:PRC

[Baf11] Vineet Bafna. Preface: Research in Computational Molecular Biology (RECOMB 2011). *Journal of Computational Biology*, 18(11):1369, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.009p.

Bansal:2013:RRH

[BAK13] Mukul S. Bansal, Eric J. Alm, and Manolis Kellis. Reconciliation revisited: Handling multiple optima when reconciling with duplication, transfer, and loss. *Journal of Computational Biology*, 20(10):738–754, October 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0073; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0073.

Baldi:1995:SMH

[Bal95] Pierre Baldi. Substitution matrices and hidden Markov models. *Journal of Computational Biology*, 2(3):487–491, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.487; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.487.

Barash:2004:SDS

[Bar04] Danny Barash. Spectral decomposition for the search and analysis of RNA secondary structure. *Journal of Computational Biology*, 11(6):1169–1174, December 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.

1089/cmb.2004.11.1169; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.1169.

Bayzid:2023:IOS

[Bay23] Md. Shamsuzzoha Bayzid. Inferring optimal species trees in the presence of gene duplication and loss: Beyond rooted gene trees. *Journal of Computational Biology*, 30(2):161–175, February 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0522; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0522.

Benham:2004:ASI

[BB04] Craig J. Benham and Chengpeng Bi. The analysis of stress-induced duplex destabilization in long genomic DNA sequences. *Journal of Computational Biology*, 11(4):519–543, August 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.519; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.519.

Bafna:2006:IAR

[BB06] Vineet Bafna and Vikas Bansal. Inference about recombination from haplotype data: Lower bounds and recombination hotspots. *Journal of Computational Biology*, 13 (2):501–521, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.501; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.501.

Baur:2015:CCA

[BB15] Brittany Baur and Serdar Bozdag. A canonical correlation analysis-based dynamic Bayesian network prior to infer gene regulatory networks from multiple types of biological data. *Journal of Computational Biology*, 22(4):289–299, April 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0296; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0296.

Ben-Bassat:2016:CDS

[BBC16] Ilan Ben-Bassat and Benny Chor. CRISPR detection from short reads using partial overlap graphs. *Journal of Compu-*

tational Biology, 23(6):461–471, June 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0226; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0226.

Berman:2004:FOG

[BBD+04] Piotr Berman, Paul Bertone, Bhaskar Dasgupta, Mark Gerstein, Ming-Yang Kao, and Michael Snyder. Fast optimal genome tiling with applications to microarray design and homology search. *Journal of Computational Biology*, 11(4):766–785, August 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.766; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.766.

Bohnenkamper:2021:CRD

[BBDS21] Leonard Bohnenkämper, Marília D. V. Braga, Daniel Doerr, and Jens Stoye. Computing the rearrangement distance of natural genomes. *Journal of Computational Biology*, 28(4):410–431, April 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Bertrand:2009:GMR

[BBEM09] Denis Bertrand, Mathieu Blanchette, and Nadia El-Mabrouk. Genetic map refinement using a comparative genomic approach. *Journal of Computational Biology*, 16(10):1475–1486, October 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0094; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0094.

Bansal:2011:DHH

[BBGS11] Mukul S. Bansal, Guy Banay, J. Peter Gogarten, and Ron Shamir. Detecting highways of horizontal gene transfer. *Journal of Computational Biology*, 18(9):1087–1114, September 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0066; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0066.

Blin:2007:GML

[BBH+07] Guillaume Blin, Eric Blais, Danny Hermelin, Pierre Guillon, Mathieu Blanchette, and Nadia El-Mabrouk. Gene maps linearization using genomic rearrangement distances. *Journal of Computational Biology*, 14(4):394–407, May 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.A002; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.A002`.

Barrett:2021:MFL

[BBH+21] Christopher Barrett, Andrei C. Bura, Qijun He, Fenix W. Huang, Thomas J. X. Li, Michael S. Waterman, and Christian M. Reidys. Multiscale feedback loops in SARS-CoV-2 viral evolution. *Journal of Computational Biology*, 28(3):248–256, March 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0343; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0343`.

Bandaru:2011:MCI

[BBN11] Pradeep Bandaru, Mukesh Bansal, and Ilya Nemenman. Mass conservation and inference of metabolic networks from high-throughput mass spectrometry data. *Journal of Computational Biology*, 18(2):147–154, February 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0222; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0222`.

Benth:2024:NIT

[BBN24] JūratĖ ŠaltytĖ Benth, Fred Espen Benth, and Espen Rostrup Nakstad. Nearly instantaneous time-varying reproduction number for contagious diseases — a direct approach based on nonlinear regression. *Journal of Computational Biology*, 31(8):727–741, August 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0414; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0414`.

Belcaid:2010:MGC

[BBP10] Mahdi Belcaid, Anne Bergeron, and Guylaine Poisson. Mosaic graphs and comparative genomics in phage communities. *Journal of Computational Biology*, 17(9):1315–1326, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0108; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0108`.

Beretta:2014:MAS

[BBV+14] Stefano Beretta, Paola Bonizzoni, Gianluca Della Vedova, Yuri Pirola, and Raffaella Rizzi. Modeling alternative splicing variants from RNA-Seq data with isoform graphs. *Journal of Computational Biology*, 21(1):16–40, January 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0112; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0112`.

Burleigh:2009:LLS

[BBWE09] J. G. Burleigh, M. S. Bansal, A. Wehe, and O. Eulenstein. Locating large-scale gene duplication events through reconciled trees: Implications for identifying ancient polyploidy events in plants. *Journal of Computational Biology*, 16(8):1071–1083, August 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0139; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0139`.

Baldi:1994:HMM

[BC94] Pierre Baldi and Yves Chauvin. Hidden Markov models of the G-protein-coupled receptor family. *Journal of Computational Biology*, 1(4):311–336, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.311; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.311`.

Bhandarkar:1996:PCP

[BCA96] Suchendra M. Bhandarkar, Sridhar Chirravuri, and Jonathan Arnold. Parallel computing of physical maps — a comparative study in SIMD and MIMD parallelism. *Journal of Computational Biology*, 3(4):503–528, January 1996. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.503; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.503`.

Bourgeade:2015:CSS

[BCA15] Laetitia Bourgeade, Cédric Chauve, and Julien Allali. Chaining sequence/structure seeds for computing RNA similarity. *Journal of Computational Biology*, 22(3):205–217, March 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0283; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0283`.

Berard:2009:CPD

[BCC+09] Sèverine Bérard, Annie Chateau, Cedric Chauve, Christophe Paul, and Eric Tannier. Computation of perfect DCJ rearrangement scenarios with linear and circular chromosomes. *Journal of Computational Biology*, 16(10):1287–1309, October 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0088; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0088`.

Benshahar:2018:BAR

[BCCHZU18] Arnon Benshahar, Vered Chalifa-Caspi, Danny Hermelin, and Michal Ziv-Ukelson. A biclique approach to reference-anchored gene blocks and its applications to genomic islands. *Journal of Computational Biology*, 25(2):214–235, February 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0108; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0108`.

Bolteau:2024:BNM

[BCD+24] Mathieu Bolteau, Lokmane Chebouba, Laurent David, Jérémie Bourdon, and Carito Guziolowski. Boolean network models of human preimplantation development. *Journal of Computational Biology*, 31(6):513–523, June 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Beretta:2018:IEA

[BCG+18] Stefano Beretta, Mauro Castelli, Ivo Gonçalves, Ivan Kel, Valentina Giansanti, and Ivan Merelli. Improving eQTL analysis using a machine learning approach for data integration: a logistic model tree solution. *Journal of Computational Biology*, 25(10):1091–1105, October 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0167; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0167`.

Baggerly:2001:IDE

[BCH+01] Keith A. Baggerly, Kevin R. Coombes, Kenneth R. Hess, David N. Stivers, Lynne V. Abruzzo, and Wei Zhang. Identifying differentially expressed genes in cDNA microarray experiments. *Journal of Computational Biology*, 8(6):639–659, November 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652701753307539; https://www.liebertpub.com/doi/pdf/10.1089/106652701753307539`.

Backofen:2007:LGR

[BCH+07] Rolf Backofen, Shihyen Chen, Danny Hermelin, Gad M. Landau, Mikhail A. Roytberg, Oren Weimann, and Kaizhong Zhang. Locality and gaps in RNA comparison. *Journal of Computational Biology*, 14(8):1074–1087, October 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0062; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0062`.

Bay:2004:TAB

[BCPS04] S. D. Bay, L. Chrisman, A. Pohorille, and J. Shrager. Temporal aggregation bias and inference of causal regulatory networks. *Journal of Computational Biology*, 11 (5):971–985, October 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.971; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.971`.

Barros-Carvalho:2017:EAE

[BCVL17] Gesiele Almeida Barros-Carvalho, Marie-Anne Van Sluys, and Fabricio Martins Lopes. An efficient approach to explore and discriminate anomalous regions in bacterial genomes based on maximum entropy. *Journal of Computational Biology*, 24 (11):1125–1133, November 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0042; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0042`.

Boden:2010:BNM

[BDBB10] Mikael Bodén, Graham Dellaire, Kevin Burrage, and Timothy L. Bailey. A Bayesian network model of proteins' association with promyelocytic leukemia (PML) nuclear bodies. *Journal of Computational Biology*, 17(4):617–630, April 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0140; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0140`.

Ben-Dor:2000:TCG

[BDBF+00] Amir Ben-Dor, Laurakay Bruhn, Nir Friedman, Iftach Nachman, Michèl Schummer, and Zohar Yakhini. Tissue classification with gene expression profiles. *Journal of Computational Biology*, 7(3–4):559–583, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Ben-Dor:1997:CRH

[BDC97] Amir Ben-Dor and Benny Chor. On constructing radiation hybrid maps. *Journal of Computational Biology*, 4 (4):517–533, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.517; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.517`.

Ben-Dor:1998:CPQ

[BDCG+98] Amir Ben-Dor, Benny Chor, Dan Graur, Ron Ophir, and Dan Pelleg. Constructing phylogenies from quartets: Elucidation of Eutherian superordinal relationships. *Journal of Computational Biology*, 5(3):377–390, January 1998. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.377; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.377`.

Ben-Dor:2003:DLS

[BDCKY03] Amir Ben-Dor, Benny Chor, Richard Karp, and Zohar Yakhini. Discovering local structure in gene expression data: The order-preserving submatrix problem. *Journal of Computational Biology*, 10(3–4):373–384, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Ben-Dor:2004:TOM

[BDHK+04] Amir Ben-Dor, Tzvika Hartman, Richard M. Karp, Benno Schwikowski, Roded Sharan, and Zohar Yakhini. Towards optimally multiplexed applications of universal arrays. *Journal of Computational Biology*, 11(2–3):476–492, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Bonizzoni:2016:MEC

[BDK+16] Paola Bonizzoni, Riccardo Dondi, Gunnar W. Klau, Yuri Pirola, Nadia Pisanti, and Simone Zaccaria. On the minimum error correction problem for haplotype assembly in diploid and polyploid genomes. *Journal of Computational Biology*, 23(9):718–736, September 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0220; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0220`.

Ben-Dor:2003:RSP

[BDKSS03] Amir Ben-Dor, Richard M. Karp, Benno Schwikowski, and Ron Shamir. The restriction scaffold problem. *Journal of Computational Biology*, 10(3–4):385–398, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Ben-Dor:2000:UDT

[BDKSY00] Amir Ben-Dor, Richard Karp, Benno Schwikowski, and Zohar Yakhini. Universal DNA tag systems: a combinatorial design scheme. *Journal of Computational Biology*, 7(3–4):503–519, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Bishop:2007:FEG

[BDM+07] Morgan A. Bishop, Arkadii G. D'Yachkov, Anthony J. Macula, Thomas E. Renz, and Vyacheslav V. Rykov. Free energy gap and statistical thermodynamic fidelity of DNA codes. *Journal of Computational Biology*, 14(8):1088–1104, October 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0083; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0083`.

Bazin:2019:NRC

[BDN19] Alexandre Bazin, Didier Debroas, and Engelbert Mephu Nguifo. A de novo robust clustering approach for amplicon-based sequence data. *Journal of Computational Biology*, 26(6):618–624, June 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0170; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0170`.

Ben-Dor:2001:CPS

[BDPSS01] A. Ben-Dor, I. Pe'er, R. Shamir, and R. Sharan. On the complexity of positional sequencing by hybridization. *Journal of Computational Biology*, 8(4):361–371, September 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652701752236188; https://www.liebertpub.com/doi/pdf/10.1089/106652701752236188`.

Ben-Dor:1999:CGE

[BDSY99] Amir Ben-Dor, Ron Shamir, and Zohar Yakhini. Clustering gene expression patterns. *Journal of Computational Biology*, 6(3–4):281–297, October 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Beaver:1995:CD

[Bea95] Donald Beaver. Computing with DNA. *Journal of Computational Biology*, 2(1):1–7, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.1; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.1`.

Benson:1997:SAT

[Ben97] Gary Benson. Sequence alignment with tandem duplication. *Journal of Computational Biology*, 4(3):351–367, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.351; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.351`.

Bentil:1998:MSM

[Ben98] Daniel E. Bentil. Modelling and simulation of motility in actomyosin systems. *Journal of Computational Biology*, 5(1):73–86, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.73; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.73`.

Benner:2021:CLR

[Ben21] Philipp Benner. Computing leapfrog regularization paths with applications to large-scale K-mer logistic regression. *Journal of Computational Biology*, 28(6):560–569, June 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0284; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0284`.

Berger:1995:APS

[Ber95] Bonnie Berger. Algorithms for protein structural motif recognition. *Journal of Computational Biology*, 2(1):125–138, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.125; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.125`.

Berger:2011:PIC

[Ber11] Bonnie Berger. Preface: 14^{th} International Conference on Research in Computational Molecular Biology (RECOMB 2010). *Journal of Computational Biology*, 18(3):205, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.006p`.

Berezovsky:2000:HRA

[BET00] Igor N. Berezovsky, Natalia G. Esipova, and Vladimir G. Tumanyan. Hierarchy of regions of amino acid sequence with respect to their role in the protein spatial structure. *Journal of Computational Biology*, 7(1–2):183–192, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Betancourt:2010:CBM

[Bet10] Marcos R. Betancourt. Comparison between molecular dynamic based and knowledge based potentials for protein side chains. *Journal of Computational Biology*, 17(7):943–952, July 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0152; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0152`.

Badretdinov:1998:HHC

[BF98] Azat Ya Badretdinov and Alexei V. Finkelstein. How homologs can help to predict protein folds even though they cannot be predicted for individual sequences. *Journal of Computational Biology*, 5(3):369–376, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.369; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.369`.

Barash:2002:CSB

[BF02] Yoseph Barash and Nir Friedman. Context-specific Bayesian clustering for gene expression data. *Journal of Computational Biology*, 9(2):169–191, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270252935403; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935403`.

Borenstein:2009:TSS

[BF09] Elhanan Borenstein and Marcus W. Feldman. Topological signatures of species interactions in metabolic networks. *Journal of Computational Biology*, 16(2):191–200, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.06TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.06TT`.

Blazewicz:1999:DSP

[BFK+99] J. Błażewicz, P. Formanowicz, M. Kasprzak, W. T. Markiewicz, and J. Węglarz. DNA sequencing with positive and negative errors. *Journal of Computational Biology*, 6(1):113–123, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.113; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.113`.

Berge:2010:MFM

[BFK+10] Claude Berge, Nicolas Froloff, Ravi Kiran Reddy Kalathur, Myriam Maumy, Olivier Poch, Wolfgang Raffelsberger, and Nicolas Wicker. Multidimensional fitting for multivariate data analysis. *Journal of Computational Biology*, 17(5):723–732, May 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0126; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0126`.

Blazewicz:2011:RPD

[BFK+11] Jacek Blazewicz, Marek Figlerowicz, Marta Kasprzak, Martyna Nowacka, and Agnieszka Rybarczyk. RNA partial degradation problem: Motivation, complexity, algorithm. *Journal of Computational Biology*, 18(6):821–834, June 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0153; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0153`.

Blekas:2005:MBP

[BFL05] Konstantinos Blekas, Dimitrios I. Fotiadis, and Aristidis Likas. Motif-based protein sequence classification using neural networks. *Journal of Computational Biology*, 12 (1):64–82, February 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.64; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.64`.

Bryant:2013:AME

[BFP13] William A. Bryant, Ali A. Faruqi, and John W. Pinney. Analysis of metabolic evolution in bacteria using whole-genome metabolic

models. *Journal of Computational Biology*, 20(10):755–764, October 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0079; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0079.

Blin:2010:FNC

[BFS10] Guillaume Blin, David Faye, and Jens Stoye. Finding nested common intervals efficiently. *Journal of Computational Biology*, 17(9):1183–1194, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0089; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0089.

Bejerano:2004:EEV

[BFT04] Gill Bejerano, Nir Friedman, and Naftali Tishby. Efficient exact p-value computation for small sample, sparse, and surprising categorical data. *Journal of Computational Biology*, 11(5):867–886, October 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.867; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.867.

Bailey:1997:SDS

[BG97] Timothy L. Bailey and Michael Gribskov. Score distributions for simultaneous matching to multiple motifs. *Journal of Computational Biology*, 4(1):45–59, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.45; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.45.

Bailey:1998:MSC

[BG98] Timothy L. Bailey and Michael Gribskov. Methods and statistics for combining motif match scores. *Journal of Computational Biology*, 5(2):211–221, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.211; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.211.

Bailey:2002:EES

[BG02] Timothy L. Bailey and Michael Gribskov. Estimating and evaluating the statistics of gapped local-alignment scores. *Journal of Computational Biology*, 9(3):575–593, June 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652702760138637; https://www.liebertpub.com/doi/pdf/10.1089/106652702760138637`.

Bern:2006:NAP

[BG06] Marshall Bern and David Goldberg. *De Novo* analysis of peptide tandem mass spectra by spectral graph partitioning. *Journal of Computational Biology*, 13(2):364–378, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.364; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.364`.

Bern:2008:IRF

[BG08] Marshall Bern and David Goldberg. Improved ranking functions for protein and modification-site identifications. *Journal of Computational Biology*, 15(7):705–719, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0119; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0119`.

Bercovici:2009:IAE

[BG09] Sivan Bercovici and Dan Geiger. Inferring ancestries efficiently in admixed populations with linkage disequilibrium. *Journal of Computational Biology*, 16(8):1141–1150, August 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0105; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0105`.

Bercovici:2011:AAA

[BG11] Sivan Bercovici and Dan Geiger. Admixture aberration analysis: Application to mapping in admixed population using pooled DNA. *Journal of Computational Biology*, 18(3):237–249, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/`

10.1089/cmb.2010.0250; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0250.

Bois:2015:PGR

[BG15] Frederic Y. Bois and Ghislaine Gayraud. Probabilistic generation of random networks taking into account information on motifs occurrence. *Journal of Computational Biology*, 22(1):25–36, January 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0175; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0175.

Bogdanowicz:2017:CPT

[BG17] Damian Bogdanowicz and Krzysztof Giaro. Comparing phylogenetic trees by matching nodes using the transfer distance between partitions. *Journal of Computational Biology*, 24(5):422–435, May 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0204; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0204.

Bogdanowicz:2023:GPM

[BG23] Damian Bogdanowicz and Krzysztof Giaro. Generalization of phylogenetic matching metrics with experimental tests of practical advantages. *Journal of Computational Biology*, 30(3):261–276, March 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0090; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0090.

Bock:2007:DSR

[BGG07] Mary Ellen Bock, Claudio Garutti, and Concettina Guerra. Discovery of similar regions on protein surfaces. *Journal of Computational Biology*, 14(3):285–299, April 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0145; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0145.

Bidot:2008:MMC

[BGH+08] C. Bidot, F. Gruy, C.-S. Haudin, F. El Hentati, B. Guy, and C. Lambert. Mathematical modeling of T-cell activation kinetic. *Journal of Computational Biology*, 15(1):105–128, January 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0125; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0125`.

Bafna:2004:NEC

[BGHY04] Vineet Bafna, Dan Gusfield, Sridhar Hannenhalli, and Shibu Yooseph. A note on efficient computation of haplotypes via perfect phylogeny. *Journal of Computational Biology*, 11(5):858–866, October 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.858; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.858`.

Bhattacharyya:2004:RSH

[BGJ+04] C. Bhattacharyya, L. R. Grate, M. I. Jordan, L. El Ghaoui, and I. S. Mian. Robust sparse hyperplane classifiers: Application to uncertain molecular profiling data. *Journal of Computational Biology*, 11(6):1073–1089, December 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.1073; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.1073`.

Bleker:2024:CSG

[BGL24] Carissa Bleker, Stephen K. Grady, and Michael A. Langston. A comparative study of gene co-expression thresholding algorithms. *Journal of Computational Biology*, 31(6):539–548, June 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Bafna:2003:HPP

[BGLY03] Vineet Bafna, Dan Gusfield, Giuseppe Lancia, and Shibu Yooseph. Haplotyping as perfect phylogeny: a direct approach. *Journal of Computational Biology*, 10(3–4):323–340, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Benhabiles:1998:DAP

[BGTSB98] Nora Benhabilès, Xavier Gallet, Annick Thomas-Soumarmon, and Robert Brasseur. A descriptive analysis of populations of three-dimensional structures calculated from primary sequences of proteins by OSIRIS. *Journal of Computational Biology*, 5(2):351–366, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.351; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.351`.

Belal:2011:TMW

[BH11] Nahla A. Belal and Lenwood S. Heath. A theoretical model for whole genome alignment. *Journal of Computational Biology*, 18(5):705–728, May 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0101; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0101`.

Badr:2014:ISR

[BH14] Eman Badr and Lenwood S. Heath. Identifying splicing regulatory elements with de Bruijn graphs. *Journal of Computational Biology*, 21(12):880–897, December 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0183; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0183`.

Baran:2015:NRB

[BH15] Yael Baran and Eran Halperin. A note on the relations between spatio-genetic models. *Journal of Computational Biology*, 22(10):905–917, October 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0080; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0080`.

Barreto-Hernadez:2011:PPO

[BHGCS11] Emiliano Barreto-Hernadez, Margarida Gama-Carvalho, and Lisete Sousa. Pre-processing optimization of RNA immunoprecipitation microarray data. *Journal of Computational Biology*, 18(10):1319–1328, October 2011. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0020; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0020.

Barrett:2018:EDS

[BHHR18] Christopher Barrett, Qijun He, Fenix W. Huang, and Christian M. Reidys. An efficient dual sampling algorithm with Hamming distance filtration. *Journal of Computational Biology*, 25(11):1179–1192, November 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0075; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0075.

Barrett:2019:BSP

[BHHR19] Christopher Barrett, Qijun He, Fenix W. Huang, and Christian M. Reidys. A Boltzmann sampler for 1-pairs with double filtration. *Journal of Computational Biology*, 26(3):173–192, March 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0095; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0095.

Bruckner:2010:TFQ

[BHK+10] Sharon Bruckner, Falk Hüffner, Richard M. Karp, Ron Shamir, and Roded Sharan. Topology-free querying of protein interaction networks. *Journal of Computational Biology*, 17(3):237–252, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0170; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0170.

Blanca:2022:SMS

[BHKM22] Antonio Blanca, Robert S. Harris, David Koslicki, and Paul Medvedev. The statistics of k-mers from a sequence undergoing a simple mutation process without spurious matches. *Journal of Computational Biology*, 29(2):155–168, February 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0431; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0431.

Biane:2025:EPM

[BHKN25] Célia Biane, Greg Hampikian, Sergey Kirgizov, and Khaydar Nurligareev. Endhered patterns in matchings and RNA. *Journal of Computational Biology*, 32(1):28–46, January 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0658; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0658`.

Bao:2018:ACR

[BHL+18] Yu Bao, Morihiro Hayashida, Pengyu Liu, Masayuki Ishitsuka, Jose C. Nacher, and Tatsuya Akutsu. Analysis of critical and redundant vertices in controlling directed complex networks using feedback vertex sets. *Journal of Computational Biology*, 25(10):1071–1090, October 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0019; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0019`.

Berger:1999:SSC

[BHPS99] Bonnie Berger, Gunnar W. Hoest, James R. Paulson, and Peter W. Shor. On the structure of the scaffolding core of bacteriophage T4. *Journal of Computational Biology*, 6(1):1–12, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.1; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.1`.

Bafna:2000:LRP

[BHRV00] Vineet Bafna, Sridhar Hannenhalli, Ken Rice, and Lisa Vawter. Ligand-receptor pairing via tree comparison. *Journal of Computational Biology*, 7(1–2):59–70, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Borguesan:2017:NSN

[BIPD17] Bruno Borguesan, Mario Inostroza-Ponta, and Márcio Dorn. NIAS-Server: Neighbors influence of amino acids and secondary structures in proteins. *Journal of Computational Biology*, 24(3):255–265, March 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0074;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0074.

Budden:2017:CTI

[BJ17] David Budden and Mitchell Jones. Cautionary tales of inapproximability. *Journal of Computational Biology*, 24(3):213–216, March 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0097; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0097.

Brazma:1998:AAD

[BJEG98] Alvis Brazma, Inge Jonassen, Ingvar Eidhammer, and David Gilbert. Approaches to the automatic discovery of patterns in biosequences. *Journal of Computational Biology*, 5(2):279–305, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.279; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.279.

Brito:2020:SGR

[BJF+20] Klairton Lima Brito, Géraldine Jean, Guillaume Fertin, Andre Rodrigues Oliveira, Ulisses Dias, and Zanoni Dias. Sorting by genome rearrangements on both gene order and intergenic sizes. *Journal of Computational Biology*, 27(2):156–174, February 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0293; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0293.

Bar-Joseph:2003:CRT

[BJGG+03] Ziv Bar-Joseph, Georg K. Gerber, David K. Gifford, Tommi S. Jaakkola, and Itamar Simon. Continuous representations of time-series gene expression data. *Journal of Computational Biology*, 10(3–4):341–356, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Bocker:2009:CMG

[BJMS09] Sebastian Böcker, Katharina Jahn, Julia Mixtacki, and Jens Stoye. Computation of median gene clusters. *Journal of Computational Biology*, 16(8):1085–1099, August 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0098; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0098.

Blum:2008:UAM

[BK08] Torsten Blum and Oliver Kohlbacher. Using atom mapping rules for an improved detection of relevant routes in weighted metabolic networks. *Journal of Computational Biology*, 15(6):565–576, July 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0044; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0044.

Bandyopadhyay:2010:GMO

[BK10] Nirmalya Bandyopadhyay and Tamer Kahveci. GBA manager: an online tool for querying low-complexity regions in proteins. *Journal of Computational Biology*, 17(1):73–77, January 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0006; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0006.

Bailey-Kellogg:2005:RGA

[BKCP05] Chris Bailey-Kellogg, Sheetal Chainraj, and Gopal Pandurangan. A random graph approach to NMR sequential assignment. *Journal of Computational Biology*, 12(6):569–583, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.569; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.569.

Bailey-Kellogg:2001:RMD

[BKKSD01] Chris Bailey-Kellogg, John J. Kelleyiii, Cliff Stein, and Bruce Randall Donald. Reducing mass degeneracy in SAR by MS by stable isotopic labeling. *Journal of Computational Biology*, 8(1):19–36, February 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701300099056; https://www.liebertpub.com/doi/pdf/10.1089/106652701300099056.

Benham:1995:HTW

[BKPW95] Craig Benham, Sampath Kannan, Michael Paterson, and Tandy Warnow. Hen's teeth and Whale's feet: Generalized charac-

ters and their compatibility. *Journal of Computational Biology*, 2(4):515–525, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.515; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.515`.

Bartholome:2009:EGI

[BKT09] Kilian Bartholomé, Clemens Kreutz, and Jens Timmer. Estimation of gene induction enables a relevance-based ranking of gene sets. *Journal of Computational Biology*, 16(7):959–967, July 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0226; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0226`.

Bailey-Kellogg:2000:NJA

[BKWK+00] Chris Bailey-Kellogg, Alik Widge, John J. Kelley, Marcelo J. Berardi, John H. Bushweller, and Bruce Randall Donald. The NOESY jigsaw: Automated protein secondary structure and main-chain assignment from sparse, unassigned NMR data. *Journal of Computational Biology*, 7(3–4):537–558, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Berger:1998:PFH

[BL98] Bonnie Berger and Tom Leighton. Protein folding in the hydrophobic–hydrophilic (*HP*) model is NP-complete. *Journal of Computational Biology*, 5(1):27–40, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.27; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.27`.

Bilu:2002:AFP

[BL02] Yonatan Bilu and Michal Linial. The advantage of functional prediction based on clustering of yeast genes and its correlation with non-sequence based classifications. *Journal of Computational Biology*, 9(2):193–210, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270252935412; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935412`.

Bashir:2010:OPA

[BLC+10a] Ali Bashir, Qing Lu, Dennis Carson, Benjamin J. Raphael, Yu-Tsueng Liu, and Vineet Bafna. Optimizing PCR assays for DNA-Based cancer diagnostics. *Journal of Computational Biology*, 17(3):369–381, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0203; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0203`.

Boisvert:2010:RSA

[BLC10b] Sébastien Boisvert, François Laviolette, and Jacques Corbeil. Ray: Simultaneous assembly of reads from a mix of high-throughput sequencing technologies. *Journal of Computational Biology*, 17(11):1519–1533, November 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0238; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0238`.

Bertrand:2008:IAG

[BLEM08] Denis Bertrand, Mathieu Lajoie, and Nadia El-Mabrouk. Inferring ancestral gene orders for a family of tandemly arrayed genes. *Journal of Computational Biology*, 15(8):1063–1077, October 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0025; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0025`.

Burden:2014:DWM

[BLF14] Conrad J. Burden, Paul Leopardi, and Sylvain Forêt. The distribution of word matches between Markovian sequences with periodic boundary conditions. *Journal of Computational Biology*, 21(1):41–63, January 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0277; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0277`.

Bigness:2022:ILR

[BLP+22] Jeremy Bigness, Xavier Loinaz, Shalin Patel, Erica Larschan, and Ritambhara Singh. Integrating long-range regulatory interactions to predict gene expression using graph convolutional

networks. *Journal of Computational Biology*, 29(5):409–424, May 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0316; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0316.

Bergemann:2004:SDA

[BLQZ04] T. L. Bergemann, R. J. Laws, F. Quiaoit, and L. P. Zhao. A statistically driven approach for image segmentation and signal extraction in cDNA microarrays. *Journal of Computational Biology*, 11(4):695–713, August 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.695; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.695.

Barrett:2016:RSS

[BLR16] Christopher L. Barrett, Thomas J. X. Li, and Christian M. Reidys. RNA secondary structures having a compatible sequence of certain nucleotide ratios. *Journal of Computational Biology*, 23(11):857–873, November 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0049; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0049.

Biswas:2024:CCB

[BMB24] Gargi Biswas, Debasish Mukherjee, and Sankar Basu. Combining complementarity and binding energetics in the assessment of protein interactions: EnCPdock — a practical manual. *Journal of Computational Biology*, 31(8):769–781, August 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0554; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0554.

Basher:2021:MPP

[BMH21] Abdur Rahman M. A. Basher, Ryan J. Mclaughlin, and Steven J. Hallam. Metabolic pathway prediction using non-negative matrix factorization with improved precision. *Journal of Computational Biology*, 28(11):1075–1103, November 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/

10.1089/cmb.2021.0258; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0258.

Biswas:2016:LMI

[BML+16] Surojit Biswas, Meredith Mcdonald, Derek S. Lundberg, Jeffery L. Dangl, and Vladimir Jojic. Learning microbial interaction networks from metagenomic count data. *Journal of Computational Biology*, 23(6):526–535, June 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0061; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0061.

Bansal:2023:SII

[BMM+23] Mukul S. Bansal, Ion I. Măndoiu, Marmar Moussa, Murray Patterson, Sanguthevar Rajasekaran, Pavel Skums, and Alexander Zelikovsky. Special issue: 11th International Computational Advances in Bio and Medical Sciences (ICCABS 2021). *Journal of Computational Biology*, 30(4):363–365, April 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/fpi/10.1089/cmb.2023.29085.msb; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.29085.msb.

Bishop:2007:GTA

[BMN+07] Morgan Bishop, Anthony J. Macula, Kayla Nimmo, Lauren Wood, Wendy K. Pogozelski, and Thomas E. Renz. Group testing to annihilate pairs applied to DNA cross-hybridization elimination using SYBR Green I. *Journal of Computational Biology*, 14(1):84–96, January 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0114; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0114.

Bonizzoni:2009:DAG

[BMP+09] Paola Bonizzoni, Giancarlo Mauri, Graziano Pesole, Ernesto Picardi, Yuri Pirola, and Raffaella Rizzi. Detecting alternative gene structures from spliced ESTs: a computational approach. *Journal of Computational Biology*, 16(1):43–66, January 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/

abs/10.1089/cmb.2008.0028; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0028.

BenHassen:2009:IST

[BMR09] Hanen Ben Hassen, Afif Masmoudi, and Ahmed Rebai. Inference in signal transduction pathways using EM algorithm and an implicit algorithm: Incomplete data case. *Journal of Computational Biology*, 16(9):1227–1240, September 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0129; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0129.

Budhlakoti:2019:CSS

[BMR+19] Neeraj Budhlakoti, Dwijesh Chandra Mishra, Anil Rai, S. B. Lal, Krishna Kumar Chaturvedi, and Rajeev Ranjan Kumar. A comparative study of single-trait and multi-trait genomic selection. *Journal of Computational Biology*, 26(10):1100–1112, October 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0032; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0032.

Bergeron:2006:ST

[BMS06] Anne Bergeron, Julia Mixtacki, and Jens Stoye. On sorting by translocations. *Journal of Computational Biology*, 13(2):567–578, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.567; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.567.

Bergeron:2010:RMS

[BMS10] Anne Bergeron, Paul Medvedev, and Jens Stoye. Rearrangement models and single-cut operations. *Journal of Computational Biology*, 17(9):1213–1225, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0091; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0091.

Booth:2004:ESA

[BMWG04] Hilary S. Booth, John H. Maindonald, Susan R. Wilson, and Jill E. Gready. An efficient Z-score algorithm for as-

sessing sequence alignments. *Journal of Computational Biology*, 11(4):616–625, August 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.616; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.616.

Bader:2001:LTA

[BMY01] David A. Bader, Bernard M. E. Moret, and Mi Yan. A linear-time algorithm for computing inversion distance between signed permutations with an experimental study. *Journal of Computational Biology*, 8(5):483–491, October 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701753216503; https://www.liebertpub.com/doi/pdf/10.1089/106652701753216503.

Bankevich:2012:SNG

[BNA+12] Anton Bankevich, Sergey Nurk, Dmitry Antipov, Alexey A. Gurevich, Mikhail Dvorkin, Alexander S. Kulikov, Valery M. Lesin, Sergey I. Nikolenko, Son Pham, Andrey D. Prjibelski, Alexey V. Pyshkin, Alexander V. Sirotkin, Nikolay Vyahhi, Glenn Tesler, Max A. Alekseyev, and Pavel A. Pevzner. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *Journal of Computational Biology*, 19(5):455–477, May 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0021; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0021.

Behrens:2012:AAW

[BNN12] Sarah Behrens, Cyril Nicaud, and Pierre Nicodème. An automaton approach for waiting times in DNA evolution. *Journal of Computational Biology*, 19(5):550–562, May 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0218; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0218.

Bader:2007:SWR

[BO07] Martin Bader and Enno Ohlebusch. Sorting by weighted reversals, transpositions, and inverted transpositions. *Journal of Computational Biology*, 14(5):615–636, June 2007.

CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R006; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R006.

Barsbey:2023:CST

[BÖB+23] Melih Barsbey, Rıza Özçelik, Alperen Bağ, Berk Atil, Arzucan Özgür, and Elif Ozkirimli. A computational software for training robust drug–target affinity prediction models: pydebiaseddta. *Journal of Computational Biology*, 30(11):1240–1245, November 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0194; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0194.

Bocker:2004:SCU

[Böc04] Sebastian Böcker. Sequencing from compomers: Using mass spectrometry for DNA *de novo* sequencing of 200+ nt. *Journal of Computational Biology*, 11(6):1110–1134, December 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.1110; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.1110.

Boenn:2018:SSS

[Boe18] Markus Boenn. ShRangeSim: Simulation of single nucleotide polymorphism clusters in next-generation sequencing data. *Journal of Computational Biology*, 25(6):613–622, June 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0007; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0007.

Bohnenkamper:2024:FLH

[Boh24] Leonard Bohnenkämper. The floor is lava: Halving natural genomes with viaducts, piers, and pontoons. *Journal of Computational Biology*, 31(4):294–311, April 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0330; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0330.

Bruno:2006:TPD

[BP06] William J. Bruno and John E. Pearson. Transformations that preserve detailed balance in Markov models. *Journal of Computational Biology*, 13(9):1574–1578, November 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1574; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1574`.

Bartolucci:2014:NCM

[BP14] Francesco Bartolucci and Silvia Pandolfi. A new constant memory recursion for hidden Markov models. *Journal of Computational Biology*, 21(2):99–117, February 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0096; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0096`.

Bonissone:2016:ICU

[BP16] Stefano R. Bonissone and Pavel A. Pevzner. Immunoglobulin classification using the colored antibody graph. *Journal of Computational Biology*, 23(6):483–494, June 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0010; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0010`.

Barrios:2017:DIG

[BP17] David Barrios and Carlos Prieto. D3GB: an interactive genome browser for R, Python, and WordPress. *Journal of Computational Biology*, 24(5):447–449, May 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0213; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0213`.

Baeissa:2020:III

[BP20] Hanadi M. Baeissa and Frances M. G. Pearl. Identifying the impact of inframe insertions and deletions on protein function in cancer. *Journal of Computational Biology*, 27(5):786–795, May 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/`

abs/10.1089/cmb.2018.0192; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0192.

Berloff:2002:SMC

[BPL02] Natalia Berloff, Markus Perola, and Kenneth Lange. Spline methods for the comparison of physical and genetic maps. *Journal of Computational Biology*, 9(3):465–475, June 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652702760138565; https://www.liebertpub.com/doi/pdf/10.1089/106652702760138565.

Berard:2003:CM

[BR03] Sèverine Bérard and Eric Rivals. Comparison of minisatellites. *Journal of Computational Biology*, 10(3–4):357–372, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Beattie:2006:BSP

[BR06] Bradley J. Beattie and Peter N. Robinson. Binary state pattern clustering: a digital paradigm for class and biomarker discovery in gene microarray studies of cancer. *Journal of Computational Biology*, 13(5):1114–1130, June 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1114; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1114.

Bolouri:2012:ICS

[BR12] Hamid Bolouri and Walter L. Ruzzo. Integration of 198 ChIP-seq datasets reveals human *cis*-regulatory regions. *Journal of Computational Biology*, 19(9):989–997, September 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0100; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0100.

Bunimovich:2023:LIC

[BR23] Leonid Bunimovich and Athulya Ram. Local immunodeficiency: Combining cross-immunoreactivity networks. *Journal of Computational Biology*, 30(4):492–501, April 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0390; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0390.

Baird:2024:GTG

[BR24] Tarrion Baird and Rahul Roychoudhuri. GS-TCGA: Gene set-based analysis of *The Cancer Genome Atlas*. *Journal of Computational Biology*, 31(3):229–240, March 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0278; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0278.

Bai:2020:OCK

[BRC20] Lianmei Bai, Yu Ren, and Tianqing Cui. Overexpression of *CDCA5*, *KIF4A*, *TPX2*, and *FOXM1* coregulated cell cycle and promoted hepatocellular carcinoma development. *Journal of Computational Biology*, 27(6):965–974, June 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0254; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0254.

Beerenwinkel:2005:LME

[BRD+05] Niko Beerenwinkel, Jörg Rahnenführer, Martin Däumer, Daniel Hoffmann, Rolf Kaiser, Joachim Selbig, and Thomas Lengauer. Learning multiple evolutionary pathways from cross-sectional data. *Journal of Computational Biology*, 12(6):584–598, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.584; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.584.

Briscoe:2019:UPF

[Bri19] James Briscoe. Understanding pattern formation in embryos: Experiment, theory, and simulation. *Journal of Computational Biology*, 26(7):696–702, July 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0090; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0090.

Browning:1998:RIC

[Bro98] Sharon Browning. Relationship information contained in gamete identity by descent data. *Journal of Computational Biology*, 5(2):323–334, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.323; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.323`.

Broet:2002:BHM

[BRR02] Philippe Broët, Sylvia Richardson, and François Radvanyi. Bayesian hierarchical model for identifying changes in gene expression from microarray experiments. *Journal of Computational Biology*, 9(4):671–683, August 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652702760277381; https://www.liebertpub.com/doi/pdf/10.1089/106652702760277381`.

Bhasin:2006:RCH

[BRR06] Manoj Bhasin, Ellis L. Reinherz, and Pedro A. Reche. Recognition and classification of histones using support vector machine. *Journal of Computational Biology*, 13 (1):102–112, January 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.102; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.102`.

Bienkowska:1999:PTS

[BRS99] Jadwiga R. Bieńkowska, Robert G. Rogers, Jr., and Temple F. Smith. Performance of threading scoring functions designed using new optimization method. *Journal of Computational Biology*, 6(3–4):299–311, October 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Bonnet:2020:DRS

[BRS20] Édouard Bonnet, Paweł Rzażewski, and Florian Sikora. Designing RNA secondary structures is hard. *Journal of Computational Biology*, 27(3):302–316, March 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0420; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0420`.

Bryant:1996:HTB

[Bry96] David Bryant. Hunting for trees in binary character sets: Efficient algorithms for extraction, enumeration, and optimization. *Journal of Computational Biology*, 3(2):275–288, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.275; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.275`.

Biswas:2015:DPA

[BRZH15] Abhishek Biswas, Desh Ranjan, Mohammad Zubair, and Jing He. A dynamic programming algorithm for finding the optimal placement of a secondary structure topology in Cryo-EM data. *Journal of Computational Biology*, 22(9):837–843, September 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0120; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0120`.

Berger:1997:IMI

[BS97] Bonnie Berger and Mona Singh. An iterative method for improved protein structural motif recognition. *Journal of Computational Biology*, 4(3):261–273, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.261; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.261`.

Benson:1998:DTM

[BS98] Gary Benson and Xiaoping Su. On the distribution of K-tuple matches for sequence homology: a constant time exact calculation of the variance. *Journal of Computational Biology*, 5(1):87–100, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.87; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.87`.

Bergeron:2006:SSP

[BS06] Anne Bergeron and Jens Stoye. On the similarity of sets of permutations and its applications to genome comparison. *Journal of Computational Biology*, 13(7):1340–1354, September 2006.

CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1340; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1340.

Behre:2009:MST

[BS09] Jörn Behre and Stefan Schuster. Modeling signal transduction in enzyme cascades with the concept of elementary flux modes. *Journal of Computational Biology*, 16(6):829–844, June 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0177; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0177.

Braga:2010:SSS

[BS10] Marília D. V. Braga and Jens Stoye. The solution space of sorting by DCJ. *Journal of Computational Biology*, 17 (9):1145–1165, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0109; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0109.

Bruner:2020:RAD

[BS20] Ariel Bruner and Roded Sharan. A robustness analysis of dynamic Boolean models of cellular circuits. *Journal of Computational Biology*, 27(2):133–143, February 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0290; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0290.

Berrar:2005:STA

[BSB+05] Daniel Berrar, Brian Sturgeon, Ian Bradbury, C. Stephen Downes, and Werner Dubitzky. Survival trees for analyzing clinical outcome in lung adenocarcinomas based on gene expression profiles: Identification of neogenin and diacylglycerol kinase α expression as critical factors. *Journal of Computational Biology*, 12(5):534–544, June 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.534; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.534.

Balaur:2017:EGD

[BSB+17] Irina Balaur, Mansoor Saqi, Ana Barat, Artem Lysenko, Alexander Mazein, Christopher J. Rawlings, Heather J. Ruskin, and Charles Auffray. EpiGeNet: a graph database of interdependencies between genetic and epigenetic events in colorectal cancer. *Journal of Computational Biology*, 24(10):969–980, October 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0095; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0095`.

Battle:2005:PDO

[BSK05] Alexis Battle, Eran Segal, and Daphne Koller. Probabilistic discovery of overlapping cellular processes and their regulation. *Journal of Computational Biology*, 12(7):909–927, September 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.909; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.909`.

Banman:2023:AMA

[BSKgG23] Andrew Banman, Nikita A. Sakhanenko, James Kunert-graf, and David J. Galas. *ApoE* modifier alleles for Alzheimer's disease discovered by information theory dependency measures: `MIST` software package. *Journal of Computational Biology*, 30(3):323–336, March 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0185; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0185`.

Bonet:2006:ASD

[BSMA06] Maria Luisa Bonet, Katherine St.John, Ruchi Mahindru, and Nina Amenta. Approximating subtree distances between phylogenies. *Journal of Computational Biology*, 13(8):1419–1434, October 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1419; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1419`.

Bataa:2024:FHS

[BSP+24] Magsarjav Bataa, Siwoo Song, Kunsoo Park, Miran Kim, Jung Hee Cheon, and Sun Kim. Finding highly similar re-

gions of genomic sequences through homomorphic encryption. *Journal of Computational Biology*, 31(3):197–212, March 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0050; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0050.

Bai:2025:OMP

[BSP+25] Lidan Bai, Jun Sun, Vasile Palade, Chao Li, Hengyang Lu, and Cong Gao. Optimizing metabolite production with neighborhood-based binary quantum-behaved particle swarm optimization and flux balance analysis. *Journal of Computational Biology*, 32(1):64–88, January 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0538; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0538.

Badr:2011:LAP

[BSS11] Ghada Badr, Krister M. Swenson, and David Sankoff. Listing all parsimonious reversal sequences: New algorithms and perspectives. *Journal of Computational Biology*, 18(9):1201–1210, September 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0133; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0133.

Blokh:2013:ASP

[BSS13] Dima Blokh, Danny Segev, and Roded Sharan. The approximability of shortest path-based graph orientations of protein–protein interaction networks. *Journal of Computational Biology*, 20(12):945–957, December 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0064; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0064.

Boroojeny:2020:GTE

[BSSZ+20a] Ali Ebrahimpour Boroojeny, Akash Shrestha, Ali Sharifi-Zarchi, Suzanne Renick Gallagher, S. Cenk Sahinalp, and Hamidreza Chitsaz. Graph traversal edit distance and extensions. *Journal of Computational Biology*, 27(3):317–329, March 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0511; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0511.

Boroojeny:2020:PPA

[BSSz+20b] Ali Ebrahimpour Boroojeny, Akash Shrestha, Ali Sharifi-zarchi, Suzanne Renick Gallagher, Süleyman Cenk Sahinalp, and Hamidreza Chitsaz. PyGTED: Python application for computing graph traversal edit distance. *Journal of Computational Biology*, 27(3):436–439, March 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0510; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0510.

Blanchette:2002:APF

[BST02] Mathieu Blanchette, Benno Schwikowski, and Martin Tompa. Algorithms for phylogenetic footprinting. *Journal of Computational Biology*, 9(2):211–223, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270252935421; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935421.

Bonet:1998:BMS

[BSWY98] Maria Bonet, Mike Steel, Tandy Warnow, and Shibu Yooseph. Better methods for solving parsimony and compatibility. *Journal of Computational Biology*, 5(3):391–407, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.391; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.391.

Buhler:2002:FMU

[BT02] Jeremy Buhler and Martin Tompa. Finding motifs using random projections. *Journal of Computational Biology*, 9(2):225–242, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270252935430; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935430.

Boden:2008:DNA

[BT08] Mikael Bodén and Rohan D. Teasdale. Determining nucleolar association from sequence by leveraging protein-protein interactions. *Journal of Computational Biology*, 15(3):291–304,

April 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0163; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0163.

Bafna:2006:CFU

[BTZ06] Vineet Bafna, Haixu Tang, and Shaojie Zhang. Consensus folding of unaligned RNA sequences revisited. *Journal of Computational Biology*, 13(2):283–295, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.283; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.283.

Buhler:2003:PSI

[Buh03] Jeremy Buhler. Provably sensitive indexing strategies for biosequence similarity search. *Journal of Computational Biology*, 10 (3–4):399–417, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Bundschuh:2002:RSE

[Bun02] Ralf Bundschuh. Rapid significance estimation in local sequence alignment with gaps. *Journal of Computational Biology*, 9(2):243–260, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270252935449; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935449.

Blanchet:2009:MBA

[BV09] Juliette Blanchet and Matthieu Vignes. A model-based approach to gene clustering with missing observation reconstruction in a Markov random field framework. *Journal of Computational Biology*, 16(3):475–486, March 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0078; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0078.

Behrens:2010:SEP

[BV10] Sarah Behrens and Martin Vingron. Studying the evolution of promoter sequences: a waiting time problem. *Journal of Computational Biology*, 17(12):1591–1606, December 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0084; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0084.

Benner:2020:MMS

[BV20] Philipp Benner and Martin Vingron. ModHMM: a modular supra-Bayesian genome segmentation method. *Journal of Computational Biology*, 27(4):442–457, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0280; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0280.

Bonizzoni:2016:LEM

[BVP+16] Paola Bonizzoni, Gianluca Della Vedova, Yuri Pirola, Marco Previtali, and Raffaella Rizzi. LSG: an external-memory tool to compute string graphs for next-generation sequencing data assembly. *Journal of Computational Biology*, 23(3):137–149, March 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0172; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0172.

Bonizzoni:2017:FFS

[BVP+17] Paola Bonizzoni, Gianluca Della Vedova, Yuri Pirola, Marco Previtali, and Raffaella Rizzi. FSG: Fast string graph construction for De Novo assembly. *Journal of Computational Biology*, 24(10):953–968, October 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0089; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0089.

Bonizzoni:2019:MMB

[BVP+19] Paola Bonizzoni, Gianluca Della Vedova, Yuri Pirola, Marco Previtali, and Raffaella Rizzi. Multithread multistring Burrows–Wheeler transform and longest common prefix array. *Journal of Computational Biology*, 26(9):948–961, September 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0230; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0230.

Viswanath:2019:IDI

[bVRN+19] bBiju Viswanath, Naren P. Rao, Janardhanan C. Narayanaswamy, Palanimuthu T. Sivakumar, Arunkandaswamy, Muralidharankesavan, Urvakhsh-Meherwan Mehta, Ganesanvenkatasubramanian, John P. John, Odity Mukherjee, Meerapurushottam, Ramakrishnankannan, Bhupesh Mehta, Thennarasukandavel, B. Binukumar, Jitendersaini, Deepak Jayarajan, A. Shyamsundar, Sydney Moirangthem, Kumar G. Vijay, Jagadishathirthalli, Prabha S. Chandra, Bangalore N. Gangadhar, Pratima Murthy, Mitradas M. Panicker, Upinder S. Bhalla, Sumantrachattarji, Vivekbenegal, Mathew Varghese, Janardhan Y. C. Reddy, Padinjat Raghu, Mahendrarao, and Sanjeev Jain. INDEX-db: The Indian Exome Reference Database (Phase I). *Journal of Computational Biology*, 26(3):225–234, March 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0199; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0199`.

Bayzid:2012:EOS

[BW12] Md. Shamsuzzoha Bayzid and Tandy Warnow. Estimating optimal species trees from incomplete gene trees under deep coalescence. *Journal of Computational Biology*, 19(6):591–605, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0037; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0037`.

Blazej:2017:RSS

[BWGM17] Paweł Błażej, Małgorzata Wnetrzak, Małgorzata Grabińska, and Paweł Mackiewicz. Representations of search spaces in the problem of mutational pressure optimization according to protein-coding sequences. *Journal of Computational Biology*, 24(11):1089–1098, November 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0017; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0017`.

Braga:2011:DCJ

[BWS11] Marília D. V. Braga, Eyla Willing, and Jens Stoye. Double cut and join with insertions and deletions. *Journal of Computational Biology*, 18(9):1167–1184, September 2011. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0118; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0118.

Behnam:2013:GIL

[BWS13] Ehsan Behnam, Michael S. Waterman, and Andrew D. Smith. A geometric interpretation for local alignment-free sequence comparison. *Journal of Computational Biology*, 20(7):471–485, July 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0280; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0280.

Bar-Yaakov:2012:UIR

[BYGI12] Nimrod Bar-Yaakov, Zehava Grossman, and Nathan Intrator. Using iterative ridge regression to explore associations between conditioned variables. *Journal of Computational Biology*, 19(5):504–518, May 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0028; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0028.

Yao:2024:PMD

[bYjHgZ+24] Hai bin Yao, Zhen jie Hou, Wen guang Zhang, Han Li, and Yan Chen. Prediction of MicroRNA-Disease potential association based on sparse learning and multilayer random walks. *Journal of Computational Biology*, 31(3):241–256, March 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0266; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0266.

Brand:2020:LRM

[BYL+20] Lodewijk Brand, Xue Yang, Kai Liu, Saad Elbeleidy, Hua Wang, Hao Zhang, and Feiping Nie. Learning robust multilabel sample specific distances for identifying HIV-1 drug resistance. *Journal of Computational Biology*, 27(4):655–672, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0329; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0329.

Brinza:2008:DVM

[BZ08] Dumitru Brinza and Alexander Zelikovsky. Design and validation of methods searching for risk factors in genotype case-control studies. *Journal of Computational Biology*, 15(1):81–90, January 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0081; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0081`.

Bezdan:2022:FSH

[BZB+22] Timea Bezdan, Miodrag Zivkovic, Nebojsa Bacanin, Amit Chhabra, and Muthusamy Suresh. Feature selection by hybrid brain storm optimization algorithm for COVID-19 classification. *Journal of Computational Biology*, 29(6):515–529, June 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0256; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0256`.

Bai:2022:SSC

[BZG+22] Tian Bai, Zhenting Zhang, Shuyu Guo, Chen Zhao, and Xiao Luo. Semi-supervised cell detection with reliable pseudo-labels. *Journal of Computational Biology*, 29(10):1061–1073, October 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0108; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0108`.

Bizjak:2016:CFM

[BZMM16] Manca Bizjak, Nikolaj Zimic, Miha Mraz, and Miha Moškon. Computational framework for modeling multiple noncooperative transcription factor binding and its application to the analysis of nuclear factor kappa B oscillatory response. *Journal of Computational Biology*, 23(12):923–933, December 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0065; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0065`.

Berman:2000:WSD

[BZW+00] Piotr Berman, Zheng Zhang, Yuri I. Wolf, Eugene V. Koonin, and Webb Miller. Winnowing sequences from a database search.

Journal of Computational Biology, 7(1–2):293–302, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Cunial:2012:PCR

[CA12] Fabio Cunial and Alberto Apostolico. Phylogeny construction with rigid gapped motifs. *Journal of Computational Biology*, 19(7):911–927, July 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0060; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0060`.

Chitsaz:2015:ELR

[CA15] Hamidreza Chitsaz and Mohammad Aminisharifabad. Exact learning of RNA energy parameters from structure. *Journal of Computational Biology*, 22(6):463–473, June 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0164; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0164`.

Chiang:2007:USR

[CAB+07] Tsung-Han Chiang, Mehmet Serkan Apaydin, Douglas L. Brutlag, David Hsu, and Jean-Claude Latombe. Using stochastic roadmap simulation to predict experimental quantities in protein folding kinetics: Folding rates and phi-values. *Journal of Computational Biology*, 14(5):578–593, June 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R004; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R004`.

Claassen:2011:PCP

[CAB11] Manfred Claassen, Ruedi Aebersold, and Joachim M. Buhmann. Proteome coverage prediction for integrated proteomics datasets. *Journal of Computational Biology*, 18(3):283–293, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0261; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0261`.

Chourasia:2023:REE

[CAC+23] Prakash Chourasia, Sarwan Ali, Simone Ciccolella, Gianluca Della Vedova, and Murray Patterson. Reads2Vec: Efficient embedding of raw high-throughput sequencing reads data. *Journal of Computational Biology*, 30(4):469–491, April 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0424; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0424`.

Calabrese:2022:QBU

[Cal22] Peter Calabrese. Quantitative biology undergraduate major at the University of Southern California. *Journal of Computational Biology*, 29(7):616–618, July 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0605; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0605`.

Cardone:2010:EIC

[CASP10] Antonio Cardone, R. Wayne Albers, Ram D. Sriram, and Harish C. Pant. Evaluation of the interaction of cyclin-dependent kinase 5 with activator p25 and with p25-derived inhibitor CIP. *Journal of Computational Biology*, 17(5):707–721, May 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0202; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0202`.

Chia:2006:PAS

[CB06] Nicholas Chia and Ralf Bundschuh. A practical approach to significance assessment in alignment with gaps. *Journal of Computational Biology*, 13(2):429–441, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.429; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.429`.

Chennubhotla:2007:MMH

[CB07] Chakra Chennubhotla and Ivet Bahar. Markov methods for hierarchical coarse-graining of large protein dynamics. *Journal of Computational Biology*, 14(6):765–776, July 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R015; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R015.

Cleary:2014:JVN

[CBG+14] John G. Cleary, Ross Braithwaite, Kurt Gaastra, Brian S. Hilbush, Stuart Inglis, Sean A. Irvine, Alan Jackson, Richard Littin, Sahar Nohzadeh-Malakshah, Mehul Rathod, David Ware, Len Trigg, and Francisco M. De La Vega. Joint variant and *De Novo* mutation identification on pedigrees from high-throughput sequencing data. *Journal of Computational Biology*, 21(6):405–419, June 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0029; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0029.

Carnevali:2012:CTH

[CBH+12] Paolo Carnevali, Jonathan Baccash, Aaron L. Halpern, Igor Nazarenko, Geoffrey B. Nilsen, Krishna P. Pant, Jessica C. Ebert, Anushka Brownley, Matt Morenzoni, Vitali Karpinchyk, Bruce Martin, Dennis G. Ballinger, and Radoje Drmanac. Computational techniques for human genome resequencing using mated gapped reads. *Journal of Computational Biology*, 19(3):279–292, March 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0201; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0201.

Cowen:2002:PBH

[CBM+02] Lenore Cowen, Phil Bradley, Matthew Menke, Jonathan King, and Bonnie Berger. Predicting the beta-helix fold from protein sequence data. *Journal of Computational Biology*, 9(2):261–276, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270252935458; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935458.

Cheloshkina:2021:RCB

[CBP21] Kseniia Cheloshkina, Islam Bzhikhatlov, and Maria Poptsova. Randomness in cancer breakpoint prediction. *Journal of Computational Biology*, 28(7):716–731, July 2021. CODEN

JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0551; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0551.

Carter:2020:CPF

[CBS+20] Brandon Carter, Maxwell Bileschi, Jamie Smith, Theo Sanderson, Drew Bryant, David Belanger, and Lucy J. Colwell. Critiquing protein family classification models using sufficient input subsets. *Journal of Computational Biology*, 27(8):1219–1231, August 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0339; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0339.

Cameron:2007:CSR

[CBW07] Michael Cameron, Yaniv Bernstein, and Hugh E. Williams. Clustered sequence representation for fast homology search. *Journal of Computational Biology*, 14(5):594–614, June 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R005; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R005.

Chattopadhyay:2003:TCP

[CC03] Sujay Chattopadhyay and Jayprokas Chakrabarti. Temporal changes in phosphoglycerate kinase coding sequences: a quantitative measure. *Journal of Computational Biology*, 10 (1):83–93, February 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703763255688; https://www.liebertpub.com/doi/pdf/10.1089/106652703763255688.

Chen:2006:FRT

[CC06] Yu Chen and Gordon M. Crippen. Fold recognition via a tree. *Journal of Computational Biology*, 13(9):1565–1573, November 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1565; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1565.

Cheng:2009:SOM

[CC09] Qiang Cheng and Jie Cheng. Sparsity optimization method for multivariate feature screening for gene expression analysis. *Journal of Computational Biology*, 16(9):1241–1252, September 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0034; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0034`.

Chen:2011:BPA

[CC11] Jiun-Rung Chen and Ye-In Chang. An up-down bit pattern approach to coregulated and negative-coregulated gene clustering of microarray data. *Journal of Computational Biology*, 18(12):1777–1791, December 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0212; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0212`.

Cohen:2012:DPS

[CC12] Eyal Cohen and Benny Chor. Detecting phylogenetic signals in eukaryotic whole genome sequences. *Journal of Computational Biology*, 19(8):945–956, August 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0122; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0122`.

Cavattoni:2023:CIM

[CC23] Margherita Cavattoni and Matteo Comin. ClassGraph: Improving metagenomic read classification with overlap graphs. *Journal of Computational Biology*, 30(6):633–647, June 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0208; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0208`.

Castellani:2021:ECE

[CCDB21] Gastone Castellani, Leon N. Cooper, Luciana Renata De Oliveira, and Brian S. Blais. Energy consumption and entropy production in a stochastic formulation of BCM learning. *Journal of Computational Biology*, 28(3):257–268, March 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0118; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0118.

Chang:2010:ICP

[CCF10] Huilan Chang, Hong-Bin Chen, and Hung-Lin Fu. Identification and classification problems on pooling designs for inhibitor models. *Journal of Computational Biology*, 17(7):927–941, July 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0138; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0138.

Carlson:2006:BBS

[CCG06] Jonathan M. Carlson, Arijit Chakravarty, and Robert H. Gross. BEAM: a beam search algorithm for the identification of *Cis*-regulatory elements in groups of genes. *Journal of Computational Biology*, 13(3):686–701, April 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.686; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.686.

Chen:2019:IPK

[CCH+19] Zide Chen, Jiehua Chen, Xuan Huang, Yi Wu, Kuiyuan Huang, Weikang Xu, Linqing Xie, Xiaoyong Zhang, and Hongyan Liu. Identification of potential key genes for hepatitis B virus-associated hepatocellular carcinoma by bioinformatics analysis. *Journal of Computational Biology*, 26(5):485–494, May 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0244; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0244.

Caprara:2004:OPS

[CCI+04] Alberto Caprara, Robert Carr, Sorin Istrail, Giuseppe Lancia, and Brian Walenz. 1001 optimal PDB structure alignments: Integer programming methods for finding the maximum contact map overlap. *Journal of Computational Biology*, 11(1):27–52, January 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652704773416876; https://www.liebertpub.com/doi/pdf/10.1089/106652704773416876.

Chen:2009:AMP

[CCJ09] Ho-Lin Chen, Anne Condon, and Hosna Jabbari. An O (n^5) algorithm for MFE prediction of kissing hairpins and 4-chains in nucleic acids. *Journal of Computational Biology*, 16(6):803–815, June 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0219; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0219`.

Chen:2019:BAD

[CCL+19] Hengxi Chen, Shuting Cheng, Chang Liu, Jing Fu, and Wei Huang. Bioinformatics analysis of differentially expressed genes, methylated genes, and miRNAs in unexplained recurrent spontaneous abortion. *Journal of Computational Biology*, 26(12):1418–1426, December 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0158; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0158`.

Chakraborty:2020:CRN

[CCMS20] Shounak Chakraborty, Stefan Canzar, Tobias Marschall, and Marcel H. Schulz. Chromatyping: Reconstructing nucleosome profiles from NOMe sequencing data. *Journal of Computational Biology*, 27(3):330–341, March 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0457; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0457`.

Choi:2017:PLN

[CCPT17] Yoonha Choi, Marc Coram, Jie Peng, and Hua Tang. A Poisson log-normal model for constructing gene covariation network using RNA-seq data. *Journal of Computational Biology*, 24(7):721–731, July 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0053; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0053`.

Chang:2009:MSC

[CCT09] Ye-In Chang, Jiun-Rung Chen, and Yueh-Chi Tsai. Mining subspace clusters from DNA microarray data using large itemset

techniques. *Journal of Computational Biology*, 16(5):745–768, May 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0161; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0161`.

Chang:2015:VCF

[CCT15] Huilan Chang, Yi-Chang Chiu, and Yi-Lin Tsai. A variation of cover-free families and its applications. *Journal of Computational Biology*, 22(7):677–686, July 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0222; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0222`.

Chang:2018:ROA

[CCYH18] Kuang-Yu Chang, Yun Cui, Siu-Ming Yiu, and Wing-Kai Hon. Reconstructing one-articulated networks with distance matrices. *Journal of Computational Biology*, 25(3):253–269, March 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0148; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0148`.

Cheng:2007:ECD

[CD07] Yongxi Cheng and Ding-Zhu Du. Efficient constructions of disjunct matrices with applications to DNA library screening. *Journal of Computational Biology*, 14(9):1208–1216, November 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0052; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0052`.

Cheng:2008:NCO

[CD08] Yongxi Cheng and Ding-Zhu Du. New constructions of one- and two-stage pooling designs. *Journal of Computational Biology*, 15(2):195–205, March 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0195; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0195`.

Chen:2011:AOA

[CD11] Hong-Bin Chen and Annalisa De Bonis. An almost optimal algorithm for generalized threshold group testing with inhibitors. *Journal of Computational Biology*, 18(6):851–864, June 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0030; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0030`.

Chen:2018:DCN

[CD18] Jie Chen and Shirong Deng. Detection of copy number variation regions using the DNA-Sequencing data from multiple profiles with correlated structure. *Journal of Computational Biology*, 25(10):1128–1140, October 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0053; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0053`.

Collins:2021:MAE

[CD21] Obiora Cornelius Collins and Kevin Jan Duffy. Mathematical analyses on the effects of control measures for a waterborne disease model with socioeconomic conditions. *Journal of Computational Biology*, 28(1):19–32, January 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0352; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0352`.

Corradin:2011:SAR

[CDC+11] Alberto Corradin, Barbara Di Camillo, Vincenzo Ciminale, Gianna Toffolo, and Claudio Cobelli. Sensitivity analysis of retrovirus HTLV-1 transactivation. *Journal of Computational Biology*, 18(2):183–193, February 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0219; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0219`.

Chauve:2008:GFE

[CDEM08] Cedric Chauve, Jean-Philippe Doyon, and Nadia El-Mabrouk. Gene family evolution by duplication, speciation, and loss. *Journal of Computational Biology*, 15(8):1043–1062, October

2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0054; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0054.

Chen:2000:NPD

[CDFC00] Kevin Chen, Dannie Durand, and Martin Farach-Colton. NOTUNG: a program for dating gene duplications and optimizing gene family trees. *Journal of Computational Biology*, 7(3–4): 429–447, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Colannino:2006:LTA

[CDH+06] Justin Colannino, Mirela Damian, Ferran Hurtado, John Iacono, Henk Meijer, Suneeta Ramaswami, and Godfried Toussaint. An $O(n \log n)$-time algorithm for the restriction scaffold assignment problem. *Journal of Computational Biology*, 13(4):979–989, May 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.979; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.979.

Chen:2016:BIM

[CDH+16] Shi-Yi Chen, Feilong Deng, Ying Huang, Xianbo Jia, Yi-Ping Liu, and Song-Jia Lai. bioOTU: an improved method for simultaneous taxonomic assignments and operational taxonomic units clustering of 16s rRNA gene sequences. *Journal of Computational Biology*, 23(4):229–238, April 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0214; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0214.

Cheng:2009:PCP

[CDKL09] Yongxi Cheng, Ding-Zhu Du, Ker-I Ko, and Guohui Lin. On the parameterized complexity of pooling design. *Journal of Computational Biology*, 16(11):1529–1537, November 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0224; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0224.

Chen:2019:IIB

[CDL+19] Qingfeng Chen, Canshang Deng, Wei Lan, Zhixian Liu, Ruiqing Zheng, Jin Liu, and Jianxin Wang. Identifying interactions between kinases and substrates based on protein–protein interaction network. *Journal of Computational Biology*, 26(8):836–845, August 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0048; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0048`.

Cao:2021:IMD

[CDQ+21] Buwen Cao, Shuguang Deng, Hua Qin, Jiawei Luo, Guanghui Li, and Cheng Liang. Inferring MicroRNA-disease associations based on the identification of a functional module. *Journal of Computational Biology*, 28(1):33–42, January 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0106; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0106`.

Chen:2016:BIB

[CDS+16] Zhi-Zhong Chen, Fei Deng, Chao Shen, Yiji Wang, and Lusheng Wang. Better ILP-Based approaches to haplotype assembly. *Journal of Computational Biology*, 23(7):537–552, July 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0035; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0035`.

Canzar:2016:RCP

[CEJM16] Stefan Canzar, Khaled Elbassioni, Mitchell Jones, and Julián Mestre. Resolving conflicting predictions from multimapping reads. *Journal of Computational Biology*, 23(3):203–217, March 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0164; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0164`.

Cole:2017:NMS

[CEK+17] Marc Cole, Steffen Eikenberry, Takahide Kato, Roman A. Sandler, Stanley M. Yamashiro, and Vasilis Z. Marmarelis.

Nonparametric model of smooth muscle force production during electrical stimulation. *Journal of Computational Biology*, 24(3):229–237, March 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0070; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0070`.

Canzar:2013:CGP

[CEKP+13] Stefan Canzar, Mohammed El-Kebir, René Pool, Khaled Elbassioni, Alpeshkumar K. Malde, Alan E. Mark, Daan P. Geerke, Leen Stougie, and Gunnar W. Klau. Charge group partitioning in biomolecular simulation. *Journal of Computational Biology*, 20(3):188–198, March 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0239; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0239`.

Cohen:1997:NTD

[CF97] Jaime Cohen and Martin Farach. Numerical taxonomy on data: Experimental results. *Journal of Computational Biology*, 4(4):547–558, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.547; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.547`.

Comin:2014:PCF

[CF14] Matteo Comin and Montse Farreras. Parallel continuous flow: a parallel suffix tree construction tool for whole genomes. *Journal of Computational Biology*, 21(4):330–344, April 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0256; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0256`.

Chen:2007:MPP

[CFB+07] Brian Y. Chen, Viacheslav Y. Fofanov, Drew H. Bryant, Bradley D. Dodson, David M. Kristensen, Andreas M. Lisewski, Marek Kimmel, Olivier Lichtarge, and Lydia E. Kavraki. The MASH pipeline for protein function prediction and an algorithm for the geometric refinement of 3D motifs. *Journal of Computational Biology*, 14(6):791–816, July 2007. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R017; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R017.

Chapuis:2013:GPU

[CFE+13] Guillaume Chapuis, Olivier Filangi, Jean-Michel Elsen, Dominique Lavenier, and Pascale Le Roy. Graphics processing unit–accelerated quantitative trait loci detection. *Journal of Computational Biology*, 20(9):672–686, September 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0136; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0136.

Chitsaz:2013:EAU

[CFH13] Hamidreza Chitsaz, Elmirasadat Forouzmand, and Gholamreza Haffari. An efficient algorithm for upper bound on the partition function of nucleic acids. *Journal of Computational Biology*, 20(7):486–494, July 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0003; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0003.

Ceselli:2012:ADM

[CFR12] Alberto Ceselli, Sandro Luciano Fornili, and Giovanni Righini. Algorithms for the design of maximum hydropathic complementarity molecules. *Journal of Computational Biology*, 19(3):261–270, March 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0084; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0084.

Chen:2008:LTP

[CFS+08] Zhixiang Chen, Bin Fu, Robert Schweller, Boting Yang, Zhiyu Zhao, and Binhai Zhu. Linear time probabilistic algorithms for the singular haplotype reconstruction problem from SNP fragments. *Journal of Computational Biology*, 15(5):535–546, June 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0003; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0003.

Chang:2013:TGT

[CFS13] Huilan Chang, Hung-Lin Fu, and ChiH-Huai Shih. Threshold group testing on inhibitor model. *Journal of Computational Biology*, 20(6):464–470, June 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0224; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0224`.

Comin:2009:BBF

[CGD09] Matteo Comin, Concettina Guerra, and Frank Dellaert. Binding balls: Fast detection of binding sites using a property of spherical Fourier transform. *Journal of Computational Biology*, 16(11):1577–1591, November 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0045; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0045`.

Christodoulakis:2007:EAC

[CGI+07] Manolis Christodoulakis, G. Brian Golding, Costas S. Iliopoulos, Yoan José Pinzón Ardila, and William F. Smyth. Efficient algorithms for counting and reporting segregating sites in genomic sequences. *Journal of Computational Biology*, 14(7):1001–1010, September 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0136; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0136`.

Chauve:2010:YAG

[CGOT10] Cedric Chauve, Haris Gavranovic, Aida Ouangraoua, and Eric Tannier. Yeast ancestral genome reconstructions: The possibilities of computational methods II. *Journal of Computational Biology*, 17(9):1097–1112, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0092; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0092`.

Crescenzi:1998:CPF

[CGP+98] Pierluigi Crescenzi, Deborah Goldman, Christos Papadimitriou, Antonio Piccolboni, and Mihalis Yannakakis. On the com-

plexity of protein folding. *Journal of Computational Biology*, 5(3):423–465, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.423; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.423`.

Chen:2014:ZSR

[CGSW14] William Y. C. Chen, Qiang-Hui Guo, Lisa H. Sun, and Jian Wang. Zigzag stacks and m-regular linear stacks. *Journal of Computational Biology*, 21(12):915–935, December 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0133; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0133`.

Chang:2012:OBI

[CGT12] Young Hwan Chang, Joe Gray, and Claire Tomlin. Optimization-based inference for temporally evolving networks with applications in biology. *Journal of Computational Biology*, 19 (12):1307–1323, December 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0190; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0190`.

Comin:2004:PCM

[CGZ04] Matteo Comin, Concettina Guerra, and Giuseppe Zanotti. PROuST: a comparison method of three-dimensional structures of proteins using indexing techniques. *Journal of Computational Biology*, 11(6):1061–1072, December 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.1061; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.1061`.

Childs:2024:PDN

[CGZD24] Henry Childs, Nathan Guerin, Pei Zhou, and Bruce R. Donald. Protocol for designing *De Novo* noncanonical peptide binders in OSPREY. *Journal of Computational Biology*, 31(10):965–974, October 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0669;`

https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0669.

Chen:2015:CAM

[CH15] Ping Chen and Xuelin Huang. Comparison of analytic methods for quantitative real-time polymerase chain reaction data. *Journal of Computational Biology*, 22(11):988–996, November 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0023; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0023.

Charleston:1995:TCL

[Cha95] M. A. Charleston. Toward a characterization of landscapes of combinatorial optimization problems, with special attention to the phylogeny problem. *Journal of Computational Biology*, 2(3):439–450, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.439; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.439.

Charleston:2001:HHP

[Cha01] Michael A. Charleston. Hitch-hiking: a parallel heuristic search strategy, applied to the phylogeny problem. *Journal of Computational Biology*, 8(1):79–91, February 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701300099137; https://www.liebertpub.com/doi/pdf/10.1089/106652701300099137.

Cheung:2004:URS

[Che04] Leo Wang-Kit Cheung. Use of runs statistics for pattern recognition in genomic DNA sequences. *Journal of Computational Biology*, 11(1):107–124, January 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652704773416911; https://www.liebertpub.com/doi/pdf/10.1089/106652704773416911.

Chen:2006:DEA

[Che06] Peter C. Y. Chen. A discrete-event approach to transcription control with dynamic event-controllability. *Journal of*

Computational Biology, 13(9):1532–1545, November 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1532; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1532`.

Chen:2012:PDP

[Che12] Yen Hung Chen. The k partition-distance problem. *Journal of Computational Biology*, 19(4):404–417, April 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0186; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0186`.

Christensen:2005:PLA

[CHJ05] Ole F. Christensen, Asger Hobolth, and Jens L. Jensen. Pseudo-likelihood analysis of codon substitution models with neighbor-dependent rates. *Journal of Computational Biology*, 12(9):1166–1182, November 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1166; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1166`.

Coombes:2002:IQS

[CHK+02] Kevin R. Coombes, W. Edward Highsmith, Tammy A. Krogmann, Keith A. Baggerly, David N. Stivers, and Lynne V. Abruzzo. Identifying and quantifying sources of variation in microarray data using high-density cDNA membrane arrays. *Journal of Computational Biology*, 9(4):655–669, August 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652702760277372; https://www.liebertpub.com/doi/pdf/10.1089/106652702760277372`.

Chew:1999:FDC

[CHKK99] L. Paul Chew, Dan Huttenlocher, Klara Kedem, and Jon Kleinberg. Fast detection of common geometric substructure in proteins. *Journal of Computational Biology*, 6(3–4):313–325, October 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Chao:1994:RDL

[CHM94] Kun-Mao Chao, Ross C. Hardison, and Webb Miller. Recent developments in linear-space alignment methods: a survey. *Journal of Computational Biology*, 1(4):271–291, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.271; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.271`.

Chor:2013:PR

[Cho13] Benny Chor. Preface: RECOMB 2012. *Journal of Computational Biology*, 20(2):63, February 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.007p`.

Charleston:1994:ESL

[CHP94] Michael A. Charleston, Michael D. Hendy, and David Penny. The effects of sequence length, tree topology, and number of taxa on the performance of phylogenetic methods. *Journal of Computational Biology*, 1(2):133–151, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.133; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.133`.

Chen:2017:AWP

[CHS17] Wenbin Chen, William Hendrix, and Nagiza F. Samatova. The application of the weighted k-partite graph problem to the multiple alignment for metabolic pathways. *Journal of Computational Biology*, 24(12):1195–1211, December 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0064; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0064`.

Chauve:2010:MCS

[CHSY10] Cedric Chauve, Utz-Uwe Haus, Tamon Stephen, and Vivija P. You. Minimal conflicting sets for the consecutive ones property in ancestral genome reconstruction. *Journal of Computational Biology*, 17(9):1167–1181, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0113;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0113.

Christodoulakis:2006:CRR

[CIM+06] M. Christodoulakis, C. Iliopoulos, L. Mouchard, K. Perdikuri, A. Tsakalidis, and K. Tsichlas. Computation of repetitions and regularities of biologically weighted sequences. *Journal of Computational Biology*, 13(6):1214–1231, July 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1214; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1214.

Chen:2021:ILI

[CJ21] Xuejun Chen and Zhenran Jiang. ISFMDA: Learning interactions of selected features-based method for predicting potential MicroRNA-Disease associations. *Journal of Computational Biology*, 28(12):1219–1227, December 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0149; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0149.

Chandrasekhar:2022:MFA

[CJ22] Arjun Chandrasekhar and Magdalena M. Julkowska. A mathematical framework for analyzing wild tomato root architecture. *Journal of Computational Biology*, 29(4):306–316, April 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0361; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0361.

Chandra:2023:GSC

[CJ23] Ghanshyam Chandra and Chirag Jain. Gap-sensitive colinear chaining algorithms for acyclic pangenome graphs. *Journal of Computational Biology*, 30(11):1182–1197, November 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0186; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0186.

Chen:2001:AIP

[CJC01] Ting Chen, Jacob D. Jaffe, and George M. Church. Algorithms for identifying protein cross-links via tandem mass

spectrometry. *Journal of Computational Biology*, 8(6):571–583, November 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652701753307494; https://www.liebertpub.com/doi/pdf/10.1089/106652701753307494`.

Chiang:2006:GTC

[CJD06] David Chiang, Aravind K. Joshi, and Ken A. Dill. A grammatical theory for the conformational changes of simple helix bundles. *Journal of Computational Biology*, 13(1):21–42, January 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.21; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.21`.

Christof:1997:BCA

[CJK+97] Thomas Christof, Michael Jünger, John Kececioglu, Petra Mutzel, and Gerhard Reinelt. A branch-and-cut approach to physical mapping of chromosomes by unique end-probes. *Journal of Computational Biology*, 4(4):433–447, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.433; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.433`.

Chen:2022:SSG

[CJP+22] Ming Chen, Wei Jiang, Yi Pan, Jianhua Dai, Yunwen Lei, and Chunyan Ji. SGFNNs: Signed graph filtering-based neural networks for predicting drug–drug interactions. *Journal of Computational Biology*, 29(10):1104–1116, October 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0113; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0113`.

Chiang:2006:GRM

[CJS06] David Chiang, Aravind K. Joshi, and David B. Searls. Grammatical representations of macromolecular structure. *Journal of Computational Biology*, 13(5):1077–1100, June 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1077; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1077`.

Cui:2012:PTA

[CJS12] Yun Cui, Jesper Jansson, and Wing-Kin Sung. Polynomial-time algorithms for building a consensus MUL-Tree. *Journal of Computational Biology*, 19(9):1073–1088, September 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0008; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0008`.

Chechik:2009:TGE

[CK09] Gal Chechik and Daphne Koller. Timing of gene expression responses to environmental changes. *Journal of Computational Biology*, 16(2):279–290, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.13TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.13TT`.

Chung:2010:NRM

[CK10] Myung-Hoon Chung and Chul Koo Kim. Non-random mating involving inheritance of social status. *Journal of Computational Biology*, 17(5):745–754, May 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0152; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0152`.

Caldas:2011:HGB

[CK11] José Caldas and Samuel Kaski. Hierarchical generative biclustering for MicroRNA expression analysis. *Journal of Computational Biology*, 18(3):251–261, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0256; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0256`.

Chudin:2006:MTV

[CKB+06] E. Chudin, S. Kruglyak, S. C. Baker, S. Oeser, D. Barker, and T. K. McDaniel. A model of technical variation of microarray signals. *Journal of Computational Biology*, 13(4):996–1003, May 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.996;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.996.

Cristea:2017:PJI

[CKB17] Simona Cristea, Jack Kuipers, and Niko Beerenwinkel. pathTiMEx: Joint inference of mutually exclusive cancer pathways and their progression dynamics. *Journal of Computational Biology*, 24(6):603–615, June 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0171; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0171.

Cunha:2015:FAA

[CKdAHdF15] Luís Felipe I. Cunha, Luis Antonio B. Kowada, Rodrigo de A. Hausen, and Celina M. H. de Figueiredo. A faster 1.375-approximation algorithm for sorting by transpositions*. *Journal of Computational Biology*, 22(11):1044–1056, November 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0298; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0298.

Clifton:2017:HSM

[CKL+17] Sara M. Clifton, Chaeryon Kang, Jingyi Jessica Li, Qi Long, Nirmish Shah, and Daniel M. Abrams. Hybrid statistical and mechanistic mathematical model guides mobile health intervention for chronic pain. *Journal of Computational Biology*, 24(7):675–688, July 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0059; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0059.

Chor:2006:MLM

[CKS06] Benny Chor, Amit Khetan, and Sagi Snir. Maximum likelihood molecular clock comb: Analytic solutions. *Journal of Computational Biology*, 13(3):819–837, April 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.819; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.819.

Califano:2012:PRS

[CKS12] Andrea Califano, Manolis Kellis, and Gustavo Stolovitzky. Preface: RECOMB Systems Biology, Regulatory Genomics, and DREAM 2011 special issue. *Journal of Computational Biology*, 19(2):101, February 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.010p`.

Califano:2013:PRS

[CKS13] Andrea Califano, Manolis Kellis, and Gustavo Stolovitzky. Preface: RECOMB Systems Biology, Regulatory Genomics, and DREAM 2012 special issue. *Journal of Computational Biology*, 20(5):373–374, May 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.008p`.

Califano:2014:RIS

[CKS14] Andrea Califano, Manolis Kellis, and Gustavo Stolovitzky. RECOMB/ISCB systems biology, regulatory genomics, and DREAM 2013 special issue. *Journal of Computational Biology*, 21(5):371–372, May 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.009p`.

Califano:2015:PRI

[CKS15] AnDrea Califano, Manolis Kellis, and Gustavo Stolovitzky. Preface: RECOMB/ISCB Systems Biology, Regulatory Genomics, and DREAM 2014 special issue. *Journal of Computational Biology*, 22(4):251–252, April 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.020P`.

Chen:2001:DPA

[CKT+01] Ting Chen, Ming-Yang Kao, Matthew Tepel, John Rush, and George M. Church. A dynamic programming approach to De Novo peptide sequencing via tandem mass spectrometry. *Journal of Computational Biology*, 8(3):325–337, June 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270152530872; https://www.liebertpub.com/doi/pdf/10.1089/10665270152530872`.

Chakrabarty:2016:DCD

[CKT16] Deeparnab Chakrabarty, Sampath Kannan, and Kevin Tian. Detecting character dependencies in stochastic models of evolution. *Journal of Computational Biology*, 23(3):180–191, March 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0099; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0099`.

Cho:2019:MDC

[CKZ+19] Soonweng Cho, Hyun-Seok Kim, Martha A. Zeiger, Christopher B. Umbricht, and Leslie M. Cope. Measuring DNA copy number variation using high-density methylation microarrays. *Journal of Computational Biology*, 26(4):295–304, April 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0143; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0143`.

Chen:2020:IBA

[CKZL20] Mengwei Chen, Chengqi Kong, Zhiyuan Zheng, and Yin Li. Identification of biomarkers associated with septic cardiomyopathy based on bioinformatics analyses. *Journal of Computational Biology*, 27(1):69–80, January 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0181; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0181`.

Churchill:1999:BRH

[CL99] Gary A. Churchill and Betty Lazareva. Bayesian restoration of a hidden Markov chain with applications to DNA sequencing. *Journal of Computational Biology*, 6(2):261–277, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.261; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.261`.

Cao:2017:UVL

[CL17] Hu Cao and Yonggang Lu. Using variable-length aligned fragment pairs and an improved transition function for flexible protein structure alignment. *Journal of Computational Biology*, 24(1):2–12, January 2017. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0135; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0135.

Chen:2021:OFB

[CL21a] Hsin-Hao Chen and Chung-Chin Lu. Optimized fluorescence-based detection in single molecule synthesis process. *Journal of Computational Biology*, 28(2):195–208, February 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0226; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0226.

Cheng:2021:ANP

[CL21b] Chu-Yu Cheng and Chung-Chin Lu. The agility of a neuron: Phase shift between sinusoidal current input and firing rate curve. *Journal of Computational Biology*, 28(2):220–234, February 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0224; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0224.

Liu:2021:ERA

[cLcSwP+21] Chun cheng Liu, Tao chuan Shih, Tun wen Pai, Chin hwa Hu, and Wen shyong Tzou. Enhanced over-representation analysis for the differential regulation of *birc5a* and *hif2* α-knockdown approaches. *Journal of Computational Biology*, 28(7):674–686, July 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0556; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0556.

Chung:2003:DMB

[CLDG03] Fan Chung, Linyuan Lu, T. Gregory Dewey, and David J. Galas. Duplication models for biological networks. *Journal of Computational Biology*, 10(5):677–687, October 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703322539024; https://www.liebertpub.com/doi/pdf/10.1089/106652703322539024.

Chikhi:2015:RBG

[CLJ+15] Rayan Chikhi, Antoine Limasset, Shaun Jackman, Jared T. Simpson, and Paul Medvedev. On the representation of de Bruijn graphs. *Journal of Computational Biology*, 22(5):336–352, May 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0160; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0160`.

Cui:2020:MIL

[CLLL20] Danni Cui, Yingying Liu, Gang Liu, and Lei Liu. A multiple-instance learning-based convolutional neural network model to detect the *IDH1* mutation in the histopathology images of glioma tissues. *Journal of Computational Biology*, 27 (8):1264–1272, August 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0410; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0410`.

Camilo:2016:HOO

[CLM+16] Cesar M. Camilo, Gustavo M. A. Lima, Fernando V. Maluf, Rafael V. C. Guido, and Igor Polikarpov. HTP-OligoDesigner: an online primer design tool for high-throughput gene cloning and site-directed mutagenesis. *Journal of Computational Biology*, 23(1):27–29, January 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0148; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0148`.

Ciach:2018:ERR

[CŁM+18] Michał Aleksander Ciach, Mateusz Krzysztof Łacki, Błażej Miasojedow, Frederik Lermyte, Dirk Valkenborg, Frank Sobott, and Anna Gambin. Estimation of rates of reactions triggered by electron transfer in top-down mass spectrometry. *Journal of Computational Biology*, 25(3):282–301, March 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0156; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0156`.

Clote:2005:EAC

[Clo05] P. Clote. An efficient algorithm to compute the landscape of locally optimal RNA secondary structures with respect to the Nussinov–Jacobson energy model. *Journal of Computational Biology*, 12(1):83–101, February 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.83; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.83`.

Clote:2006:CSS

[Clo06] P. Clote. Combinatorics of saturated secondary structures of RNA. *Journal of Computational Biology*, 13(9):1640–1657, November 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1640; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1640`.

Chen:2005:MRP

[CLR+05] Zhi-Zhong Chen, Guohui Lin, Romeo Rizzi, Jianjun Wen, Dong Xu, Ying Xu, and Tao Jiang. More reliable protein NMR peak assignment via improved 2-interval scheduling. *Journal of Computational Biology*, 12(2):129–146, March 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.129; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.129`.

Collins:2011:QHR

[CLS11] Joshua Collins, Simone Linz, and Charles Semple. Quantifying hybridization in realistic time. *Journal of Computational Biology*, 18(10):1305–1318, October 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0166; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0166`.

Clark:2002:CAG

[CLSW02] Terry Clark, Sanggyu Lee, L. Ridgway Scott, and San Ming Wang. Computational analysis of gene identification with SAGE. *Journal of Computational Biology*, 9(3):513–526, June 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652702760138600; https://www.liebertpub.com/doi/pdf/10.1089/106652702760138600.

Chen:2020:APP

[CLT+20] Xiaoxia Chen, Hao Li, Lichao Tian, Qinwei Li, Jinxiang Luo, and Yongqiang Zhang. Analysis of the physicochemical properties of acaricides based on Lipinski's rule of five. *Journal of Computational Biology*, 27(9):1397–1406, September 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0323; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0323.

Csuros:2004:PGI

[CM04] Miklós Csürös and Aleksandar Milosavljevic. Pooled genomic indexing (PGI): Analysis and design of experiments. *Journal of Computational Biology*, 11(5):1001–1021, October 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.1001; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.1001.

Campo:2023:NIT

[CMK23] David S. Campo, Alexander Mosa, and Yury Khudyakov. A novel information-theory-based genetic distance that approximates phenotypic differences. *Journal of Computational Biology*, 30(4):420–431, April 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0395; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0395.

Carmel:2014:WCC

[CMLTZU14] Amir Carmel, Noa Musa-Lempel, Dekel Tsur, and Michal Ziv-Ukelson. The worst case complexity of maximum parsimony. *Journal of Computational Biology*, 21(11):799–808, November 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0128; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0128.

Chen:2025:FBI

[CMS+25] Xiang Chen, Yibing Ma, Yongle Shi, Bai Zhang, Hanwen Wu, and Jie Gao. Fuzzy-based identification of transition cells to infer cell trajectory for single-cell transcriptomics. *Journal of Computational Biology*, 32(3):253–273, March 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0432; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0432`.

Chen:2012:PSI

[CMSZ12] Ting Chen, Paul Marjoram, Fengzhu Sun, and Jasmine Xianghong Zhou. Preface: Special issue. *Journal of Computational Biology*, 19(6):575–576, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.6pre`.

Chernomor:2015:CCT

[CMvH15] Olga Chernomor, Bui Quang Minh, and Arndt von Haeseler. Consequences of common topological rearrangements for partition trees in phylogenomic inference. *Journal of Computational Biology*, 22(12):1129–1142, December 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0146; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0146`.

Castro:2017:UNM

[CN17] Christina J. Castro and Terry Fei Fan Ng. U_{50}: a new metric for measuring assembly output based on non-overlapping, target-specific contigs. *Journal of Computational Biology*, 24 (11):1071–1080, November 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0013; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0013`.

Chowdhury:2011:SSF

[CNCK11] Salim A. Chowdhury, Rod K. Nibbe, Mark R. Chance, and Mehmet Koyutürk. Subnetwork state functions define dysregulated subnetworks in cancer. *Journal of Computational Biology*, 18(3):263–281, March 2011. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0269; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0269.

Costa:2018:SMS

[COL+18] José M. J. Costa, Helcio R. B. Orlande, Viviane O. F. Lione, Antonio G. F. Lima, Tayná C. S. Cardoso, and Leonardo A. B. Varón. Simultaneous model selection and model calibration for the proliferation of tumor and normal cells during in vitro chemotherapy experiments. *Journal of Computational Biology*, 25(12):1285–1300, December 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0130; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0130.

Conklin:2004:RHC

[Con04] Darrell Conklin. Recognition of the helical cytokine fold. *Journal of Computational Biology*, 11(6):1189–1200, December 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.1189; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.1189.

Costa:2018:MGF

[Cos18] Evaldo Bezerra Costa. MELC genomics: a framework for De Novo genome assembly. *Journal of Computational Biology*, 25(2):194–199, February 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0102; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0102.

Costa:2015:ETS

[COV+15] Jose M. J. Costa, Helcio R. B. Orlande, Haroldo F. Campos Velho, Suani T. R. de Pinho, George S. Dulikravich, Renato M. Cotta, and Silvio H. da Cunha Neto. Estimation of tumor size evolution using particle filters. *Journal of Computational Biology*, 22(7):649–665, July 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0003; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0003.

Cowen:2020:PSI

[Cow20] Lenore J. Cowen. Preface special issue: RECOMB 2019. *Journal of Computational Biology*, 27(4):441, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.29027.ljc`.

Chatterji:2005:LMO

[CP05] Sourav Chatterji and Lior Pachter. Large multiple organism gene finding by collapsed Gibbs sampling. *Journal of Computational Biology*, 12(6):599–608, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.599; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.599`.

Cunha:2019:GRM

[CP19] Luís Felipe I. Cunha and Fábio Protti. Genome rearrangements on multigenomic models: Applications of graph convexity problems. *Journal of Computational Biology*, 26(11):1214–1222, November 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0091; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0091`.

Campanelli:2024:WPR

[CPFP24] Alessio Campanelli, Giulio Ermanno Pibiri, Jason Fan, and Rob Patro. Where the patterns are: Repetition-aware compression for colored de Bruijn graphs. *Journal of Computational Biology*, 31(10):1022–1044, October 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0714; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0714`.

Chitra:2022:NPN

[CPR22] Uthsav Chitra, Tae Yoon Park, and Benjamin J. Raphael. NetMix2: a principled network propagation algorithm for identifying altered subnetworks. *Journal of Computational Biology*, 29(12):1305–1323, December 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0336;`

https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0336.

Choi:2010:DLM

[CQG10] Hyungwon Choi, Zhaohui S. Qin, and Debashis Ghosh. A double-layered mixture model for the joint analysis of DNA copy number and gene expression data. *Journal of Computational Biology*, 17(2):121–137, February 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0019; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0019.

Castelo:2009:REM

[CR09] Robert Castelo and Alberto Roverato. Reverse engineering molecular regulatory networks from microarray data with qp-graphs. *Journal of Computational Biology*, 16 (2):213–227, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.08TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.08TT.

Clement:2018:VCA

[CRB18] Nathan Clement, Muhibur Rasheed, and Chandrajit Lal Bajaj. Viral capsid assembly: a quantified uncertainty approach. *Journal of Computational Biology*, 25(1):51–71, January 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0218; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0218.

Chiappetta:2004:BSS

[CRT04] P. Chiappetta, M. C. Roubaud, and B. Torrésani. Blind source separation and the analysis of microarray data. *Journal of Computational Biology*, 11(6):1090–1109, December 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.1090; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.1090.

Cerisier:2017:CVL

[CRT+17] Natacha Cerisier, Leslie Regad, Dhoha Triki, Anne-Claude Camproux, and Michel Petitjean. Cavity versus ligand shape

descriptors: Application to urokinase binding pockets. *Journal of Computational Biology*, 24(11):1134–1137, November 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0061; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0061.

Cawley:2000:DST

[CS00] Simon E. Cawley and Terence P. Speed. DNA sequencing with transposons. *Journal of Computational Biology*, 7(5):717–729, October 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701446161; https://www.liebertpub.com/doi/pdf/10.1089/106652701446161.

Cohen:2003:NSA

[CS03] Barry Cohen and Steven Skiena. Natural selection and algorithmic design of mRNA. *Journal of Computational Biology*, 10 (3–4):419–432, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Clausen:2015:DDE

[CS15] Rudy Clausen and Amarda Shehu. A data-driven evolutionary algorithm for mapping multibasin protein energy landscapes. *Journal of Computational Biology*, 22(9):844–860, September 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0107; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0107.

Chen:1998:HOM

[CSA98] Cheng Che Chen, Jas Winder Pal Singh, and Russ B. Altman. Hierarchical organization of molecular structure computations. *Journal of Computational Biology*, 5(3):409–422, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.409; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.409.

Chen:2020:MMI

[CSH+20] Zhenghao Chen, Ilya Soifer, Hugo Hilton, Leeat Keren, and Vladimir Jojic. Modeling multiplexed images with

Spatial–LDA reveals novel tissue microenvironments. *Journal of Computational Biology*, 27(8):1204–1218, August 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0340; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0340`.

Cosentino:2012:SBG

[CSP+12] Carlo Cosentino, Luca Salerno, Antonio Passanti, Alessio Merola, Declan G. Bates, and Francesco Amato. Structural bistability of the GAL regulatory network and characterization of its domains of attraction. *Journal of Computational Biology*, 19(2):148–162, February 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0251; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0251`.

Cai:2021:SIIa

[CSPZ21a] Zhipeng Cai, Pavel Skums, Yuri Porozov, and Alexander Zelikovsky. Special issue: 16th International Symposium on Bioinformatics Research and Applications (ISBRA 2020). *Journal of Computational Biology*, 28(7):636, July 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.29038.zc`.

Cai:2021:SIIb

[CSPZ21b] Zhipeng Cai, Pavel Skums, Yuri Porozov, and Alexander Zelikovsky. Special issue: 16th International Symposium on Bioinformatics Research and Applications (ISBRA 2020). *Journal of Computational Biology*, 28(8):745–746, August 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.29041.zc`.

Costa:2020:APA

[CST20] Evaldo Bezerra Costa, Gabriel Pereira Silva, and Marcello Goulart Teixeira. An approach to parallel algorithms for long DNA sequences alignment on manycore architecture. *Journal of Computational Biology*, 27(8):1248–1252, August 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/`

10.1089/cmb.2019.0362; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0362.

Csuros:2002:FRE

[Csu02] Miklós Csurös. Fast recovery of evolutionary trees with thousands of nodes. *Journal of Computational Biology*, 9(2):277–297, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270252935467; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935467.

Cai:2018:SIP

[CSZ18] Zhipeng Cai, Pavel Skums, and Alexander Zelikovsky. *Special Issue* preface: 13th International Symposium on Bioinformatics Research and Applications (ISBRA 2017). *Journal of Computational Biology*, 25(3):251–252, March 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.29012.zc.

Cai:2019:PIS

[CSZ19] Zhipeng Cai, Pavel Skums, and Alexander Zelikovsky. Preface: 14th International Symposium on Bioinformatics Research and Applications (ISBRA 2018). *Journal of Computational Biology*, 26(8):767–768, August 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.29022.zc.

Cai:2020:PSI

[CSZ20] Zhipeng Cai, Pavel Skums, and Alexander Zelikovsky. Preface special issue: 15th International Symposium on Bioinformatics Research and Applications (ISBRA 2019). *Journal of Computational Biology*, 27(2):131–132, February 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.29024.zc.

Cai:2022:ISB

[CSZ22] Zhipeng Cai, Pavel Skums, and Alexander Zelikovsky. 17th international symposium on bioinformatics research and applications (ISBRA 2021). *Journal of Computational Biology*, 29(10):1059–1060, October 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.29070.zc.

Cai:2023:SIPb

[CSZ23a] Zhipeng Cai, Pavel Skums, and Alexander Zeilkovsky. Special issue, part 2: 18th International Symposium on Bioinformatics Research and Applications (ISBRA 2022). *Journal of Computational Biology*, 30(9):949–950, September 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.29099.az`.

Cai:2023:SIPa

[CSZ23b] Zhipeng Cai, Pavel Skums, and Alexander Zelikovsky. Special issue, part I: 18th International Symposium on Bioinformatics Research and Applications (ISBRA 2022). *Journal of Computational Biology*, 30(8):829–830, August 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.29095.az`.

Chor:2007:BNC

[CT07] Benny Chor and Tamir Tuller. Biological networks: Comparison, conservation, and evolution via relative description length. *Journal of Computational Biology*, 14(6):817–838, July 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R018; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R018`.

Caylak:2021:PET

[CTC21a] Gizem Caylak, Oznur Tastan, and A. Ercument Cicek. Potpourri: an epistasis test prioritization algorithm via diverse SNP selection. *Journal of Computational Biology*, 28(4):365–377, April 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Caylak:2021:TDC

[CTC21b] Gizem Caylak, Oznur Tastan, and A. Ercument Cicek. A tool for detecting complementary single nucleotide polymorphism pairs in genome-wide association studies for epistasis testing. *Journal of Computational Biology*, 28(4):378–380, April 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Ciau-Uitz:2019:GRN

[CUP19] Aldo Ciau-Uitz and Roger Patient. Gene regulatory networks governing the generation and regeneration of blood. *Journal of Computational Biology*, 26(7):719–725, July 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0114; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0114`.

Comin:2011:ICM

[CV11] Matteo Comin and Davide Verzotto. The irredundant class method for remote homology detection of protein sequences. *Journal of Computational Biology*, 18(12):1819–1829, December 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0171; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0171`.

Croydon-veleslavov:2024:RDS

[CvS24] Ivan A. Croydon-veleslavov and Michael P. H. Stumpf. Repeated decision stumping distils simple rules from single-cell data. *Journal of Computational Biology*, 31(1):21–40, January 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0613; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0613`.

Chen:2009:IBK

[CW09] Xi Chen and Lily Wang. Integrating biological knowledge with gene expression profiles for survival prediction of cancer. *Journal of Computational Biology*, 16(2):265–278, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.12TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.12TT`.

Chen:2013:UTM

[CW13] Zhi-Zhong Chen and Lusheng Wang. An ultrafast tool for minimum reticulate networks. *Journal of Computational Biology*, 20(1):38–41, January 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0240;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0240.

Chen:2020:LRM

[CW20] Chian Chen and Hsiuying Wang. Logistic regression method for ligand discovery. *Journal of Computational Biology*, 27(6):934–940, June 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0232; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0232.

Cameron:2006:DFA

[CWC06] Michael Cameron, Hugh E. Williams, and Adam Cannane. A deterministic finite automaton for faster protein hit detection in BLAST. *Journal of Computational Biology*, 13(4):965–978, May 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.965; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.965.

Chen:2022:SMM

[CWH+22] Liang Chen, Hui Wan, Qiuyan He, Shun He, and Minghua Deng. Statistical methods for microbiome compositional data network inference: a survey. *Journal of Computational Biology*, 29(7):704–723, July 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0406; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0406.

Chen:2021:CIS

[CWJ+21] Zhineng Chen, Sai Wang, Caiyan Jia, Kai Hu, Xiongjun Ye, Xuanya Li, and Xieping Gao. CRDet: Improving signet ring cell detection by reinforcing the classification branch. *Journal of Computational Biology*, 28(7):732–743, July 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0555; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0555.

Chen:2013:SFM

[CWL13] Shijian Chen, Anqi Wang, and Lei M. Li. SEME: a fast mapper of illumina sequencing reads with statistical evaluation. *Journal of Computational Biology*, 20(11):847–860, November 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0111; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0111`.

Chakraborty:2024:PPA

[CWR24] Amit K. Chakraborty, Hao Wang, and Pouria Ramazi. From policy to prediction: Assessing forecasting accuracy in an integrated framework with machine learning and disease models. *Journal of Computational Biology*, 31(11):1104–1117, November 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0377; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0377`.

Chen:2015:PCA

[CWRF15] Derek E. Chen, Darryl L. Willick, Joseph B. Ruckel, and Wely B. Floriano. Principal component analysis of binding energies for single-point mutants of hT2R16 bound to an agonist correlate with experimental mutant cell response. *Journal of Computational Biology*, 22(1):37–53, January 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0192; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0192`.

Chen:2021:EDM

[CWS+21] Yanwei Chen, Keke Wang, Mengyuan Shang, Shuangshuang Zhao, Zheng Zhang, Haizhen Yang, Zheming Chen, Rui Du, Qilong Wang, and Baoding Chen. Exploration of DNA methylation-driven genes in papillary thyroid carcinoma based on the cancer genome atlas. *Journal of Computational Biology*, 28(1):99–114, January 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0471; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0471`.

Wang:2023:ASL

[cWxLlS+23] Zhen chang Wang, Jin xing Liu, Jun liang Shang, Ling yun Dai, Chun hou Zheng, and Juan Wang. ARGLRR: a sparse low-rank representation single-cell RNA-Sequencing data clustering method combined with a new graph regularization. *Journal of Computational Biology*, 30(8):848–860, August 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0077; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0077`.

Chen:2016:CPN

[CWYB16] Duo Chen, Jiasong Wang, Ming Yan, and Forrest Sheng Bao. A complex prime numerical representation of amino acids for protein function comparison. *Journal of Computational Biology*, 23(8):669–677, August 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0178; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0178`.

Chen:2016:EFR

[CXW16] Jiawen Chen, Zhong-Ru Xie, and Yinghao Wu. Elucidating the functional roles of spatial organization in cross-membrane signal transduction by a hybrid simulation method. *Journal of Computational Biology*, 23(7):566–584, July 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0227; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0227`.

Cai:2009:SMS

[CY09] Xiaodong Cai and Zhi-Min Yuan. Stochastic modeling and simulation of the p53-MDM2/MDMX loop. *Journal of Computational Biology*, 16(7):917–933, July 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0231; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0231`.

Chen:2010:CCG

[CY10] Xin Chen and Jian-Yi Yang. Constructing consensus genetic maps in comparative analysis. *Journal of Computational Bi-*

ology, 17(11):1561–1573, November 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0268; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0268`.

Cheng:2017:GAM

[CY17] Wen Cheng and Changhui Yan. A graph approach to mining biological patterns in the binding interfaces. *Journal of Computational Biology*, 24(1):31–39, January 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0128; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0128`.

Chang:2020:BAS

[CYF+20] Xin Chang, Mei-Feng Yang, Wei Fan, Li-Sheng Wang, Jun Yao, Zhao-Shen Li, and De-Feng Li. Bioinformatic analysis suggests that three hub genes may be a vital prognostic biomarker in pancreatic ductal adenocarcinoma. *Journal of Computational Biology*, 27(11):1595–1609, November 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0367; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0367`.

Chuang:2012:HBC

[CYLY12] Li-Yeh Chuang, Cheng-Huei Yang, Jung-Chike Li, and Cheng-Hong Yang. A hybrid BPSO-CGA approach for gene selection and classification of microarray data. *Journal of Computational Biology*, 19(1):68–82, January 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0064; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0064`.

Chandola:2011:NSI

[CYP+11] Himanshu Chandola, Anthony K. Yan, Shobha Potluri, Bruce R. Donald, and Chris Bailey-Kellogg. NMR structural inference of symmetric homo-oligomers. *Journal of Computational Biology*, 18(12):1757–1775, December 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0327;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0327.

Chuang:2009:TSB

[CYY09] Li-Yeh Chuang, Cheng-Huei Yang, and Cheng-Hong Yang. Tabu search and binary particle swarm optimization for feature selection using microarray data. *Journal of Computational Biology*, 16(12):1689–1703, December 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0211; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0211.

Chen:2023:NAL

[CYY23] Zhijie Chen, Tianhao Yan, and Zhanwen Yang. Numerical analysis of linearly implicit methods for discontinuous nonlinear Gurtin–MacCamy model. *Journal of Computational Biology*, 30(5):588–608, May 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0331; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0331.

Cong:2020:PRP

[CYZ+20] Ruochen Cong, Jushun Yang, Jie Zhou, Jianhua Shi, Yihua Zhu, Jianfeng Zhu, Jing Xiao, Ping Wang, Ying He, and Bosheng He. The potential role of protein tyrosine phosphatase, receptor type C (CD45) in the intestinal ischemia–reperfusion injury. *Journal of Computational Biology*, 27(8):1303–1312, August 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0244; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0244.

Chan:2010:ISW

[CZC10] Hock Peng Chan, Nancy Ruonan Zhang, and Louis H. Y. Chen. Importance sampling of word patterns in DNA and protein sequences. *Journal of Computational Biology*, 17 (12):1697–1709, December 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0233; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0233.

Castro:2019:FPM

[CZNF19] Guilherme Torres Castro, Luis Enrique Zárate, Cristiane Neri Nobre, and Henrique Cota Freitas. A fast parallel K-modes algorithm for clustering nucleotide sequences to predict translation initiation sites. *Journal of Computational Biology*, 26(5):442–456, May 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0245; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0245`.

Chen:2015:FGO

[CZS15] Quan Chen, Xianghong J. Zhou, and Fengzhu Sun. Finding genetic overlaps among diseases based on ranked gene lists. *Journal of Computational Biology*, 22(2):111–123, February 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0149; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0149`.

Chen:2019:SEN

[CZW+19] Qingyu Chen, Xiuzhen Zhang, Yu Wan, Justin Zobel, and Karin Verspoor. Search effectiveness in nonredundant sequence databases: Assessments and solutions. *Journal of Computational Biology*, 26(6):605–617, June 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0198; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0198`.

Chung:2019:MIC

[CZY19] Dahye Chung, Kaiyuan Zhang, and Jihoon Yang. Method for identifying cancer-related genes using gene similarity-based collaborative filtering. *Journal of Computational Biology*, 26(8):875–881, August 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0115; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0115`.

Dancik:1999:NPS

[DAC+99] Vlado Dančík, Theresa A. Addona, Karl R. Clauser, James E. Vath, and Pavel A. Pevzner. *De Novo* peptide sequencing via

tandem mass spectrometry. *Journal of Computational Biology*, 6(3–4):327–342, October 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Duong:2019:WSE

[DAE+19] Dat Duong, Wasi Uddin Ahmad, Eleazar Eskin, Kai-Wei Chang, and Jingyi Jessica Li. Word and sentence embedding tools to measure semantic similarity of gene ontology terms by their definitions. *Journal of Computational Biology*, 26(1):38–52, January 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0093; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0093`.

Diaz:2008:APP

[DAL+08] María Elena Díaz, Guillermo Ayala, Teresa León, Roberto Zoncu, and Derek Toomre. Analyzing protein-protein spatial-temporal dependencies from image sequences using fuzzy temporal random sets. *Journal of Computational Biology*, 15 (9):1221–1236, November 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0055; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0055`.

Dragomir:2023:PIM

[DAR23] Dakota Dragomir, Elizabeth S. Allman, and John A. Rhodes. Parameter identifiability of a multitype pure-birth model of speciation. *Journal of Computational Biology*, 30(3):277–292, March 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0330; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0330`.

Datta:2009:SFU

[DB09] Ritendra Datta and Marshall Bern. Spectrum fusion: Using multiple mass spectra for De Novo peptide sequencing. *Journal of Computational Biology*, 16(8):1169–1182, August 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0122; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0122`.

Dougherty:2002:ICA

[DBB+02] Edward R. Dougherty, Junior Barrera, Marcel Brun, Seungchan Kim, Roberto M. Cesar, Yidong Chen, Michael Bittner, and Jeffrey M. Trent. Inference from clustering with application to gene-expression microarrays. *Journal of Computational Biology*, 9(1):105–126, January 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270252833217; https://www.liebertpub.com/doi/pdf/10.1089/10665270252833217`.

Diallo:2009:WGS

[DBBM09] Abdoulaye Baniré Diallo, Dunarel Badescu, Mathieu Blanchette, and Vladimir Makarenkov. A whole genome study and identification of specific carcinogenic regions of the human papilloma viruses. *Journal of Computational Biology*, 16 (10):1461–1473, October 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0091; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0091`.

Devkota:2024:AIS

[DBHC24] Kapil Devkota, Anselm Blumer, Xiaozhe Hu, and Lenore Cowen. Approximate IsoRank for scalable and functionally meaningful cross-species alignments of protein interaction networks. *Journal of Computational Biology*, 31(10):990–1007, October 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0673; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0673`.

Dost:2012:AMS

[DBL+12] Banu Dost, Nuno Bandeira, Xiangqian Li, Zhouxin Shen, Steven P. Briggs, and Vineet Bafna. Accurate mass spectrometry based protein quantification via shared peptides. *Journal of Computational Biology*, 19(4):337–348, April 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0267; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0267`.

Dynerman:2009:CCG

[DBM09] David Dynerman, Erick Butzlaff, and Julie C. Mitchell. CUSA and CUDE: GPU-Accelerated methods for estimating solvent accessible surface area and desolvation. *Journal of Computational Biology*, 16(4):523–537, April 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0157; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0157`.

Dojer:2011:BBS

[DBT11] Norbert Dojer, Przemysław Biecek, and Jerzy Tiuryn. Bibillboard: Symmetrization and careful choice of informant species results in higher accuracy of regulatory element prediction. *Journal of Computational Biology*, 18(6):809–819, June 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0299; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0299`.

Dai:2017:SST

[DBW17] Zheng Dai, David Becerra, and Jérôme Waldispühl. On stable states in a topologically driven protein folding model. *Journal of Computational Biology*, 24(9):851–862, September 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0034; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0034`.

Deng:2016:DTE

[DC16a] Feilong Deng and Shi-Yi Chen. dbHT-Trans: an efficient tool for filtering the protein-encoding transcripts assembled by RNA-Seq according to search for homologous proteins. *Journal of Computational Biology*, 23(1):1–9, January 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0137; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0137`.

Drinkwater:2016:RRA

[DC16b] Benjamin Drinkwater and Michael A. Charleston. RASCAL: a randomized approach for coevolutionary analysis. *Journal of Computational Biology*, 23(3):218–227, March 2016.

CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0111; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0111.

Dong:2019:DFC

[DCD19] Chaoxuan Dong, Xiao-Yan Chen, and Chao-Yi Dong. Discerning functional connections in the pulsed neural networks with the dynamic Bayesian network structure search method based on a genetic algorithm. *Journal of Computational Biology*, 26(11):1243–1252, November 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0147; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0147.

Doyon:2009:SGS

[DCH09] Jean-Philippe Doyon, Cedric Chauve, and Sylvie Hamel. Space of gene/species trees reconciliations and parsimonious models. *Journal of Computational Biology*, 16(10):1399–1418, October 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0095; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0095.

Dizaji:2021:DLS

[DCH21] Kamran Ghasedi Dizaji, Wei Chen, and Heng Huang. Deep large-scale multitask learning network for gene expression inference. *Journal of Computational Biology*, 28(5):485–500, May 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Donze:2010:PSN

[DCL10] Alexandre Donzé, Gilles Clermont, and Christopher J. Langmead. Parameter synthesis in nonlinear dynamical systems: Application to systems biology. *Journal of Computational Biology*, 17(3):325–336, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0172; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0172.

Dong:2018:CTG

[DCL18] Yan Dong, Hongbao Cao, and Zhigang Liang. A curated target gene pool assisting early disease prediction and patient-specific treatment for small cell lung cancer. *Journal of Computational Biology*, 25(6):576–585, June 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0071; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0071`.

Do:2008:SBN

[DCP+08] Huy Hoang Do, Kwok Pui Choi, Franco P. Preparata, Wing Kin Sung, and Louxin Zhang. Spectrum-based *De Novo* repeat detection in genomic sequences. *Journal of Computational Biology*, 15(5):469–488, June 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0013; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0013`.

Dai:2021:NME

[DCP+21] Wei Dai, Bingxi Chen, Wei Peng, Xia Li, Jiancheng Zhong, and Jianxin Wang. A novel multi-ensemble method for identifying essential proteins. *Journal of Computational Biology*, 28(7):637–649, July 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0527; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0527`.

Deng:2004:IPM

[DCS04] Minghua Deng, Ting Chen, and Fengzhu Sun. An integrated probabilistic model for functional prediction of proteins. *Journal of Computational Biology*, 11(2–3):463–475, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Devillers:2011:RAW

[DCSE11] Hugo Devillers, Hélène Chiapello, Sophie Schbath, and Meriem El Karoui. Robustness assessment of whole bacterial genome segmentations. *Journal of Computational Biology*, 18(9):1155–1165, September 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0115;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0115.

Deforche:2007:ERC

[DCV+07] Koen Deforche, Ricardo Camacho, Kristel Van Laethem, Beth Shapiro, Yves Moreau, Andrew Rambaut, Anne-Mieke Vandamme, and Philippe Lemey. Estimating the relative contribution of dNTP pool imbalance and APOBEC3G/3F editing to HIV evolution *In Vivo*. *Journal of Computational Biology*, 14(8):1105–1114, October 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0073; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0073.

Deng:2017:GWS

[DCW+17] Feilong Deng, Shi-Yi Chen, Zhou-Lin Wu, Yongsong Hu, Xianbo Jia, and Song-Jia Lai. GFFview: a Web server for parsing and visualizing annotation information of eukaryotic genome. *Journal of Computational Biology*, 24(10):1060–1064, October 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0216; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0216.

Danford:2011:DRO

[DDA+11] Timothy Danford, Robin Dowell, Sudeep Agarwala, Paula Grisafi, Gerald Fink, and David Gifford. Discovering regulatory overlapping RNA transcripts. *Journal of Computational Biology*, 18(3):295–303, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0267; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0267.

Deng:2020:PNB

[DDC+20] Chao Deng, Timothy Daley, Peter Calabrese, Jie Ren, and Andrew D. Smith. Predicting the number of bases to attain sufficient coverage in high-throughput sequencing experiments. *Journal of Computational Biology*, 27(7):1130–1143, July 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0264; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0264.

Dhankhar:2021:SSA

[DDK21] Poonam Dhankhar, Vikram Dalal, and Viney Kumar. Screening of severe acute respiratory syndrome coronavirus 2 RNA-Dependent RNA polymerase inhibitors using computational approach. *Journal of Computational Biology*, 28 (12):1228–1247, December 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0639; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0639`.

Doan:2010:NLT

[DEH10] Duong D. Doan, Patricia A. Evans, and Joseph D. Horton. A near-linear time algorithm for haplotype determination on general pedigrees. *Journal of Computational Biology*, 17(10):1451–1465, October 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0133; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0133`.

Deichmann:2019:SIG

[Dei19a] Guest Editor Ute Deichmann. *Special Issue*: Genomic regulation: Experiments, computational modeling, and philosophy. *Journal of Computational Biology*, 26(7):625–628, July 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.29021.ud; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.29021.ud`.

Deichmann:2019:GME

[Dei19b] Ute Deichmann. From Gregor Mendel to Eric Davidson: Mathematical models and basic principles in biology. *Journal of Computational Biology*, 26(7):637–652, July 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0087; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0087`.

Dewey:2001:SAA

[Dew01] T. Gregory Dewey. A sequence alignment algorithm with an arbitrary gap penalty function. *Journal of Computational Biology*, 8(2):177–190, April 2001. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701300312931; https://www.liebertpub.com/doi/pdf/10.1089/106652701300312931.

Ding:2006:LTA

[DFG06] Zhihong Ding, Vladimir Filkov, and Dan Gusfield. A linear-time algorithm for the perfect phylogeny haplotyping (PPH) problem. *Journal of Computational Biology*, 13(2):522–553, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.522; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.522.

Dyer:1994:PUS

[DFS94] Martin Dyer, Alan Frieze, and Stephen Suen. The probability of unique solutions of sequencing by hybridization. *Journal of Computational Biology*, 1(2):105–110, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.105; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.105. See corrigendum [DFS96].

Dyer:1995:OCL

[DFS95] Martin Dyer, Alan Frieze, and Stephen Suen. Ordering clone libraries in computational biology. *Journal of Computational Biology*, 2(2):207–218, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.207; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.207.

Dyer:1996:CPU

[DFS96] Martin Dyer, Alan Frieze, and Stephen Suen. Corrigendum to *Probability of Unique Solutions of Sequencing by Hybridization*. *Journal of Computational Biology*, 3(2):331, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.331. See [DFS94].

Desper:2002:FAP

[DG02] Richard Desper and Olivier Gascuel. Fast and accurate phylogeny reconstruction algorithms based on the minimum-evolution principle. *Journal of Computational Biology*, 9(5):

687–705, October 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652702761034136; https://www.liebertpub.com/doi/pdf/10.1089/106652702761034136.

deAndres-Galiana:2016:DBR

[dGFMS16] Enrique J. deAndrés Galiana, Juan Luis Fernández-Martínez, and Stephen T. Sonis. Design of biomedical robots for phenotype prediction problems. *Journal of Computational Biology*, 23(8):678–692, August 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0008; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0008.

Deandres-Galiana:2016:IMP

[DGFMSS16] Enrique J. Deandrés-Galiana, Juan Luis Fernández-Martínez, Leorey N. Saligan, and Stephen T. Sonis. Impact of microarray preprocessing techniques in unraveling biological pathways. *Journal of Computational Biology*, 23(12):957–968, December 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0042; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0042.

Devauchelle:2001:RMA

[DGH+01] C. Devauchelle, A. Grossmann, A. Hénaut, M. Holschneider, M. Monnerot, J. L. Risler, and B. Torrésani. Rate matrices for analyzing large families of protein sequences. *Journal of Computational Biology*, 8(4):381–399, September 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701752236205; https://www.liebertpub.com/doi/pdf/10.1089/106652701752236205.

Deng:2013:BPP

[DGW+13] Lei Deng, Jihong Guan, Xiaoming Wei, Yuan Yi, Qiangfeng Cliff Zhang, and Shuigeng Zhou. Boosting prediction performance of protein–protein interaction hot spots by using structural neighborhood properties. *Journal of Computational Biology*, 20(11):878–891, November 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0083;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0083.

Drasdo:2000:SLS

[DHL00] Dirk Drasdo, Terence Hwa, and Michael Lässig. Scaling laws and similarity detection in sequence alignment with gaps. *Journal of Computational Biology*, 7(1–2):115–141, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Dancik:1997:HFC

[DHM97] Vlado Dančík, Sridhar Hannenhalli, and S. Muthukrishnan. Hardness of flip-cut problems from optical mapping. *Journal of Computational Biology*, 4(2):119–125, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.119; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.119.

DYachkov:2005:CPD

[DHM+05] A. D'Yachkov, Frank Hwang, Antony Macula, Pavel Vilenkin, and Chih-Wen Weng. A construction of pooling designs with some happy surprises. *Journal of Computational Biology*, 12(8):1129–1136, October 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1129; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1129.

Durand:2006:HMM

[DHV06] Dannie Durand, Bjarni V. Halldórsson, and Benjamin Vernot. A hybrid micro–macroevolutionary approach to gene tree reconstruction. *Journal of Computational Biology*, 13(2):320–335, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.320; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.320.

Du:2006:NCT

[DHWZ06] Ding-Zhu Du, F. K. Hwang, Weili Wu, and Taieb Znati. New construction for transversal design. *Journal of Computational Biology*, 13(4):990–995, May 2006. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.990; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.990.

Doniger:2002:PCP

[DHY02] Scott Doniger, Thomas Hofmann, and Joanne Yeh. Predicting CNS permeability of drug molecules: Comparison of neural network and support vector machine algorithms. *Journal of Computational Biology*, 9(6):849–864, December 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270260518317; https://www.liebertpub.com/doi/pdf/10.1089/10665270260518317.

deJong:2002:MSG

[dJ02] Hidde de Jong. Modeling and simulation of genetic regulatory systems: a literature review. *Journal of Computational Biology*, 9(1):67–103, January 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270252833208; https://www.liebertpub.com/doi/pdf/10.1089/10665270252833208.

Desper:1999:ITM

[DJK+99] Richard Desper, Feng Jiang, Olli-P. Kallioniemi, Holger Moch, Christos H. Papadimitriou, and Alejandro A. Schäffer. Inferring tree models for oncogenesis from comparative genome hybridization data. *Journal of Computational Biology*, 6(1):37–51, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.37; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.37.

Desper:2000:DBR

[DJK+00] Richard Desper, Feng Jiang, Olli-P. Kallioniemi, Holger Moch, Christos H. Papadimitriou, and Alejandro A. Schäffer. Distance-based reconstruction of tree models for oncogenesis. *Journal of Computational Biology*, 7(6):789–803, December 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270050514936; https://www.liebertpub.com/doi/pdf/10.1089/10665270050514936.

DeBlasio:2018:ALR

[DK18] Dan DeBlasio and John Kececioglu. Adaptive local realignment of protein sequences. *Journal of Computational Biology*, 25(7):780–793, July 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0045; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0045`.

Doerr:2017:NGS

[DKA+17] Daniel Doerr, Luis Antonio B. Kowada, Eloi Araujo, Shachi Deshpande, Simone Dantas, Bernard M. E. Moret, and Jens Stoye. New genome similarity measures based on conserved gene adjacencies. *Journal of Computational Biology*, 24(6):616–634, June 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0065; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0065`.

Dong:2015:CAS

[DKC15] Hui Dong, Jin Seob Kim, and Gregory S. Chirikjian. Computational analysis of SAXS data acquisition. *Journal of Computational Biology*, 22(9):787–805, September 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0115; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0115`.

Dombi:2009:AFT

[DKF09] József Dombi and Attila Kertész-Farkas. Applying fuzzy technologies to equivalence learning in protein classification. *Journal of Computational Biology*, 16(4):611–623, April 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0147; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0147`.

Deblasio:2020:MAT

[DKK20] Dan Deblasio, Kwanho Kim, and Carl Kingsford. More accurate transcript assembly via parameter advising. *Journal of Computational Biology*, 27(8):1181–1189, August 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0286; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0286.

Ding:2014:CPR

[DLD+14] Yang Ding, William A. Lorenz, Ivan Dotu, Evan Senter, and Peter Clote. Computing the probability of RNA hairpin and multiloop formation. *Journal of Computational Biology*, 21(3):201–218, March 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0148; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0148.

Du:2022:NMH

[DLFS22] Yuxuan Du, Sarah M. Laperriere, Jed Fuhrman, and Fengzhu Sun. Normalizing metagenomic Hi-C data and detecting spurious contacts using zero-inflated negative binomial regression. *Journal of Computational Biology*, 29(2):106–120, February 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0439; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0439.

David:2012:CBD

[DLL+12] Olivier David, Catherine Larédo, Raphaël Leblois, Brigitte Schaeffer, and Nicolas Vergne. Coalescent-based DNA barcoding: Multilocus analysis and robustness. *Journal of Computational Biology*, 19(3):271–278, March 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0122; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0122.

Ding:2024:SLS

[DLL+24] Jiayuan Ding, Lingxiao Li, Qiaolin Lu, Julian Venegas, Yixin Wang, Lidan Wu, Wei Jin, Hongzhi Wen, Renming Liu, Wenzhuo Tang, Xinnan Dai, Zhaoheng Li, and ... See all authors. SpatialCTD: a large-scale tumor microenvironment spatial transcriptomic dataset to evaluate cell type deconvolution for immuno-oncology. *Journal of Computational Biology*, 31(9):871–885, September 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Delgado:2010:CSA

[DLM10] João Delgado, Inês Lynce, and Vasco Manquinho. Computing the summed adjacency disruption number between two genomes with duplicate genes. *Journal of Computational Biology*, 17(9):1243–1265, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0098; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0098`.

Dimitrova:2010:DTS

[DLML10] Elena S. Dimitrova, M. Paola Vera Licona, John McGee, and Reinhard Laubenbacher. Discretization of time series data. *Journal of Computational Biology*, 17(6):853–868, June 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0023; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0023`.

Didier:2006:LDS

[DLPH06] Gilles Didier, Ivan Laprevotte, Maude Pupin, and Alain Hénaut. Local decoding of sequences and alignment-free comparison. *Journal of Computational Biology*, 13(8):1465–1476, October 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1465; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1465`.

Dhar:2017:CHO

[DM17] Amrit Dhar and Vladimir N. Minin. Calculating higher-order moments of phylogenetic stochastic mapping summaries in linear time. *Journal of Computational Biology*, 24(5):377–399, May 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0172; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0172`.

Dey:2020:GBA

[DM20] Lopamudra Dey and Anirban Mukhopadhyay. A graph-based approach for finding the dengue infection pathways in humans using protein–protein interactions. *Journal of Computational Biology*, 27(5):755–768, May 2020. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0171; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0171.

Diallo:2007:EHA

[DMB07] Abdoulaye Banire Diallo, Vladimir Makarenkov, and Mathieu Blanchette. Exact and heuristic algorithms for the indel maximum likelihood problem. *Journal of Computational Biology*, 14(4):446–461, May 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.A006; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.A006.

DeSouzaJacomini:2017:GNF

[DMDR17] Ricardo De Souza Jacomini, David Correa Martins, Jr., Felipe Leno Da Silva, and Anna Helena Reali Costa. GeNICE: a novel framework for gene network inference by clustering, exhaustive search, and multivariate analysis. *Journal of Computational Biology*, 24(8):809–830, August 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0022; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0022.

Dalgaard:1997:SMP

[DMHM97] Jacob Z. Dalgaard, Michael J. Moser, Richard Hughey, and I. Saira Mian. Statistical modeling, phylogenetic analysis and structure prediction of a protein splicing domain common to inteins and hedgehog proteins. *Journal of Computational Biology*, 4(2):193–214, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.193; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.193.

DYachkov:2006:NGI

[DMP+06] Arkadii G. D'Yachkov, Anthony J. Macula, Wendy K. Pogozelski, Thomas E. Renz, Vyacheslav V. Rykov, and David C. Torney. New t-gap insertion-deletion-like metrics for DNA hybridization thermodynamic modeling. *Journal of Computational Biology*, 13(4):866–881, May 2006. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.866; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.866.

Dror:2003:BET

[DMR+03] Ron O. Dror, Jonathan G. Murnick, Nicola J. Rinaldi, Voichita D. Marinescu, Ryan M. Rifkin, and Richard A. Young. Bayesian estimation of transcript levels using a general model of array measurement noise. *Journal of Computational Biology*, 10 (3–4):433–452, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

deMontgolfier:2014:EIG

[dMRR14] Fabien de Montgolfier, Mathieu Raffinot, and Irena Rusu. Easy identification of generalized common and conserved nested intervals. *Journal of Computational Biology*, 21(7):520–533, July 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0146; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0146.

DeMol:2009:RMS

[DMTV09] Christine De Mol, Sofia Mosci, Magali Traskine, and Alessandro Verri. A regularized method for selecting nested groups of relevant genes from microarray data. *Journal of Computational Biology*, 16(5):677–690, May 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0171; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0171.

Dediu:2017:PSA

[DMV17] Adrian-Horia Dediu and Carlos Martín-Vide. Preface: Selected articles of the Second International Conference on Algorithms for Computational Biology (AlCoB 2015). *Journal of Computational Biology*, 24(2):91–92, February 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.29005.ahd.

Donmez:2017:CIS

[DMW+17] Nilgun Donmez, Salem Malikic, Alexander W. Wyatt, Martin E. Gleave, Colin C. Collins, and S. Cenk Sahinalp. Clonal-

ity inference from single tumor samples using low-coverage sequence data. *Journal of Computational Biology*, 24(6):515–523, June 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0148; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0148`.

Diallo:2019:SPW

[DND+19] Abdoulaye Baniré Diallo, Engelbert Mephu Nguifo, Wajdi Dhifli, Elham Azizi, Sandhya Prabhakaran, and Wesley Tansey. Selected papers from the Workshop on Computational Biology: Joint with the International Joint Conference on Artificial Intelligence and the International Conference on Machine Learning, 2018. *Journal of Computational Biology*, 26(6):507–508, June 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.29020.abd`.

Diallo:2017:PSP

[DNZ17] Abdoulaye Baniré Diallo, Engelbert Mephu Nguifo, and Mohammed J. Zaki. Preface: Selected papers from the Workshop Bioinformatics and Artificial Intelligence Joined with the International Joint Conference on Artificial Intelligence. *Journal of Computational Biology*, 24(8):733, August 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.29008.abd`.

Davidson:1995:CIB

[DOB95] S. B. Davidson, C. Overton, and P. Buneman. Challenges in integrating biological data sources. *Journal of Computational Biology*, 2(4):557–572, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.557; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.557`.

Dunlavy:2005:HHO

[DOKT05] Daniel M. Dunlavy, Dianne P. O'leary, Dmitri Klimov, and D. Thirumalai. HOPE: a homotopy optimization method for protein structure prediction. *Journal of Computational Biology*, 12(10):1275–1288, December 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (elec-

tronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1275; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1275.

Domanic:2007:NAD

[DP07] Nevzat Onur Domaniç and Franco P. Preparata. A novel approach to the detection of genomic approximate tandem repeats in the Levenshtein metric. *Journal of Computational Biology*, 14(7):873–891, September 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0018; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0018.

Dehnert:2005:GPB

[DPHH05] Manuel Dehnert, Rainer Plaumann, Werner E. Helm, and Marc-Th. Hütt. Genome phylogeny based on short-range correlations in DNA sequences. *Journal of Computational Biology*, 12(5):545–553, June 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.545; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.545.

Dill:1997:PSE

[DPR97] K. A. Dill, A. T. Phillips, and J. B. Rosen. Protein structure and energy landscape dependence on sequence using a continuous energy function. *Journal of Computational Biology*, 4(3):227–239, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.227; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.227.

Delfino:2020:ESS

[DPS+20] Francesco Delfino, Yuri Porozov, Eugene Stepanov, Gaik Tamazian, and Valentina Tozzini. Evolutionary switches structural transitions via coarse-grained models. *Journal of Computational Biology*, 27(2):189–199, February 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0338; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0338.

Desai:2020:CSU

[DPSW20] Heta P. Desai, Anuja P. Parameshwaran, Rajshekhar Sunderraman, and Michael Weeks. Comparative study using neural networks for 16S ribosomal gene classification. *Journal of Computational Biology*, 27(2):248–258, February 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0436; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0436`.

Day:2011:RPG

[DQS+11] Ryan Day, Xiaotao Qu, Rosemarie Swanson, Zach Bohannan, Robert Bliss, and Jerry Tsai. Relative packing groups in template-based structure prediction: Cooperative effects of true positive constraints. *Journal of Computational Biology*, 18(1):17–26, January 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0078; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0078`.

Disanto:2015:CHL

[DR15] Filippo Disanto and Noah A. Rosenberg. Coalescent histories for lodgepole species trees. *Journal of Computational Biology*, 22(10):918–929, October 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0015; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0015`.

Disanto:2017:EAC

[DR17] Filippo Disanto and Noah A. Rosenberg. Enumeration of ancestral configurations for matching gene trees and species trees. *Journal of Computational Biology*, 24(9):831–850, September 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0159; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0159`.

DeVoe:2025:AAC

[DRT+25] Elias DeVoe, Honey V. Reddi, Bradley W. Taylor, Samantha Stachowiak, Jennifer L. Geurts, Ben George, Reza Shaker,

Raul Urrutia, and Michael T. Zimmermann. An analytical approach that combines knowledge from germline and somatic mutations enhances tumor genomic reanalyses in precision oncology. *Journal of Computational Biology*, 32(1):89–103, January 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0461; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0461`.

Durand:2003:TGC

[DS03] Dannie Durand and David Sankoff. Tests for gene clustering. *Journal of Computational Biology*, 10(3–4):453–482, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Dejori:2004:IIP

[DS04] Mathäus Dejori and Martin Stetter. Identifying interventional and pathogenic mechanisms by generative inverse modeling of gene expression profiles. *Journal of Computational Biology*, 11(6):1135–1148, December 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.1135; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.1135`.

Devillers:2012:SSM

[DS12] Hugo Devillers and Sophie Schbath. Separating significant matches from spurious matches in DNA sequences. *Journal of Computational Biology*, 19(1):1–12, January 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0070; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0070`.

Demongeot:2019:BDC

[DS19] Jacques Demongeot and Hervé Seligmann. Bias for 3′-dominant codon directional asymmetry in theoretical minimal RNA rings. *Journal of Computational Biology*, 26(9):1003–1012, September 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0256; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0256`.

Demetci:2022:SSCb

[DSC+22] Pinar Demetci, Rebecca Santorella, Manav Chakravarthy, Bjorn Sandstede, and Ritambhara Singh. SCOTv2: Single-cell multiomic alignment with disproportionate cell-type representation. *Journal of Computational Biology*, 29(11):1213–1228, November 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0270; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0270`.

Dost:2008:QTQ

[DSG+08] Banu Dost, Tomer Shlomi, Nitin Gupta, Eytan Ruppin, Vineet Bafna, and Roded Sharan. QNet: a tool for querying protein interaction networks. *Journal of Computational Biology*, 15(7):913–925, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0172; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0172`.

Dhifli:2014:SPS

[DSN14] Wajdi Dhifli, Rabie Saidi, and Engelbert Mephu Nguifo. Smoothing 3D protein structure motifs through graph mining and amino acid similarities. *Journal of Computational Biology*, 21(2):162–172, February 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0092; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0092`.

Demetci:2022:SSCa

[DSS+22a] Pinar Demetci, Rebecca Santorella, Björn Sandstede, William Stafford Noble, and Ritambhara Singh. SCOT: Single-cell multiomics alignment with optimal transport. *Journal of Computational Biology*, 29(1):3–18, January 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0446; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0446`.

Demetci:2022:SCM

[DSS+22b] Pinar Demetci, Rebecca Santorella, Björn Sandstede, William Stafford Noble, and Ritambhara Singh. Single-cell multiomics integration

by SCOT. *Journal of Computational Biology*, 29(1):19–22, January 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0477; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0477.

Dixit:2012:FPM

[DSV12] Narendra M. Dixit, Piyush Srivastava, and Nisheeth K. Vishnoi. A finite population model of molecular evolution: Theory and computation. *Journal of Computational Biology*, 19 (10):1176–1202, October 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0064; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0064.

Dana:2012:EMS

[DT12] Alexandra Dana and Tamir Tuller. Efficient manipulations of synonymous mutations for controlling translation rate: an analytical approach. *Journal of Computational Biology*, 19 (2):200–231, February 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0275; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0275.

Dutkowski:2013:PMN

[DT13] Janusz Dutkowski and Jerzy Tiuryn. A probabilistic model of neutral and selective dynamics of protein network evolution. *Journal of Computational Biology*, 20(9):631–642, September 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0295; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0295.

Deac:2019:ACM

[DVS19] Andreea Deac, Petar Veličković, and Pietro Sormanni. Attentive cross-modal paratope prediction. *Journal of Computational Biology*, 26(6):536–545, June 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0175; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0175.

Duan:2020:MBC

[DWK+20] Xin Duan, Kejun Wang, Jia Ke, Ping Lan, Feng Gao, and Xiaojian Wu. Multiomics-based colorectal cancer molecular subtyping using local scaling network fusion. *Journal of Computational Biology*, 27(8):1295–1302, August 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0252; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0252`.

Dias:2022:EMF

[DWMT22] Fernando H. C. Dias, Lucia Williams, Brendan Mumey, and Alexandru I. Tomescu. Efficient minimum flow decomposition via integer linear programming. *Journal of Computational Biology*, 29(11):1252–1267, November 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0257; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0257`.

Dew:2005:TAM

[DWS05] Ian M. Dew, Brian Walenz, and Granger Sutton. A tool for analyzing mate pairs in assemblies (TAMPA). *Journal of Computational Biology*, 12(5):497–513, June 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.497; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.497`.

Dong:2020:IMG

[DYLK20] Xihua Dong, Xiaoou Yu, Hua Li, and Hui Kang. Identification of marker genes and pathways in patients with primary biliary cholangitis. *Journal of Computational Biology*, 27(6):923–933, June 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0230; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0230`.

Deng:2003:PPF

[DZM+03] Minghua Deng, Kui Zhang, Shipra Mehta, Ting Chen, and Fengzhu Sun. Prediction of protein function using protein–protein interaction data. *Journal of Computational Biology*, 10(6):947–960, December 2003. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703322756168; https://www.liebertpub.com/doi/pdf/10.1089/106652703322756168.

Du:2024:IMH

[DZS24] Yuxuan Du, Wenxuan Zuo, and Fengzhu Sun. Imputing metagenomic Hi-C contacts facilitates the integrative contig binning through constrained random walk with restart. *Journal of Computational Biology*, 31(10):1008–1021, October 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0663; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0663.

Eng:2009:NDM

[EAA+09] Catherine Eng, Charu Asthana, Bertrand Aigle, Sébastien Hergalant, Jean-François Mari, and Pierre Leblond. A new data mining approach for the detection of bacterial promoters combining stochastic and combinatorial methods. *Journal of Computational Biology*, 16(9):1211–1225, September 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0122; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0122.

Eriksen:2024:TRI

[EAFM24] Casper Asbjørn Eriksen, Jakob Lykke Andersen, Rolf Fagerberg, and Daniel Merkle. Toward the reconciliation of inconsistent molecular structures from biochemical databases. *Journal of Computational Biology*, 31(6):498–512, June 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Elmarakeby:2017:BEC

[EAM+17] Haitham Elmarakeby, Mostafa Arefiyan, Elijah Myers, Song Li, Ruth Grene, and Lenwood S. Heath. Beacon Editor: Capturing signal transduction pathways using the systems biology graphical notation activity flow language. *Journal of Computational Biology*, 24(12):1226–1229, December 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0095; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0095.

Erten:2011:VAP

[EBK11] Sinan Erten, Gurkan Bebek, and Mehmet Koyutürk. Vavien: an algorithm for prioritizing candidate disease genes based on topological similarity of proteins in interaction networks. *Journal of Computational Biology*, 18(11):1561–1574, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0154; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0154`.

Espitia:2022:MMH

[EBS+22] Cristian C. Espitia, Miguel A. Botina, Marco A. Solarte, Ivan Hernandez, Ricardo A. Riascos, and João F. Meyer. Mathematical model of HIV/AIDS considering sexual preferences under antiretroviral therapy, a case study in San Juan de Pasto, Colombia. *Journal of Computational Biology*, 29(5):483–493, May 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0323; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0323`.

Eduati:2012:DMM

[EdCK+12] Federica Eduati, Barbara di Camillo, Michael Karbiener, Marcel Scheideler, Davide Corà, Michele Caselle, and Gianna Toffolo. Dynamic modeling of miRNA-mediated feed-forward loops. *Journal of Computational Biology*, 19(2):188–199, February 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0274; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0274`.

Editor:2024:RSC

[Edi24] Tomas VinarGuest Editor. RECOMB satellite conference on comparative genomics (RECOMB-CG 2023). *Journal of Computational Biology*, 31(4):275–276, April 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.29113.tv`.

Ehler:2012:LLB

[EFM12] M. Ehler, F. Filbir, and H. N. Mhaskar. Locally learning biomedical data using diffusion frames. *Journal of Computational Biology*, 19(11):1251–1264, November 2012. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0187; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0187.

Eskin:2013:EEA

[EHC+13] Itamar Eskin, Farhad Hormozdiari, Lucia Conde, Jacques Riby, Christine F. Skibola, Eleazar Eskin, and Eran Halperin. eALPS: Estimating abundance levels in pooled sequencing using available genotyping data. *Journal of Computational Biology*, 20(11):861–877, November 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0105; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0105.

Elder:2024:AEO

[EHFK24] C. S. Elder, Minh Hoang, Mohsen Ferdosi, and Carl Kingsford. Approximate and exact optimization algorithms for the Beltway and Turnpike problems with duplicated, missing, partially labeled, and uncertain measurements. *Journal of Computational Biology*, 31(10):908–926, October 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0661; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0661.

Efrat:2002:GAA

[EHK+02] Alon Efrat, Frank Hoffmann, Klaus Kriegel, Christof Schultz, and Carola Wenk. Geometric algorithms for the analysis of 2D-electrophoresis gels. *Journal of Computational Biology*, 9(2):299–315, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270252935476; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935476.

Eidhammer:2000:SCS

[EJT00] Ingvar Eidhammer, Inge Jonassen, and William R. Taylor. Structure comparison and structure patterns. *Journal of Computational Biology*, 7(5):685–716, October 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701446152; https://www.liebertpub.com/doi/pdf/10.1089/106652701446152.

Elhai:2001:DBR

[Elh01] Jeff Elhai. Determination of bias in the relative abundance of oligonucleotides in DNA sequences. *Journal of Computational Biology*, 8(2):151–175, April 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652701300312922; https://www.liebertpub.com/doi/pdf/10.1089/106652701300312922`.

Elhai:2011:HCR

[Elh11] Jeff Elhai. Humans, computers, and the route to biological insights: Regaining our capacity for surprise. *Journal of Computational Biology*, 18(7):867–878, July 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0194; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0194`.

Elias:2006:SIM

[Eli06] Isaac Elias. Settling the intractability of multiple alignment. *Journal of Computational Biology*, 13(7):1323–1339, September 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1323; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1323`.

Elliott:2020:KSP

[Ell20] Lloyd T. Elliott. Kinship solutions for partially observed multiphenotype data. *Journal of Computational Biology*, 27 (9):1461–1470, September 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0440; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0440`.

Eres:2004:PPD

[ELP04] Revital Eres, Gad M. Landau, and Laxmi Parida. Permutation pattern discovery in biosequences. *Journal of Computational Biology*, 11(6):1050–1060, December 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.1050; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.1050`.

Eddy:1995:MDH

[EMD95] Sean R. Eddy, Graeme Mitchison, and Richard Durbin. Maximum discrimination hidden Markov models of sequence consensus. *Journal of Computational Biology*, 2(1):9–23, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.9; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.9`.

Eulenstein:1998:DBM

[EMV98] O. Eulenstein, B. Mirkin, and M. Vingron. Duplication-based measures of difference between gene and species trees. *Journal of Computational Biology*, 5(1):135–148, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.135; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.135`.

Emek:2022:SIB

[EN22] Yuval Emek and Saket Navlakha. Special issue: Biological Distributed Algorithms 2021. *Journal of Computational Biology*, 29 (4):305, April 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.29060.ye`.

Eskin:2002:USM

[ENS02] Eleazar Eskin, William Stafford Noble, and Yoram Singer. Using substitution matrices to estimate probability distributions for biological sequences. *Journal of Computational Biology*, 9(6):775–791, December 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270260518263; https://www.liebertpub.com/doi/pdf/10.1089/10665270260518263`.

Eskin:2003:PFC

[ENS03] Eleazar Eskin, William Stafford Noble, and Yoram Singer. Protein family classification using sparse Markov transducers. *Journal of Computational Biology*, 10(2):187–213, April 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652703321825964; https://www.liebertpub.com/doi/pdf/10.1089/106652703321825964`.

Escobar:2018:PPP

[EOD+18] Juan José Escobar, Julio Ortega, Antonio Francisco Díaz, Jesús González, and Miguel Damas. A power–performance perspective to multiobjective electroencephalogram feature selection on heterogeneous parallel platforms. *Journal of Computational Biology*, 25(8):882–893, August 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0080; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0080`.

Escalier:1998:PMI

[EPSV98] Vincent Escalier, Joél Pothier, Henri Soldano, and Alain Viari. Pairwise and multiple identification of three-dimensional common substructures in proteins. *Journal of Computational Biology*, 5(1):41–56, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.41; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.41`.

Erdmann:2005:PSK

[Erd05] Michael A. Erdmann. Protein similarity from knot theory: Geometric convolution and line weavings. *Journal of Computational Biology*, 12(6):609–637, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.609; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.609`.

Erives:2009:NHS

[Eri09] Albert Erives. Non-homologous structured CRMs from the *Ciona* genome. *Journal of Computational Biology*, 16 (2):369–377, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.20TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.20TT`.

Erwin:2019:PGT

[Erw19] Douglas H. Erwin. Prospects for a general theory of evolutionary novelty. *Journal of Computational Biology*, 26(7):735–744,

July 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0089; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0089.

Emmert-Streib:2006:ACK

[ES06] Frank Emmert-Streib. Algorithmic computation of knot polynomials of secondary structure elements of proteins. *Journal of Computational Biology*, 13(8):1503–1512, October 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1503; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1503.

Emmert-Streib:2007:CFS

[ES07] Frank Emmert-Streib. The chronic fatigue syndrome: a comparative pathway analysis. *Journal of Computational Biology*, 14(7):961–972, September 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0041; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0041.

Elias:2007:RAG

[ET07] Isaac Elias and Tamir Tuller. Reconstruction of ancestral genomic sequences using likelihood. *Journal of Computational Biology*, 14(2):216–237, March 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0101; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0101.

Ershov:2019:IHS

[ETLK19] Vasily Ershov, Artem Tarasov, Alla Lapidus, and Anton Korobeynikov. IonHammer: Homopolymer-space Hamming clustering for IonTorrent read error correction. *Journal of Computational Biology*, 26(2):124–127, February 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0152; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0152.

Engel:2019:CGB

[EVLZU19] Jonathan Engel, Isana Veksler-Lublinsky, and Michal Ziv-Ukelson. Constrained gene block discovery and its application to prokaryotic genomes. *Journal of Computational Biology*, 26(7):745–766, July 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0096; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0096`.

Evans:1998:CCP

[EZ98] Steven N. Evans and Xiaowen Zhou. Constructing and counting phylogenetic invariants. *Journal of Computational Biology*, 5(4):713–724, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.713; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.713`.

Eghbal-Zadeh:2019:DEE

[EZFP+19] Hamid Eghbal-Zadeh, Lukas Fischer, Niko Popitsch, Florian Kromp, Sabine Taschner-Mandl, Teresa Gerber, Eva Bozsaky, Peter F. Ambros, Inge M. Ambros, Gerhard Widmer, and Bernhard A. Moser. DeepSNP: an end-to-end deep neural network with attention-based localization for breakpoint detection in single-nucleotide polymorphism array genomic data. *Journal of Computational Biology*, 26(6):572–596, June 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0172; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0172`.

Frazier:2012:CAI

[FA12] Zachary Frazier and Frank Alber. A computational approach to increase time scales in Brownian dynamics–based reaction-diffusion modeling. *Journal of Computational Biology*, 19(6):606–618, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0027; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0027`.

Farhoodi:2017:MLA

[FADH17] Roshanak Farhoodi, Bahar Akbal-Delibas, and Nurit Haspel. Machine learning approaches for predicting protein complex similarity. *Journal of Computational Biology*, 24(1):40–51, January 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0137; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0137`.

Farach:1997:RCD

[Far97] Martin Farach. Recognizing circular decomposable metrics. *Journal of Computational Biology*, 4(2):157–162, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.157; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.157`.

Fasman:1994:RGD

[Fas94] Kenneth H. Fasman. Restructuring the genome data base: a model for a federation of biological databases. *Journal of Computational Biology*, 1(2):165–171, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.165; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.165`.

Falconnet:2012:AEE

[FB12] Mikael Falconnet and Sarah Behrens. Accurate estimations of evolutionary times in the context of strong CpG hypermutability. *Journal of Computational Biology*, 19(5):519–531, May 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0135; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0135`.

Figueroa:2004:CBF

[FBJ04] Andres Figueroa, James Borneman, and Tao Jiang. Clustering binary fingerprint vectors with missing values for DNA array data analysis. *Journal of Computational Biology*, 11 (5):887–901, October 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.887;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.887.

Frasca:2015:UUA

[FBV15] Marco Frasca, Alberto Bertoni, and Giorgio Valentini. UNIPred: Unbalance-aware network integration and prediction of protein functions. *Journal of Computational Biology*, 22(12): 1057–1074, December 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0110; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0110.

Feltes:2019:CEC

[FCGD19] Bruno César Feltes, Eduardo Bassani Chandelier, Bruno Iochins Grisci, and Márcio Dorn. CuMiDa: an extensively curated microarray database for benchmarking and testing of machine learning approaches in cancer research. *Journal of Computational Biology*, 26(4):376–386, April 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0238; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0238.

Flygare:2013:IAI

[FCR+13] Steven Flygare, Michael Campbell, Robert Mars Ross, Barry Moore, and Mark Yandell. ImagePlane: an automated image analysis pipeline for high-throughput screens using the planarian *Schmidtea mediterranea*. *Journal of Computational Biology*, 20(8):583–592, August 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0025; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0025.

Fan:2012:ICP

[FCS12] Jia-Hao Fan, Jianer Chen, and Sing-Hoi Sze. Identifying complexes from protein interaction networks according to different types of neighborhood density. *Journal of Computational Biology*, 19(12):1284–1294, December 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0195; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0195.

Fu:2007:MHT

[FCV+07] Zheng Fu, Xin Chen, Vladimir Vacic, Peng Nan, Yang Zhong, and Tao Jiang. MSOAR: a high-throughput ortholog assignment system based on genome rearrangement. *Journal of Computational Biology*, 14(9):1160–1175, November 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0048; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0048`.

Fischer:2018:SRA

[FDB18] Carlos N. Fischer, Victor De A.Campos, and Victor H. Barella. On the search for retrotransposons: Alternative protocols to obtain sequences to learn profile hidden Markov models. *Journal of Computational Biology*, 25(5):517–527, May 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0219; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0219`.

Feltes:2021:BTM

[FDD21] Bruno César Feltes, Joice De Faria Poloni, and Márcio Dorn. Benchmarking and testing machine learning approaches with BARRA:CuRDa, a *Curated RNA-Seq Database* for cancer research. *Journal of Computational Biology*, 28 (9):931–944, September 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0463; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0463`.

Fuss:2007:DSF

[FDDK07] Hendrik Fuß, Werner Dubitzky, C. Stephen Downes, and Mary Jo Kurth. Deactivation of Src family kinases: Hypothesis testing using a Monte Carlo sensitivity analysis of systems-level properties. *Journal of Computational Biology*, 14(9):1185–1200, November 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0095; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0095`.

Faria:2015:RAP

[FdSdSR+15] Alexandre Wagner Chagas Faria, Alisson Marques da Silva, Thiago de Souza Rodrigues, Marcelo Azevedo Costa, and Antonio Padua Braga. A ranking approach for probe selection and classification of microarray data with artificial neural networks. *Journal of Computational Biology*, 22(10):953–961, October 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0125; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0125`.

Fan:2020:VKE

[FDW20] Jianye Fan, Shoubin Dong, and Bo Wang. Variant-kudu: an efficient tool kit leveraging distributed bitmap index for analysis of massive genetic variation datasets. *Journal of Computational Biology*, 27(9):1350–1360, September 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0344; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0344`.

Fiosina:2020:EDL

[FFB20] Jelena Fiosina, Maksims Fiosins, and Stefan Bonn. Explainable deep learning for augmentation of small RNA expression profiles. *Journal of Computational Biology*, 27(2):234–247, February 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0320; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0320`.

Ferdous:2024:MFW

[FFM24] Jannatul Ferdous, George Matthew Fricke, and Melanie E. Moses. More is faster: Why population size matters in biological search. *Journal of Computational Biology*, 31(5):429–444, May 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0296; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0296`.

Franzese:2022:SDT

[FFSL22] Nicholas Franzese, Jason Fan, Roded Sharan, and Mark D. M. Leiserson. ScalpelSig designs targeted genomic panels from data to detect activity of mutational signatures.

Journal of Computational Biology, 29(1):56–73, January 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0453; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0453`.

Fishelson:2004:OEG

[FG04] Maayan Fishelson and Dan Geiger. Optimizing exact genetic linkage computations. *Journal of Computational Biology*, 11(2–3):263–275, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Frieze:2002:OSH

[FH02] Alan M. Frieze and Bjarni V. Halldórsson. Optimal sequencing by hybridization in rounds. *Journal of Computational Biology*, 9(2):355–369, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270252935502; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935502`.

Fukunaga:2018:NMA

[FH18] Tsukasa Fukunaga and Michiaki Hamada. A novel method for assessing the statistical significance of RNA-RNA interactions between two long RNAs. *Journal of Computational Biology*, 25(9):976–986, September 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0260; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0260`.

Firoz:2011:AAS

[FHKR11] Jesun Sahariar Firoz, Masud Hasan, Ashik Zinnat Khan, and M. Sohel Rahman. The 1.375 approximation algorithm for sorting by transpositions can run in $O(n \log n)$ time. *Journal of Computational Biology*, 18(8):1007–1011, August 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0042; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0042`.

Fekete:2000:PRB

[FHS00] Martin Fekete, Ivo L. Hofacker, and Peter F. Stadler. Prediction of RNA base pairing probabilities on massively parallel comput-

ers. *Journal of Computational Biology*, 7(1–2):171–182, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Fang:2017:GCD

[FHZD17] Huaying Fang, Chengcheng Huang, Hongyu Zhao, and Minghua Deng. gCoda: Conditional dependence network inference for compositional data. *Journal of Computational Biology*, 24(7):699–708, July 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0054; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0054`.

Fickett:1995:OGH

[Fic95] James W. Fickett. ORFs and genes: How strong a connection? *Journal of Computational Biology*, 2(1):117–123, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.117; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.117`.

Fonseca-Junior:2018:PNB

[FJAOB18] Néli J. Fonseca-Júnior, Marcelo Q. L. Afonso, Lucas C. Oliveira, and Lucas Bleicher. PFstats: a network-based open tool for protein family analysis. *Journal of Computational Biology*, 25(5):480–486, May 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0181; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0181`.

Fasulo:1999:AAM

[FJK+99] Dan Fasulo, Tao Jiang, Richard M. Karp, Reuben J. Settergren, and Ed Thayer. An algorithmic approach to multiple complete digest mapping. *Journal of Computational Biology*, 6(2):187–207, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.187; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.187`.

Ferre:2006:FMP

[FK06] Sébastien Ferré and Ross D. King. Finding motifs in protein secondary structure for use in function prediction. *Journal of Computational Biology*, 13(3):719–731, April 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.719; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.719`.

Friedel:2009:BIU

[FKZ09] Caroline C. Friedel, Jan Krumsiek, and Ralf Zimmer. Bootstrapping the interactome: Unsupervised identification of protein complexes in yeast. *Journal of Computational Biology*, 16(8):971–987, August 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0023; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0023`.

Forsten:1994:PAL

[FL94] Kimberly E. Forsten and Douglas A. Lauffenburger. Probability of autocrine ligand capture by cell-surface receptors: Implications for ligand secretion measurements. *Journal of Computational Biology*, 1(1):15–23, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.15; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.15`.

Fusi:2017:FMG

[FL17] Nicolo Fusi and Jennifer Listgarten. Flexible modeling of genetic effects on function-valued traits. *Journal of Computational Biology*, 24(6):524–535, June 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0174; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0174`.

Feng:2011:IIS

[FLJ11] Jianxing Feng, Wei Li, and Tao Jiang. Inference of isoforms from short sequence reads. *Journal of Computational Biology*, 18(3):305–321, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0243;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0243.

Faulhammer:2000:FEL

[FLL00] Dirk Faulhammer, Richard J. Lipton, and Laura F. Landweber. Fidelity of enzymatic ligation for DNA computing. *Journal of Computational Biology*, 7(6):839–848, December 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270050514963; https://www.liebertpub.com/doi/pdf/10.1089/10665270050514963.

Friedman:2000:UBN

[FLNP00] Nir Friedman, Michal Linial, Iftach Nachman, and Dana Pe'er. Using Bayesian networks to analyze expression data. *Journal of Computational Biology*, 7(3–4):601–620, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Ferretti:1994:SBC

[FLS94] V. Ferretti, B. F. Lang, and D. Sankoff. Skewed base compositions, asymmetric transition matrices, and phylogenetic invariants. *Journal of Computational Biology*, 1(1):77–92, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.77; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.77.

Fu:2021:JCS

[FLT+21] Xuecong Fu, Haoyun Lei, Yifeng Tao, Kerstin Heselmeyer-haddad, Irianna Torres, Michael Dean, Thomas Ried, and Russell Schwartz. Joint clustering of single-cell sequencing and fluorescence in situ hybridization data for reconstructing clonal heterogeneity in cancers. *Journal of Computational Biology*, 28(11):1035–1051, November 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0255; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0255.

Frey:2006:GGM

[FMH06] Brendan J. Frey, Quaid D. Morris, and Timothy R. Hughes. GenRate: a generative model that reveals novel transcripts in genome-tiling microarray data. *Journal of Computational*

Biology, 13(2):200–214, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.200; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.200.

Feng:2008:CDA

[FNC08] Jian Feng, Daniel Q. Naiman, and Bret Cooper. Combined dynamic arrays for storing and searching semi-ordered tandem mass spectrometry data. *Journal of Computational Biology*, 15(4):457–468, May 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0011; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0011.

Flannick:2009:APL

[FND+09] Jason Flannick, Antal Novak, Chuong B. Do, Balaji S. Srinivasan, and Serafim Batzoglou. Automatic parameter learning for multiple local network alignment. *Journal of Computational Biology*, 16(8):1001–1022, August 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0099; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0099.

Friedman:2002:SEA

[FNPP02] Nir Friedman, Matan Ninio, Itsik Pe'er, and Tal Pupko. A structural EM algorithm for phylogenetic inference. *Journal of Computational Biology*, 9(2):331–353, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270252935494; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935494.

Fomin:2016:SARa

[Fom16a] Eduard Fomin. A simple approach to the reconstruction of a set of points from the multiset of n^2 pairwise distances in n^2 steps for the sequencing problem: I. Theory. *Journal of Computational Biology*, 23(9):769–775, September 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0044; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0044.

Fomin:2016:SARb

[Fom16b] Eduard Fomin. A simple approach to the reconstruction of a set of points from the multiset of n^2 pairwise distances in n^2 steps for the sequencing problem: II. algorithm. *Journal of Computational Biology*, 23(12):934–942, December 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0046; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0046`.

Fomin:2019:SAR

[Fom19] Eduard Fomin. A simple approach to the reconstruction of a set of points from the multiset of pairwise distances in n^2 steps for the sequencing problem: III. noise inputs for the Beltway case. *Journal of Computational Biology*, 26(1):68–75, January 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0078; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0078`.

Fionda:2011:BNQ

[FP11] Valeria Fionda and Luigi Palopoli. Biological network querying techniques: Analysis and comparison. *Journal of Computational Biology*, 18(4):595–625, April 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0144; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0144`.

Faure:2013:NSP

[FPD13] Emmanuel Faure, Isabelle S. Peter, and Eric H. Davidson. A new software package for predictive gene regulatory network modeling and redesign. *Journal of Computational Biology*, 20(6):419–423, June 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0297; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0297`.

Fosso:2018:UTA

[FPRV18] Bruno Fosso, Graziano Pesole, Francesc Rosselló, and Gabriel Valiente. Unbiased taxonomic annotation of metagenomic samples. *Journal of Computational Biology*, 25(3):348–360, March

2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0144; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0144.

Flomin:2022:DSA

[FPS22] Dan Flomin, David Pellow, and Ron Shamir. Data set-adaptive minimizer order reduces memory usage in k-mer counting. *Journal of Computational Biology*, 29(8):825–838, August 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0599; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0599.

Feldmann:2022:CAR

[FPSD22] Michael Feldmann, Andreas Padalkin, Christian Scheideler, and Shlomi Dolev. Coordinating amoebots via reconfigurable circuits. *Journal of Computational Biology*, 29(4):317–343, April 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0363; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0363.

Frieze:1999:ORS

[FPU99] Alan M. Frieze, Franco P. Preparata, and Eli Upfal. Optimal reconstruction of a sequence from its probes. *Journal of Computational Biology*, 6(3–4):361–368, October 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Fu:2014:SIR

[FR14] Benjamin M. M. Fu and Christian M. Reidys. Shapes of interacting RNA complexes. *Journal of Computational Biology*, 21(9):649–664, September 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0107; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0107.

Firoozbakht:2017:IAI

[FRD+17] Forough Firoozbakht, Iman Rezaeian, Michele D'agnillo, Lisa Porter, Luis Rueda, and Alioune Ngom. An integrative approach for identifying network biomarkers of breast cancer subtypes using genomic, interactomic, and transcriptomic

data. *Journal of Computational Biology*, 24(8):756–766, August 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0010; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0010`.

Freschi:2011:IBN

[Fre11] Valerio Freschi. Improved biological network reconstruction using graph Laplacian regularization. *Journal of Computational Biology*, 18(8):987–996, August 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0232; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0232`.

Forst:1999:EMN

[FS99] Christian V. Forst and Klaus Schulten. Evolution of metabolisms: a new method for the comparison of metabolic pathways using genomics information. *Journal of Computational Biology*, 6(3–4):343–360, October 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Filkov:2008:SMM

[FS08] Vladimir Filkov and Nameeta Shah. A simple model of the modular structure of transcriptional regulation in yeast. *Journal of Computational Biology*, 15(4):393–405, May 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0020; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0020`.

Ferraro:2014:PRS

[FSD+14] Maria Brigida Ferraro, Marco Savarese, Giuseppina Di Fruscio, Vincenzo Nigro, and Mario Rosario Guarracino. Prediction of rare single-nucleotide causative mutations for muscular diseases in pooled next-generation sequencing experiments. *Journal of Computational Biology*, 21(9):665–675, September 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0037; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0037`.

Feng:2020:IAD

[FSW+20] Ye Feng, Chunyu Shi, Dayu Wang, Xuefeng Wang, and Zhi Chen. Integrated analysis of DNA copy number changes and gene expression identifies key genes in gastric cancer. *Journal of Computational Biology*, 27(6):877–887, June 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0149; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0149`.

Filkov:2002:ATM

[FSZ02] Vladimir Filkov, Steven Skiena, and Jizu Zhi. Analysis techniques for microarray time-series data. *Journal of Computational Biology*, 9(2):317–330, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270252935485; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935485`.

Frenkel:2007:ENF

[FT07] Zakharia M. Frenkel and Edward N. Trifonov. Evolutionary networks in the formatted protein sequence space. *Journal of Computational Biology*, 14(8):1044–1057, October 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0066; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0066`.

Fonseca:2016:PRN

[FvdBB16] Rasmus Fonseca, Henry van den Bedem, and Julie Bernauer. Probing RNA native conformational ensembles with structural constraints. *Journal of Computational Biology*, 23(5):362–371, May 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0201; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0201`.

Faller:2003:NDM

[FVTH03] D. Faller, H. U. Voss, J. Timmer, and U. Hobohm. Normalization of DNA-Microarray data by nonlinear correlation maximization. *Journal of Computational Biology*, 10(5):

751–762, October 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703322539079; https://www.liebertpub.com/doi/pdf/10.1089/106652703322539079.

Fonseca:2012:BVP

[FW12] Rasmus Fonseca and Paweł Winter. Bounding volumes for proteins: a comparative study. *Journal of Computational Biology*, 19(10):1203–1213, October 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0104; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0104.

Wang:2023:FAS

[fW23] Biing feng Wang. Fast algorithms for the simplified partial digest problem. *Journal of Computational Biology*, 30(1):41–51, January 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0641; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0641.

Fan:2018:PCN

[FYJ18] Jun Fan, Jing Yang, and Zhenran Jiang. Prediction of central nervous system side effects through drug permeability to blood–brain barrier and recommendation algorithm. *Journal of Computational Biology*, 25(4):435–443, April 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0149; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0149.

Zou:2020:IFE

[fZbMqW+20] Yang fan Zou, Ling bing Meng, Qing qing Wang, Zhao kai He, Chen hao Hu, Meng jie Shan, Deng yuan Wang, and Xin Yu. Identification and functional enrichment analysis of potential diagnostic and therapeutic targets in adamantinomatous craniopharyngioma. *Journal of Computational Biology*, 27(1):55–68, January 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0184; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0184.

Fan:2020:IPB

[FZF+20] Zongjiang Fan, Wanqiu Zhao, Shengning Fan, Chunxiao Li, Jing Qiao, and Yongqing Xu. Identification of potential biomarkers for intervertebral disc degeneration using the genome-wide expression analysis. *Journal of Computational Biology*, 27(9):1341–1349, September 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0103; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0103`.

Ghrifi:2019:CSA

[GAWI19] Fatima Ghrifi, Loubna Allam, Lakhlili Wiame, and Azeddine Ibrahimi. Curcumin-synthetic analogs library screening by docking and quantitative structure–activity relationship studies for AXL tyrosine kinase inhibition in cancers. *Journal of Computational Biology*, 26(10):1156–1167, October 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0052; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0052`.

Gross:2006:UMA

[GB06] Samuel S. Gross and Michael R. Brent. Using multiple alignments to improve gene prediction. *Journal of Computational Biology*, 13(2):379–393, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.379; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.379`.

Gog:2008:FAT

[GB08] Simon Gog and Martin Bader. Fast algorithms for transforming back and forth between a signed permutation and its equivalent simple permutation. *Journal of Computational Biology*, 15(8):1029–1041, October 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0040; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0040`.

Guthals:2015:GFA

[GBB15] Adrian Guthals, Christina Boucher, and Nuno Bandeira. The generating function approach for peptide identification in spectral networks. *Journal of Computational Biology*, 22(5):353–366, May 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0165; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0165`.

Gusfield:2007:DTP

[GBBS07] Dan Gusfield, Vikas Bansal, Vineet Bafna, and Yun S. Song. A decomposition theory for phylogenetic networks and incompatible characters. *Journal of Computational Biology*, 14 (10):1247–1272, December 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0137; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0137`.

Gogoshin:2017:NAS

[GBR17] Grigoriy Gogoshin, Eric Boerwinkle, and Andrei S. Rodin. New algorithm and software (BNOmics) for inferring and visualizing Bayesian networks from heterogeneous big biological and genetic data. *Journal of Computational Biology*, 24(4):340–356, April 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0100; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0100`.

Guo:2015:CSR

[GC15] Ziyi Guo and Brian Yuan Chen. Conformational sampling reveals amino acids with a steric influence on specificity. *Journal of Computational Biology*, 22(9):861–875, September 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0117; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0117`.

Ghavidel:2015:NHM

[GCB15] Fatemeh Zamanzad Ghavidel, Jürgen Claesen, and Tomasz Burzykowski. A nonhomogeneous hidden Markov model for gene mapping based on next-generation sequencing data.

Journal of Computational Biology, 22(2):178–188, February 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0258; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0258`.

Gorczak:2020:CFA

[GCB20] Katarzyna Górczak, Jürgen Claesen, and Tomasz Burzykowski. A conceptual framework for abundance estimation of genomic targets in the presence of ambiguous short sequencing reads. *Journal of Computational Biology*, 27(8):1232–1247, August 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0272; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0272`.

Gu:2020:SPR

[GCD20] Yifan Gu, Guoqing Chen, and Yibao Du. Screening of prognosis-related genes in primary breast carcinoma using genomic expression data. *Journal of Computational Biology*, 27(7):1030–1040, July 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0131; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0131`.

Gillett:1995:FCS

[GDHC95] Will Gillett, Jim Daues, Liz Hanks, and Rob Capra. Fragment collapsing and splitting while assembling high-resolution restriction maps. *Journal of Computational Biology*, 2 (2):185–205, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.185; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.185`.

Gui:2015:IHC

[GDL+15] Tuantuan Gui, Xiao Dong, Rudong Li, Yixue Li, and Zhen Wang. Identification of hepatocellular carcinoma–related genes with a machine learning and network analysis. *Journal of Computational Biology*, 22(1):63–71, January 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0122; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0122`.

Ge:2004:EBS

[GE04] Nanxiang Ge and Charles B. Epstein. An empirical Bayesian significance test of cDNA library data. *Journal of Computational Biology*, 11(6):1175–1188, December 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.1175; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.1175`.

Gorecki:2014:DPM

[GE14] Paweł Górecki and Oliver Eulenstein. DrML: Probabilistic modeling of gene duplications. *Journal of Computational Biology*, 21(1):89–98, January 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0078; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0078`.

Godin:2017:MPA

[GE17] Noa Godin and Jerry Eichler. The mitochondrial protein atlas: a database of experimentally verified information on the human mitochondrial proteome. *Journal of Computational Biology*, 24(9):906–916, September 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0011; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0011`.

Gelfand:1995:PFD

[Gel95] M. S. Gelfand. Prediction of function in DNA sequence analysis. *Journal of Computational Biology*, 2(1):87–115, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.87; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.87`.

Georgiev:2009:IND

[Geo09] Alexander G. Georgiev. Interpretable numerical descriptors of amino acid space. *Journal of Computational Biology*, 16(5):703–723, May 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0173;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0173.

Gartner:2016:IVC

[GF16] Kerstin Gärtner and Andreas Futschik. Improved versions of common estimators of the recombination rate. *Journal of Computational Biology*, 23(9):756–768, September 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0039; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0039.

Galvez:2016:SBA

[GFE+16] Sergio Gálvez, Adis Ferusic, Francisco J. Esteban, Pilar Hernández, Juan A. Caballero, and Gabriel Dorado. Speeding-up bioinformatics algorithms with heterogeneous architectures: Highly heterogeneous Smith-Waterman (HHeterSW). *Journal of Computational Biology*, 23(10):801–809, October 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0237; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0237.

Greenspan:2004:MBI

[GG04] Gideon Greenspan and Dan Geiger. Model-based inference of haplotype block variation. *Journal of Computational Biology*, 11(2–3):493–504, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Goldberg:1995:FSA

[GGKS95] Paul W. Goldberg, Martin C. Golumbic, Haim Kaplan, and Ron Shamir. Four strikes against physical mapping of DNA. *Journal of Computational Biology*, 2(1):139–152, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.139; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.139.

Gonzalez:2012:EMA

[GGM12] M. González, C. Gutiérrez, and R. Martínez. Expectation-maximization algorithm for determining natural selection of Y-linked genes through two-sex branching processes. *Journal of Computational Biology*, 19(9):1015–1026, September

2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0242; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0242.

Giaquinta:2013:FMT

[GGU13] Emanuele Giaquinta, Szymon Grabowski, and Esko Ukkonen. Fast matching of transcription factor motifs using generalized position weight matrix models. *Journal of Computational Biology*, 20(9):621–630, September 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0289; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0289.

Girdlestone:2016:DWA

[GH16] Christopher Girdlestone and Steven Hayward. The DynDom3D Webserver for the analysis of domain movements in multimeric proteins. *Journal of Computational Biology*, 23(1):21–26, January 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0143; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0143.

Gao:2012:BLP

[GHJ+12] Qinghui Gao, Christine Ho, Yingmin Jia, Jingyi Jessica Li, and Haiyan Huang. Biclustering of linear patterns in gene expression data. *Journal of Computational Biology*, 19(6):619–631, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0032; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0032.

Giladi:2010:ETI

[GHM+10] Eldar Giladi, John Healy, Gene Myers, Chris Hart, Philipp Kapranov, Doron Lipson, Steve Roels, Edward Thayer, and Stan Letovsky. Error tolerant indexing and alignment of short reads with covering template families. *Journal of Computational Biology*, 17(10):1397–1411, October 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0005; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0005.

Greenberg:1995:PMS

[GI95] David S. Greenberg and Sorin Istrail. Physical mapping by STS hybridization: Algorithmic strategies and the challenge of software evaluation. *Journal of Computational Biology*, 2(2):219–273, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.219; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.219`.

Guerra:2021:RSM

[GJL+21] Concettina Guerra, Sarang Joshi, Yinquan Lu, Francesco Palini, Umberto Ferraro Petrillo, and Jarek Rossignac. Rank-similarity measures for comparing gene prioritizations: a case study in autism. *Journal of Computational Biology*, 28(3):283–295, March 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0244; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0244`.

Guo:2022:NSO

[GJL+22] Qianghui Guo, Yinglie Jin, Mengqin Li, Lisa Hui Sun, and Yanyan Xu. On the number of saturated and optimal extended 2-regular simple stacks in the Nussinov–Jacobson energy model. *Journal of Computational Biology*, 29(5):425–440, May 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0421; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0421`.

Galtier:2004:MMM

[GJM04] N. Galtier and A. Jean-Marie. Markov-modulated Markov chains and the covarion process of molecular evolution. *Journal of Computational Biology*, 11(4):727–733, August 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.727; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.727`.

Gunewardena:2006:EPT

[GJZ06] Sumedha Gunewardena, Peter Jeavons, and Zhaolei Zhang. Enhancing the prediction of transcription factor binding sites by incorporating structural properties and nucleotide covariations.

Journal of Computational Biology, 13(4):929–945, May 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.929; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.929.

Goutsias:2006:STR

[GK06] John Goutsias and Seungchan Kim. Stochastic transcriptional regulatory systems with time delays: a mean-field approximation. *Journal of Computational Biology*, 13(5):1049–1076, June 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1049; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1049.

Garren:2018:BTC

[GK18] Jeonifer M. Garren and Jaejik Kim. Bootstrapping time-course gene expression data for gene networks: Application to gene relevance networks. *Journal of Computational Biology*, 25(12):1374–1384, December 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0029; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0029.

Gonnet:2000:EMM

[GKB00] Gaston H. Gonnet, Chantal Korostensky, and Steve Benner. Evaluation measures of multiple sequence alignments. *Journal of Computational Biology*, 7(1–2):261–276, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Guerin:2022:RNO

[GKD22] Nathan Guerin, Teresa Kaserer, and Bruce R. Donald. RESISTOR: a new OSPREY module to predict resistance mutations. *Journal of Computational Biology*, 29(12):1346–1352, December 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0254; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0254.

Gniewek:2012:OPP

[GKG12] Paweł Gniewek, Andrzej Kolinski, and Dominik Gront. Optimization of profile-to-profile alignment parameters for one-

dimensional threading. *Journal of Computational Biology*, 19(7):879–886, July 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0307; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0307`.

Galas:2021:TIT

[GKgUS21] David J. Galas, James Kunert-graf, Lisa Uechi, and Nikita A. Sakhanenko. Toward an information theory of quantitative genetics. *Journal of Computational Biology*, 28(6):527–559, June 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0032; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0032`.

Gelfand:1998:ADC

[GKKS98] Israel Gelfand, Alexander Kister, Casimir Kulikowski, and Ognyan Stoyanov. Algorithmic determination of core positions in the V_L and V_H domains of immunoglobulin molecules. *Journal of Computational Biology*, 5(3):467–477, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.467; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.467`.

Gupta:2010:HIG

[GKM+10] Arvind Gupta, Mohammad M. Karimi, Ján Maňuch, Ladislav Stacho, and Xiaohong Zhao. Haplotype inferring via galled-tree networks is NP-Complete. *Journal of Computational Biology*, 17(10):1435–1449, October 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0117; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0117`.

Golding:2023:CMC

[GKMS23] G. Brian Golding, Holly Koponen, Neerja Mhaskar, and W. F. Smyth. Computing maximal covers for protein sequences. *Journal of Computational Biology*, 30(2):149–160, February 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0520; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0520`.

Gupta:1995:IPS

[GKS95] Sandeep K. Gupta, John D. Kececioglu, and Alejandro A. Schäffer. Improving the practical space and time efficiency of the shortest-paths approach to sum-of-pairs multiple sequence alignment. *Journal of Computational Biology*, 2 (3):459–472, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.459; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.459`.

Gu:2009:OEP

[GLJW09] Junfeng Gu, Honglin Li, Hualiang Jiang, and Xicheng Wang. Optimizing energy potential for protein fold recognition with parametric evaluation function. *Journal of Computational Biology*, 16(3):427–442, March 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0128; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0128`.

Geraci:2009:KBS

[GLM+09] Filippo Geraci, Mauro Leoncini, Manuela Montangero, Marco Pellegrini, and M. Elena Renda. K-Boost: a scalable algorithm for high-quality clustering of microarray gene expression data. *Journal of Computational Biology*, 16(6):859–873, June 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0201; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0201`.

Guo:2016:NRR

[GLM16] Wenchuan Guo, Zhenqiu Liu, and Shujie Ma. Nonparametric regularized regression for phenotype-associated taxa selection and network construction with metagenomic count data. *Journal of Computational Biology*, 23(11):877–890, November 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0023; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0023`.

Gouveia:2020:RBM

[GLM20] Filipe Gouveia, Inês Lynce, and Pedro T. Monteiro. Revision of Boolean models of regulatory networks using stable state observations. *Journal of Computational Biology*, 27(2):144–155, February 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0289; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0289`.

Graca:2010:HIP

[GLMSO10] Ana Graça, Inês Lynce, João Marques-Silva, and Arlindo L. Oliveira. Haplotype inference by pure parsimony: a survey. *Journal of Computational Biology*, 17(8):969–992, August 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0101; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0101`.

Guo:2013:DPC

[GLMW13] Fei Guo, Shuai Cheng Li, Wenji Ma, and Lusheng Wang. Detecting protein conformational changes in interactions via scaling known structures. *Journal of Computational Biology*, 20(10):765–779, October 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0069; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0069`.

Griffiths:1996:AIS

[GM96] R. C. Griffiths and P. Marjoram. Ancestral inference from samples of DNA sequences with recombination. *Journal of Computational Biology*, 3(4):479–502, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.479; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.479`.

Gronau:2007:NJA

[GM07] Ilan Gronau and Shlomo Moran. Neighbor joining algorithms for inferring phylogenies via LCA distances. *Journal of Computational Biology*, 14(1):1–15, January 2007. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0115; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0115.

Gold:2008:RTG

[GMC08] David Gold, Bani Mallick, and Kevin Coombes. Real-time gene expression: Statistical challenges in design and inference. *Journal of Computational Biology*, 15(6):611–623, July 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0220; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0220.

Gamermann:2014:NAP

[GMC+14] Daniel Gamermann, Arnaud Montagud, J. Alberto Conejero, Javier F. Urchueguía, and Pedro Fernández de Córdoba. New approach for phylogenetic tree recovery based on genome-scale metabolic networks. *Journal of Computational Biology*, 21(7):508–519, July 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0150; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0150.

Goryachev:2001:UMD

[GME01] Andrew B. Goryachev, Pascale F. Macgregor, and Aled M. Edwards. Unfolding of microarray data. *Journal of Computational Biology*, 8(4):443–461, September 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701752236232; https://www.liebertpub.com/doi/pdf/10.1089/106652701752236232.

Gebert:2008:IGG

[GMF+08] Jutta Gebert, Susanne Motameny, Ulrich Faigle, Christian V. Forst, and Rainer Schrader. Identifying genes of gene regulatory networks using formal concept analysis. *Journal of Computational Biology*, 15(2):185–194, March 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0107; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0107.

Garcia-Maya:2020:IWB

[GML20] Brenda Ivette Garcia-Maya and Nikolaos Limnios. Identification of words in biological sequences under the semi-Markov hypothesis. *Journal of Computational Biology*, 27(5):683–697, May 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0253; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0253`.

Gupta:2005:SAI

[GMS05] Arvind Gupta, Ján Maňuch, and Ladislav Stacho. Structure-approximating inverse protein folding problem in the 2D HP model. *Journal of Computational Biology*, 12(10):1328–1345, December 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1328; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1328`.

Gupta:2012:AHI

[GMSZ12] Arvind Gupta, Ján Maňuch, Ladislav Stacho, and Xiaohong Zhao. Algorithm for haplotype inference via galled-tree networks with simple galls. *Journal of Computational Biology*, 19(4):439–454, April 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0145; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0145`.

Gusev:2020:ASS

[GMVC20] Yury Gusev, Svyatoslav Mazilov, Irina Volokhina, and Mikhail Chumakov. Agrobacterial, single-stranded DNA-Binding protein VirE2 and its complexes. *Journal of Computational Biology*, 27(5):675–682, May 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0243; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0243`.

Gronau:2010:ADM

[GMY10] Ilan Gronau, Shlomo Moran, and Irad Yavneh. Adaptive distance measures for resolving K2P quartets: Metric separation versus stochastic noise. *Journal of Computational Biology*, 17(11):1509–1518, November 2010. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0236; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0236.

Grover:2012:BTO

[GNI12] Dhruv Grover and Juan Nunez-Iglesias. Betamax: Towards optimal sampling strategies for high-throughput screens. *Journal of Computational Biology*, 19(6):776–784, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0036; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0036.

Gilbert:2001:ETC

[GNME01] Peter B. Gilbert, Vladimir A. Novitsky, Monty A. Montano, and Max Essex. An efficient test for comparing sequence diversity between two populations. *Journal of Computational Biology*, 8(2):123–139, April 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701300312904; https://www.liebertpub.com/doi/pdf/10.1089/106652701300312904.

Giaquinta:2013:EEA

[GP13] Emanuele Giaquinta and Laura Pozzi. An effective exact algorithm and a new upper bound for the number of contacts in the hydrophobic-polar two-dimensional lattice model. *Journal of Computational Biology*, 20(8):593–609, August 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0266; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0266.

Gong:2020:MDM

[GP20] Boying Gong and Elizabeth Purdom. MethCP: Differentially methylated region detection with change point models. *Journal of Computational Biology*, 27(4):458–471, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0326; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0326.

Gelfand:1996:RGH

[GPAR96] M. S. Gelfand, L. I. Podolsky, T. V. Astakhova, and M. A. Roytberg. Recognition of genes in human DNA sequences. *Journal of Computational Biology*, 3(2):223–234, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.223; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.223`.

Grusea:2011:CPA

[GPCP11] S. Grusea, E. Pardoux, O. Chabrol, and P. Pontarotti. Compound Poisson approximation and testing for gene clusters with multigene families. *Journal of Computational Biology*, 18(4):579–594, April 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0043; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0043`.

Gonzalez-Perez:2017:CAS

[GPOP+17] Pedro P. González-Pérez, Daniel J. Orta, Irving Peña, Eduardo C. Flores, José U. Ramírez, Hiram I. Beltrán, and Salomón J. Alas. A computational approach to studying protein folding problems considering the crucial role of the intracellular environment. *Journal of Computational Biology*, 24(10):995–1013, October 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0115; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0115`.

Grossi:2011:MSM

[GPP+11] Roberto Grossi, Andrea Pietracaprina, Nadia Pisanti, Geppino Pucci, Eli Upfal, and Fabio Vandin. MADMX: a strategy for maximal dense motif extraction. *Journal of Computational Biology*, 18(4):535–545, April 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0177; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0177`.

Goncalves:2012:OAS

[GPRR12] Emanuel Gonçalves, Rui Pereira, Isabel Rocha, and Miguel Rocha. Optimization approaches for the *In Silico* discov-

ery of optimal targets for gene over/underexpression. *Journal of Computational Biology*, 19(2):102–114, February 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0265; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0265.

Ge:2009:BNA

[GQ09] Hao Ge and Min Qian. Boolean network approach to negative feedback loops of the p53 pathways: Synchronized dynamics and stochastic limit cycles. *Journal of Computational Biology*, 16(1):119–132, January 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0181; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0181.

Gu:2024:DEP

[GQEk24] Xinyu Gu, Yuanyuan Qi, and Mohammed El-kebir. DERNA enables Pareto optimal RNA design. *Journal of Computational Biology*, 31(3):179–196, March 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0283; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0283.

Grandison:2009:AZM

[GRM09] Scott Grandison, Carl Roberts, and Richard J. Morris. The application of 3D Zernike moments for the description of "model-free" molecular structure, functional motion, and structural reliability. *Journal of Computational Biology*, 16(3):487–500, March 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0083; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0083.

Grundy:1998:HDF

[Gru98] William Noble Grundy. Homology detection via family pairwise search. *Journal of Computational Biology*, 5 (3):479–491, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.479; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.479.

Gill:2014:CDG

[GSA14] Nivit Gill, Shailendra Singh, and Trilok C. Aseri. Computational disease gene prioritization: An appraisal. *Journal of Computational Biology*, 21(6):456–465, June 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0158; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0158`.

Gogolewski:2019:TRP

[GSCG19] Krzysztof Gogolewski, Maciej Sykulski, Neo Christopher Chung, and Anna Gambin. Truncated robust principal component analysis and noise reduction for single cell RNA sequencing data. *Journal of Computational Biology*, 26(8):782–793, August 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0255; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0255`.

Gigrich:2017:NAA

[GSH17] James Gigrich, Shahryar Sarkani, and Thomas Holzer. A new approach in applying systems engineering tools and analysis to determine hepatocyte toxicogenomics risk levels to human health. *Journal of Computational Biology*, 24(3):238–254, March 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0073; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0073`.

Gustfield:1994:MEL

[GSLW94] Dan Gustfield, David Shmoys, Jan Karel Lenstra, and Tandy Warnow. In memoriam Eugene L. Lawler. *Journal of Computational Biology*, 1(4):255–256, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.255`.

Gao:2011:ORO

[GSN11] Song Gao, Wing-Kin Sung, and Niranjan Nagarajan. Opera: Reconstructing optimal genomic scaffolds with high-throughput paired-end sequences. *Journal of Computational Biology*, 18 (11):1681–1691, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0170;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0170.

Gortler:2020:LFL

[GSS+20] Franziska Görtler, Marian Schön, Jakob Simeth, Stefan Solbrig, Tilo Wettig, Peter J. Oefner, Rainer Spang, and Michael Altenbuchinger. Loss-function learning for digital tissue deconvolution. *Journal of Computational Biology*, 27(3):342–355, March 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0462; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0462.

Galas:2014:DCS

[GSSI14] David J. Galas, Nikita A. Sakhanenko, Alexander Skupin, and Tomasz Ignac. Describing the complexity of systems: Multivariable "set complexity" and the information basis of systems biology. *Journal of Computational Biology*, 21(2):118–140, February 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0039; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0039.

Grainger:2010:RER

[GST10] Ben Grainger, Michael I. Sadowski, and William R. Taylor. Re-evaluating the "rules" of protein topology. *Journal of Computational Biology*, 17(10):1371–1384, October 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0265; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0265.

Graudenzi:2011:RAB

[GSV+11a] A. Graudenzi, R. Serra, M. Villani, A. Colacci, and S. A. Kauffman. Robustness analysis of a Boolean model of gene regulatory network with memory. *Journal of Computational Biology*, 18(4):559–577, April 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0224; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0224.

Graudenzi:2011:DPB

[GSV+11b] Alex Graudenzi, Roberto Serra, Marco Villani, Chiara Damiani, Annamaria Colacci, and Stuart A. Kauffman. Dynamical properties of a Boolean model of gene regulatory network with memory. *Journal of Computational Biology*, 18(10):1291–1303, October 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0069; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0069`.

Gopal:2021:IRD

[GSV21] Jeyakodi Gopal, Vigneshwar Suriya Prakash Sinnarasan, and Amouda Venkatesan. Identification of repurpose drugs by computational analysis of disease–gene–drug associations. *Journal of Computational Biology*, 28(10):975–984, October 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0356; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0356`.

Guo:2016:EER

[GSW16] Qiang-Hui Guo, Lisa H. Sun, and Jian Wang. Enumeration of extended m-regular linear stacks. *Journal of Computational Biology*, 23(12):943–956, December 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0041; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0041`.

Goz:2016:EDE

[GT16] Eli Goz and Tamir Tuller. Evidence of a direct evolutionary selection for strong folding and mutational robustness within HIV coding regions. *Journal of Computational Biology*, 23(8):641–650, August 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0052; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0052`.

Giurcarneanu:2004:FIG

[GTA+04] Ciprian Doru Giurcărneanu, Ioan Tăbuş, Jaakko Astola, Juha Ollila, and Mauno Vihinen. Fast iterative gene clustering based on information theoretic criteria for selecting

the cluster structure. *Journal of Computational Biology*, 11(4):660–682, August 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.660; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.660.

Gibney:2022:HSA

[GTA22] Daniel Gibney, Sharma V. Thankachan, and Srinivas Aluru. On the hardness of sequence alignment on de Bruijn graphs. *Journal of Computational Biology*, 29(12):1377–1396, December 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0411; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0411.

Gambin:2006:ACD

[GTT06] Anna Gambin, Jerzy Tiuryn, and Jerzy Tyszkiewicz. Alignment with context dependent scoring function. *Journal of Computational Biology*, 13(1):81–101, January 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.81; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.81.

Gu:2001:MMF

[Gu01] Xun Gu. Mathematical modeling for functional divergence after gene duplication. *Journal of Computational Biology*, 8(3):221–234, June 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270152530827; https://www.liebertpub.com/doi/pdf/10.1089/10665270152530827.

Guigo:1998:AGP

[Gui98] Roderic Guigó. Assembling genes from predicted exons in linear time with dynamic programming. *Journal of Computational Biology*, 5(4):681–702, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.681; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.681.

Guo:2015:NFP

[Guo15] Yuzhen Guo. The noncompacted folding of proteins by modified elastic net algorithm. *Journal of Computational Biology*, 22(7):609–618, July 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0290; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0290`.

Gusfield:2001:IHS

[Gus01] Dan Gusfield. Inference of haplotypes from samples of diploid populations: Complexity and algorithms. *Journal of Computational Biology*, 8(3):305–323, June 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270152530863; https://www.liebertpub.com/doi/pdf/10.1089/10665270152530863`.

Gusfield:2005:PSR

[Gus05] Dan Gusfield. Preface: Special RECOMB 2004 issue. *Journal of Computational Biology*, 12(6):567–568, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.567`.

Gusfield:2010:MSP

[Gus10] Dan Gusfield. The multi-state perfect phylogeny problem with missing and removable data: Solutions via integer-programming and chordal graph theory. *Journal of Computational Biology*, 17(3):383–399, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0200; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0200`.

Gan:2022:CIS

[GVA22] Luqin Gan, Giuseppe Vinci, and Genevera I. Allen. Correlation imputation for single-cell RNA-seq. *Journal of Computational Biology*, 29(5):465–482, May 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0403; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0403`.

Gafurov:2024:FCA

[GVMB24] Askar Gafurov, Tomáš VinaŘ, Paul Medvedev, and BroŇa Brejová. Fast context-aware analysis of genome annotation colocalization. *Journal of Computational Biology*, 31(10):946–964, October 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0667; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0667`.

Gat-Viks:2006:PMI

[GVTRS06] Irit Gat-Viks, Amos Tanay, Daniela Raijman, and Ron Shamir. A probabilistic methodology for integrating knowledge and experiments on biological networks. *Journal of Computational Biology*, 13(2):165–181, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.165; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.165`.

Gat-Viks:2004:MAH

[GVTS04] Irit Gat-Viks, Amos Tanay, and Ron Shamir. Modeling and analysis of heterogeneous regulation in biological networks. *Journal of Computational Biology*, 11(6):1034–1049, December 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.1034; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.1034`.

Goldstein:1994:APS

[GW94] Larry Goldstein and Michael S. Waterman. Approximations to profile score distributions. *Journal of Computational Biology*, 1(2):93–104, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.93; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.93`.

Golightly:2006:BSI

[GW06] Andrew Golightly and Darren J. Wilkinson. Bayesian sequential inference for stochastic kinetic biochemical network models. *Journal of Computational Biology*, 13(3):838–851, April 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.`

1089/cmb.2006.13.838; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.838.

Ge:2021:SAA

[GWA+21] Songwei Ge, Haohan Wang, Amir Alavi, Eric Xing, and Ziv Bar-joseph. Supervised adversarial alignment of single-cell RNA-seq data. *Journal of Computational Biology*, 28(5):501–513, May 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Ge:2019:PGI

[GWL+19] Fangfang Ge, Yi Wang, Huayang Li, Rui Zhang, Xiaotong Wang, Qingyun Li, Zhenchang Liang, and Long Yang. PlantGQ: an integrative database of G-quadruplex in plant. *Journal of Computational Biology*, 26(9):1013–1019, September 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0010; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0010.

Guo:2021:CSE

[GWM+21a] Yuzhi Guo, Jiaxiang Wu, Hehuan Ma, Sheng Wang, and Junzhou Huang. Comprehensive study on enhancing low-quality position-specific scoring matrix with deep learning for accurate protein structure property prediction: Using bagging multiple sequence alignment learning. *Journal of Computational Biology*, 28(4):346–361, April 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Guo:2021:ENE

[GWM+21b] Yuzhi Guo, Jiaxiang Wu, Hehuan Ma, Sheng Wang, and Junzhou Huang. EPTool: a new enhancing PSSM tool for protein secondary structure prediction. *Journal of Computational Biology*, 28(4):362–364, April 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Guo:2018:AAP

[GWX18] Qianghui Guo, Jian Wang, and Zhao Xu. Approximation algorithms for protein folding in the hydrophobic-polar model on 3D hexagonal prism lattice. *Journal of Computational Biology*, 25(5):487–498, May 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0185;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0185.

Goulet:2023:COU

[GYA+23] Dennis R. Goulet, Yongqi Yan, Palak Agrawal, Andrew B. Waight, Amanda Nga sze Mak, and Yi Zhu. Codon optimization using a recurrent neural network. *Journal of Computational Biology*, 30(1):70–81, January 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0458; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0458.

Guo:2015:DNF

[GYD+15] Xuan Guo, Ning Yu, Xiaojun Ding, Jianxin Wang, and Yi Pan. DIME: a novel framework for *De Novo* metagenomic sequence assembly. *Journal of Computational Biology*, 22(2):159–177, February 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0251; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0251.

Gunawan:2019:CPN

[GYZ19] Andreas D. M. Gunawan, Hongwei Yan, and Louxin Zhang. Compression of phylogenetic networks and algorithm for the tree containment problem. *Journal of Computational Biology*, 26(3):285–294, March 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0220; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0220.

Gao:2024:PPI

[GZLY24] Qian Gao, Chi Zhang, Ming Li, and Tianfei Yu. Protein–protein interaction prediction model based on ProtBert-BiGRU-Attention. *Journal of Computational Biology*, 31(9):797–814, September 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Guan:2016:EPE

[GZN16] Boxin Guan, Changsheng Zhang, and Jiaxu Ning. EDGA: a population evolution direction-guided genetic algorithm

for protein–ligand docking. *Journal of Computational Biology*, 23(7):585–596, July 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0190; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0190.

Gong:2016:CSE

[GZW+16] Huichao Gong, Sai Zhang, Jiangdian Wang, Haipeng Gong, and Jianyang Zeng. Constructing structure ensembles of intrinsically disordered proteins from chemical shift data. *Journal of Computational Biology*, 23(5):300–310, May 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0184; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0184.

Gu:2021:SGS

[GZW+21] Wenyan Gu, Aizhong Zhou, Lusheng Wang, Shiwei Sun, Xuefeng Cui, and Daming Zhu. SVLR: Genome structural variant detection using long-read sequencing data. *Journal of Computational Biology*, 28(8):774–788, August 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0048; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0048.

Ganjdanesh:2022:MGP

[GZY+22] Alireza Ganjdanesh, Jipeng Zhang, Sarah Yan, Wei Chen, and Heng Huang. Multimodal genotype and phenotype data integration to improve partial data-based longitudinal prediction. *Journal of Computational Biology*, 29(12):1324–1345, December 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0378; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0378.

Hamada:2012:CBA

[HA12] Michiaki Hamada and Kiyoshi Asai. A classification of bioinformatics algorithms from the viewpoint of maximizing expected accuracy (MEA). *Journal of Computational Biology*, 19(5):532–549, May 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0197;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0197.

Hamada:2012:DUR

[Ham12] Michiaki Hamada. Direct updating of an RNA base-pairing probability matrix with marginal probability constraints. *Journal of Computational Biology*, 19(12):1265–1276, December 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0215; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0215.

Hassani:2022:OSF

[HAM+22] Hossein Hassani, Zakieh Avazzadeh, J. A. Tenreiro Machado, Praveen Agarwal, and Maryam Bakhtiar. Optimal solution of a fractional HIV/AIDS epidemic mathematical model. *Journal of Computational Biology*, 29(3):276–291, March 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0253; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0253.

Hansen:2009:SML

[Han09] Niels Richard Hansen. Statistical models for local occurrences of RNA structures. *Journal of Computational Biology*, 16(6):845–858, June 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0180; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0180.

Hossain:2012:NNI

[HAP12] M. Shahriar Hossain, Monika Akbar, and Nicholas F. Polys. Narratives in the network: Interactive methods for mining cell signaling networks. *Journal of Computational Biology*, 19(9):1043–1059, September 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0244; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0244.

He:2018:SIP

[HASL18] Jing He, Kamal Al Nasr, Weitao Sun, and Yonggang Lu. *Special Issue* preface: The 9th Computational Structural Bioinfor-

matics Workshop. *Journal of Computational Biology*, 25(1):1–2, January 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.29010.jh.

Halldorsson:2011:CPS

[HATI11] Bjarni V. Halldórsson, Derek Aguiar, Ryan Tarpine, and Sorin Istrail. The Clark phaseable sample size problem: Long-range phasing and loss of heterozygosity in GWAS. *Journal of Computational Biology*, 18(3):323–333, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0288; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0288.

Havilio:2006:SDB

[Hav06] Moshe Havilio. Signal deconvolution based expression-detection and background adjustment for microarray data. *Journal of Computational Biology*, 13(1):63–80, January 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.63; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.63.

Hickey:2011:PMS

[HB11] Glenn Hickey and Mathieu Blanchette. A probabilistic model for sequence alignment with context-sensitive indels. *Journal of Computational Biology*, 18(11):1449–1464, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0157; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0157.

Hide:1994:BED

[HBD94] Winston Hide, John Burke, and Daniel B. Da Vison. Biological evaluation of d^2, an algorithm for high-performance sequence comparison. *Journal of Computational Biology*, 1(3):199–215, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.199; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.199.

Heath:2011:AEI

[HBK11] Allison P. Heath, George N. Bennett, and Lydia E. Kavraki. An algorithm for efficient identification of branched metabolic pathways. *Journal of Computational Biology*, 18(11):1575–1597, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0165; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0165`.

Haimovich:2006:WAD

[HBRW06] Adrian D. Haimovich, Bruce Byrne, Ramakrishna Ramaswamy, and William J. Welsh. Wavelet analysis of DNA walks. *Journal of Computational Biology*, 13(7):1289–1298, September 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1289; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1289`.

Huan:2005:CGR

[HBW+05] Jun Huan, Deepak Bandyopadhyay, Wei Wang, Jack Snoeyink, Jan Prins, and Alexander Tropsha. Comparing graph representations of protein structure for mining family-specific residue-based packing motifs. *Journal of Computational Biology*, 12(6):657–671, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.657; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.657`.

Huang:2005:AAH

[HCC05] Yao-Ting Huang, Kun-Mao Chao, and Ting Chen. An approximation algorithm for haplotype inference by maximum parsimony. *Journal of Computational Biology*, 12(10):1261–1274, December 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1261; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1261`.

Hoque:2009:EHM

[HCS09] Tamjidul Hoque, Madhu Chetty, and Abdul Sattar. Extended HP model for protein structure prediction. *Journal of Computational Biology*, 16(1):85–103, January 2009. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0082; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0082.

He:2009:URU

[HCX09] Yi He, Changjun Chen, and Yi Xiao. United-residue (UNRES) Langevin dynamics simulations of trpzip2 folding. *Journal of Computational Biology*, 16(12):1719–1730, December 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0070; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0070.

Holmes:1998:DPA

[HD98] Ian Holmes and Richard Durbin. Dynamic programming alignment accuracy. *Journal of Computational Biology*, 5 (3):493–504, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.493; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.493.

Herant:2010:CTD

[HD10] Marc Herant and Micah Dembo. Cytopede: a three-dimensional tool for modeling cell motility on a flat surface. *Journal of Computational Biology*, 17(12):1639–1677, December 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0271; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0271.

Hallen:2016:CCO

[HD16] Mark A. Hallen and Bruce R. Donald. comets (constrained optimization of multistate energies by tree search): a provable and efficient protein design algorithm to optimize binding affinity and specificity with respect to sequence. *Journal of Computational Biology*, 23(5):311–321, May 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0188; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0188.

Han:2008:SAP

[HDBZ08] Buhm Han, Banu Dost, Vineet Bafna, and Shaojie Zhang. Structural alignment of pseudoknotted RNA. *Journal of Computational Biology*, 15(5):489–504, June 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0214; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0214`.

Heath:1997:MCM

[Hea97] S. C. Heath. Markov chain Monte Carlo methods for radiation hybrid mapping. *Journal of Computational Biology*, 4(4):505–515, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.505; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.505`.

Hussain:2019:PDT

[HFUH19] Shahid Hussain, Javed Ferzund, and Raza Ul-Haq. Prediction of drug target sensitivity in cancer cell lines using Apache Spark. *Journal of Computational Biology*, 26(8):882–889, August 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0102; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0102`.

He:2005:ICG

[HG05] Xin He and Michael H. Goldwasser. Identifying conserved gene clusters in the presence of homology families. *Journal of Computational Biology*, 12(6):638–656, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.638; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.638`.

Halldorsson:2011:ADH

[HG11] Bjarni V. Halldórsson and Daníel F. Gudbjartsson. An algorithm for detecting high frequency copy number polymorphisms using SNP arrays. *Journal of Computational Biology*, 18(8):955–966, August 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0317;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0317.

Huang:2018:NRT

[HG18] Hsin-Hsiung Huang and Senthil B. Girimurugan. A novel real-time genome comparison method using discrete wavelet transform. *Journal of Computational Biology*, 25(4):405–416, April 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0115; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0115.

Halperin:2006:HEH

[HH06] Eran Halperin and Elad Hazan. HAPLOFREQ — estimating haplotype frequencies efficiently. *Journal of Computational Biology*, 13(2):481–500, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.481; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.481.

Hu:2014:PSP

[HH14] Wei Hu and John Hu. Prediction of siRNA potency using sparse logistic regression. *Journal of Computational Biology*, 21(6):420–427, June 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0115; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0115.

Hung:2006:CUC

[HHC06] Chun-Min Hung, Yueh-Min Huang, and Ming-Shi Chang. CSAM: Using clustering-hashing-signal anchoring method to explore human novel genes. *Journal of Computational Biology*, 13(10):1775–1789, December 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1775; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1775.

He:2017:PSA

[HHC17] Jing He, Nurit Haspel, and Brian Chen. Preface: Selected articles from 2015 Computational Structural Bioinformatics

Workshop. *Journal of Computational Biology*, 24(1):1, January 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.29004.jh`.

He:2013:HSO

[HHE13] Dan He, Buhm Han, and Eleazar Eskin. Hap-seq: an optimal algorithm for haplotype phasing with imputation using sequencing data. *Journal of Computational Biology*, 20(2):80–92, February 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0091; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0091`.

Halperin:2003:HLT

[HHHS03] Eran Halperin, Shay Halperin, Tzvika Hartman, and Ron Shamir. Handling long targets and errors in sequencing by hybridization. *Journal of Computational Biology*, 10(3–4):483–497, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Horng:2002:RSD

[HHJ+02] Jorng-Tzong Horng, Hsien-Da Huang, Ming-Hui Jin, Li-Cheng Wu, and Shir-Ly Huang. The repetitive sequence database and mining putative regulatory elements in gene promoter regions. *Journal of Computational Biology*, 9(4): 621–640, August 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652702760277354; https://www.liebertpub.com/doi/pdf/10.1089/106652702760277354`.

Huang:2013:RMT

[HHJ+13] Yan Huang, Yin Hu, Corbin D. Jones, James N. MacLeod, Derek Y. Chiang, Yufeng Liu, Jan F. Prins, and Jinze Liu. A robust method for transcript quantification with RNA-Seq data. *Journal of Computational Biology*, 20(3):167–187, March 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0230; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0230`.

Hjelm:2006:NPN

[HHL06] Marcus Hjelm, Mattias Höglund, and Jens Lagergren. New probabilistic network models and algorithms for oncogenesis. *Journal of Computational Biology*, 13(4):853–865, May 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.853; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.853`.

Hong:2009:APP

[HHP+09] Huixiao Hong, Qilong Hong, Roger Perkins, Leming Shi, Hong Fang, Zhenqiang Su, Yvonne Dragan, James C. Fuscoe, and Weida Tong. The accurate prediction of protein family from amino acid sequence by measuring features of sequence fragments. *Journal of Computational Biology*, 16 (12):1671–1688, December 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0115; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0115`.

Hashemifar:2016:JAM

[HHX16] Somaye Hashemifar, Qixing Huang, and Jinbo Xu. Joint alignment of multiple protein–protein interaction networks via convex optimization. *Journal of Computational Biology*, 23(11):903–911, November 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0025; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0025`.

He:2018:ALM

[HHZ+18] Jin-Hua He, Ze-Ping Han, Mao-Xian Zou, Li Wang, Yu Bing Lv, Jia Bin Zhou, Ming-Rong Cao, and Yu-Guang Li. Analyzing the LncRNA, miRNA, and mRNA regulatory network in prostate cancer with bioinformatics software. *Journal of Computational Biology*, 25(2):146–157, February 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0093; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0093`.

Hart:1996:FPF

[HI96] William E. Hart and Sorin C. Istrail. Fast protein folding in the hydrophobic–hydrophilic model within three-eighths of optimal. *Journal of Computational Biology*, 3(1):53–96, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.53; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.53`.

Hart:1997:LLS

[HI97a] William E. Hart and Sorin Istrail. Lattice and off-lattice side chain models of protein folding: Linear time structure prediction better than 86% of optimal. *Journal of Computational Biology*, 4(3):241–259, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.241; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.241`.

Hart:1997:RPN

[HI97b] William E. Hart and Sorin Istrail. Robust proofs of NP-Hardness for protein folding: General lattices and energy potentials. *Journal of Computational Biology*, 4(1):1–22, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.1; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.1`.

Hobolth:2005:AHM

[HJ05] Asger Hobolth and Jens Ledet Jensen. Applications of hidden Markov models for characterization of homologous DNA sequences with a common gene. *Journal of Computational Biology*, 12(2):186–203, March 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.186; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.186`.

Huo:2014:CTM

[HJ14] Yunzhang Huo and Ping Ji. Continuous-time Markov chain–based flux analysis in metabolism. *Journal of Computational Biology*, 21(9):691–698, September 2014. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0073; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0073.

Hallen:2017:LLU

[HJD17] Mark A. Hallen, Jonathan D. Jou, and Bruce R. Donald. LUTE (local unpruned tuple expansion): Accurate continuously flexible protein design with general energy functions and rigid rotamer-like efficiency. *Journal of Computational Biology*, 24(6):536–546, June 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0136; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0136.

Helmkamp:2012:ICD

[HJR12] Laura J. Helmkamp, Ethan M. Jewett, and Noah A. Rosenberg. Improvements to a class of distance matrix methods for inferring species trees from gene trees. *Journal of Computational Biology*, 19(6):632–649, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0042; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0042.

Heckerman:2007:LIA

[HKL07] David Heckerman, Carl Kadie, and Jennifer Listgarten. Leveraging information across HLA alleles/supertypes improves epitope prediction. *Journal of Computational Biology*, 14(6):736–746, July 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R013; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R013.

Haus:2008:CKS

[HKS08] Utz-Uwe Haus, Steffen Klamt, and Tamon Stephen. Computing knock-out strategies in metabolic networks. *Journal of Computational Biology*, 15(3):259–268, April 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0229; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0229.

Huang:2004:DLS

[HKZ+04] Haiyan Huang, Ming-Chih J. Kao, Xianghong Zhou, Jun S. Liu, and Wing H. Wong. Determination of local statistical significance of patterns in Markov sequences with application to promoter element identification. *Journal of Computational Biology*, 11(1):1–14, January 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652704773416858; https://www.liebertpub.com/doi/pdf/10.1089/106652704773416858`.

Hwang:2003:ETP

[HL03] F. K. Hwang and Y. C. Liu. Error-tolerant pooling designs with inhibitors. *Journal of Computational Biology*, 10 (2):231–236, April 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652703321825982; https://www.liebertpub.com/doi/pdf/10.1089/106652703321825982`.

Huang:2010:SRG

[HL10] Yen-Lin Huang and Chin Lung Lu. Sorting by reversals, generalized transpositions, and translocations using permutation groups. *Journal of Computational Biology*, 17(5):685–705, May 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0025; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0025`.

Huang:2013:MVT

[HL13] Hong Huang and Yongji Li. MASTtreedist: Visualization of tree space based on maximum agreement subtree. *Journal of Computational Biology*, 20(1):42–49, January 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0243; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0243`.

Hsiao:2016:SAF

[HL16a] Ya-Chun Hsiao and Li-Yu Daisy Liu. A stepwise approach of finding dependent variables via coefficient of intrinsic dependence. *Journal of Computational Biology*, 23(1):42–55, January 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/`

abs/10.1089/cmb.2015.0150; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0150.

Hu:2016:CPT

[HL16b] Yucheng Hu and John S. Lowengrub. Collective properties of a transcription initiation model under varying environment. *Journal of Computational Biology*, 23(1):56–66, January 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0144; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0144.

Hernandez-lopez:2020:TDT

[HlAM20] Ana A. Hernandez-lopez, Claudio Alberti, and Marco Mattavelli. Toward a dynamic threshold for quality score distortion in reference-based alignment. *Journal of Computational Biology*, 27(2):288–300, February 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0333; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0333.

Hescott:2010:EBP

[HLCS10] B. J. Hescott, M. D. M. Leiserson, L. J. Cowen, and D. K. Slonim. Evaluating between-pathway models with expression data. *Journal of Computational Biology*, 17(3):477–487, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0178; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0178.

Huang:2018:AMW

[HLG18] Xinrui Huang, Sha Li, and Song Gao. Applying a modified wavelet shrinkage filter to improve cryo-electron microscopy imaging. *Journal of Computational Biology*, 25 (9):1050–1058, September 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0060; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0060.

Heger:2004:ADV

[HLH04] Andreas Heger, Michael Lappe, and Liisa Holm. Accurate detection of very sparse sequence motifs. *Journal of Computational*

Biology, 11(5):843–857, October 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.843; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.843.

Hohm:2006:MEM

[HLH06] Tim Hohm, Philipp Limbourg, and Daniel Hoffmann. A multiobjective evolutionary method for the design of peptidic mimotopes. *Journal of Computational Biology*, 13 (1):113–125, January 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.113; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.113.

Hedjazi:2013:SDA

[HLK+13] Lyamine Hedjazi, Marie-Veronique Le Lann, Tatiana Kempowsky, Florence Dalenc, Joseph Aguilar-Martin, and Gilles Favre. Symbolic data analysis to defy low signal-to-noise ratio in microarray data for breast cancer prognosis. *Journal of Computational Biology*, 20(8):610–620, August 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0249; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0249.

Holtby:2013:LLM

[HLL13] Daniel Holtby, Shuai Cheng Li, and Ming Li. LoopWeaver: Loop modeling by the weighted scaling of verified proteins. *Journal of Computational Biology*, 20(3):212–223, March 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0078; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0078.

Heinonen:2011:CAM

[HLMR11] Markus Heinonen, Sampsa Lappalainen, Taneli Mielikäinen, and Juho Rousu. Computing atom mappings for biochemical reactions without subgraph isomorphism. *Journal of Computational Biology*, 18(1):43–58, January 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0216;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0216.

Huber:2008:CDM

[HLMS08] Katharina T. Huber, Martin Lott, Vincent Moulton, and Andreas Spillner. The complexity of deriving multi-labeled trees from bipartitions. *Journal of Computational Biology*, 15(6):639–651, July 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0088; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0088.

Han:2014:CS

[HLR14] Hillary S. W. Han, Thomas J. X. Li, and Christian M. Reidys. Combinatorics of γ-structures. *Journal of Computational Biology*, 21(8):591–608, August 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0128; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0128.

Hu:2025:AAC

[HLY25] Yingxin Hu, Yanjun Liu, and Yuefei Yang. Adaptive arithmetic coding-based encoding method toward high-density DNA storage. *Journal of Computational Biology*, 32(3):298–315, March 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0697; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0697.

Hochberg:2014:DSP

[HM14] Robert Hochberg and Treena Larrew Milam. Data structures for parsimony correlation and biosequence co-evolution. *Journal of Computational Biology*, 21(4):361–369, April 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0107; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0107.

Huang:2007:BIM

[HMF07] Jim C. Huang, Quaid D. Morris, and Brendan J. Frey. Bayesian inference of MicroRNA targets from sequence and expression data. *Journal of Computational Biology*, 14(5):550–563, June

2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R002; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R002.

Hoang:2024:DCO

[HMK24] Minh Hoang, Guillaume Marçais, and Carl Kingsford. Density and conservation optimization of the generalized masked-minimizer sketching scheme. *Journal of Computational Biology*, 31(1):2–20, January 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0212; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0212.

Hayes:2021:CVD

[HMN21] Matthew Hayes, Derrick Mullins, and Angela Nguyen. Complex variant discovery using discordant cluster normalization. *Journal of Computational Biology*, 28(2):185–194, February 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0249; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0249.

Horesh:2006:DAC

[HMU06] Yair Horesh, Ramit Mehr, and Ron Unger. Designing an $A*$ algorithm for calculating edit distance between rooted-unordered trees. *Journal of Computational Biology*, 13(6):1165–1176, July 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1165; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1165.

Hasegawa:2014:EDA

[HMY+14] Takanori Hasegawa, Tomoya Mori, Rui Yamaguchi, Seiya Imoto, Satoru Miyano, and Tatsuya Akutsu. An efficient data assimilation schema for restoration and extension of gene regulatory networks using time-course observation data. *Journal of Computational Biology*, 21(11):785–798, November 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0171; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0171.

Hayashi:2019:ANB

[HMY+19] Shuto Hayashi, Takuya Moriyama, Rui Yamaguchi, Shinichi Mizuno, Mitsuhiro Komura, Satoru Miyano, Hidewaki Nakagawa, and Seiya Imoto. ALPHLARD-NT: Bayesian method for human leukocyte antigen genotyping and mutation calling through simultaneous analysis of normal and tumor whole-genome sequence data. *Journal of Computational Biology*, 26(9):923–937, September 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0224; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0224`.

Haus:2009:LIP

[HNTW09] Utz-Uwe Haus, Kathrin Niermann, Klaus Truemper, and Robert Weismantel. Logic integer programming models for signaling networks. *Journal of Computational Biology*, 16(5):725–743, May 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0163; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0163`.

Huson:1999:DCF

[HNW99] Daniel H. Huson, Scott M. Nettles, and Tandy J. Warnow. Disk-covering, a fast-converging method for phylogenetic tree reconstruction. *Journal of Computational Biology*, 6(3–4):369–386, October 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Horton:2001:TBB

[Hor01] Paul Horton. Tsukuba BB: a branch and bound algorithm for local multiple alignment of DNA and protein sequences. *Journal of Computational Biology*, 8(3):283–303, June 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270152530854; https://www.liebertpub.com/doi/pdf/10.1089/10665270152530854`.

Hendy:1996:CFL

[HP96] Michael D. Hendy and David Penny. Complete families of linear invariants for some stochastic models of sequence evolution, with and without the molecular clock assumption. *Journal of Computational Biology*, 3(1):19–31, January 1996. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.19; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.19.

Hochbaum:1997:PCE

[HP97] Dorit S. Hochbaum and Anu Pathria. Path costs in evolutionary tree reconstruction. *Journal of Computational Biology*, 4(2):163–175, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.163; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.163.

Haubold:2009:EMD

[HPDLW09] Bernhard Haubold, Peter Pfaffelhuber, Mirjana Domazet-Losō, and Thomas Wiehe. Estimating mutation distances from unaligned genomes. *Journal of Computational Biology*, 16(10):1487–1500, October 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0106; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0106.

Hanson:2020:GKY

[HPL+20] Jack Hanson, Kuldip K. Paliwal, Thomas Litfin, Yuedong Yang, and Yaoqi Zhou. Getting to know your neighbor: Protein structure prediction comes of age with contextual machine learning. *Journal of Computational Biology*, 27(5):796–814, May 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0193; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0193.

Huang:2009:FNR

[HPR09] Fenix W. D. Huang, Wade W. J. Peng, and Christian M. Reidys. Folding 3-noncrossing RNA pseudoknot structures. *Journal of Computational Biology*, 16(11):1549–1575, November 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0194; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0194.

Huynen:1996:BPP

[HPVS96] Martijn A. Huynen, Alan Perelson, Wayne A. Vieira, and Peter F. Stadler. Base pairing probabilities in a complete HIV-1 RNA. *Journal of Computational Biology*, 3 (2):253–274, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.253; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.253`.

Heath:2003:SHC

[HPY03] Samuel A. Heath, Franco P. Preparata, and Joel Young. Sequencing by hybridization by cooperating direct and reverse spectra. *Journal of Computational Biology*, 10(3–4):499–508, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Huang:2006:LPW

[HQ06] Shuguang Huang and Yongming Qu. The loss in power when the test of differential expression is performed under a wrong scale. *Journal of Computational Biology*, 13(3):786–797, April 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.786; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.786`.

Han:2008:PRS

[HR08] Hillary S. W. Han and Christian M. Reidys. Pseudoknot RNA structures with arc-length ≥ 4. *Journal of Computational Biology*, 15(9):1195–1208, November 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0051; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0051`.

Han:2012:DRS

[HR12a] Hillary S. W. Han and Christian M. Reidys. The 5'-3' distance of RNA secondary structures. *Journal of Computational Biology*, 19(7):867–878, July 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0301;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0301.

Han:2012:PTE

[HR12b] Hillary S. W. Han and Christian M. Reidys. A phase transition in energy-filtered RNA secondary structures. *Journal of Computational Biology*, 19(10):1105–1119, October 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0151; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0151.

Hill:2022:ITB

[HR22] Max Hill and Sebastien Roch. Inconsistency of triplet-based and quartet-based species tree estimation under intralocus recombination. *Journal of Computational Biology*, 29 (11):1173–1197, November 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0265; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0265.

Hart:2000:SFA

[HRSC00] Reece K. Hart, Ajay K. Royyuru, Gustavo Stolovitzky, and Andrea Califano. Systematic and fully automated identification of protein sequence patterns. *Journal of Computational Biology*, 7(3–4):585–600, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Hsieh:2014:FAC

[HS14] Mu-Fen Hsieh and Sing-Hoi Sze. Finding alignments of conserved graphlets in protein interaction networks. *Journal of Computational Biology*, 21(3):234–246, March 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0130; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0130.

Hashmi:2015:IIM

[HS15] Irina Hashmi and Amarda Shehu. idDock+: Integrating machine learning in probabilistic search for protein–protein docking. *Journal of Computational Biology*, 22(9):806–822, September 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-

8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0108; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0108.

Hasegawa:2023:ECB

[HS23] Nozomi Hasegawa and Kana Shimizu. Efficient colored de Bruijn graph for indexing reads. *Journal of Computational Biology*, 30(6):648–662, June 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0259; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0259.

Holloway:2013:AGO

[HSAEM13] Patrick Holloway, Krister Swenson, David Ardell, and Nadia El-Mabrouk. Ancestral genome organization: an alignment approach. *Journal of Computational Biology*, 20(4):280–295, April 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0292; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0292.

Hormozdiari:2010:PPI

[HSBS10] Fereydoun Hormozdiari, Raheleh Salari, Vineet Bafna, and S. Cenk Sahinalp. Protein-protein interaction network evaluation for identifying potential drug targets. *Journal of Computational Biology*, 17(5):669–684, May 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0032; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0032.

Hoberman:2005:SAS

[HSD05] Rose Hoberman, David Sankoff, and Dannie Durand. The statistical analysis of spatially clustered genes under the maximum gap criterion. *Journal of Computational Biology*, 12 (8):1083–1102, October 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1083; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1083.

Henderson:1997:FGD

[HSF97] John Henderson, Steven Salzberg, and Kenneth H. Fasman. Finding genes in DNA with a hidden Markov model. *Journal of Computational Biology*, 4(2):127–141, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.127; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.127`.

Heber:2000:CSP

[HSF+00] Steffen Heber, Jens Stoye, Marcus Frohme, Jörg Hoheisel, and Martin Vingron. Contig selection in physical mapping. *Journal of Computational Biology*, 7(3–4):395–408, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Hammoud:2022:CPT

[HSG22] Muhsen Hammoud, Charles Morphy D. Santos, and João Paulo Gois. Comparing phylogenetic trees side by side through iPhyloC, a new interactive Web-based framework. *Journal of Computational Biology*, 29(3):292–303, March 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0351; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0351`.

Hormozdiari:2009:EID

[HSH+09] Fereydoun Hormozdiari, Raheleh Salari, Michael Hsing, Alexander Schönhuth, Simon K. Chan, S. Cenk Sahinalp, and Artem Cherkasov. The effect of insertions and deletions on wirings in protein-protein interaction networks: a large-scale study. *Journal of Computational Biology*, 16(2):159–167, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.03TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.03TT`.

Hirsch:2011:BDA

[HSH11] Michael Hirsch, Bernhard Schölkopf, and Michael Habeck. A blind deconvolution approach for improving the resolution of Cryo-EM density maps. *Journal of Computational Biology*, 18(3):335–346, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0264;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0264.

Haque:2014:ICL

[HSH14] M. Muksitul Haque, Michael K. Skinner, and Lawrence B. Holder. Imbalanced class learning in epigenetics. *Journal of Computational Biology*, 21(7):492–507, July 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0008; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0008.

He:2015:CSB

[HSHC15] Jing He, Amarda Shehu, Nurit Haspel, and Brian Chen. The 7th computational structural bioinformatics workshop. *Journal of Computational Biology*, 22(9):785–786, September 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.28999.jh.

Hirsch:2007:OSS

[HSL07] Michael Hirsch, Stephen Swift, and Xiohui Liu. Optimal search space for clustering gene expression data via consensus. *Journal of Computational Biology*, 14(10):1327–1341, December 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0153; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0153.

Hou:2024:VRG

[HSL+24] Xiaodi Hou, Guoming Sang, Zhi Liu, Xiaobo Li, and Yijia Zhang. Visual recalibration and gating enhancement network for radiology report generation. *Journal of Computational Biology*, 31(6):486–497, June 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Haussler:2018:FPL

[HSOE+18] David Haussler, Maciej Smuga-Otto, Jordan M. Eizenga, Benedict Paten, Adam M. Novak, Sergei Nikitin, Maria Zueva, and Dmitrii Miagkov. A flow procedure for linearization of genome sequence graphs. *Journal of Computational Biology*, 25(7):664–676, July 2018. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0248; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0248.

Huang:2017:SIS

[HTH+17] Haiyan Huang, Hua Tang, Jing Huang, Bin Chen, Ruixiao Liu, Rui (Sammi) Tang, Ying Lu, and Peng Yang. Special issue: Selected papers of the Inaugural DahShu Data Science Symposium: Computational Precision Health (CPH 2017). *Journal of Computational Biology*, 24(7):635–636, July 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.29007.hh.

Harjule:2022:TEM

[HTM+22] Priyanka Harjule, Manva Mohd. Tokir, Tanuj Mehta, Shivam Gurjar, Anupam Kumar, and Basant Agarwal. Texture enhancement of medical images for efficient disease diagnosis with optimized fractional derivative masks. *Journal of Computational Biology*, 29(6):545–564, June 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0267; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0267.

Han:2022:LSH

[HTY22] Wontack Han, Haixu Tang, and Yuzhen Ye. Locality-sensitive hashing-based k-mer clustering for identification of differential microbial markers related to host phenotype. *Journal of Computational Biology*, 29(7):738–751, July 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0640; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0640.

He:2012:NAT

[HTZ+12] Yichao He, Haiyan Tian, Xinlu Zhang, Zhiwei Wang, and Suogang Gao. Nonadaptive algorithms for threshold group testing with inhibitors and error-tolerance. *Journal of Computational Biology*, 19(7):903–910, July 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0229;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0229.

Hart:2013:CSS

[HTZ+13] Steven N. Hart, Terry M. Therneau, Yuji Zhang, Gregory A. Poland, and Jean-Pierre Kocher. Calculating sample size estimates for RNA sequencing data. *Journal of Computational Biology*, 20(12):970–978, December 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0283; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0283.

Huang:2008:SAA

[Hua08] Xiaoqiu Huang. Sequence alignment with an appropriate substitution matrix. *Journal of Computational Biology*, 15(2):129–138, March 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0155; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0155.

Huang:2010:SIS

[Hua10] Shuguang Huang. Statistical issues in subpopulation analysis of high content imaging data. *Journal of Computational Biology*, 17(7):879–894, July 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0071; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0071.

Huang:2015:MRR

[Hua15] Chia-Hui Huang. Medical reasoning with rough-set influence diagrams. *Journal of Computational Biology*, 22(8):752–764, August 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0293; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0293.

Hubbell:2001:MSH

[Hub01] Earl Hubbell. Multiplex sequencing by hybridization. *Journal of Computational Biology*, 8(2):141–149, April 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.

1089/106652701300312913; https://www.liebertpub.com/doi/pdf/10.1089/106652701300312913.

Heath:2003:SSS

[HV03] Lenwood S. Heath and John Paul C. Vergara. Sorting by short swaps. *Journal of Computational Biology*, 10(5): 775–789, October 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703322539097; https://www.liebertpub.com/doi/pdf/10.1089/106652703322539097.

Havukkala:2007:RIP

[HV07] Ilkka Havukkala and Stijn Vanderlooy. On the reliable identification of plant sequences containing a polyadenylation site. *Journal of Computational Biology*, 14(9):1229–1245, November 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0058; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0058.

Huang:2009:MSN

[HV09] Xiaoqiu Huang and Martin Vingron. Maximum similarity: a new formulation of phylogenetic reconstruction. *Journal of Computational Biology*, 16(7):887–896, July 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0232; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0232.

Helman:2004:BNC

[HVAW04] Paul Helman, Robert Veroff, Susan R. Atlas, and Cheryl Willman. A Bayesian network classification methodology for gene expression data. *Journal of Computational Biology*, 11(4):581–615, August 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.581; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.581.

Halioui:2017:GDG

[HVD17] Ahmed Halioui, Petko Valtchev, and Abdoulaye Baniré Diallo. T-GOWler: Discovering generalized process models within

texts. *Journal of Computational Biology*, 24(8):799–808, August 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0085; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0085.

He:2013:BBB

[HVPBK13] Lu He, Fabio Vandin, Gopal Pandurangan, and Chris Bailey-Kellogg. Ballast: a ball-based algorithm for structural motifs. *Journal of Computational Biology*, 20(2):137–151, February 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0246; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0246.

Husmeier:2001:DRD

[HW01] Dirk Husmeier and Frank Wright. Detection of recombination in DNA multiple alignments with hidden Markov models. *Journal of Computational Biology*, 8(4):401–427, September 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701752236214; https://www.liebertpub.com/doi/pdf/10.1089/106652701752236214.

He:2013:IIP

[HWH+13] Dan He, Zhanyong Wang, Buhm Han, Laxmi Parida, and Eleazar Eskin. IPED: Inheritance path-based pedigree reconstruction algorithm using genotype data. *Journal of Computational Biology*, 20(10):780–791, October 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0080; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0080.

Hoinka:2020:AOW

[HWP20] Jan Hoinka, Yijie Wang, and Teresa M. Przytycka. AptaBlocks online: a Web-based toolkit for the in silico design of oligonucleotide sticky bridges. *Journal of Computational Biology*, 27(3):356–360, March 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0470; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0470.

Holley:2018:DAF

[HWSH18] Guillaume Holley, Roland Wittler, Jens Stoye, and Faraz Hach. Dynamic alignment-free and reference-free read compression. *Journal of Computational Biology*, 25(7):825–836, July 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0068; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0068`.

Hu:2020:PMI

[HWW+20] Guozhang Hu, Rui Wang, Bo Wei, Le Wang, Qi Yang, Daliang Kong, and Chao Du. Prognostic markers identification in glioma by gene expression profile analysis. *Journal of Computational Biology*, 27(1):81–90, January 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0217; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0217`.

Huang:2021:IID

[HWZ+21] Qiuyue Huang, Jun Wang, Xiangliang Zhang, Maozu Guo, and Guoxian Yu. IsoDA: Isoform–disease association prediction by multiomics data fusion. *Journal of Computational Biology*, 28(8):804–819, August 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0626; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0626`.

Hao:2017:RFD

[HXL+17] Yangyang Hao, Xiaoling Xuei, Lang Li, Harikrishna Nakshatri, Howard J. Edenberg, and Yunlong Liu. RareVar: a framework for detecting low-frequency single-nucleotide variants. *Journal of Computational Biology*, 24(7):637–646, July 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0057; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0057`.

Hu:2020:CAI

[HXL+20] Maolin Hu, Jiangling Xie, Zhifeng Liu, Xuan Wang, Ming Liu, and Jianye Wang. Comprehensive analysis identifying Wnt ligands gene family for biochemical recurrence in

prostate adenocarcinoma and construction of a nomogram. *Journal of Computational Biology*, 27(12):1656–1667, December 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0397; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0397`.

Huang:2023:HDP

[HXY+23] An Huang, Xiaolan Xie, Xiaojun Yao, Huanxiang Liu, Xiaoqi Wang, and Shaoliang Peng. HF-DDI: Predicting drug–drug interaction events based on multimodal hybrid fusion. *Journal of Computational Biology*, 30(9):961–971, September 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0068; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0068`.

Hernandez:2016:DSG

[HY16a] Troy Hernandez and Jie Yang. Descriptive statistics of the genome: Phylogenetic classification of viruses. *Journal of Computational Biology*, 23(10):810–820, October 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0132; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0132`.

Hu:2016:SEU

[HY16b] Yucheng Hu and Gongrong Yang. Sequence evolution under constraints: Lessons learned from Sudoku. *Journal of Computational Biology*, 23(10):830–840, October 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0218; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0218`.

Hu:2019:CMC

[HYJ+19] Xi Hu, Wenling Yi, Ling Jiang, Sijia Wu, Yan Zhang, Jianqiang Du, Tianyou Ma, Tong Wang, and Xiaoming Wu. Classification of metaphase chromosomes using deep convolutional neural network. *Journal of Computational Biology*, 26(5):473–484, May 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/`

abs/10.1089/cmb.2018.0212; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0212.

He:2010:OBP

[HYY+10] Zengyou He, Chao Yang, Can Yang, Robert Z. Qi, Jason Po-Ming Tam, and Weichuan Yu. Optimization-based peptide mass fingerprinting for protein mixture identification. *Journal of Computational Biology*, 17(3):221–235, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0160; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0160.

Hertzberg:2005:FMP

[HZGD05] Libi Hertzberg, Or Zuk, Gad Getz, and Eytan Domany. Finding motifs in promoter regions. *Journal of Computational Biology*, 12(3):314–330, April 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.314; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.314.

Hsu:2010:EMD

[HZH+10] Chih-Hao Hsu, Yu Zhang, Ross C. Hardison, Eric D. Green, and Webb Miller. An effective method for detecting gene conversion events in whole genomes. *Journal of Computational Biology*, 17(9):1281–1297, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0103; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0103.

Hoang:2022:DLS

[HZK22] Minh Hoang, Hongyu Zheng, and Carl Kingsford. Differentiable learning of sequence-specific minimizer schemes with DeepMinimizer. *Journal of Computational Biology*, 29(12):1288–1304, December 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0275; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0275.

Hu:2022:CAH

[HZL22] Ran Hu, Xianghong Jasmine Zhou, and Wenyuan Li. Computational analysis of high-dimensional DNA methylation

data for cancer prognosis. *Journal of Computational Biology*, 29(8):769–781, August 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0002; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0002.

Han:2006:PDRa

[HZNF06a] Pengfei Han, Xiuzhen Zhang, Raymond S. Norton, and Zhi-Ping Feng. Predicting disordered regions in proteins based on decision trees of reduced amino acid composition. *Journal of Computational Biology*, 13(9):1579–1590, November 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1579; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1579.

Han:2006:PDRb

[HZNF06b] Pengfei Han, Xiuzhen Zhang, Raymond S. Norton, and Zhi-Ping Feng. Predicting disordered regions in proteins based on decision trees of reduced amino acid composition. *Journal of Computational Biology*, 13(10):1723–1734, December 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1723; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1723.

Illner:2014:BBS

[IFT14] Katrin Illner, Christiane Fuchs, and Fabian J. Theis. Bayesian blind source separation for data with network structure. *Journal of Computational Biology*, 21(11):855–865, November 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0117; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0117.

Ibrahim:2012:TBS

[IJCL12] Maysson Al-Haj Ibrahim, Sabah Jassim, Michael Anthony Cawthorne, and Kenneth Langlands. A topology-based score for pathway enrichment. *Journal of Computational Biology*, 19(5):563–573, May 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0182;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0182.

Ieong:2003:PRS

[IKL+03] Samuel Ieong, Ming-Yang Kao, Tak-Wah Lam, Wing-Kin Sung, and Siu-Ming Yiu. Predicting RNA secondary structures with arbitrary pseudoknots by maximizing the number of stacking pairs. *Journal of Computational Biology*, 10(6): 981–995, December 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703322756186; https://www.liebertpub.com/doi/pdf/10.1089/106652703322756186.

Ilan:2020:ATR

[Ila20] Yaron Ilan. Advanced tailored randomness: a novel approach for improving the efficacy of biological systems. *Journal of Computational Biology*, 27(1):20–29, January 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0231; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0231.

Irvahn:2014:PSM

[IM14] Jan Irvahn and Vladimir N. Minin. Phylogenetic stochastic mapping without matrix exponentiation. *Journal of Computational Biology*, 21(9):676–690, September 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0062; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0062.

Ilatovskiy:2009:GWS

[IP09] Andrey Ilatovskiy and Michael Petukhov. Genome-wide search for local DNA segments with anomalous GC-Content. *Journal of Computational Biology*, 16(4):555–564, April 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0159; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0159.

Istrail:2019:HDR

[IP19] Sorin Istrail and Isabelle S. Peter. How does the regulatory genome work? *Journal of Computational Biology*, 26(7):685–695, July 2019. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0097; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0097.

Islam:2018:QTC

[IPH18] Tunazzina Islam, Michael Poteat, and Jing He. Quantification of twist from the central lines of β-strands. *Journal of Computational Biology*, 25(1):114–120, January 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0174; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0174.

Istrail:2022:SIP

[IPSV22] Sorin Istrail, Pavel Pevzner, Fengzhu Sun, and Martin Vingron. Special issue: Professor Michael Waterman's 80th birthday, part 1. *Journal of Computational Biology*, 29(7):599–600, July 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.29065.si.

Iv:2022:EIC

[IR22] Frederick A. Matsen Iv and Peter L. Ralph. Enabling inference for context-dependent models of mutation by bounding the propagation of dependency. *Journal of Computational Biology*, 29(8):802–824, August 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0644; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0644.

Innis:2021:GPC

[IRCA21] Sarah E. Innis, Kelsie Reinaltt, Mete Civelek, and Warren D. Anderson. GSEAplot: a package for customizing gene set enrichment analysis in R. *Journal of Computational Biology*, 28(6):629–631, June 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0426; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0426.

Ihuegbu:2012:FSD

[ISB12] Nnamdi E. Ihuegbu, Gary D. Stormo, and Jeremy Buhler. Fast, sensitive discovery of conserved genome-wide motifs. *Journal of Computational Biology*, 19(2):139–147, February 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0249; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0249`.

Istrail:1999:LSA

[ISK99] S. Istrail, R. Schwartz, and J. King. Lattice simulations of aggregation funnels for protein folding. *Journal of Computational Biology*, 6(2):143–162, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.143; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.143`.

Istrail:1999:SRI

[Ist99] Sorin Istrail. Special RECOMB'99 issue. *Journal of Computational Biology*, 6(3–4):279, October 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Istrail:2019:EDR

[Ist19] Sorin Istrail. Eric Davidson's regulatory genome for computer science: Causality, logic, and proof principles of the genomic *cis*-regulatory code. *Journal of Computational Biology*, 26(7):653–684, July 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0144; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0144`.

Istrail:2020:PSI

[Ist20] Sorin Istrail. Preface special issue: RECOMB 2018. *Journal of Computational Biology*, 27(3):301, March 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.29026.si`.

Iorio:2009:IND

[ITdB09] Francesco Iorio, Roberto Tagliaferri, and Diego di Bernardo. Identifying network of drug mode of action by gene ex-

pression profiling. *Journal of Computational Biology*, 16 (2):241–251, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.10TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.10TT.

Ideker:2000:TDE

[ITSH00] Trey Ideker, Vesteinn Thorsson, Andrew F. Siegel, and Leroy E. Hood. Testing for differentially-expressed genes by maximum-likelihood analysis of microarray data. *Journal of Computational Biology*, 7(6):805–817, December 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270050514945; https://www.liebertpub.com/doi/pdf/10.1089/10665270050514945.

Idury:1995:NAD

[IW95] Ramana M. Idury and Michael S. Waterman. A new algorithm for DNA sequence assembly. *Journal of Computational Biology*, 2(2):291–306, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.291; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.291.

Jakaitiene:2017:BBM

[JAG17] Audrone Jakaitiene, Mariano Avino, and Mario Rosario Guarracino. Beta-binomial model for the detection of rare mutations in pooled next-generation sequencing experiments. *Journal of Computational Biology*, 24(4):357–367, April 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0106; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0106.

Jahn:2011:ECA

[Jah11] Katharina Jahn. Efficient computation of approximate gene clusters based on reference occurrences. *Journal of Computational Biology*, 18(9):1255–1274, September 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0132; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0132.

Jisna:2024:UAU

[JAJ24] V. A. Jisna, Abhaysing Pawar Ajay, and P. B. Jayaraj. Using Attention-UNet models to predict protein contact maps. *Journal of Computational Biology*, 31(7):691–702, July 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

James:2010:MAG

[JB10] Scott C. James and Varun Boriah. Modeling algae growth in an open-channel raceway. *Journal of Computational Biology*, 17(7):895–906, July 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0078`; `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0078`.

Jow:2010:IGM

[JBBW10] Howsun Jow, Madhuchhanda Bhattacharjee, Richard Boys, and Darren Wilkinson. The integration of genetic maps using Bayesian inference. *Journal of Computational Biology*, 17(6):825–840, June 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0243`; `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0243`.

Joshi:2015:MSN

[JBM15] Anagha Joshi, Yvonne Beck, and Tom Michoel. Multi-species network inference improves gene regulatory network reconstruction for early embryonic development in *Drosophila*. *Journal of Computational Biology*, 22(4):253–265, April 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0290`; `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0290`.

Jiang:2022:TSG

[JC22] Wei Jiang and Liang Chen. Tissue specificity of gene expression evolves across mammal species. *Journal of Computational Biology*, 29(8):880–891, August 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0592`; `https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0592`.

Jiao:2022:GWC

[JCBX22] Rong Jiao, Xiangning Chen, Eric Boerwinkle, and Momiao Xiong. Genome-wide causation studies of complex diseases. *Journal of Computational Biology*, 29(8):908–931, August 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0676; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0676`.

Jabbari:2008:NER

[JCZ08] Hosna Jabbari, Anne Condon, and Shelly Zhao. Novel and efficient RNA secondary structure prediction using hierarchical folding. *Journal of Computational Biology*, 15(2):139–163, March 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0198; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0198`.

Jia:2005:RPM

[JD05] Yuting Jia and T. Gregory Dewey. A random polymer model of the statistical significance of structure alignment. *Journal of Computational Biology*, 12(3):298–313, April 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.298; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.298`.

Jaakkola:2000:DFD

[JDH00] Tommi Jaakkola, Mark Diekhans, and David Haussler. A discriminative framework for detecting remote protein homologies. *Journal of Computational Biology*, 7(1–2):95–114, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Jain:2018:FAA

[JDK+18] Chirag Jain, Alexander Dilthey, Sergey Koren, Srinivas Aluru, and Adam M. Phillippy. A fast approximate algorithm for mapping long reads to large reference databases. *Journal of Computational Biology*, 25(7):766–779, July 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0036; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0036`.

Jia:2004:NSF

[JDSB04] Yuting Jia, T. Gregory Dewey, Ilya N. Shindyalov, and Philip E. Bourne. A new scoring function and associated statistical significance for structure alignment by CE. *Journal of Computational Biology*, 11(5):787–799, October 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.787; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.787`.

Jaimovich:2006:TIP

[JEMF06] Ariel Jaimovich, Gal Elidan, Hanah Margalit, and Nir Friedman. Towards an integrated protein–protein interaction network: a relational Markov network approach. *Journal of Computational Biology*, 13(2):145–164, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.145; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.145`.

Jensen:2009:NLM

[Jen09] Jens Ledet Jensen. A note on the linear memory Baum–Welch algorithm. *Journal of Computational Biology*, 16(9):1209–1210, September 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0178; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0178`.

Jiang:2020:ITA

[JFLL20] Fangping Jiang, Hong Fan, Lian Luo, and Yun Li. An integrative transcriptome analysis reveals consistently dysregulated long noncoding RNAs and their transcriptional regulation relationships in heart failure. *Journal of Computational Biology*, 27(6):958–964, June 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0246; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0246`.

Jenkins:2011:ISD

[JG11] Paul A. Jenkins and Robert C. Griffiths. Inference from samples of DNA sequences using a two-locus model. *Journal of Computational Biology*, 18(1):109–127, January 2011.

CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0231; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0231.

Joyce:2012:ESL

[JGB12] Paul Joyce, Alan Genz, and Erkan Ozge Buzbas. Efficient simulation and likelihood methods for non-neutral multi-allele models. *Journal of Computational Biology*, 19(6):650–661, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0033; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0033.

Jang:2011:TFA

[JGL11] Richard Jang, Xin Gao, and Ming Li. Towards fully automated structure-based NMR resonance assignment of ^{15}N-labeled proteins from automatically picked peaks. *Journal of Computational Biology*, 18(3):347–363, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0251; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0251.

Jain:2022:ACC

[JGT22] Chirag Jain, Daniel Gibney, and Sharma V. Thankachan. Algorithms for colinear chaining with overlaps and gap costs. *Journal of Computational Biology*, 29(11):1237–1251, November 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0266; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0266.

Jindalertudomdee:2016:EMS

[JHA16] Jira Jindalertudomdee, Morihiro Hayashida, and Tatsuya Akutsu. Enumeration method for structural isomers containing user-defined structures based on breadth-first search approach. *Journal of Computational Biology*, 23(8):625–640, August 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0056; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0056.

Jou:2020:MAR

[JHLD20] Jonathan D. Jou, Graham T. Holt, Anna U. Lowegard, and Bruce R. Donald. Minimization-aware recursive $K*$: a novel, provable algorithm that accelerates ensemble-based protein design and provably approximates the energy landscape. *Journal of Computational Biology*, 27(4):550–564, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0315; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0315`.

Juyal:2023:RVV

[JHN+23] Akshay Juyal, Roya Hosseini, Daniel Novikov, Mark Grinshpon, and Alex Zelikovsky. Reconstruction of viral variants via Monte Carlo clustering. *Journal of Computational Biology*, 30(9):1009–1018, September 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0154; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0154`.

Jansson:2006:LGS

[JHS06] Jesper Jansson, Ngo Trung Hieu, and Wing-Kin Sung. Local gapped subforest alignment and its application in finding RNA structural motifs. *Journal of Computational Biology*, 13(3):702–718, April 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.702; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.702`.

Jiang:2011:ZED

[Jia11] Minghui Jiang. The zero exemplar distance problem. *Journal of Computational Biology*, 18(9):1077–1086, September 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0097; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0097`.

Jou:2016:BNP

[JJGD16] Jonathan D. Jou, Swati Jain, Ivelin S. Georgiev, and Bruce R. Donald. BWM*: a novel, provable, ensemble-based dynamic

programming algorithm for sparse approximations of computational protein design. *Journal of Computational Biology*, 23(6):413–424, June 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0194; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0194`.

Jung:2021:BEE

[JJH+21] Jinuk Jung, Hyunwhan Joe, Kyungsik Ha, Jin muk Lim, and Hong gee Kim. Biomedical entity explorer: a Web server for biomedical entity exploration. *Journal of Computational Biology*, 28(6):619–628, June 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0364; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0364`.

Jasrotia:2020:GWA

[JJY+20] Rahul Singh Jasrotia, Sarika Jaiswal, Pramod Kumar Yadav, Mustafa Raza, Mir Asif Iquebal, Anil Rai, and Dinesh Kumar. Genome-wide analysis of HSP70 family protein in *Vigna radiata* and coexpression analysis under abiotic and biotic stress. *Journal of Computational Biology*, 27(5):738–754, May 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0166; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0166`.

Joshi:1996:PLI

[JK96] Rajani R. Joshi and K. Krishnanand. Probabilistic learning in immune network: Weighted tree matching model. *Journal of Computational Biology*, 3(1):143–162, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.143; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.143`.

Janes:2004:CSR

[JKG+04] Kevin A. Janes, Jason R. Kelly, Suzanne Gaudet, John G. Albeck, Peter K. Sorger, and Douglas A. Lauffenburger. Cue-signal-response analysis of TNF-Induced apoptosis by partial least squares regression of dynamic multivariate data. *Journal of Computational Biology*, 11(4):544–561, August 2004. CODEN

JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.544; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.544.

Jeong:2023:SIC

[JLmR+23] Hyundoo Jeong, José Lugo-martinez, Anna Ritz, Yijie Wang, and Chi Zhang. *Special Issue* computational network biology: Modeling, analysis, and control (CNB-MAC) Workshop (2022). *Journal of Computational Biology*, 30(7):737, July 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.29090.hj.

Jiang:2002:GED

[JLMZ02] Tao Jiang, Guohui Lin, Bin Ma, and Kaizhong Zhang. A general edit distance between RNA structures. *Journal of Computational Biology*, 9(2):371–388, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270252935511; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935511.

Jansson:2018:DCR

[JLRS18] Jesper Jansson, Andrzej Lingas, Ramesh Rajaby, and Wing-Kin Sung. Determining the consistency of resolved triplets and fan triplets. *Journal of Computational Biology*, 25(7):740–754, July 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0256; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0256.

Jiang:2024:QMS

[JLSL24] Hao Jiang, Jingxin Liu, You Song, and Jinzhi Lei. Quantitative modeling of stemness in single-cell RNA sequencing data: a nonlinear one-class support vector machine method. *Journal of Computational Biology*, 31(1):41–57, January 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0484; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0484.

Jiang:2008:CRP

[JLY08] Xianyang Jiang, Dominique Lavenier, and Stephen S.-T. Yau. Coding region prediction based on a universal DNA sequence representation method. *Journal of Computational Biology*, 15 (10):1237–1256, December 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0041; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0041`.

Jain:1995:NSC

[JM95] Mudita Jain and Eugene W. Myers. A note on scoring clones given a probe ordering. *Journal of Computational Biology*, 2(1):33–37, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.33; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.33`.

Jain:1997:ACI

[JM97] Mudita Jain and Eugene W. Myers. Algorithms for computing and integrating physical maps using unique probes. *Journal of Computational Biology*, 4(4):449–466, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.449; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.449`.

Jelovic:2018:FSS

[JMEB18] Ana M. Jelovic, Nenad S. Mitic, Samira Eshafah, and Milos V. Beljanski. Finding statistically significant repeats in nucleic acids and proteins. *Journal of Computational Biology*, 25(4):375–387, April 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0046; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0046`.

Jain:2023:HAM

[JMPR23] Shipra Jain, Kawal Preet Kaur Malhotra, Sumeet Patiyal, and Gajendra Pal Singh Raghava. A highly accurate model for screening prostate cancer using propensity index panel of ten

genes. *Journal of Computational Biology*, 30(12):1305–1314, December 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/fpi/10.1089/cmb.2023.0040; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0040.

Jha:2021:SII

[JMR+21] Sumit Kumar Jha, Ion Măndoiu, Sanguthevar Rajasekaran, Pavel Skums, and Alexander Zelikovsky. Special issue: 10th International Computational Advances in Bio and Medical Sciences (ICCABS 2020). *Journal of Computational Biology*, 28 (11):1033–1034, November 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.29048.skj.

Jonsson:2017:VMC

[JÖNK17] Viktor Jonsson, Tobias Österlund, Olle Nerman, and Erik Kristiansson. Variability in metagenomic count data and its influence on the identification of differentially abundant genes. *Journal of Computational Biology*, 24(4):311–326, April 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0180; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0180.

Joshi:1996:SOC

[Jos96] Rajani R. Joshi. A self-organizing cognitive network of antibody repertoire development. *Journal of Computational Biology*, 3(4):529–545, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.529; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.529.

Jasra:2015:BID

[JPB+15] Ajay Jasra, Adam Persing, Alexandros Beskos, Kari Heine, and Maria De Iorio. Bayesian inference for duplication–mutation with complementarity network models. *Journal of Computational Biology*, 22(11):1025–1033, November 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0072; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0072.

Jastrzebski:2023:IRP

[JPLD23] Jan Pawel Jastrzebski, Stefano Pascarella, Aleksandra Lipka, and Slawomir Dorocki. `IncRna`: The R package for optimizing lncRNA identification processes. *Journal of Computational Biology*, 30(12):1322–1326, December 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0091; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0091`.

Jaklic:2006:CCB

[JPR06] Gašper Jaklič, Tomaž Pisanski, and Milan Randić. Characterization of complex biological systems by matrix invariants. *Journal of Computational Biology*, 13(9):1558–1564, November 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1558; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1558`.

Jossinet:2015:P

[JPW15] Fabrice Jossinet, Yann Ponty, and Jérôme Waldispühl. Preface. *Journal of Computational Biology*, 22(3):189, March 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.010P`.

Qiao:2024:FLM

[jQLsY+24] Tian jing Qiao, Feng Li, Sha sha Yuan, Ling yun Dai, and Juan Wang. A fusion learning model based on deep learning for single-cell RNA sequencing data clustering. *Journal of Computational Biology*, 31(6):576–588, June 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Jewett:2012:IIG

[JR12] Ethan M. Jewett and Noah A. Rosenberg. iGLASS: an improvement to the GLASS method for estimating species trees from gene trees. *Journal of Computational Biology*, 19(3):293–315, March 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0231; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0231`.

Johnston:2016:PDP

[JR16] Sean B. Johnston and Ronald T. Raines. PTENpred: a designer protein impact predictor for PTEN-related disorders. *Journal of Computational Biology*, 23(12):969–975, December 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0058; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0058`.

Jansson:2017:MPA

[JR17] Jesper Jansson and Ramesh Rajaby. A more practical algorithm for the rooted triplet distance. *Journal of Computational Biology*, 24(2):106–126, February 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0185; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0185`.

Jun:2009:BNG

[JRH+09] Jin Jun, Paul Ryvkin, Edward Hemphill, Ion Mandoiu, and Craig Nelson. The birth of new genes by RNA- and DNA-mediated duplication during mammalian evolution. *Journal of Computational Biology*, 16(10):1429–1444, October 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0073; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0073`.

Jung:2010:PEM

[JRH+10] Juhyun Jung, Taewoo Ryu, Yongdeuk Hwang, Eunjung Lee, and Doheon Lee. Prediction of extracellular matrix proteins based on distinctive sequence and domain characteristics. *Journal of Computational Biology*, 17(1):97–105, January 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0236; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0236`.

Jun:2009:DMD

[JRHN09] Jin Jun, Paul Ryvkin, Edward Hemphill, and Craig Nelson. Duplication mechanism and disruptions in flanking regions determine the fate of mammalian gene duplicates. *Journal of Computational Biology*, 16(9):1253–1266, September

2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0074; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0074.

Jansson:2019:EAR

[JRS19] Jesper Jansson, Ramesh Rajaby, and Wing-Kin Sung. An efficient algorithm for the rooted triplet distance between galled trees. *Journal of Computational Biology*, 26(9): 893–907, September 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0033; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0033.

Jonsson:2003:AML

[JS03] Henrik Jönsson and Bo Söderberg. An approximate maximum likelihood approach, applied to phylogenetic trees. *Journal of Computational Biology*, 10(5):737–749, October 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703322539060; https://www.liebertpub.com/doi/pdf/10.1089/106652703322539060.

Jean:2009:MSG

[JSN09] Géraldine Jean, David James Sherman, and Macha Nikolski. Mining the semantics of genome super-blocks to infer ancestral architectures. *Journal of Computational Biology*, 16(9):1267–1284, September 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0046; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0046.

Jia:2020:IAM

[JSZ+20] Xiaochen Jia, Yehui Shi, Yuehong Zhu, Wenjing Meng, Lihong He, Yongsheng Jia, and Zhongsheng Tong. Integrated analysis of mRNA–miRNA–lncRNA ceRNA network in human HR+/Her-2- breast cancer and triple negative breast cancer. *Journal of Computational Biology*, 27(7):1055–1066, July 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0152; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0152.

Jiang:2010:PRS

[JTL+10] Minghui Jiang, Pedro J. Tejada, Ramoni O. Lasisi, Shanhong Cheng, and D. Scott Fechser. K-partite RNA secondary structures. *Journal of Computational Biology*, 17(7):915–925, July 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0119; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0119`.

Jevremovic:2010:APE

[JTSB10] Dimitrije Jevremovic, Cong T. Trinh, Friedrich Srienc, and Daniel Boley. On algebraic properties of extreme pathways in metabolic networks. *Journal of Computational Biology*, 17(2):107–119, February 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0020; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0020`.

Just:2001:CCM

[Jus01] Winfried Just. Computational complexity of multiple sequence alignment with SP-Score. *Journal of Computational Biology*, 8(6):615–623, November 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652701753307511; https://www.liebertpub.com/doi/pdf/10.1089/106652701753307511`.

Just:2006:RED

[Jus06] Winfried Just. Reverse engineering discrete dynamical systems from data sets with random input vectors. *Journal of Computational Biology*, 13(8):1435–1456, October 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1435; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1435`.

Jia:2024:III

[JWL24] Jianhua Jia, Genqiang Wu, and Meifang Li. iGly-IDN: Identifying Lysine glycation sites in proteins based on improved DenseNet. *Journal of Computational Biology*, 31 (2):161–174, February 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0112;`

https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0112.

Jiao:2010:EPE

[JZ10] Shuo Jiao and Shunpu Zhang. Estimating the proportion of equivalently expressed genes in microarray data based on transformed test statistics. *Journal of Computational Biology*, 17(2):177–187, February 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0060; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0060.

Jain:2020:CSG

[JZGA20] Chirag Jain, Haowen Zhang, Yu Gao, and Srinivas Aluru. On the complexity of sequence-to-graph alignment. *Journal of Computational Biology*, 27(4):640–654, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0066; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0066.

Jukan:2020:VPC

[JZL+20] Nermin Jukan, David Zagoršek, Julija Lazarevič, Irena Preložnik Zupan, Nataša Debeljak, and Miha Moškon. ViDis: a platform for constructing and sharing of medical algorithms. *Journal of Computational Biology*, 27(6):941–947, June 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0238; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0238.

Jia:2019:IFC

[JZZ+19] Xi Jia, Qian Zhao, Yuanyuan Zhang, Yiping Dong, Li Lei, Ramone A. Williamson, Yutiantian Lei, Xinyue Tan, Dan Zhang, and Jinsong Hu. Identification of a five-CpG signature with diagnostic value in thyroid cancer. *Journal of Computational Biology*, 26(12):1409–1417, December 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0165; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0165.

Koskinen:2015:IDC

[KABH15] Kaisa Koskinen, Petri Auvinen, K. Johanna Björkroth, and Jenni Hultman. Inconsistent denoising and clustering algorithms for amplicon sequence data. *Journal of Computational Biology*, 22(8):743–751, August 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0268; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0268`.

Kim:2017:CVD

[KAC17] Jin Seob Kim, Bijan Afsari, and Gregory S. Chirikjian. Cross-validation of data compatibility between small angle X-ray scattering and cryo-electron microscopy. *Journal of Computational Biology*, 24(1):13–30, January 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0139; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0139`.

Kim:2019:MPP

[KAD+19] Baekdoo Kim, Thahmina Ali, Changsu Dong, Carlos Lijeron, Raja Mazumder, Claudia Wultsch, and Konstantinos Krampis. *miCloud*: a plug-n-play, extensible, on-premises bioinformatics cloud for seamless execution of complex next-generation sequencing data analysis pipelines. *Journal of Computational Biology*, 26(3):280–284, March 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0218; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0218`.

Karp:1995:SDI

[Kar95] Peter D. Karp. A strategy for database interoperation. *Journal of Computational Biology*, 2(4):573–586, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.573; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.573`.

Kato:2009:DPA

[KAS09] Yuki Kato, Tatsuya Akutsu, and Hiroyuki Seki. Dynamic programming algorithms and grammatical modeling for pro-

tein beta-sheet prediction. *Journal of Computational Biology*, 16(7):945–957, July 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0228; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0228`.

Keith:2008:DSR

[KASM08] Jonathan M. Keith, Peter Adams, Stuart Stephen, and John S. Mattick. Delineating slowly and rapidly evolving fractions of the *Drosophila* genome. *Journal of Computational Biology*, 15(4):407–430, May 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0173; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0173`.

Kinsella:2012:CBF

[KB12] Marcus Kinsella and Vineet Bafna. Combinatorics of the breakage–fusion–bridge mechanism. *Journal of Computational Biology*, 19(6):662–678, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0020; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0020`.

Kokas:2019:SNF

[KBČ19] Filip Zavadil Kokáš, Véronique Bergougnoux, and Mária Majeská Čudejková. SATrans: New free available software for annotation of transcriptome and functional analysis of differentially expressed genes. *Journal of Computational Biology*, 26(2):117–123, February 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0149; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0149`.

Kowalczyk:2011:PMT

[KBCBS11] Adam Kowalczyk, Justin Bedo, Thomas Conway, and Bryan Beresford-Smith. The Poisson margin test for normalization-free significance analysis of NGS data. *Journal of Computational Biology*, 18(3):391–400, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0272;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0272.

Kanj:2018:SNN

[KBG18] Sawsan Kanj, Thomas Brüls, and Stéphane Gazut. Shared nearest neighbor clustering in a locality sensitive hashing framework. *Journal of Computational Biology*, 25(2):236–250, February 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0113; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0113.

Kaminski:2007:PGM

[KBJ07] Naftali Kaminski and Ziv Bar-Joseph. A patient-gene model for temporal expression profiles in clinical studies. *Journal of Computational Biology*, 14(3):324–338, April 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0001; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0001.

Kechin:2017:CNT

[KBKF17] Andrey Kechin, Uljana Boyarskikh, Alexander Kel, and Maxim Filipenko. cutPrimers: a new tool for accurate cutting of primers from reads of targeted next generation sequencing. *Journal of Computational Biology*, 24(11):1138–1143, November 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0096; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0096.

Kalhor:2024:RFC

[KBLS24] Reza Kalhor, Guillaume Beslon, Manuel Lafond, and Celine Scornavacca. A rigorous framework to classify the postduplication fate of paralogous genes. *Journal of Computational Biology*, 31(9):815–833, September 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Kalaev:2009:FAA

[KBS09] Maxim Kalaev, Vineet Bafna, and Roded Sharan. Fast and accurate alignment of multiple protein networks. *Journal of Computational Biology*, 16(8):989–999, August 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0136; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0136.

Kaufman:2005:CPA

[KBZ+05] Menachem Kaufman, David Bloch, Naomi Zurgil, Yana Shafran, and Mordechai Deutsch. A cluster pattern algorithm for the analysis of multiparametric cell assays. *Journal of Computational Biology*, 12(7):1014–1028, September 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1014; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1014.

Kelly:1996:BAA

[KC96] Colleen Kelly and Gary A. Churchill. Biases in amino acid replacement matrices and alignment scores due to rate heterogeneity. *Journal of Computational Biology*, 3 (2):307–318, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.307; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.307.

Kim:2018:SPR

[KC18] Jin Seob Kim and Gregory S. Chirikjian. Symmetrical parameterization of rigid body transformations for biomolecular structures. *Journal of Computational Biology*, 25(1):72–88, January 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0166; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0166.

Kellis:2011:P

[KCBJ11] Manolis Kellis, Andrea Califano, and Ziv Bar-Joseph. Preface. *Journal of Computational Biology*, 18(2):131, February 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.005p.

Kazakiewicz:2019:MNB

[KCG+19] Denis Kazakiewicz, Jürgen Claesen, Katarzyna Górczak, Dariusz Plewczynski, and Tomasz Burzykowski. A multivariate

negative-binomial model with random effects for differential gene-expression analysis of correlated mRNA sequencing data. *Journal of Computational Biology*, 26(12):1339–1348, December 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0168; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0168`.

Krishnapuram:2004:JCF

[KCH04] Balaji Krishnapuram, Lawrence Carin, and Alexander J. Hartemink. Joint classifier and feature optimization for comprehensive cancer diagnosis using gene expression data. *Journal of Computational Biology*, 11(2–3):227–242, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Kececioglu:2013:AEP

[KD13] John Kececioglu and Dan DeBlasio. Accuracy estimation and parameter advising for protein multiple sequence alignment. *Journal of Computational Biology*, 20(4):259–279, April 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0007; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0007`.

Kim:2002:SFS

[KDB+02] Seungchan Kim, Edward R. Dougherty, Junior Barrera, Yidong Chen, Michael L. Bittner, and Jeffrey M. Trent. Strong feature sets from small samples. *Journal of Computational Biology*, 9(1):127–146, January 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270252833226; https://www.liebertpub.com/doi/pdf/10.1089/10665270252833226`.

Knuppel:1994:TRP

[KDL+94] R. Knüppel, P. Dietze, W. Lehnberg, K. Frech, and E. Wingender. TRANSFAC retrieval program: a network model database of eukaryotic transcription regulating sequences and proteins. *Journal of Computational Biology*, 1(3):191–198, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.191; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.191`.

Kostem:2013:EIS

[KE13] Emrah Kostem and Eleazar Eskin. Efficiently identifying significant associations in genome-wide association studies. *Journal of Computational Biology*, 20(10):817–830, October 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0087; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0087.

Kearney:1997:SPC

[Kea97] Paul E. Kearney. A six-point condition for ordinal matrices. *Journal of Computational Biology*, 4(2):143–156, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.143; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.143.

Keich:2005:SFA

[Kei05] Uri Keich. sFFT: a faster accurate computation of the p-value of the entropy score. *Journal of Computational Biology*, 12(4):416–430, May 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.416; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.416.

Keith:2006:SEG

[Kei06] Jonathan M. Keith. Segmenting eukaryotic genomes with the generalized Gibbs sampler. *Journal of Computational Biology*, 13(7):1369–1383, September 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1369; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1369.

Kaiser:2015:NAE

[KEL15] Florian Kaiser, Alexander Eisold, and Dirk Labudde. A novel algorithm for enhanced structural motif matching in proteins. *Journal of Computational Biology*, 22(7):698–713, July 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0263; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0263.

Kerr:2003:LMM

[Ker03] M. Kathleen Kerr. Linear models for microarray data analysis: Hidden similarities and differences. *Journal of Computational Biology*, 10(6):891–901, December 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652703322756131; https://www.liebertpub.com/doi/pdf/10.1089/106652703322756131`.

Knapp:2011:ICD

[KFC+11] B. Knapp, S. Frantal, M. Cibena, W. Schreiner, and P. Bauer. Is an intuitive convergence definition of molecular dynamics simulations solely based on the root mean square deviation possible? *Journal of Computational Biology*, 18(8):997–1005, August 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0237; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0237`.

Kooperberg:2002:IBC

[KFDT02] Charles Kooperberg, Thomas G. Fazzio, Jeffrey J. Delrow, and Toshio Tsukiyama. Improved background correction for spotted DNA microarrays. *Journal of Computational Biology*, 9(1):55–66, January 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270252833190; https://www.liebertpub.com/doi/pdf/10.1089/10665270252833190`.

Ku:2004:CLL

[KFR04] Jason Ku, Xiao-Jiang Feng, and Herschel Rabitz. Closed-loop learning control of bio-networks. *Journal of Computational Biology*, 11(4):642–659, August 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.642; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.642`.

Khanghahi:2024:BHO

[KG24] Maryam Jafari Khanghahi and Reza Khoshsiar Ghaziani. Bifurcations and homoclinic orbits of a model consisting of vegetation–prey–predator populations. *Journal of Computational Biology*, 31(11):1118–1145, November 2024. CODEN

JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0485; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0485.

Konopka:2014:ESP

[KGK14] Bogumil M. Konopka, Tomasz Golda, and Małgorzata Kotulska. Evaluating the significance of protein functional similarity based on gene ontology. *Journal of Computational Biology*, 21(11):809–822, November 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0181; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0181.

Kamisetty:2015:LSD

[KGLBK15] Hetunandan Kamisetty, Bornika Ghosh, Christopher James Langmead, and Chris Bailey-Kellogg. Learning sequence determinants of protein:protein interaction specificity with sparse graphical models. *Journal of Computational Biology*, 22(6):474–486, June 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0289; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0289.

Kluge:2009:MEA

[KGN09] Bogusaw Kluge, Anna Gambin, and Wojciech Niemiro. Modeling exopeptidase activity from LC-MS data. *Journal of Computational Biology*, 16(2):395–406, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.22TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.22TT.

Kosesoy:2018:PWS

[KGÖ18] İrfan Kösesoy, Murat Gök, and Cemil Öz. PROSES: a Web server for sequence-based protein encoding. *Journal of Computational Biology*, 25(10):1120–1122, October 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0049; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0049.

Khan:2014:SPE

[Kha14] Abdul Arif Khan. *In Silico* prediction of *Escherichia coli* proteins targeting the host cell nucleus, with special reference to their role in colon cancer etiology. *Journal of Computational Biology*, 21(6):466–475, June 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0001; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0001`.

Kirkpatrick:2010:HIC

[KHK10] Bonnie Kirkpatrick, Eran Halperin, and Richard M. Karp. Haplotype inference in complex pedigrees. *Journal of Computational Biology*, 17(3):269–280, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0174; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0174`.

Kayano:2013:MOA

[KIYM13] Mitsunori Kayano, Seiya Imoto, Rui Yamaguchi, and Satoru Miyano. Multi-omics approach for estimating metabolic networks using low-order partial correlations. *Journal of Computational Biology*, 20(8):571–582, August 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0043; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0043`.

Kong:2022:PDL

[KJmZ+22] Lupeng Kong, Fusong Ju, Wei mou Zheng, Jianwei Zhu, Shiwei Sun, Jinbo Xu, and Dongbo Bu. ProALIGN: Directly learning alignments for protein structure prediction via exploiting context-specific alignment motifs. *Journal of Computational Biology*, 29(2):92–105, February 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0430; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0430`.

Kelley:2011:EBP

[KK11] David R. Kelley and Carl Kingsford. Extracting between-pathway models from E-MAP interactions using expected graph

compression. *Journal of Computational Biology*, 18(3):379–390, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0268; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0268.

Kim:2018:EDS

[KK18] Yoonji Kim and Jaejik Kim. Estimation of dynamic systems for gene regulatory networks from dependent time-course data. *Journal of Computational Biology*, 25(9):987–996, September 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0062; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0062.

Kim:2022:INC

[KK22] Yujung Kim and Jaejik Kim. Identification of new clusters from labeled data using mixture models. *Journal of Computational Biology*, 29(6):585–596, June 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0443; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0443.

Krieger:2023:SHD

[KK23] Spencer Krieger and John Kececioglu. Shortest hyperpaths in directed hypergraphs for reaction pathway inference. *Journal of Computational Biology*, 30(11):1198–1225, November 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0242; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0242.

Krieger:2024:ROM

[KK24] Spencer Krieger and John Kececioglu. Robust optimal metabolic factories. *Journal of Computational Biology*, 31 (10):1045–1086, October 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0748; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0748.

Konagurthu:2015:SSL

[KKA+15] Arun S. Konagurthu, Parthan Kasarapu, Lloyd Allison, James H. Collier, and Arthur M. Lesk. On sufficient statistics of least-squares superposition of vector sets. *Journal of Computational Biology*, 22(6):487–497, June 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0154; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0154`.

Khan:2022:IRA

[KKC+22] Shahbaz Khan, Milla Kortelainen, Manuel Cáceres, Lucia Williams, and Alexandru I. Tomescu. Improving RNA assembly via safety and completeness in flow decompositions. *Journal of Computational Biology*, 29(12):1270–1287, December 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0261; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0261`.

Kanlaya:2023:CDC

[KKe23] Arunothai Kanlaya and Chakkrid Klin-eam. Constructing double cyclic codes over F2+uF2 for DNA codes. *Journal of Computational Biology*, 30(10):1112–1130, October 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0151; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0151`.

Kumari:2018:PRP

[KKK18] Bandana Kumari, Ravindra Kumar, and Manish Kumar. Prediction of rare palmitoylation events in proteins. *Journal of Computational Biology*, 25(9):997–1008, September 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0069; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0069`.

Kim:2020:HMS

[KKM+20] Younhun Kim, Frederic Koehler, Ankur Moitra, Elchanan Mossel, and Govind Ramnarayan. How many subpopulations is too many? Exponential lower bounds for inferring population histories. *Journal of Computational Biology*, 27(4):613–625, April

2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0318; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0318.

Koyuturk:2006:DCI

[KKS+06] Mehmet Koyutürk, Yohan Kim, Shankar Subramaniam, Wojciech Szpankowski, and Ananth Grama. Detecting conserved interaction patterns in biological networks. *Journal of Computational Biology*, 13(7):1299–1322, September 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1299; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1299.

Kang:2015:PAD

[KKS+15] Kyoung-Tak Kang, Sung-Hwan Kim, Juhyun Son, Young Han Lee, and Heoung-Jae Chun. Probabilistic approach for determining the material properties of meniscal attachments *In Vivo* using magnetic resonance imaging and a finite element model. *Journal of Computational Biology*, 22(12):1097–1107, December 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0126; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0126.

Kunev:2022:ASN

[KKS22] Martin Kunev, Petr Kuznetsov, and Denis Sheynikhovich. Agreement in spiking neural networks. *Journal of Computational Biology*, 29(4):358–369, April 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0365; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0365.

Koyuturk:2006:PAP

[KKT+06] Mehmet Koyutürk, Yohan Kim, Umut Topkara, Shankar Subramaniam, Wojciech Szpankowski, and Ananth Grama. Pairwise alignment of protein interaction networks. *Journal of Computational Biology*, 13(2):182–199, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.182;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.182.

Kececioglu:2010:APS

[KKW10] John Kececioglu, Eagu Kim, and Travis Wheeler. Aligning protein sequences with predicted secondary structure. *Journal of Computational Biology*, 17(3):561–580, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0222; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0222.

Kruglyak:1998:FML

[KL98] Leonid Kruglyak and Eric S. Lander. Faster multipoint linkage analysis using Fourier transforms. *Journal of Computational Biology*, 5(1):1–7, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.1; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.1.

Kuo:2011:DDC

[KLC+11] Hsien-Chi Kuo, Po-Yu Lin, Ting-Chiun Chung, Chin-Mei Chao, Liang-Chuan Lai, Mong-Hsun Tsai, and Eric Y. Chuang. DBCAT: Database of CpG islands and analytical tools for identifying comprehensive methylation profiles in cancer cells. *Journal of Computational Biology*, 18(8):1013–1017, August 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0038; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0038.

Kleinberg:1999:EAP

[Kle99] Jon M. Kleinberg. Efficient algorithms for protein sequence design and the analysis of certain evolutionary fitness landscapes. *Journal of Computational Biology*, 6(3–4):387–404, October 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Kirkpatrick:2011:PRU

[KLKH11] Bonnie Kirkpatrick, Shuai Cheng Li, Richard M. Karp, and Eran Halperin. Pedigree reconstruction using identity by descent.

Journal of Computational Biology, 18(11):1481–1493, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0156; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0156.

Kannan:2011:PTA

[KLM11] Lavanya Kannan, Hua Li, and Arcady Mushegian. A polynomial-time algorithm computing lower and upper bounds of the rooted subtree prune and regraft distance. *Journal of Computational Biology*, 18(5):743–757, May 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0045; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0045.

Kist:2018:DMP

[KLO18] Andreas M. Kist, Angelika Lampert, and Andrias O. O'Reilly. DIsulfide mapping PLanner software tool. *Journal of Computational Biology*, 25(4):430–434, April 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0129; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0129.

Kose:2023:GDA

[KLR23] Tunç Başar Köse, Jiarong Li, and Anna Ritz. Growing directed acyclic graphs: Optimization functions for pathway reconstruction algorithms. *Journal of Computational Biology*, 30(7):814–828, July 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0376; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0376.

Kim:2015:SSS

[KLS15] Sera Kim, Kyeongjun Lee, and Hokeun Sun. Statistical selection strategy for risk and protective rare variants associated with complex traits. *Journal of Computational Biology*, 22(11):1034–1043, November 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0091; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0091.

Kim:2013:MDD

[KLV+13] Jaejik Kim, Jiaxu Li, Srirangapatnam G. Venkatesh, Douglas S. Darling, and Grzegorz A. Rempala. Model discrimination in dynamic molecular systems: Application to parotid De-differentiation network. *Journal of Computational Biology*, 20(7):524–539, July 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0222; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0222`.

Koch:1996:AFM

[KLW96] Ina Koch, Thomas Lengauer, and Egon Wanke. An algorithm for finding maximal common subtopologies in a set of protein structures. *Journal of Computational Biology*, 3(2):289–306, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.289; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.289`.

Kent:2006:CSE

[KLZU06] Carmel Kent, Gad M. Landau, and Michal Ziv-Ukelson. On the complexity of sparse exon assembly. *Journal of Computational Biology*, 13(5):1013–1027, June 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1013; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1013`.

Kuwahara:2008:PPT

[KM08] Hiroyuki Kuwahara and Chris J. Myers. Production-passage-time approximation: a new approximation method to accelerate the simulation process of enzymatic reactions. *Journal of Computational Biology*, 15(7):779–792, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0135; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0135`.

Kuhnle:2020:ECC

[KMB+20] Alan Kuhnle, Taher Mun, Christina Boucher, Travis Gagie, Ben Langmead, and Giovanni Manzini. Efficient construc-

tion of a complete index for pan-genomics read alignment. *Journal of Computational Biology*, 27(4):500–513, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0309; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0309`.

Kerr:2000:AVG

[KMC00] M. Kathleen Kerr, Mitchell Martin, and Gary A. Churchill. Analysis of variance for gene expression microarray data. *Journal of Computational Biology*, 7(6):819–837, December 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270050514954; https://www.liebertpub.com/doi/pdf/10.1089/10665270050514954`.

Kshirsagar:2017:MMC

[KMCKS17] Meghana Kshirsagar, Keerthiram Murugesan, Jaime G. Carbonell, and Judith Klein-Seetharaman. Multitask matrix completion for learning protein interactions across diseases. *Journal of Computational Biology*, 24(6):501–514, June 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0201; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0201`.

Karasikov:2020:SBR

[KMJ+20] Mikhail Karasikov, Harun Mustafa, Amir Joudaki, Sara Javadzadeh-no, Gunnar Rätsch, and André Kahles. Sparse binary relation representations for genome graph annotation. *Journal of Computational Biology*, 27(4):626–639, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0324; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0324`.

Khanna:2017:DCA

[KMM17] Radhika Khanna, Sangeeta Mittal, and Sujata Mohanty. Development of computer algorithm for editing of next generation sequencing metagenome data. *Journal of Computational Biology*, 24(9):882–894, September 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0179;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0179.

Karami:2020:NAS

[KMMF20] Amirhossein Karami, Afshin Fayyaz Movaghar, Sabine Mercier, and Louis Ferre. New approximate statistical significance of gapped alignments based on the greedy extension model. *Journal of Computational Biology*, 27(9):1361–1372, September 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0203; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0203.

Kahng:2004:SHD

[KMP+04] Andrew B. Kahng, Ion I. Măndoiu, Pavel A. Pevzner, Sherief Reda, and Alexander Z. Zelikovsky. Scalable heuristics for design of DNA probe arrays. *Journal of Computational Biology*, 11(2–3):429–447, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Kennedy:2008:GED

[KMP08] Justin Kennedy, Ion Măndoiu, and Bogdan Paşaniuc. Genotype error detection using hidden Markov models of haplotype diversity. *Journal of Computational Biology*, 15(9):1155–1171, November 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0133; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0133.

Khodabakhshi:2009:IPF

[KMRG09a] Alireza Hadj Khodabakhshi, Ján Maňuch, Arash Rafiey, and Arvind Gupta. Inverse protein folding in 3D hexagonal prism lattice under HPC model. *Journal of Computational Biology*, 16(6):769–802, June 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0202; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0202.

Khodabakhshi:2009:SSA

[KMRG09b] Alireza Hadj Khodabakhshi, Ján Maňuch, Arash Rafiey, and Arvind Gupta. Stable structure-approximating inverse protein folding in 2D hydrophobic-polar-cysteine (HPC) model.

Journal of Computational Biology, 16(1):19–30, January 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0096; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0096.

Kambhampati:2022:COT

[KMUK22] Sandeep Kambhampati, Sean Murphy, Hideki Uosaki, and Chulan Kwon. Cross-organ transcriptomic comparison reveals universal factors during maturation. *Journal of Computational Biology*, 29(9):1031–1044, September 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0349; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0349.

Kim:2010:WBF

[KMZ+10] Bong-Rae Kim, Timothy McMurry, Wei Zhao, Rongling Wu, and Arthur Berg. Wavelet-based functional clustering for patterns of high-dimensional dynamic gene expression. *Journal of Computational Biology*, 17(8):1067–1080, August 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0270; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0270.

Khandai:2022:DSC

[KNmS+22] Kaustubh Khandai, Cristian Navarro-martinez, Brendan Smith, Rebecca Buonopane, Soyong Ashley Byun, and Murray Patterson. Determining significant correlation between pairs of extant characters in a small parsimony framework. *Journal of Computational Biology*, 29(10):1132–1154, October 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0141; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0141.

Klie:2014:BCE

[KNS14] Sebastian Klie, Zoran Nikoloski, and Joachim Selbig. Biological cluster evaluation for gene function prediction. *Journal of Computational Biology*, 21(6):428–445, June 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/

10.1089/cmb.2009.0129; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0129.

Kong:2007:GCF

[Kon07] Yong Kong. Generalized correlation functions and their applications in selection of optimal multiple spaced seeds for homology search. *Journal of Computational Biology*, 14(2):238–254, March 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0008; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0008.

Kong:2009:SDP

[Kon09a] Yong Kong. Statistical distributions of pyrosequencing. *Journal of Computational Biology*, 16(1):31–42, January 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0106; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0106.

Kong:2009:SDS

[Kon09b] Yong Kong. Statistical distributions of sequencing by synthesis with probabilistic nucleotide incorporation. *Journal of Computational Biology*, 16(6):817–827, June 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0215; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0215.

Kovac:2014:CRP

[Kov14] Jakub Kováč. On the complexity of rearrangement problems under the breakpoint distance. *Journal of Computational Biology*, 21(1):1–15, January 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0004; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0004.

Karp:1996:IAM

[KP96] Peter D. Karp and Suzanne Paley. Integrated access to metabolic and genomic data. *Journal of Computational Biology*, 3(1):191–212, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.191;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.191.

Kellis:2004:MCG

[KPB+04] Manolis Kellis, Nick Patterson, Bruce Birren, Bonnie Berger, and Eric S. Lander. Methods in comparative genomics: Genome correspondence, gene identification and regulatory motif discovery. *Journal of Computational Biology*, 11(2–3):319–355, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Kumar:2022:MLP

[KPP+22] Harshit Kumar, Manjit Panigrahi, Anuradha Panwar, Divya Rajawat, Sonali Sonejita Nayak, K. A. Saravanan, Kaiho Kaisa, Subhashree Parida, Bharat Bhushan, and Triveni Dutt. Machine-learning prospects for detecting selection signatures using population genomics data. *Journal of Computational Biology*, 29(9):943–960, September 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0447; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0447.

Karp:2000:ACD

[KPS00] Richard M. Karp, Itsik Pe'er, and Ron Shamir. An algorithm combining discrete and continuous methods for optical mapping. *Journal of Computational Biology*, 7 (5):745–760, October 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701446189; https://www.liebertpub.com/doi/pdf/10.1089/106652701446189.

Koonin:2011:CPT

[KPW11] Eugene V. Koonin, Pere Puigbò, and Yuri I. Wolf. Comparison of phylogenetic trees and search for a central trend in the "forest of life". *Journal of Computational Biology*, 18(7):917–924, July 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0185; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0185.

Kucherov:2011:RLC

[KPZU11] Gregory Kucherov, Tamar Pinhas, and Michal Ziv-Ukelson. Regular language constrained sequence alignment revisited.

Journal of Computational Biology, 18(5):771–781, May 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0291; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0291.

Karlebach:2024:CMB

[KR24] Guy Karlebach and Peter N. Robinson. Computing minimal Boolean models of gene regulatory networks. *Journal of Computational Biology*, 31(2):117–127, February 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0122; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0122.

Kundeti:2014:BLM

[KRD14] Vamsi Kundeti, Sanguthevar Rajasekaran, and Hieu Dinh. Border length minimization problem on a square array. *Journal of Computational Biology*, 21(6):446–455, June 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0127; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0127.

Kirkpatrick:2012:CPG

[KRF+12] Bonnie Kirkpatrick, Yakir Reshef, Hilary Finucane, Haitao Jiang, Binhai Zhu, and Richard M. Karp. Comparing pedigree graphs. *Journal of Computational Biology*, 19(9):998–1014, September 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0254; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0254.

Kruglyak:1998:MSH

[Kru98] Semyon Kruglyak. Multistage sequencing by hybridization. *Journal of Computational Biology*, 5(1):165–171, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.165; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.165.

Krupska:2017:IOE

[Kru17] Aldona Krupska. Influence of oscillatory enzyme activity on the reaction kinetics: Mathematical model. *Journal of Computational Biology*, 24(10):1065–1070, October 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0001; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0001`.

Kim:1999:ASP

[KS99] Sun Kim and Alberto Maria Segre. AMASS: a structured pattern matching approach to shotgun sequence assembly. *Journal of Computational Biology*, 6(2):163–186, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.163; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.163`.

Karp:2000:AOM

[KS00] Richard M. Karp and Ron Shamir. Algorithms for optical mapping. *Journal of Computational Biology*, 7(1–2):303–316, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Kimmel:2005:BFH

[KS05] Gad Kimmel and Ron Shamir. A block-free hidden Markov model for genotypes and its application to disease association. *Journal of Computational Biology*, 12(10):1243–1260, December 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1243; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1243`.

Konagurthu:2006:OSP

[KS06] Arun S. Konagurthu and Peter J. Stuckey. Optimal sum-of-pairs multiple sequence alignment using incremental Carrillo and Lipman bounds. *Journal of Computational Biology*, 13(3):668–685, April 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.668; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.668`.

Kao:2011:NEM

[KS11] Wei-Chun Kao and Yun S. Song. naiveBayesCall: an efficient model-based base-calling algorithm for high-throughput sequencing. *Journal of Computational Biology*, 18(3):365–377, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0247; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0247`.

Karlebach:2012:CLM

[KS12] Guy Karlebach and Ron Shamir. Constructing logical models of gene regulatory networks by integrating transcription Factor–DNA interactions with expression data: an entropy-based approach. *Journal of Computational Biology*, 19(1):30–41, January 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0100; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0100`.

Kosaraju:1998:AAG

[KSB98] S. Rao Kosaraju, Alejandro A. Schäffer, and Leslie G. Biesecker. Approximation algorithms for a genetic diagnostics problem. *Journal of Computational Biology*, 5(1):9–26, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.9; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.9`.

Koyuturk:2007:ASC

[KSG07] Mehmet Koyutürk, Wojciech Szpankowski, and Ananth Grama. Assessing significance of connectivity and conservation in protein interaction networks. *Journal of Computational Biology*, 14(6):747–764, July 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R014; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R014`.

Kozanitis:2011:CGS

[KSK+11] Christos Kozanitis, Chris Saunders, Semyon Kruglyak, Vineet Bafna, and George Varghese. Compressing genomic sequence fragments using SlimGene. *Journal of Computational*

Biology, 18(3):401–413, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0253; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0253.

Karni:2009:NBM

[KSS09] Shaul Karni, Hermona Soreq, and Roded Sharan. A network-based method for predicting disease-causing genes. *Journal of Computational Biology*, 16(2):181–189, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.05TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.05TT.

Kimura:2009:CRS

[KSSK09] Kouichi Kimura, Yutaka Suzuki, Sumio Sugano, and Asako Koike. Computation of rank and select functions on hierarchical binary string and its application to genome mapping problems for short-read DNA sequences. *Journal of Computational Biology*, 16(11):1601–1613, November 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0146; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0146.

Knill:1996:IPE

[KST96] E. Knill, A. Schliep, and D. C. Torney. Interpretation of pooling experiments using the Markov chain Monte Carlo method. *Journal of Computational Biology*, 3(3):395–406, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.395; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.395.

Shieh:2022:ILP

[kSyPhC+22] Yi kung Shieh, Dao yuan Peng, Yu han Chen, Tsung wei Wu, and Chin Lung Lu. An integer linear programming approach for scaffolding based on exemplar breakpoint distance. *Journal of Computational Biology*, 29(9):961–973, September 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0399; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0399.

Kruglyak:2001:NES

[KT01] Semyon Kruglyak and Haixu Tang. A new estimator of significance of correlation in time series data. *Journal of Computational Biology*, 8(5):463–470, October 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652701753216486; https://www.liebertpub.com/doi/pdf/10.1089/106652701753216486`.

Koepke:2013:EIE

[KT13] Hoyt Koepke and Elizabeth Thompson. Efficient identification of equivalences in dynamic graphs and pedigree structures. *Journal of Computational Biology*, 20(8):551–570, August 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0032; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0032`.

Kavya:2019:SAD

[KTSS19] Vaddadi Naga Sai Kavya, Kshitij Tayal, Rajgopal Srinivasan, and Naveen Sivadasan. Sequence alignment on directed graphs. *Journal of Computational Biology*, 26(1):53–67, January 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0264; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0264`.

Kanhaiya:2020:IDT

[KTT20] Krishna Kanhaiya and Dwitiya Tyagi-Tiwari. Identification of drug targets in breast cancer metabolic network. *Journal of Computational Biology*, 27(6):975–986, June 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0258; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0258`.

Kumar:2022:SIC

[Kum22] Sandeep Kumar. Special issue: Computational intelligence. *Journal of Computational Biology*, 29(6):495–496, June 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.29063.sk`.

Khanin:2008:CMP

[KV08] Raya Khanin and Veronica Vinciotti. Computational modeling of post-transcriptional gene regulation by MicroRNAs. *Journal of Computational Biology*, 15(3):305–316, April 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0184; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0184`.

Kadumuri:2017:LGU

[KV17] Rajashekar Varma Kadumuri and Ramakrishna Vadrevu. LoopX: a graphical user interface-based database for comprehensive analysis and comparative evaluation of loops from protein structures. *Journal of Computational Biology*, 24 (10):1043–1049, October 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0197; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0197`.

Kopp:2019:DMM

[KV19] Wolfgang Kopp and Martin Vingron. DNA motif match statistics without Poisson approximation. *Journal of Computational Biology*, 26(8):846–865, August 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0144; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0144`.

Ke:2023:GBR

[KV23] Ziqi Ke and Haris Vikalo. Graph-based reconstruction and analysis of disease transmission networks using viral genomic data. *Journal of Computational Biology*, 30(7):796–813, July 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0373; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0373`.

Keles:2006:MTM

[KVDC06] Sündüz Keleş, Mark J. Van Der Laan, Sandrine Dudoit, and Simon E. Cawley. Multiple testing methods for ChIP–Chip high density oligonucleotide array data. *Journal of Computational Biology*, 13(3):579–613, April 2006. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.579; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.579.

Kupczok:2008:EAG

[KVK08] Anne Kupczok, Arndt Von Haeseler, and Steffen Klaere. An exact algorithm for the geodesic distance between phylogenetic trees. *Journal of Computational Biology*, 15(6):577–591, July 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0068; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0068.

Kakourou:2014:CAI

[KVM14] Alexia Kakourou, Werner Vach, and Bart Mertens. Combination approaches improve predictive performance of diagnostic rules for mass-spectrometry proteomic data. *Journal of Computational Biology*, 21(12):898–914, December 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0125; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0125.

Khayatian:2024:RFD

[KVZ24] Elahe Khayatian, Gabriel Valiente, and Louxin Zhang. The k-Robinson–Foulds dissimilarity measures for comparison of labeled trees. *Journal of Computational Biology*, 31(4):328–344, April 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0312; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0312.

Khanin:2006:HSF

[KW06] Raya Khanin and Ernst Wit. How scale-free are biological networks. *Journal of Computational Biology*, 13(3):810–818, April 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.810; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.810.

Kannan:2014:ECP

[KW14] Lavanya Kannan and Ward C. Wheeler. Exactly computing the parsimony scores on phylogenetic networks us-

ing dynamic programming. *Journal of Computational Biology*, 21(4):303–319, April 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0134; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0134`. See correction [Ano14].

Kuang:2021:DLS

[KW21] Shuzhen Kuang and Liangjiang Wang. Deep learning of sequence patterns for CCCTC-binding factor-mediated chromatin loop formation. *Journal of Computational Biology*, 28(2):133–145, February 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0225; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0225`.

Kim:2011:BDU

[KWA11] Hoon Kim, John Watkinson, and Dimitris Anastassiou. Biomarker discovery using statistically significant gene sets. *Journal of Computational Biology*, 18(10):1329–1338, October 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0085; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0085`.

Keele:1994:CDM

[KWB+94] J. W. Keele, J. E. Wray, D. W. Behrens, G. A. Rohrer, S. L. F. Sunden, S. M. Kappes, M. D. Bishop, R. T. Stone, L. J. Alexander, and C. W. Beattie. A conceptual database model for genomic research. *Journal of Computational Biology*, 1(1):65–76, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.65; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.65`.

Kirk:2013:BRP

[KWB+13] Paul Kirk, Aviva Witkover, Charles R. M. Bangham, Sylvia Richardson, Alexandra M. Lewin, and Michael P. H. Stumpf. Balancing the robustness and predictive performance of biomarkers. *Journal of Computational Biology*, 20(12): 979–989, December 2013. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0018; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0018.

Kothiyal:2019:MIS

[KWBN19] Prachi Kothiyal, Wendy S. W. Wong, Dale L. Bodian, and John E. Niederhuber. Mendelian inconsistent signatures from 1314 ancestrally diverse family trios distinguish biological variation from sequencing error. *Journal of Computational Biology*, 26(5):405–419, May 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0253; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0253.

Kovac:2011:RDM

[KWBS11] Jakub Kováč, Robert Warren, Marília D. V. Braga, and Jens Stoye. Restricted DCJ model: Rearrangement problems with chromosome reincorporation. *Journal of Computational Biology*, 18(9):1231–1241, September 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0116; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0116.

Karakas:2010:BCL

[KWM10] Mert Karakaş, Nils Woetzel, and Jens Meiler. BCL::Contact — low confidence fold recognition hits boost protein contact prediction and *De Novo* structure determination. *Journal of Computational Biology*, 17(2):153–168, February 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0030; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0030.

Kim:2006:PMAa

[KX06a] Nak-Kyeong Kim and Jun Xie. Protein multiple alignment incorporating primary and secondary structure information. *Journal of Computational Biology*, 13(9):1615–1629, November 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1615; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1615.

Kim:2006:PMAb

[KX06b] Nak-Kyeong Kim and Jun Xie. Protein multiple alignment incorporating primary and secondary structure information. *Journal of Computational Biology*, 13(10):1735–1748, December 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1735; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1735`.

Kim:2014:EGS

[KX14] Seyoung Kim and Eric P. Xing. Exploiting genome structure in association analysis. *Journal of Computational Biology*, 21(4):345–360, April 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0224; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0224`.

Kamisetty:2008:FEE

[KXL08] Hetunandan Kamisetty, Eric P. Xing, and Christopher J. Langmead. Free energy estimates of all-atom protein structures using generalized belief propagation. *Journal of Computational Biology*, 15(7):755–766, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0131; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0131`.

Kang:2010:DPA

[KYSE10] Eun Yong Kang, Chun Ye, Ilya Shpitser, and Eleazar Eskin. Detecting the presence and absence of causal relationships between expression of yeast genes with very few samples. *Journal of Computational Biology*, 17(3):533–546, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0176; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0176`.

Kang:2010:EAM

[KZE10] Hyun Min Kang, Noah A. Zaitlen, and Eleazar Eskin. EMINIM: an adaptive and memory-efficient algorithm for genotype imputation. *Journal of Computational Biology*, 17(3):547–560,

March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0199; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0199.

Lipson:2006:ECI

[LABD+06] Doron Lipson, Yonatan Aumann, Amir Ben-Dor, Nathan Linial, and Zohar Yakhini. Efficient calculation of interval scores for DNA copy number data analysis. *Journal of Computational Biology*, 13(2):215–228, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.215; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.215.

Lavallee-Adam:2010:DLR

[LACB10] Mathieu Lavallée-Adam, Benoit Coulombe, and Mathieu Blanchette. Detection of locally over-represented GO terms in protein-protein interaction networks. *Journal of Computational Biology*, 17(3):443–457, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0165; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0165.

Levtov:2014:DNU

[LAF+14] Nissan Levtov, Sandeep Amberkar, Zakharia M. Frenkel, Lars Kaderali, and Zeev Volkovich. Detecting non-uniform clusters in large-scale interaction graphs. *Journal of Computational Biology*, 21(2):173–183, February 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0095; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0095.

Lai:2012:CPA

[Lai12] Yinglei Lai. Change-point analysis of paired allele-specific copy number variation data. *Journal of Computational Biology*, 19(6):679–693, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0031; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0031.

Li:2009:BAP

[LAL+09] Yong Fuga Li, Randy J. Arnold, Yixue Li, Predrag Radivojac, Quanhu Sheng, and Haixu Tang. A Bayesian approach to protein inference problem in shotgun proteomics. *Journal of Computational Biology*, 16(8):1183–1193, August 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0018; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0018`.

Lam:2003:PAS

[LAP03] Fumei Lam, Marina Alexandersson, and Lior Pachter. Picking alignments from (Steiner) trees. *Journal of Computational Biology*, 10(3–4):509–520, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Lartillot:2006:CGS

[Lar06] Nicolas Lartillot. Conjugate Gibbs sampling for Bayesian phylogenetic models. *Journal of Computational Biology*, 13 (10):1701–1722, December 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1701; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1701`.

Lathrop:1999:ALG

[Lat99] Richard H. Lathrop. An anytime local-to-global optimization algorithm for protein threading in o(m^2 $\tilde{n}^2$) space. *Journal of Computational Biology*, 6(3–4):405–418, October 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Ligabue-Braun:2018:EPR

[LBBV+18] Rodrigo Ligabue-Braun, Bruno Borguesan, Hugo Verli, Mathias J. Krause, and Márcio Dorn. Everyone is a protagonist: Residue conformational preferences in high-resolution protein structures. *Journal of Computational Biology*, 25(4):451–465, April 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0182; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0182`.

LopezGarciaDeLomana:2010:SAG

[LBDVF10] Adrián López García De Lomana, Qasim K. Beg, G. De Fabritiis, and Jordi Villà-Freixa. Statistical analysis of global connectivity and activity distributions in cellular networks. *Journal of Computational Biology*, 17(7):869–878, July 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0240; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0240`.

Lajoie:2007:DIH

[LBEMG07] Mathieu Lajoie, Denis Bertrand, Nadia El-Mabrouk, and Olivier Gascuel. Duplication and inversion history of a tandemly repeated genes family. *Journal of Computational Biology*, 14(4):462–478, May 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.A007; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.A007`.

Lin:2011:LCS

[LBJM11] Tien-Ho Lin, Ziv Bar-Joseph, and Robert F. Murphy. Learning cellular sorting pathways using protein interactions and sequence motifs. *Journal of Computational Biology*, 18(11):1709–1722, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0193; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0193`.

Leng:1994:PSS

[LBN94] Bing Leng, Bruce G. Buchanan, and Hugh B. Nicholas. Protein secondary structure prediction using two-level case-based reasoning. *Journal of Computational Biology*, 1(1):25–38, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.25; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.25`.

Lam:2017:EVI

[LBSB17] Ham Ching Lam, Xuan Bi, Srinand Sreevatsan, and Daniel Boley. Evolution and vaccination of influenza virus. *Journal of Computational Biology*, 24(8):787–798, August 2017.

CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0025; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0025.

Li:2011:FNO

[LBXL11] Shuai Cheng Li, Dongbo Bu, Jinbo Xu, and Ming Li. Finding nearly optimal GDT scores. *Journal of Computational Biology*, 18(5):693–704, May 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0123; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0123.

Liu:2003:CCA

[LC03a] Agatha H. Liu and Andrea Califano. CASTOR: Clustering algorithm for sequence taxonomical organization and relationships. *Journal of Computational Biology*, 10(1):21–45, February 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703763255651; https://www.liebertpub.com/doi/pdf/10.1089/106652703763255651.

Lu:2003:SAN

[LC03b] Bingwen Lu and Ting Chen. A suboptimal algorithm for *De Novo* peptide sequencing via tandem mass spectrometry. *Journal of Computational Biology*, 10(1):1–12, February 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703763255633; https://www.liebertpub.com/doi/pdf/10.1089/106652703763255633.

Lacey:2009:SEP

[LC09] Michelle R. Lacey and Jason Calmes. A sharp error probability estimate for the reconstruction of phylogenetic quartets by the four-point method. *Journal of Computational Biology*, 16(3):443–456, March 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0123; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0123.

Lopes:2011:GEC

[LCD11] Fabrício M. Lopes, Roberto M. Cesar, Jr., and Luciano Da F.Costa. Gene expression complex networks: Synthesis, identification, and analysis. *Journal of Computational Biology*, 18(10):1353–1367, October 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0118; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0118`.

Llados:2018:SCC

[LCG18] Jordi Lladós, Fernando Cores, and Fernando Guirado. Scalable consistency in T-coffee through Apache Spark and Cassandra database. *Journal of Computational Biology*, 25(8):894–906, August 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0084; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0084`.

Li:2022:TLB

[LCG+22] Hongjia Li, Ge Chen, Shan Gao, Jintao Li, Xiaohua Wan, and Fa Zhang. A transfer learning-based classification model for particle pruning in cryo-electron microscopy. *Journal of Computational Biology*, 29(10):1117–1131, October 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0101; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0101`.

Li:2023:AST

[LCG+23] Yi Li, Mandy Chen, Joshy George, Edison T. Liu, and R. Krishna Murthy Karuturi. Adaptive sentinel testing in workplace for COVID-19 pandemic. *Journal of Computational Biology*, 30(4):376–390, April 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0291; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0291`.

Liu:2009:CGM

[LCGW09] Yan Liu, Jaime Carbonell, Vanathi Gopalakrishnan, and Peter Weigele. Conditional graphical models for protein structural motif recognition. *Journal of Computational Biol-*

ogy, 16(5):639–657, May 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0176; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0176.

Lv:2017:ATF

[LCL+17] Shengqing Lv, Yimin Chen, Zeyu Li, Jiahui Lu, Mingke Gao, and Rongrong Lu. Application of time-frequency domain transform to three-dimensional interpolation of medical images. *Journal of Computational Biology*, 24(11):1112–1124, November 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0038; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0038.

Li:2016:DFS

[LCW16] Yifeng Li, Chih-Yu Chen, and Wyeth W. Wasserman. Deep feature selection: Theory and application to identify enhancers and promoters. *Journal of Computational Biology*, 23(5):322–336, May 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0189; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0189.

Liu:2006:PFR

[LCWG06] Yan Liu, Jaime Carbonell, Peter Weigele, and Vanathi Gopalakrishnan. Protein fold recognition using segmentation conditional random fields (SCRFs). *Journal of Computational Biology*, 13(2):394–406, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.394; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.394.

Leung:2005:NCP

[LCXC05] Ming-Ying Leung, Kwok Pui Choi, Aihua Xia, and Louis H. Y. Chen. Nonrandom clusters of palindromes in herpesvirus genomes. *Journal of Computational Biology*, 12(3):331–354, April 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.331; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.331.

Leung:2005:FMI

[LCY+05] Henry C. M. Leung, Francis Y. L. Chin, S. M. Yiu, Roni Rosenfeld, and W. W. Tsang. Finding motifs with insufficient number of strong binding sites. *Journal of Computational Biology*, 12(6):686–701, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.686; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.686`.

Lubomirski:2007:CAA

[LDB+07] Mariusz Lubomirski, Michael R. D'Andrea, Stanley M. Belkowski, Javier Cabrera, James M. Dixon, and Dhammika Amaratunga. A consolidated approach to analyzing data from high-throughput protein microarrays with an application to immune response profiling in humans. *Journal of Computational Biology*, 14(3):350–359, April 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0116; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0116`.

Li:2022:UTU

[LDBj22] Dongshunyi Li, Jun Ding, and Ziv Bar-joseph. UNIFAN: a tool for unsupervised single-cell clustering and annotation. *Journal of Computational Biology*, 29(11):1229–1232, November 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0251; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0251`.

Li:2012:AIF

[LDLZ12] Wenyuan Li, Chao Dai, Chun-Chi Liu, and Xianghong Jasmine Zhou. Algorithm to identify frequent coupled modules from two-layered network series: Application to study transcription and splicing coupling. *Journal of Computational Biology*, 19(6):710–730, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0025; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0025`.

Lavi:2012:NIC

[LDS12] Ofer Lavi, Gideon Dror, and Ron Shamir. Network-induced classification kernels for gene expression profile analysis. *Journal of Computational Biology*, 19(6):694–709, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0065; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0065`.

Lee:1998:ERS

[LDW98] Jae K. Lee, Vlado Dančík, and Michael S. Waterman. Estimation for restriction sites observed by optical mapping using reversible-jump Markov chain Monte Carlo. *Journal of Computational Biology*, 5(3):505–515, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.505; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.505`.

Liu:2014:WMM

[LDW+14] Lizhen Liu, Xuemin Dai, Hanshi Wang, Wei Song, and Jingli Lu. A weighted multipath measurement based on gene ontology for estimating gene products similarity. *Journal of Computational Biology*, 21(12):964–974, December 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0143; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0143`.

Lengauer:2002:PSR

[Len02] Thomas Lengauer. Preface: Special RECOMB 2001 issue. *Journal of Computational Biology*, 9(2):147–148, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/10665270252935386`.

Letovsky:1995:BIM

[Let95] Stanley Letovsky. Beyond the information maze. *Journal of Computational Biology*, 2(4):539–546, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.539; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.539`.

Lilien:2003:PDC

[LFD03] Ryan H. Lilien, Hany Farid, and Bruce R. Donald. Probabilistic disease classification of expression-dependent proteomic data from mass spectrometry of human serum. *Journal of Computational Biology*, 10(6):925–946, December 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652703322756159; https://www.liebertpub.com/doi/pdf/10.1089/106652703322756159`.

Li:2011:ILR

[LFJ11] Wei Li, Jianxing Feng, and Tao Jiang. IsoLasso: a LASSO regression approach to RNA-Seq based transcriptome assembly. *Journal of Computational Biology*, 18(11):1693–1707, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0171; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0171`.

Liu:1998:DCS

[LFT+98] Qinghua Liu, Anthony G. Frutos, Andrew J. Thiel, Robert M. Corn, and Lloyd M. Smith. DNA computing on surfaces: Encoding information at the single base level. *Journal of Computational Biology*, 5(2):269–278, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.269; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.269`.

Leibovich:2022:ODS

[LG22] Zehavit Leibovich and Ilan Gronau. Optimal design of synthetic DNA sequences without unwanted binding sites. *Journal of Computational Biology*, 29(9):974–986, September 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0417; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0417`.

Liu:2009:SPG

[LGC+09] Zhenqiu Liu, Ronald B. Gartenhaus, Xue-Wen Chen, Charles D. Howell, and Ming Tan. Survival prediction and gene identification with penalized global AUC maximization. *Journal of Computational Biology*, 16(12):1661–1670, December

2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0188; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0188.

Li:2010:EEC

[LGD+10] Zengti Li, Suogang Gao, Hongjie Du, Feng Zou, and Weili Wu. Efficient error-correcting pooling designs constructed from pseudo-symplectic spaces over a finite field. *Journal of Computational Biology*, 17(10):1413–1423, October 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0206; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0206.

Li:2019:IKB

[LGD+19] Feng Li, Peiyuan Guo, Keqin Dong, Peng Guo, Haoyuan Wang, and Xianqiang Lv. Identification of key biomarkers and potential molecular mechanisms in renal cell carcinoma by bioinformatics analysis. *Journal of Computational Biology*, 26(11):1278–1295, November 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0145; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0145.

Liu:2020:CRF

[LGS20] Xiyuan Liu, Di Gao, and Gang Shen. Conditional random fields with least absolute shrinkage and selection operator to classifying the barley genes based on expression level affected by the fungal infection. *Journal of Computational Biology*, 27(11):1581–1594, November 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0428; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0428.

Lu:2003:TCO

[LH03] Wei-Fu Lu and Wen-Lian Hsu. A test for the consecutive ones property on noisy data — application to physical mapping and sequence assembly. *Journal of Computational Biology*, 10(5):709–735, October 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.

liebertpub.com/doi/abs/10.1089/106652703322539051; https://www.liebertpub.com/doi/pdf/10.1089/106652703322539051.

Libeskind-Hadas:2024:PDP

[LH24] Ran Libeskind-Hadas. Pairwise distances and the problem of multiple optima. *Journal of Computational Biology*, 31(7):638–650, July 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Ljungberg:2002:EAQ

[LHC02] Kajsa Ljungberg, Sverker Holmgren, and Örjan Carlborg. Efficient algorithms for quantitative trait loci mapping problems. *Journal of Computational Biology*, 9(6):793–804, December 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270260518272; https://www.liebertpub.com/doi/pdf/10.1089/10665270260518272.

Libeskind-Hadas:2009:CCR

[LHC09] Ran Libeskind-Hadas and Michael A. Charleston. On the computational complexity of the reticulate cophylogeny reconstruction problem. *Journal of Computational Biology*, 16(1):105–117, January 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0084; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0084.

Liu:2019:CAC

[LHC19] Bao-Xinzi Liu, Guan-Jiang Huang, and Hai-Bo Cheng. Comprehensive analysis of core genes and potential mechanisms in rectal cancer. *Journal of Computational Biology*, 26(11):1262–1277, November 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0073; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0073.

Lobo:2016:MMC

[LHL16] Daniel Lobo, Jennifer Hammelman, and Michael Levin. MoCha: Molecular characterization of unknown pathways. *Journal of Computational Biology*, 23(4):291–297, April 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0211; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0211.

Lee:2022:RNM

[LHW+22] Sunho Lee, Seokchol Hong, Jonathan Woo, Jae hak Lee, Kyunghee Kim, Lucia Kim, Kunsoo Park, and Jongsun Jung. RDscan: a new method for improving germline and somatic variant calling based on read depth distribution. *Journal of Computational Biology*, 29(9):987–1000, September 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0269; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0269.

Ling:2008:EIM

[LHXH08] Xu Ling, Xin He, Dong Xin, and Jiawei Han. Efficiently identifying max-gap clusters in pairwise genome comparison. *Journal of Computational Biology*, 15(6):593–609, July 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0010; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0010.

Li:2008:PSS

[Li08] Jing Li. Prioritize and select SNPs for association studies with multi-stage designs. *Journal of Computational Biology*, 15(3):241–257, April 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0090; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0090.

Li:2009:GGA

[Li09] Leping Li. GADEM: a genetic algorithm guided formation of spaced dyads coupled with an EM algorithm for motif discovery. *Journal of Computational Biology*, 16(2):317–329, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.16TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.16TT.

Liebermeister:2005:PPC

[Lie05] Wolfram Liebermeister. Predicting physiological concentrations of metabolites from their molecular structure. *Journal of Computational Biology*, 12(10):1307–1315, December 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1307; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1307`.

Lippert:2005:SEW

[Lip05] Ross A. Lippert. Space-efficient whole genome comparisons with Burrows–Wheeler transforms. *Journal of Computational Biology*, 12(4):407–415, May 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.407; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.407`.

Li:2005:CEK

[LJ05a] Haifeng Li and Tao Jiang. A class of edit kernels for SVMs to predict translation initiation sites in eukaryotic mRNAs. *Journal of Computational Biology*, 12(6):702–718, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.702; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.702`.

Li:2005:CMR

[LJ05b] Jing Li and Tao Jiang. Computing the minimum recombinant haplotype configuration from incomplete genotype data on a pedigree by integer linear programming. *Journal of Computational Biology*, 12(6):719–739, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.719; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.719`.

Li:2020:DTI

[LJCZ20] Baoshan Li, Yi Jiang, Jingxin Chu, and Qian Zhou. Drug-target interaction network analysis of gene-phenotype connectivity maintained by genistein. *Journal of Computational Biology*, 27(12):1678–1687, December 2020. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0443; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0443.

Laserson:2011:GNA

[LJK11] Jonathan Laserson, Vladimir Jojic, and Daphne Koller. Genovo: *De Novo* assembly for metagenomes. *Journal of Computational Biology*, 18(3):429–443, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0244; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0244.

Leelananda:2016:PDS

[LJK16] Sumudu P. Leelananda, Robert L. Jernigan, and Andrzej Kloczkowski. Predicting designability of small proteins from graph features of contact maps. *Journal of Computational Biology*, 23(5):400–411, May 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0209; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0209.

Liu:2020:MSB

[LJL+20] Lixin Liu, Haitao Jiang, Peiqiang Liu, Binhai Zhu, and Daming Zhu. Maximum stacking base pairs: Hardness and approximation by nonlinear linear programming-rounding. *Journal of Computational Biology*, 27(2):200–211, February 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0288; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0288.

Li:2020:PNA

[LJP20] Lei Li, Linhua Jiang, and Sihua Peng. Protein network analysis of the fifth chromosome of zebrafish. *Journal of Computational Biology*, 27(5):729–737, May 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0157; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0157.

Lee:2024:GSM

[LK24] Hajoung Lee and Jaejik Kim. A gene selection method considering measurement errors. *Journal of Computational Biology*, 31(1):71–82, January 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0041; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0041`.

Laimighofer:2016:UPF

[LKBT16] Michael Laimighofer, Jan Krumsiek, Florian Buettner, and Fabian J. Theis. Unbiased prediction and feature selection in high-dimensional survival regression. *Journal of Computational Biology*, 23(4):279–290, April 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0192; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0192`.

Liu:2021:NFS

[LKC21] Shaoxun Liu, Yi Kou, and Lin Chen. Novel few-shot learning neural network for predicting carbohydrate-active enzyme affinity toward fructo-oligosaccharides. *Journal of Computational Biology*, 28(12):1208–1218, December 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0091; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0091`.

Li:2021:NRL

[LKL21] Caesar Z. Li, Eric S. Kawaguchi, and Gang Li. A new ℓ_0-regularized log-linear Poisson graphical model with applications to RNA sequencing data. *Journal of Computational Biology*, 28(9):880–891, September 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0558; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0558`.

Li:2004:HRS

[LKW04] Lei M. Li, Jong Hyun Kim, and Michael S. Waterman. Haplotype reconstruction from SNP alignment. *Journal of Computational Biology*, 11(2–3):505–516, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Li:2005:EBP

[LL05a] Lei M. Li and Henry Horng-Shing Lu. Explore biological pathways from noisy array data by directed acyclic Boolean networks. *Journal of Computational Biology*, 12 (2):170–185, March 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.170; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.170`.

Liu:2005:FCB

[LL05b] Jian Liu and Ming Li. Finding cancer biomarkers from mass spectrometry data by decision lists. *Journal of Computational Biology*, 12(7):971–979, September 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.971; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.971`.

Li:2011:HRL

[LL11] Xin Li and Jing Li. Haplotype reconstruction in large pedigrees with untyped individuals through IBD inference. *Journal of Computational Biology*, 18(11):1411–1421, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0167; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0167`.

Li:2019:ICG

[LL19a] Qi Li and Zhengqiang Luo. Identification of candidate genes for skeletal muscle injury prevention in two different types. *Journal of Computational Biology*, 26(10):1080–1089, October 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0022; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0022`.

Li:2019:TRN

[LL19b] Qi Li and Zhengqiang Luo. Transcriptional regulatory network analysis to reveal the key genes involved in skeletal muscle injury. *Journal of Computational Biology*, 26(10):1090–1099, October 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/`

abs/10.1089/cmb.2019.0025; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0025.

Liu:2019:KGI

[LL19c] Xinxin Liu and Xinqiang Li. Key genes involved in diabetic nephropathy investigated by microarray analysis. *Journal of Computational Biology*, 26(12):1438–1447, December 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0182; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0182.

Liu:2023:SJS

[LL23] Yi Liu and Gang Li. Sure joint screening for high dimensional Cox's proportional hazards model under the case-cohort design. *Journal of Computational Biology*, 30(6):663–677, June 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0416; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0416.

Lin:2005:EAS

[LLCT05] Ying Chih Lin, Chin Lung Lu, Hwan-You Chang, and Chuan Yi Tang. An efficient algorithm for sorting by block-interchanges and its application to the evolution of vibrio species. *Journal of Computational Biology*, 12(1):102–112, February 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.102; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.102.

Liu:2016:SIC

[LLD+16] Zhenqiu Liu, Shili Lin, Nan Deng, Dermot P. B. McGovern, and Steven Piantadosi. Sparse inverse covariance estimation with L_0 penalty for network construction with omics data. *Journal of Computational Biology*, 23(3):192–202, March 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0102; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0102.

Lei:2020:TCN

[LLG+20] Haoyun Lei, Bochuan Lyu, E. Michael Gertz, Alejandro A. Schäffer, Xulian Shi, Kui Wu, Guibo Li, Liqin Xu, Yong

Hou, Michael Dean, and Russell Schwartz. Tumor copy number deconvolution integrating bulk and single-cell sequencing data. *Journal of Computational Biology*, 27(4):565–598, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0302; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0302`.

Lo:2019:IPL

[LLJS19] Shih-Chiang Lo, Feng-You Liu, Wun-Sin Jhang, and Che-Chi Shu. The insight into protein-ligand interactions, a novel way of buffering protein noise in gene expression. *Journal of Computational Biology*, 26(1):86–95, January 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0103; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0103`.

Lee:2016:ENR

[LLKX16] Seunghak Lee, Aurélie Lozano, Prabhanjan Kambadur, and Eric P. Xing. An efficient nonlinear regression approach for genome-wide detection of marginal and interacting genetic variations. *Journal of Computational Biology*, 23(5):372–389, May 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0202; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0202`.

Lu:2020:TSE

[LLL+20] Ying Lu, Qixiu Lu, Houlin Liu, Jixiang Yu, Chunlei Xin, Yingping Liu, Yanfang Liu, and Linlin Fan. Time-series expression analysis of epidermal stem cells from high fat diet mice. *Journal of Computational Biology*, 27(5):769–778, May 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0172; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0172`.

Lam:2011:GAD

[LLS11a] Fumei Lam, Charles H. Langley, and Yun S. Song. On the genealogy of asexual diploids. *Journal of Computational Biology*, 18(3):415–428, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0270;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0270.

Li:2011:FMM

[LLS11b] Meng-Rong Li, Yu-Ju Lin, and Tzong-Hann Shieh. The flux model of the movement of tumor cells and healthy cells using a system of nonlinear heat equations. *Journal of Computational Biology*, 18(12):1831–1839, December 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0050; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0050.

Li:2019:DSF

[LLS+19] Huiyu Li, Sheng-Jun Li, Junliang Shang, Jin-Xing Liu, and Chun-Hou Zheng. A dynamic scale-free network particle swarm optimization for extracting features on multi-omics data. *Journal of Computational Biology*, 26(8):769–781, August 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0185; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0185.

Lee:2019:RBN

[LLSH19] Kyu Min Lee, Minhyeok Lee, Junhee Seok, and Sung Won Han. Regression-based network estimation for high-dimensional genetic data. *Journal of Computational Biology*, 26(4):336–349, April 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0225; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0225.

Liu:2006:GWT

[LLT06] Zhenqiu Liu, Shili Lin, and Ming Tan. Genome-wide tagging SNPs with entropy-based Monte Carlo method. *Journal of Computational Biology*, 13(9):1606–1614, November 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1606; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1606.

Lv:2025:CCM

[LLT+25] Ya Lv, Jin Liu, Xu Tian, Pei Yang, and Yi Pan. CFINet: Cross-modality MRI feature interaction network for pseudopro-

gression prediction of glioblastoma. *Journal of Computational Biology*, 32(2):212–224, February 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0518; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0518.

Li:2003:IPS

[LLW03] Xueliang Li, Zimao Li, and Lusheng Wang. The inverse problems for some topological indices in combinatorial chemistry. *Journal of Computational Biology*, 10(1): 47–55, February 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703763255660; https://www.liebertpub.com/doi/pdf/10.1089/106652703763255660.

Liu:2018:SWF

[LLW18] Qie Liu, Min Liu, and Wenfa Wu. Strong/weak feature recognition of promoters based on position weight matrix and ensemble set-valued models. *Journal of Computational Biology*, 25(10):1152–1160, October 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0067; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0067.

Li:2020:RMR

[LLW+20] Zhicheng Li, Shijian Li, Xian Wei, Xubiao Peng, and Qing Zhao. Recovering the missing regions in crystal structures from the nuclear magnetic resonance measurement data using matrix completion method. *Journal of Computational Biology*, 27(5):709–717, May 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0107; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0107.

Li:2019:SAS

[LLWZ19] Zhicheng Li, Shijian Li, Xian Wei, and Qing Zhao. Scaled alternating steepest descent algorithm applied for protein structure determination from nuclear magnetic resonance data. *Journal of Computational Biology*, 26(9):1020–1029, September 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0013; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0013.

Liu:2019:RSD

[LLZ19] Huan Liu, Li Liu, and Hong Zhu. The role of significantly deregulated MicroRNAs in recurrent cervical cancer based on bioinformatic analysis of the cancer genome atlas data. *Journal of Computational Biology*, 26(4):387–395, April 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0241; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0241.

Li:2003:SIM

[LM03] Jia Li and Webb Miller. Significance of interspecies matches when evolutionary rate varies. *Journal of Computational Biology*, 10(3–4):537–554, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Lin:2011:NGE

[LM11] Yu Lin and Bernard M. E. Moret. A new genomic evolutionary model for rearrangements, duplications, and losses that applies across eukaryotes and prokaryotes. *Journal of Computational Biology*, 18(9):1055–1064, September 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0098; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0098.

Lijoi:2008:BNA

[LMP08] Antonio Lijoi, Ramsés H. Mena, and Igor Prünster. A Bayesian nonparametric approach for comparing clustering structures in EST libraries. *Journal of Computational Biology*, 15(10):1315–1327, December 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0043; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0043.

Leung:1996:USD

[LMS96] Ming-Ying Leung, Genevieve M. Marsh, and Terence P. Speed. Over- and underrepresentation of short DNA words

in herpesvirus genomes. *Journal of Computational Biology*, 3(3):345–360, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.345; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.345`.

Lunter:2003:EAS

[LMSH03] G. A. Lunter, I. Miklós, Y. S. Song, and J. Hein. An efficient algorithm for statistical multiple alignment on arbitrary phylogenetic trees. *Journal of Computational Biology*, 10(6):869–889, December 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652703322756122; https://www.liebertpub.com/doi/pdf/10.1089/106652703322756122`.

Lin:2001:AAS

[LMT01] Kuang Lin, Alex C. W. May, and William R. Taylor. Amino acid substitution matrices from an artificial neural network model. *Journal of Computational Biology*, 8(5):471–481, October 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652701753216495; https://www.liebertpub.com/doi/pdf/10.1089/106652701753216495`.

Lippert:2005:SEC

[LMW05] Ross A. Lippert, Clark M. Mobarry, and Brian P. Walenz. A space-efficient construction of the Burrows–Wheeler transform for genomic data. *Journal of Computational Biology*, 12(7):943–951, September 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.943; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.943`.

Legried:2021:PTS

[LMWR21] Brandon Legried, Erin K. Molloy, Tandy Warnow, and Sébastien Roch. Polynomial-time statistical estimation of species trees under gene duplication and loss. *Journal of Computational Biology*, 28(5):452–468, May 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Liben-Nowell:2001:SSD

[LN01] David Liben-Nowell. On the structure of syntenic distance. *Journal of Computational Biology*, 8(1):53–67, February 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652701300099092; https://www.liebertpub.com/doi/pdf/10.1089/106652701300099092`.

Liao:2003:CPS

[LN03] Li Liao and William Stafford Noble. Combining pairwise sequence similarity and support vector machines for detecting remote protein evolutionary and structural relationships. *Journal of Computational Biology*, 10(6):857–868, December 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652703322756113; https://www.liebertpub.com/doi/pdf/10.1089/106652703322756113`.

Leibowitz:2001:MGE

[LNW01] Nathaniel Leibowitz, Ruth Nussinov, and Haim J. Wolfson. MUSTA — a general, efficient, automated method for multiple structure alignment and detection of common motifs: Application to proteins. *Journal of Computational Biology*, 8(2):93–121, April 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652701300312896; https://www.liebertpub.com/doi/pdf/10.1089/106652701300312896`.

Lyngso:2000:RPP

[LP00] Rune B. Lyngsø and Christian N. S. Pedersen. RNA pseudoknot prediction in energy-based models. *Journal of Computational Biology*, 7(3–4):409–427, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Lorenz:2008:ARS

[LPC08] W. A. Lorenz, Y. Ponty, and P. Clote. Asymptotics of RNA shapes. *Journal of Computational Biology*, 15(1):31–63, January 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0153; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0153`.

Lee:2014:DSV

[LPFT14] Heewook Lee, Ellen Popodi, Patricia L. Foster, and Haixu Tang. Detection of structural variants involving repetitive regions in the reference genome. *Journal of Computational Biology*, 21(3):219–233, March 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0129; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0129`.

Landau:2005:GPA

[LPW05] Gad M. Landau, Laxmi Parida, and Oren Weimann. Gene proximity analysis across whole genomes via PQ trees[1]. *Journal of Computational Biology*, 12(10):1289–1306, December 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1289; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1289`.

Lim:2023:QCT

[LQ23] Hong Seo Lim and Peng Qiu. Quantifying cell-type-specific differences of single-cell datasets using uniform manifold approximation and projection for dimension reduction and Shapley additive exPlanations. *Journal of Computational Biology*, 30(7):738–750, July 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0366; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0366`.

Luaces:2010:EGB

[LQPE+10] Oscar Luaces, José R. Quevedo, Miguel Pérez-Enciso, Jorge Díez, Juan José Del Coz, and Antonio Bahamonde. Explaining the genetic basis of complex quantitative traits through prediction models. *Journal of Computational Biology*, 17 (12):1711–1723, December 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0161; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0161`.

Lermen:2000:PUA

[LR00] Martin Lermen and Knut Reinert. The practical use of the $A*$ algorithm for exact multiple sequence alignment. *Journal of Computational Biology*, 7(5):655–671, October 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652701446134; https://www.liebertpub.com/doi/pdf/10.1089/106652701446134`.

Ledent:2005:CHM

[LR05] Sabrina Ledent and Stéphane Robin. Checking homogeneity of motifs' distribution in heterogeneous sequences. *Journal of Computational Biology*, 12(6):672–685, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.672; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.672`.

Lebatteux:2019:TAF

[LRD19] Dylan Lebatteux, Amine M. Remita, and Abdoulaye Baniré Diallo. Toward an alignment-free method for feature extraction and accurate classification of viral sequences. *Journal of Computational Biology*, 26(6):519–535, June 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0239; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0239`.

Levy:2007:ICA

[LRL+07] Dan Levy, Christopher Reeder, Bradford Loucas, Lynn Hlatky, Allen Chen, Michael Cornforth, and Rainer Sachs. Interpreting chromosome aberration spectra. *Journal of Computational Biology*, 14(2):144–155, March 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0127; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0127`.

Lin:2011:FAP

[LRM11] Y. Lin, V. Rajan, and B. M. E. Moret. Fast and accurate phylogenetic reconstruction from high-resolution whole-genome data and a novel robustness estimator. *Journal of Computational Biology*, 18(9):1131–1139, September 2011. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0114; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0114.

Lu:2010:CSE

[LRNBJ10] Yong Lu, Roni Rosenfeld, Gerard J. Nau, and Ziv Bar-Joseph. Cross species expression analysis of innate immune response. *Journal of Computational Biology*, 17(3):253–268, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0147; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0147.

Lees:2007:GMA

[LRSG07] Karen Lees, Stephen Roberts, Pari Skamnioti, and Sarah Gurr. Gene microarray analysis using angular distribution decomposition. *Journal of Computational Biology*, 14(1):68–83, January 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0098; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0098.

Lenhof:1998:PAR

[LRV98] Hans-Peter Lenhof, Knut Reinert, and Martin Vingron. A polyhedral approach to RNA sequence structure alignment. *Journal of Computational Biology*, 5(3):517–530, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.517; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.517.

Llabres:2021:GRF

[LRV21] Mercè Llabrés, Francesc Rosselló, and Gabriel Valiente. The generalized Robinson–Foulds distance for phylogenetic trees. *Journal of Computational Biology*, 28(12):1181–1195, December 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0342; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0342.

Lin:1997:AHA

[LS97] Shili Lin and Terence P. Speed. An algorithm for haplotype analysis. *Journal of Computational Biology*, 4(4):535–546, January

1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.535; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.535.

Laub:1998:FIE

[LS98] Michael T. Laub and Douglas W. Smith. Finding intron/exon splice junctions using INFO, INterruption finder and organizer. *Journal of Computational Biology*, 5(2):307–321, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.307; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.307.

Lotan:2004:APS

[LS04] Itay Lotan and Fabian Schwarzer. Approximation of protein structure for fast similarity measures. *Journal of Computational Biology*, 11(2–3):299–317, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Linhart:2005:DPD

[LS05] Chaim Linhart and Ron Shamir. The degenerate primer design problem: Theory and applications. *Journal of Computational Biology*, 12(4):431–456, May 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.431; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.431.

Lee:2008:RFI

[LS08a] Wah-Heng Lee and Wing-Kin Sung. RB-Finder: an improved distance-based sliding window method to detect recombination breakpoints. *Journal of Computational Biology*, 15(7):881–898, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0154; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0154.

Lu:2008:MSA

[LS08b] Yue Lu and Sing-Hoi Sze. Multiple sequence alignment based on profile alignment of intermediate sequences. *Journal of Computational Biology*, 15(7):767–777, September 2008.

CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0132; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0132.

Lee:2017:SPR

[LS17] Gira Lee and Hokeun Sun. Selection probability for rare variant association studies. *Journal of Computational Biology*, 24(5):400–411, May 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0222; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0222.

Liang:2023:WSP

[LS23] Xianglong Liang and Hokeun Sun. Weighted selection probability to prioritize susceptible rare variants in multi-phenotype association studies with application to a soybean genetic data set. *Journal of Computational Biology*, 30(10):1075–1088, October 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0487; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0487.

Lilien:2005:NEB

[LSAD05] Ryan H. Lilien, Brian W. Stevens, Amy C. Anderson, and Bruce R. Donald. A novel ensemble-based scoring and search algorithm for protein redesign and its application to modify the substrate specificity of the Gramicidin synthetase A phenylalanine adenylation enzyme. *Journal of Computational Biology*, 12(6):740–761, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.740; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.740.

Lai:2003:MPM

[LSAS03] Yinglei Lai, Deepali Shinde, Norman Arnheim, and Fengzhu Sun. The mutation process of microsatellites during the polymerase chain reaction. *Journal of Computational Biology*, 10(2):143–155, April 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703321825937; https://www.liebertpub.com/doi/pdf/10.1089/106652703321825937.

Lall:2018:SAP

[LSBS18] Snehalika Lall, Debajyoti Sinha, Sanghamitra Bandyopadhyay, and Debarka Sengupta. Structure-aware principal component analysis for single-cell RNA-seq data. *Journal of Computational Biology*, 25(12):1365–1373, December 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0027; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0027`.

Li:2004:EVD

[LSG04] Wentian Li, Fengzhu Sun, and Ivo Grosse. Extreme value distribution based gene selection criteria for discriminant microarray data analysis using logistic regression. *Journal of Computational Biology*, 11(2–3):215–226, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Lotan:2004:ADS

[LSHL04] Itay Lotan, Fabian Schwarzer, Dan Halperin, and Jean-Claude Latombe. Algorithm and data structures for efficient energy maintenance during Monte Carlo simulation of proteins. *Journal of Computational Biology*, 11(5):902–932, October 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.902; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.902`.

Li:2016:MPL

[LSL+16] Haiou Li, Lu Sun, Sheng Luo, Xiaoyan Xia, and Qiang Lyu. Modeling protein loop structure by cyclic coordinate descent-based approach. *Journal of Computational Biology*, 23(2):123–136, February 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0145; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0145`.

Lawhorn:2018:SCA

[LSRR18] Chelsea M. Lawhorn, Rachel Schomaker, Jonathan T. Rowell, and Olav Rueppell. Simple comparative analyses of differentially expressed gene lists May overestimate gene overlap. *Journal of Computational Biology*, 25(6):606–612, June 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0262; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0262.

Landau:2001:AAT

[LSS01] Gad M. Landau, Jeanette P. Schmidt, and Dina Sokol. An algorithm for approximate tandem repeats. *Journal of Computational Biology*, 8(1):1–18, February 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701300099038; https://www.liebertpub.com/doi/pdf/10.1089/106652701300099038.

Liu:2018:MPP

[LSSD18] Lizhen Liu, Xiaowu Sun, Wei Song, and Chao Du. A method for predicting protein complexes from dynamic weighted protein–protein interaction networks. *Journal of Computational Biology*, 25(6):586–605, June 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0114; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0114.

Lee:2017:CTS

[LST+17] Minhyeok Lee, Junhee Seok, Donghyun Tae, Hua Zhong, and Sung Won Han. A comparison of two-stage approaches based on penalized regression for estimating gene networks. *Journal of Computational Biology*, 24(7):709–720, July 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0052; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0052.

Li:2005:EHT

[LSY+05] Lang Li, Huidong Shi, Constantin Yiannoutsos, Tim Hui-Ming Huang, and Kenneth P. Nephew. Epigenetic hypothesis tests for methylation and acetylation in a triple microarray system. *Journal of Computational Biology*, 12(3):370–390, April 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.370; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.370.

Leiserson:2011:IMC

[LTCH11] Mark D. M. Leiserson, Diana Tatar, Lenore J. Cowen, and Benjamin J. Hescott. Inferring mechanisms of compensation from E-MAP and SGA data using local search algorithms for max cut. *Journal of Computational Biology*, 18(11):1399–1409, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0191; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0191`.

Lam:2010:IAR

[LTI10] Fumei Lam, Ryan Tarpine, and Sorin Istrail. The imperfect ancestral recombination graph reconstruction problem: Upper bounds for recombination and homoplasy. *Journal of Computational Biology*, 17(6):767–781, June 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0249; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0249`.

Liu:2020:IBA

[LTL20] Shanshan Liu, Wenjuan Tian, and Burong Li. Integrative bioinformatics analysis identifies NEK2 as a potential biomarker in head and neck squamous cell carcinoma. *Journal of Computational Biology*, 27(1):100–108, January 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0208; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0208`.

Larson:2020:INN

[LTS20] Gary Larson, Jeffrey L. Thorne, and Scott Schmidler. Incorporating nearest-neighbor site dependence into protein evolution models. *Journal of Computational Biology*, 27(3):361–375, March 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0500; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0500`.

Lu:2015:CSI

[LTSA15] Wei Lu, Takeyuki Tamura, Jiangning Song, and Tatsuya Akutsu. Computing smallest intervention strategies for

multiple metabolic networks in a Boolean model. *Journal of Computational Biology*, 22(2):85–110, February 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0274; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0274`.

Landry:2024:FPT

[LTsL24] Kaari Landry, Olivier Tremblay-savard, and Manuel Lafond. A fixed-parameter tractable algorithm for finding agreement cherry-reduced subnetworks in level-1 orchard networks. *Journal of Computational Biology*, 31(4):360–379, April 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0317; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0317`.

Li-Thiao-Te:2012:FDC

[LTTS12] Sébastien Li-Thiao-Té and Benno Schwikowski. Feature detection with controlled error rates in LC/MS images. *Journal of Computational Biology*, 19(4):349–364, April 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0125; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0125`.

Li:2018:MMH

[LTZ18] Lingling Li, Tianhai Tian, and Xinan Zhang. Mutation mechanisms of human breast cancer. *Journal of Computational Biology*, 25(4):396–404, April 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0111; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0111`.

Lu:2015:EAC

[Lu15] Chin Lung Lu. An efficient algorithm for the contig ordering problem under algebraic rearrangement distance. *Journal of Computational Biology*, 22(11):975–987, November 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0073; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0073`.

Levy:2004:CDD

[LVC+04] Dan Levy, Mariel Vazquez, Michael Cornforth, Bradford Loucas, Rainer K. Sachs, and Javier Arsuaga. Comparing DNA damage-processing pathways by computer analysis of chromosome painting data. *Journal of Computational Biology*, 11(4):626–641, August 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.626; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.626`.

Li:2007:QMS

[LVS+07] Haifeng Li, Anton Valouev, David C. Schwartz, Michael S. Waterman, and Lei M. Li. A quantile method for sizing optical maps. *Journal of Computational Biology*, 14(3):255–266, April 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0006; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0006`.

Lu:2012:PSS

[LW12] I-Lin Lu and Hsiuying Wang. Protein-specific scoring method for ligand discovery. *Journal of Computational Biology*, 19 (11):1215–1226, November 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0188; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0188`.

Liu:2022:SST

[LW22] Baqiao Liu and Tandy Warnow. Scalable species tree inference with external constraints. *Journal of Computational Biology*, 29(7):664–678, July 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0543; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0543`.

Li:2014:IRO

[LWC+14] Chuan-Xi Li, Ru-Jing Wang, Peng Chen, He Huang, and Ya-Ru Su. Interaction relation ontology learning. *Journal of Computational Biology*, 21(1):80–88, January 2014. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0009; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0009.

Liu:2010:EGW

[LWLJ10] Lan Liu, Yonghui Wu, Stefano Lonardi, and Tao Jiang. Efficient genome-wide TagSNP selection across populations via the linkage disequilibrium criterion. *Journal of Computational Biology*, 17(1):21–37, January 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0228; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0228.

Li:2019:RMQ

[LWLL19] Yufang Li, Aoshen Wu, Gang Liu, and Lei Liu. A review of methods to quantify the genomic similarity of topological associating domains. *Journal of Computational Biology*, 26(11):1326–1338, November 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0129; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0129.

Larson:2018:ISN

[LWN+18] Nicholas B. Larson, Chen Wang, Jie Na, Ross A. Rowsey, William Edward Highsmith, Nicole L. Hoppman, Jean-Pierre Kocher, and Eric W. Klee. Improving single-nucleotide polymorphism-based fetal fraction estimation of maternal plasma circulating cell-free DNA using Bayesian hierarchical models. *Journal of Computational Biology*, 25(9):1040–1049, September 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0056; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0056.

Liu:2018:PMD

[LWZ18] Yue Liu, Shu-Lin Wang, and Jun-Feng Zhang. Prediction of microbe–disease associations by graph regularized nonnegative matrix factorization. *Journal of Computational Biology*, 25(12):1385–1394, December 2018. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0072; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0072.

Liu:2021:COP

[LWZ21] Junfeng Liu, Yi Wang, and Hongyu Zhao. Calculating orthologous protein-coding sequence set probability using the Poisson process. *Journal of Computational Biology*, 28(10):961–974, October 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0507; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0507.

Liu:2020:AGE

[LXL+20] Ying Liu, Shenghua Xiong, Shiying Liu, Jie Chen, Hao Yang, Gang Liu, and Gengmi Li. Analysis of gene expression in bladder cancer: Possible involvement of mitosis and complement and coagulation cascades signaling pathway. *Journal of Computational Biology*, 27(6):987–998, June 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0237; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0237.

Li:2024:SNM

[LXS24] Juntao Li, Shan Xiang, and Xuekun Song. Screening nonlinear miRNA features of breast cancer by using ensemble regularized polynomial logistic regression. *Journal of Computational Biology*, 31(7):670–690, July 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Leung:2009:PPC

[LXYC09] Henry C. M. Leung, Qian Xiang, S. M. Yiu, and Francis Y. L. Chin. Predicting protein complexes from PPI data: a core-attachment approach. *Journal of Computational Biology*, 16(2):133–144, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.01TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.01TT.

Loewenstern:1999:SLE

[LY99] David Loewenstern and Peter N. Yianilos. Significantly lower entropy estimates for natural DNA sequences. *Journal of Computational Biology*, 6(1):125–142, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.125; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.125`.

Leung:2015:IMH

[LYC15] Henry C. M. Leung, Siu-Ming Yiu, and Francis Y. L. Chin. IDBA-MTP: a hybrid metatranscriptomic assembler based on protein information. *Journal of Computational Biology*, 22(5):367–376, May 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0139; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0139`.

Liang:2019:BDA

[LYF+19] Wei Liang, Yuxiao Yang, Yusi Fang, Zhongying Zhao, and Jie Hu. Bayesian detection of abnormal asynchrony of division between sister cells in mutant *Caenorhabditis elegans* embryos. *Journal of Computational Biology*, 26(5):495–505, May 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0246; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0246`.

Liang:2019:IMD

[LYH+19] Xiao Liang, William Chad Young, Ling-Hong Hung, Adrian E. Raftery, and Ka Yee Yeung. Integration of multiple data sources for gene network inference using genetic perturbation data. *Journal of Computational Biology*, 26(10):1113–1129, October 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0036; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0036`.

Langmead:2004:PTN

[LYL+04] Christopher James Langmead, Anthony Yan, Ryan Lilien, Lincong Wang, and Bruce Randall Donald. A polynomial-time nuclear vector replacement algorithm for automated NMR reso-

nance assignments. *Journal of Computational Biology*, 11(2–3):277–298, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Langmead:2003:PIR

[LYMD03] Christopher James Langmead, Anthony K. Yan, C. Robertson McClung, and Bruce Randall Donald. Phase-independent rhythmic analysis of genome-wide expression patterns. *Journal of Computational Biology*, 10(3–4):521–536, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Leung:2013:IMN

[LYPC13] Henry C. M. Leung, Siu-Ming Yiu, John Parkinson, and Francis Y. L. Chin. IDBA-MT: *De Novo* assembler for metatranscriptomic data generated from next-generation sequencing technology. *Journal of Computational Biology*, 20(7):540–550, July 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0042; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0042`.

Lo:2020:PMT

[LYS20] Shih-Chiang Lo, Chao-Xuan You, and Che-Chi Shu. A practicable method of tuning the noise intensity at protein level. *Journal of Computational Biology*, 27(9):1452–1460, September 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0151; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0151`.

Liu:2010:SMR

[LZ10] Xin Liu and Ya-Pu Zhao. Substitution matrices of residue triplets derived from protein blocks. *Journal of Computational Biology*, 17(12):1679–1687, December 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0035; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0035`.

Li:2015:IGW

[LZBK15] Xueling Li, Min Zhu, Allan R. Brasier, and Andrzej S. Kudlicki. Inferring genome-wide functional modulatory network: a case

study on NF-κB/RelA transcription factor. *Journal of Computational Biology*, 22(4):300–312, April 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0299; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0299`.

Li:2023:CTD

[LZC+23] Fang-Zhen Li, Xue-Fen Zhang, Hui-Ying Cai, Ling-Qiang Ran, Hai-Yan Zhou, and Zhi-E Liu. Chromosome three-dimensional structure reconstruction: an iterative ShRec3D algorithm. *Journal of Computational Biology*, 30(5):575–587, May 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0179; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0179`.

Lippert:2005:FAG

[LZF+05] Ross A. Lippert, Xiaoyue Zhao, Liliana Florea, Clark Mobarry, and Sorin Istrail. Finding anchors for genomic sequence comparison. *Journal of Computational Biology*, 12(6):762–776, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.762; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.762`.

Li:2015:HPG

[LZHC15] Bo Li, Xianfang Zheng, Chuancui Hu, and Yunxia Cao. Human papillomavirus genome-wide identification of T-cell epitopes for peptide vaccine development against cervical cancer: an integration of computational analysis and experimental assay. *Journal of Computational Biology*, 22(10):962–974, October 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0287; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0287`.

Li:2023:AIC

[LZL+23] Xiaobo Li, Yijia Zhang, Xingwang Li, Xianwei Pan, Jian Wang, and Mingyu Lu. Automatic international classification of diseases coding via note-code interaction network with denoising mechanism. *Journal of Computational Biology*, 30(8):912–925,

August 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0079; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0079.

Ling:2024:SFA

[LZL24] Zhao Ling, Yu Wei Zhang, and Shuai Cheng Li. SuperTAD-Fast: Accelerating topologically associating domains detection through discretization. *Journal of Computational Biology*, 31(9): 784–796, September 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Lee:2009:SLE

[LZS09] J. William Lee, Tomasz Zemojtel, and Eugene Shakhnovich. Systems-level evidence of transcriptional co-regulation of yeast protein complexes. *Journal of Computational Biology*, 16 (2):331–339, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.17TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.17TT.

Luo:2012:NGI

[LZX12] Li Luo, Yun Zhu, and Momiao Xiong. A novel genome-information content-based statistic for genome-wide association analysis designed for next-generation sequencing data. *Journal of Computational Biology*, 19(6):731–744, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0035; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0035.

Liu:2023:EMA

[LZY+23] Da Liu, Yijia Zhang, Ming Yang, Jianyuan Yuan, and Wen Qu. Extracting mutant-affected protein–protein interactions via Gaussian-enhanced representation and contrastive learning. *Journal of Computational Biology*, 30(9):972–984, September 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0080; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0080.

Ma:2011:RHL

[Ma11] Jian Ma. Reconstructing the history of large-scale genomic changes: Biological questions and computational challenges. *Journal of Computational Biology*, 18(7):879–893, July 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0189; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0189`.

Melkman:2013:ISA

[MA13] Avraham A. Melkman and Tatsuya Akutsu. An improved satisfiability algorithm for nested canalyzing functions and its application to determining a singleton attractor of a Boolean network. *Journal of Computational Biology*, 20(12):958–969, December 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0060; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0060`.

Marongiu:2019:MCL

[MA19] Luigi Marongiu and Heike Allgayer. Mingle: a command line utility for merging multi-fasta files. *Journal of Computational Biology*, 26(4):396–404, April 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0243; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0243`.

Mallios:1998:ISD

[Mal98] Ronna R. Mallios. Iterative stepwise discriminant analysis: a meta-algorithm for detecting quantitative sequence motifs. *Journal of Computational Biology*, 5(4):703–711, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.703; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.703`.

Mamitsuka:1996:LMH

[Mam96] Hiroshi Mamitsuka. A learning method of hidden Markov models for sequence discrimination. *Journal of Computational Biology*, 3(3):361–373, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.361;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.361.

Mier:2016:FFW

[MAN16] Pablo Mier and Miguel A. Andrade-Navarro. FastaHerder2: Four ways to research protein function and evolution with clustering and clustered databases. *Journal of Computational Biology*, 23(4):270–278, April 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0191; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0191.

Martin:1994:ECD

[Mar94] Daniela R. Martin. Equivalence classes for the double-digest problem with coincident cut sites. *Journal of Computational Biology*, 1(3):241–253, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.241; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.241.

Markowitz:1995:HMB

[Mar95] Victor M. Markowitz. Heterogeneous molecular biology databases. *Journal of Computational Biology*, 2(4):537–538, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.537.

Matsen:2010:CAR

[Mat10] Frederick A. Matsen. constNJ: an algorithm to reconstruct sets of phylogenetic trees satisfying pairwise topological constraints. *Journal of Computational Biology*, 17(6):799–818, June 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0201; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0201.

Medvedev:2009:MLG

[MB09] Paul Medvedev and Michael Brudno. Maximum likelihood genome assembly. *Journal of Computational Biology*, 16 (8):1101–1116, August 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0047;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0047.

Martinez:2018:FLT

[MBC+18] Héctor Martínez, Sergio Barrachina, Maribel Castillo, Enrique S. Quintana-Ortí, Jordi Rambla de Argila, Xavier Farré, and Arcadi Navarro. FaST-LMM for two-way epistasis tests on high-performance clusters. *Journal of Computational Biology*, 25(8):862–870, August 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0087; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0087.

Mumey:2003:NMM

[MBK+03] Brendan M. Mumey, Brian W. Bailey, Bonnie Kirkpatrick, Algirdas J. Jesaitis, Thomas Angel, and Edward A. Dratz. A new method for mapping discontinuous antibody epitopes to reveal structural features of proteins. *Journal of Computational Biology*, 10(3–4):555–567, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Min:2009:LRW

[MBLZ09] Renqiang Min, Anthony Bonner, Jingjing Li, and Zhaolei Zhang. Learned random-walk kernels and empirical-map kernels for protein sequence classification. *Journal of Computational Biology*, 16(3):457–474, March 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0031; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0031.

Miller:1994:CAS

[MBR+94] Webb Miller, Mark Boguski, Balaji Raghavachari, Zheng Zhang, and Ross C. Hardison. Constructing aligned sequence blocks. *Journal of Computational Biology*, 1(1):51–64, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.51; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.51.

Misra:2011:GBP

[MBRS11a] Navodit Misra, Guy Blelloch, R. Ravi, and Russell Schwartz. Generalized Buneman pruning for inferring the most parsi-

monious multi-state phylogeny. *Journal of Computational Biology*, 18(3):445–457, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0254; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0254.

Misra:2011:OBS

[MBRS11b] Navodit Misra, Guy Blelloch, R. Ravi, and Russell Schwartz. An optimization-based sampling scheme for phylogenetic trees. *Journal of Computational Biology*, 18(11):1599–1609, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0164; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0164.

Muggleton:2001:GRU

[MBS+01] S. H. Muggleton, C. H. Bryant, A. Srinivasan, A. Whittaker, S. Topp, and C. Rawlings. Are grammatical representations useful for learning from biological sequence data? — a case study. *Journal of Computational Biology*, 8(5): 493–521, October 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701753216512; https://www.liebertpub.com/doi/pdf/10.1089/106652701753216512.

Messer:2007:ELR

[MBVA07] Philipp W. Messer, Ralf Bundschuh, Martin Vingron, and Peter F. Arndt. Effects of long-range correlations in DNA on sequence alignment score statistics. *Journal of Computational Biology*, 14(5):655–668, June 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R008; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R008.

Ma:2008:UAC

[MC08] Patrick C. H. Ma and Keith C. C. Chan. UPSEC: an algorithm for classifying unaligned protein sequences into functional families. *Journal of Computational Biology*, 15(4):431–443, May 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0113; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0113.

Ma:2010:DIM

[MC10] Patrick C. H. Ma and Keith C. C. Chan. Discovering interesting motif-sets for multi-class protein sequence classification. *Journal of Computational Biology*, 17(5):733–743, May 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0213; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0213`.

McGrane:2016:BNE

[MC16] Martin McGrane and Michael A. Charleston. Biological network edit distance. *Journal of Computational Biology*, 23 (9):776–788, September 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0062; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0062`.

Marathe:2001:CDW

[MCC01] Amit Marathe, Anne E. Condon, and Robert M. Corn. On combinatorial DNA word design. *Journal of Computational Biology*, 8(3):201–219, June 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270152530818; https://www.liebertpub.com/doi/pdf/10.1089/10665270152530818`.

McCrow:2009:APU

[McC09] John P. McCrow. Alignment of phylogenetically unambiguous indels in *Shewanella*. *Journal of Computational Biology*, 16(11):1517–1528, November 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0188; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0188`.

Mishra:2019:INS

[MCH+19] Avinash Mishra, Megan Cross, Andreas Hofmann, Mark J. Coster, Abdul Karim, and Abdul Sattar. Identification of a novel scaffold for inhibition of dipeptidyl peptidase-4. *Journal of Computational Biology*, 26(12):1470–1486, December 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/`

10.1089/cmb.2019.0201; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0201.

McPeek:2012:BGI

[McP12] Mary Sara McPeek. BLUP genotype imputation for case-control association testing with related individuals and missing data. *Journal of Computational Biology*, 19(6):756–765, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0024; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0024.

Mian:2000:RRA

[MD00] I. S. Mian and I. Dubchak. Representing and reasoning about protein families using generative and discriminative methods. *Journal of Computational Biology*, 7(6):849–862, December 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270050514972; https://www.liebertpub.com/doi/pdf/10.1089/10665270050514972.

Mercier:2001:EDL

[MD01] S. Mercier and J. J. Daudin. Exact distribution for the local score of one i.i.d. random sequence. *Journal of Computational Biology*, 8(4):373–380, September 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701752236197; https://www.liebertpub.com/doi/pdf/10.1089/106652701752236197.

Myers:2003:TDF

[MD03] Gene Myers and Richard Durbin. A table-driven, full-sensitivity similarity search algorithm. *Journal of Computational Biology*, 10(2):103–117, April 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703321825919; https://www.liebertpub.com/doi/pdf/10.1089/106652703321825919.

Mongin:2011:MAB

[MDB11] Emmanuel Mongin, Ken Dewar, and Mathieu Blanchette. Mapping association between long-range *cis*-regulatory regions and their target genes using synteny. *Journal of Computational Biology*, 18(9):1115–1130, September 2011. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0088; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0088.

Marcais:2024:SMS

[MDK24] Guillaume Marçais, Dan DeBlasio, and Carl Kingsford. Sketching methods with small window guarantee using minimum decycling sets. *Journal of Computational Biology*, 31(7):597–615, July 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Mishra:2018:CNN

[MDL+18] Rashika Mishra, Ovidiu Daescu, Patrick Leavey, Dinesh Rakheja, and Anita Sengupta. Convolutional neural network for histopathological analysis of osteosarcoma. *Journal of Computational Biology*, 25(3):313–325, March 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0153; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0153.

Mohebbi:2021:HMT

[MDMC21] Mohammad Mohebbi, Liang Ding, Russell L. Malmberg, and Liming Cai. Human MicroRNA target prediction via multi-hypotheses learning. *Journal of Computational Biology*, 28 (2):117–132, February 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0227; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0227.

Mertens:2006:MSP

[MDTD06] Bart J. A. Mertens, M. E. De Noo, R. A. E. M. Tollenaar, and A. M. Deelder. Mass spectrometry proteomic diagnosis: Enacting the double cross-validatory paradigm. *Journal of Computational Biology*, 13(9):1591–1605, November 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1591; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1591.

Ma:2024:PBP

[MDWZ24] Han Ma, Yanyan Du, Zong Wang, and Qimin Zhang. Positivity and boundedness preserving numerical scheme for a stochastic multigroup susceptible-infected-recovering epidemic model with age structure. *Journal of Computational Biology*, 31(12):1259–1290, December 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0443; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0443`.

Manolopoulou:2012:PAI

[ME12] Ioanna Manolopoulou and Brent C. Emerson. Phylogeographic ancestral inference using the coalescent model on haplotype trees. *Journal of Computational Biology*, 19(6):745–755, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0038; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0038`.

Mohammed:2024:SVD

[MEF24] Isra Mohammed, Murtada K. Elbashir, and Areeg S. Faggad. Singular value decomposition-based penalized multinomial regression for classifying imbalanced medulloblastoma subgroups using methylation data. *Journal of Computational Biology*, 31(5):458–471, May 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0198; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0198`.

Metzler:2006:RVG

[Met06] Dirk Metzler. Robust E-values for gapped local alignments. *Journal of Computational Biology*, 13(4):882–896, May 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.882; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.882`.

Mellem:2019:MMD

[MFJ+19] Daniel Mellem, Frank Fischer, Sören Jaspers, Horst Wenck, and Michael Rübhausen. Mitochondrial morphologies driven by

energy-consuming cell sites in a spatially and time-resolved quality model. *Journal of Computational Biology*, 26(1):76–85, January 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0086; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0086`.

Moerkerke:2006:SSD

[MG06] B. Moerkerke and E. Goetghebeur. Selecting "significant" differentially expressed genes from the combined perspective of the null and the alternative. *Journal of Computational Biology*, 13(9):1513–1531, November 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1513; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1513`.

Morgulis:2006:FSD

[MGSA06] Aleksandr Morgulis, E. Michael Gertz, Alejandro A. Schäffer, and Richa Agarwala. A fast and symmetric DUST implementation to mask low-complexity DNA sequences. *Journal of Computational Biology*, 13(5):1028–1040, June 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1028; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1028`.

Mazza:2014:EII

[MGVS14] Arnon Mazza, Irit Gat-Viks, and Roded Sharan. Elucidating influenza inhibition pathways via network reconstruction. *Journal of Computational Biology*, 21(5):394–404, May 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0147; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0147`.

Martin:2007:IVR

[MGW+07] Francis L. Martin, Matthew J. German, Ernst Wit, Thomas Fearn, Narasimhan Ragavan, and Hubert M. Pollock. Identifying variables responsible for clustering in discriminant analysis of data from infrared microspectroscopy of a biological sample. *Journal of Computational Biology*, 14(9):1176–1184, November 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0057; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0057.

Mcloughlin:2022:SDE

[MH22] Aidan Mcloughlin and Haiyan Huang. Shared differential expression-based distance reflects global cell type relationships in single-cell RNA sequencing data. *Journal of Computational Biology*, 29(8):867–879, August 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0652; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0652.

Moon:2022:SSD

[MHL22] Sehwan Moon, Jeongyoung Hwang, and Hyunju Lee. SDGCCA: Supervised deep generalized canonical correlation analysis for multi-omics integration. *Journal of Computational Biology*, 29(8):892–907, August 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0598; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0598.

Mazowita:2006:SRM

[MHS06] Matthew Mazowita, Lani Haque, and David Sankoff. Stability of rearrangement measures in the comparison of genome sequences. *Journal of Computational Biology*, 13(2):554–566, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.554; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.554.

Milosavljevic:1995:DSR

[Mil95] Aleksandar Milosavljević. DNA sequence recognition by hybridization to short oligomers. *Journal of Computational Biology*, 2(2):355–370, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.355; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.355.

Miyano:2006:PSR

[Miy06] Satoru Miyano. Preface: Special RECOMB 2005 issue. *Journal of Computational Biology*, 13(2):131–132, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.131`.

Mongia:2022:DGD

[MJCM22] Aanchal Mongia, Stuti Jain, Emilie Chouzenoux, and Angshul Majumdar. DeepVir: Graphical deep matrix factorization for in silico antiviral repositioning — application to COVID-19. *Journal of Computational Biology*, 29(5):441–452, May 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0108; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0108`.

Ma:2024:TRS

[MJR+24] Hehuan Ma, Feng Jiang, Yu Rong, Yuzhi Guo, and Junzhou Huang. Toward robust self-training paradigm for molecular prediction tasks. *Journal of Computational Biology*, 31(3):213–228, March 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0187; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0187`.

Miardan:2023:EPD

[MJS23] Mona Meghdari Miardan, Arash Jamshidpey, and David Sankoff. Escape from parsimony of a double-cut-and-join genome evolution process. *Journal of Computational Biology*, 30(2):118–130, February 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0468; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0468`.

Mei:2024:UCD

[MJS24] Biao Mei, Yu Jiang, and Yifan Sun. Unveiling commonalities and differences in genetic regulations via two-way fusion. *Journal of Computational Biology*, 31(9):834–870, September 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Maximova:2006:NAN

[MK06] Tatiana Maximova and Chen Keasar. A novel algorithm for non-bonded-list updating in molecular simulations. *Journal of Computational Biology*, 13(5):1041–1048, June 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1041; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1041`.

Marhon:2011:GPB

[MK11] Sajid A. Marhon and Stefan C. Kremer. Gene prediction based on DNA spectral analysis: a literature review. *Journal of Computational Biology*, 18(4):639–676, April 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0184; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0184`.

Manescu:2016:SLA

[MK16] David Manescu and Uri Keich. A symmetric length-aware enrichment test. *Journal of Computational Biology*, 23(6):508–525, June 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0038; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0038`.

Mun:2020:MRM

[MKB+20] Taher Mun, Alan Kuhnle, Christina Boucher, Travis Gagie, Ben Langmead, and Giovanni Manzini. Matching reads to many genomes with the r-index. *Journal of Computational Biology*, 27(4):514–518, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0316; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0316`.

Menke:2005:WPN

[MKBC05] Matthew Menke, Jonathan King, Bonnie Berger, and Lenore Cowen. Wrap-and-pack: a new paradigm for beta structural motif recognition with application to recognizing beta trefoils. *Journal of Computational Biology*, 12(6):777–795, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (elec-

tronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.777; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.777.

Milewski:2017:ENS

[MKKK+17] Marek C. Milewski, Karol Kamel, Anna Kurzynska-Kokorniak, Marcin K. Chmielewski, and Marek Figlerowicz. EvOligo: a novel software to design and group libraries of oligonucleotides applicable for nucleic acid-based experiments. *Journal of Computational Biology*, 24(10):1014–1028, October 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0154; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0154.

Makarenkov:2000:CAT

[ML00] Vladimir Makarenkov and Bruno Leclerc. Comparison of additive trees using circular orders. *Journal of Computational Biology*, 7(5):731–744, October 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701446170; https://www.liebertpub.com/doi/pdf/10.1089/106652701446170.

Makarenkov:2004:PTR

[ML04] Vladimir Makarenkov and Pierre Legendre. From a phylogenetic tree to a reticulated network. *Journal of Computational Biology*, 11(1):195–212, January 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652704773416966; https://www.liebertpub.com/doi/pdf/10.1089/106652704773416966.

Minary:2010:CON

[ML10] Peter Minary and Michael Levitt. Conformational optimization with natural degrees of freedom: a novel stochastic chain closure algorithm. *Journal of Computational Biology*, 17(8):993–1010, August 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0016; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0016.

Mallawaarachchi:2022:ABM

[ML22] Vijini Mallawaarachchi and Yu Lin. Accurate binning of metagenomic contigs using composition, coverage, and as-

sembly graphs. *Journal of Computational Biology*, 29(12): 1357–1376, December 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0262; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0262`.

Mann:2010:IBG

[MLC10] Scott Mann, Jinyan Li, and Yi-Ping Phoebe Chen. Insights into bacterial genome composition through variable target GC content profiling. *Journal of Computational Biology*, 17(1):79–96, January 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0058; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0058`.

Ma:2017:JBM

[MLOT17] Tianzhou Ma, Faming Liang, Steffi Oesterreich, and George C. Tseng. A joint Bayesian model for integrating microarray and RNA sequencing transcriptomic data. *Journal of Computational Biology*, 24(7):647–662, July 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0056; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0056`.

Movaghar:2012:SST

[MLS+12] Afshin Fayyaz Movaghar, Guillaume Launay, Sophie Schbath, Jean-François Gibrat, and François Rodolphe. Statistical significance of threading scores. *Journal of Computational Biology*, 19(1):13–29, January 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0236; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0236`.

Moravec:2023:TPS

[MLS+23] Jiří C. Moravec, Robert Lanfear, David L. Spector, Sarah D. Diermeier, and Alex Gavryushkin. Testing for phylogenetic signal in single-cell RNA-Seq data. *Journal of Computational Biology*, 30(4):518–537, April 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0357;`

https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0357.

Mohimani:2011:MNS

[MLY+11] Hosein Mohimani, Wei-Ting Liu, Yu-Liang Yang, Susana P. Gaudêncio, William Fenical, Pieter C. Dorrestein, and Pavel A. Pevzner. Multiplex De Novo sequencing of peptide antibiotics. *Journal of Computational Biology*, 18(11):1371–1381, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0158; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0158.

Menconi:2006:CBA

[MM06] Giulia Menconi and Roberto Marangoni. A compression-based approach for coding sequences identification. I. Application to prokaryotic genomes. *Journal of Computational Biology*, 13(8):1477–1488, October 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1477; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1477.

Moussa:2019:LSI

[MM19] Marmar Moussa and Ion I. Măndoiu. Locality sensitive imputation for single cell RNA-Seq data. *Journal of Computational Biology*, 26(8):822–835, August 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0236; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0236.

Moussa:2021:STI

[MM21] Marmar Moussa and Ion I. Măndoiu. SC1: a tool for interactive Web-based single-cell RNA-Seq data analysis. *Journal of Computational Biology*, 28(8):820–841, August 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0051; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0051.

Malikic:2021:SHT

[MMA+21] Salem Malikić, Farid Rashidi Mehrabadi, Erfan Sadeqi Azer, Mohammad Haghir Ebrahimabadi, and Suleyman Cenk Sahi-

nalp. Studying the history of tumor evolution from single-cell sequencing data by exploring the space of binary matrices. *Journal of Computational Biology*, 28(9):857–879, September 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0595; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0595`.

Maghawry:2014:NPS

[MMG14] Huda A. Maghawry, Mostafa G. M. Mostafa, and Tarek F. Gharib. A new protein structure representation for efficient protein function prediction. *Journal of Computational Biology*, 21(12):936–946, December 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0137; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0137`.

Mian:1998:SMP

[MMHC98] I. Saira Mian, Michael J. Moser, William R. Holley, and Aloke Chatterjee. Statistical modelling and phylogenetic analysis of a deaminase domain. *Journal of Computational Biology*, 5(1):57–72, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.57; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.57`.

Melnyk:2021:AZI

[MMK+21] Andrew Melnyk, Fatemeh Mohebbi, Sergey Knyazev, Bikram Sahoo, Roya Hosseini, Pavel Skums, Alex Zelikovsky, and Murray Patterson. From alpha to zeta: Identifying variants and subtypes of SARS-CoV-2 via clustering. *Journal of Computational Biology*, 28(11):1113–1129, November 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0302; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0302`.

Matur:2015:AAS

[MMKH15] Meltem Gölgeli Matur, Johannes Müller, Christina Kuttler, and Burkhard A. Hense. An approximative approach for single cell spatial modeling of quorum sensing. *Journal of Computational Biology*, 22(3):227–235, March 2015. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0198; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0198.

Mandoiu:2021:SII

[MMN+21] Ion Mandoiu, T. M. Murali, Giri Narasimhan, Sanguthevar Rajasekaran, Pavel Skums, and Alexander Zelikovsky. Special issue: 9th International Computational Advances in Bio and Medical Sciences (ICCABS 2019). *Journal of Computational Biology*, 28(2):115–116, February 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2021.29034.im.

Minarsky:2018:TM

[MMPS18] Andrey Minarsky, Nadya Morozova, Robert Penner, and Christophe Soulé. Theory of morphogenesis. *Journal of Computational Biology*, 25(4):444–450, April 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0150; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0150.

Mirkin:1995:BCM

[MMS95] Boris Mirkin, Ilya Muchnik, and Temple F. Smith. A biologically consistent model for comparing molecular phylogenies. *Journal of Computational Biology*, 2(4):493–507, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.493; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.493.

Mardia:2008:SVP

[MN08] Kanti V. Mardia and Vysaul B. Nyirongo. Simulating virtual protein C_α traces with applications. *Journal of Computational Biology*, 15(9):1209–1220, November 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0092; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0092.

Muller:2015:CRS

[MN15] Robert Müller and Markus E. Nebel. Combinatorics of RNA secondary structures with base triples. *Journal of Computa-*

tional Biology, 22(7):619–648, July 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0022; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0022.

Mirarab:2015:PUL

[MNG+15] Siavash Mirarab, Nam Nguyen, Sheng Guo, Li-San Wang, Junhyong Kim, and Tandy Warnow. PASTA: Ultra-large multiple sequence alignment for nucleotide and amino-acid sequences. *Journal of Computational Biology*, 22(5):377–386, May 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0156; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0156.

Mehan:2009:INA

[MNIK+09] Michael R. Mehan, Juan Nunez-Iglesias, Mrinal Kalakrishnan, Michael S. Waterman, and Xianghong Jasmine Zhou. An integrative network approach to map the transcriptome to the phenome. *Journal of Computational Biology*, 16(8):1023–1034, August 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0037; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0037.

Makinen:2010:SRH

[MNSV10] Veli Mäkinen, Gonzalo Navarro, Jouni Sirén, and Niko Välimäki. Storage and retrieval of highly repetitive sequence collections. *Journal of Computational Biology*, 17(3):281–308, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0169; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0169.

Morange:2019:TMT

[Mor19] Michel Morange. A time to model and a time to experiment. *Journal of Computational Biology*, 26(7):629–636, July 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0133; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0133.

Mossel:2003:IRA

[Mos03] Elchanan Mossel. On the impossibility of reconstructing ancestral data and phylogenies. *Journal of Computational Biology*, 10(5):669–676, October 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652703322539015; https://www.liebertpub.com/doi/pdf/10.1089/106652703322539015`.

Miller:1994:QCD

[MP94] Mark J. Miller and John I. Powell. A quantitative comparison of DNA sequence assembly programs. *Journal of Computational Biology*, 1(4):257–269, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.257; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.257`.

Manuch:2011:CGC

[MP11] Ján Maňuch and Murray Patterson. The complexity of the gapped consecutive-ones property problem for matrices of bounded maximum degree. *Journal of Computational Biology*, 18(9):1243–1253, September 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0128; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0128`.

More:2016:IDP

[MP16] Ravi P. More and Hemant J. Purohit. The identification of discriminating patterns from 16s rRNA gene to generate signature for bacillus genus. *Journal of Computational Biology*, 23(8):651–661, August 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0002; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0002`.

Medvedev:2011:PBG

[MPC+11] Paul Medvedev, Son Pham, Mark Chaisson, Glenn Tesler, and Pavel Pevzner. Paired de Bruijn graphs: a novel approach for incorporating mate pair information into genome assemblers. *Journal of Computational Biology*, 18(11):1625–1634, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-

8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0151; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0151.

Madec:2016:GOS

[MPG+16] Morgan Madec, François Pecheux, Yves Gendrault, Elise Rosati, Christophe Lallement, and Jacques Haiech. GeNeDA: an open-source workflow for design automation of gene regulatory networks inspired from microelectronics. *Journal of Computational Biology*, 23(10):841–855, October 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0229; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0229.

Morgante:2005:SMS

[MPVZ05] Michele Morgante, Alberto Policriti, Nicola Vitacolonna, and Andrea Zuccolo. Structured motifs search. *Journal of Computational Biology*, 12(8):1065–1082, October 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1065; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1065.

Mefford:2020:EEA

[MPZ+20] Joel Mefford, Danny Park, Zhili Zheng, Arthur Ko, Mika Ala-Korpela, Markku Laakso, Päivi Pajukanta, Jian Yang, John Witte, and Noah Zaitlen. Efficient estimation and applications of cross-validated genetic predictions to polygenic risk scores and linear mixed models. *Journal of Computational Biology*, 27(4):599–612, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0325; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0325.

Mao:2023:GRN

[MPZL23] Guo Mao, Zhengbin Pang, Ke Zuo, and Jie Liu. Gene regulatory network inference using convolutional neural networks from scRNA-seq data. *Journal of Computational Biology*, 30(5):619–631, May 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0355;

https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0355.

Markowitz:1995:CHM

[MR95] Victor M. Markowitz and Otto Ritter. Characterizing heterogeneous molecular biology database systems. *Journal of Computational Biology*, 2(4):547–556, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.547; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.547.

Ma:2008:CRP

[MR08a] Gang Ma and Christian M. Reidys. Canonical RNA pseudoknot structures. *Journal of Computational Biology*, 15 (10):1257–1273, December 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0121; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0121.

Murali:2008:NLB

[MR08b] T. M. Murali and Corban G. Rivera. Network Legos: Building blocks of cellular wiring diagrams. *Journal of Computational Biology*, 15(7):829–844, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0139; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0139.

Mehrzadi:2024:MGM

[MRG+24] Arash Mehrzadi, Elham Rezaee, Sajjad Gharaghani, Zeynab Fakhar, and Seyed Mohsen Mirhosseini. A molecular generative model of COVID-19 main protease inhibitors using long short-term memory-based recurrent neural network. *Journal of Computational Biology*, 31(1):83–98, January 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0064; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0064.

Mercatanti:2002:MPA

[MRM+02] Alberto Mercatanti, Giuseppe Rainaldi, Laura Mariani, Roberto Marangoni, and Lorenzo Citti. A method for prediction of

accessible sites on an mRNA sequence for target selection of hammerhead ribozymes. *Journal of Computational Biology*, 9(4):641–653, August 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652702760277363; https://www.liebertpub.com/doi/pdf/10.1089/106652702760277363`.

Majumdar:2020:IFS

[MRM20] Sayanti Guha Majumdar, Anil Rai, and Dwijesh C. Mishra. Integrated framework for selection of additive and nonadditive genetic markers for genomic selection. *Journal of Computational Biology*, 27(6):845–855, June 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0223; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0223`.

Ma:2008:DRC

[MRR+08] Jian Ma, Aakrosh Ratan, Brian J. Raney, Bernard B. Suh, Louxin Zhang, Webb Miller, and David Haussler. DUPCAR: Reconstructing contiguous ancestral regions with duplications. *Journal of Computational Biology*, 15(8):1007–1027, October 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0069; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0069`.

Morad:2018:SAI

[MRS+18] Fatima A. Morad, Omran M. Rashidi, Saida S. Sadath, Faisal A. Al-Allaf, Mohammad Athar, Mohamed N. Alama, Sherif E. Edris, Nabeel S. Bondagji, Noor A. Shaik, Babajan Banaganapalli, and Zuhier Awan. In silico approach to investigate the structural and functional attributes of familial hypercholesterolemia variants reported in the Saudi population. *Journal of Computational Biology*, 25(2):170–181, February 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0018; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0018`.

Mitchell:2023:EUM

[MRY+23] Audrey Mitchell, Marco Ruiz, Soua Yang, Chen Wang, and Jaime I. Davila. Excerno: Using mutational signatures in

sequencing data to filter false variants caused by clinical archival. *Journal of Computational Biology*, 30(4):366–375, April 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0394; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0394`.

Mayraz:1999:CPM

[MS99] Guy Mayraz and Ron Shamir. Construction of physical maps from oligonucleotide fingerprints data. *Journal of Computational Biology*, 6(2):237–252, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.237; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.237`.

Marsan:2000:AES

[MS00] Laurent Marsan and Marie-France Sagot. Algorithms for extracting structured motifs using a suffix tree with an application to promoter and regulatory site consensus identification. *Journal of Computational Biology*, 7(3–4):345–362, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Michailidis:2003:ARB

[MS03] George Michailidis and Kerby Shedden. The application of rule-based methods to class prediction problems in genomics. *Journal of Computational Biology*, 10(5):689–698, October 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652703322539033; https://www.liebertpub.com/doi/pdf/10.1089/106652703322539033`.

Ma:2024:RSI

[MS24] Jian Ma and Mona Singh. RECOMB 2024 special issue. *Journal of Computational Biology*, 31(10):907, October 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0809`.

Molineris:2010:NAI

[MSB+10] Ivan Molineris, Gabriele Sales, Federico Bianchi, Ferdinando Di Cunto, and Michele Caselle. A new approach for the identification of processed pseudogenes. *Journal of Computational Biology*, 17(5):755–765, May 2010. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0027; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0027.

Macula:2008:NIP

[MSBR08] Anthony J. Macula, Alexander Schliep, Morgan A. Bishop, and Thomas E. Renz. New, improved, and practical k-stem sequence similarity measures for probe design. *Journal of Computational Biology*, 15(5):525–534, June 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0208; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0208.

Mongia:2020:DDM

[MSM20] Aanchal Mongia, Debarka Sengupta, and Angshul Majumdar. deepMc: Deep matrix completion for imputation of single-cell RNA-seq data. *Journal of Computational Biology*, 27(7):1011–1019, July 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0278; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0278.

Marbach:2009:GRS

[MSMF09] Daniel Marbach, Thomas Schaffter, Claudio Mattiussi, and Dario Floreano. Generating realistic *In Silico* gene networks for performance assessment of reverse engineering methods. *Journal of Computational Biology*, 16(2):229–239, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.09TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.09TT.

Moretti:2019:ATF

[MSMP19] Antonio Moretti, Andrew Stirn, Gabriel Marks, and Itsik Pe'er. Autoencoding topographic factors. *Journal of Computational Biology*, 26(6):546–560, June 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0176; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0176.

Mohanty:2020:IMT

[MSN+20] Partha Sarathi Mohanty, Sandeep Sharma, Farah Naaz, Dilip Kumar, Archana Raikwar, and Shripad A. Patil. Inhibition of *Mycobacterium tuberculosis* tRNA-ligases using siRNA-based gene silencing method: a computational approach. *Journal of Computational Biology*, 27(1):91–99, January 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0156; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0156`.

Manes:2023:ESP

[MSNl23] Nathan P. Manes, Jian Song, and Aleksandra Nita-lazar. EnsMOD: a software program for omics sample outlier detection. *Journal of Computational Biology*, 30(6):726–735, June 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0243; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0243`.

Mehta:2022:PJM

[MSR22] Rohan S. Mehta, Mike Steel, and Noah A. Rosenberg. The probability of joint monophyly of samples of gene lineages for all species in an arbitrary species tree. *Journal of Computational Biology*, 29(7):679–703, July 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0647; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0647`.

Melkus:2024:THW

[MSRS24] Gatis Melkus, Andrejs Sizovs, Peteris Rucevskis, and Sandra Silina. Transcriptional hubs within cliques in ensemble Hi-C chromatin interaction networks. *Journal of Computational Biology*, 31(6):589–596, June 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Manuch:2010:TLB

[MSS10] Ján Maňuch, Ladislav Stacho, and Christine Stoll. Two lower bounds for self-assemblies at temperature 1. *Journal of Computational Biology*, 17(6):841–852, June 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0067;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0067.

Myasnikova:2021:QAD

[MSS21] Ekaterina M. Myasnikova, Marat A. Sabirov, and Alexander V. Spirov. Quantitative analysis of the dynamics of maternal gradients in the early *Drosophila* embryo. *Journal of Computational Biology*, 28(8):747–757, August 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0571; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0571.

Mahbub:2022:QBG

[MSS+22] Sazan Mahbub, Shashata Sawmya, Arpita Saha, Rezwana Reaz, M. Sohel Rahman, and Md. Shamsuzzoha Bayzid. Quartet based gene tree imputation using deep learning improves phylogenomic analyses despite missing data. *Journal of Computational Biology*, 29(11):1156–1172, November 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0212; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0212.

Myers:1996:PMA

[MSZM96] Gene Myers, Sanford Selznick, Zheng Zhang, and Webb Miller. Progressive multiple alignment with constraints. *Journal of Computational Biology*, 3(4):563–572, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.563; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.563.

Meng:2011:SAH

[MSZW11] Lu Meng, Fengzhu Sun, Xuegong Zhang, and Michael S. Waterman. Sequence alignment as hypothesis testing. *Journal of Computational Biology*, 18(5):677–691, May 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0328; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0328.

Mott:1999:ASG

[MT99] Richard Mott and Roger Tribe. Approximate statistics of gapped alignments. *Journal of Computational Biology*, 6(1):91–112, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.91; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.91`.

Mandoiu:2006:EAA

[MT06] Ion I. Măndoiu and Dragoş Trincă. Exact and approximation algorithms for DNA tag set design. *Journal of Computational Biology*, 13(3):732–744, April 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.732; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.732`.

Marras:2011:MLP

[MTC11] Elisabetta Marras, Antonella Travaglione, and Enrico Capobianco. Manifold learning in protein interactomes. *Journal of Computational Biology*, 18(1):81–96, January 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0258; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0258`.

Mori:2012:CBM

[MTF+12] Tomoya Mori, Takeyuki Tamura, Daiji Fukagawa, Atsuhiro Takasu, Etsuji Tomita, and Tatsuya Akutsu. A clique-based method using dynamic programming for computing edit distance between unordered trees. *Journal of Computational Biology*, 19(10):1089–1104, October 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0133; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0133`.

Matroud:2011:ASM

[MTH11] Atheer A. Matroud, Christopher P. Tuffley, and Michael D. Hendy. An algorithm to solve the motif alignment problem for approximate nested tandem repeats in biological sequences.

Journal of Computational Biology, 18(9):1211–1218, September 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0101; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0101.

Mukherjee:2003:EDS

[MTR+03] Sayan Mukherjee, Pablo Tamayo, Simon Rogers, Ryan Rifkin, Anna Engle, Colin Campbell, Todd R. Golub, and Jill P. Mesirov. Estimating dataset size requirements for classifying DNA microarray data. *Journal of Computational Biology*, 10(2):119–142, April 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703321825928; https://www.liebertpub.com/doi/pdf/10.1089/106652703321825928.

McDermott:2009:BHI

[MTYH09] Jason E. McDermott, Ronald C. Taylor, Hyunjin Yoon, and Fred Heffron. Bottlenecks and hubs in inferred networks are important for virulence in *Salmonella typhimurium*. *Journal of Computational Biology*, 16(2):169–180, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.04TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.04TT.

Muller:2000:MAA

[MV00] Tobias Müller and Martin Vingron. Modeling amino acid replacement. *Journal of Computational Biology*, 7(6):761–776, December 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270050514918; https://www.liebertpub.com/doi/pdf/10.1089/10665270050514918.

Miller:2004:SRI

[MV04] Webb Miller and Martin Vingron. Special RECOMB 2003 issue. *Journal of Computational Biology*, 11(2–3):213, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Menegaux:2019:CED

[MV19] Romain Menegaux and Jean-Philippe Vert. Continuous embeddings of DNA sequencing reads and application to metage-

nomics. *Journal of Computational Biology*, 26(6):509–518, June 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0174; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0174`.

Mooney:2006:PSM

[MVP06] Catherine Mooney, Alessandro Vullo, and Gianluca Pollastri. Protein structural motif prediction in multidimensional ϕ–ψ space leads to improved secondary structure prediction. *Journal of Computational Biology*, 13(8):1489–1502, October 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1489; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1489`.

Martin-Vide:2019:P

[MVVR19] Carlos Martín-Vide and Miguel A. Vega-Rodríguez. Preface. *Journal of Computational Biology*, 26(9):891–892, September 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.29023.cmv`.

Mohl:2010:LPA

[MWB10] Mathias Möhl, Sebastian Will, and Rolf Backofen. Lifting prediction to alignment of RNA pseudoknots. *Journal of Computational Biology*, 17(3):429–442, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0168; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0168`.

Meidanis:2002:LBR

[MWD02] João Meidanis, Maria M. T. Walter, and Zanoni Dias. A lower bound on the reversal and transposition diameter. *Journal of Computational Biology*, 9(5):743–745, October 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652702761034163; https://www.liebertpub.com/doi/pdf/10.1089/106652702761034163`.

Murray:2022:EDS

[MWL22] Keith T. Murray, Mien Brabeeba Wang, and Nancy Lynch. Emergence of direction-selective retinal cell types in task-

optimized deep learning models. *Journal of Computational Biology*, 29(4):370–381, April 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0368; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0368`.

McGuire:2000:BMD

[MWP00] Gráinne McGuire, Frank Wright, and Michael J. Prentice. A Bayesian model for detecting past recombination events in DNA multiple alignments. *Journal of Computational Biology*, 7(1–2): 159–170, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Mazza:2016:FAM

[MWRS16] Arnon Mazza, Allon Wagner, Eytan Ruppin, and Roded Sharan. Functional alignment of metabolic networks. *Journal of Computational Biology*, 23(5):390–399, May 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0203; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0203`.

Mao:2019:PPA

[MWZ19] Guo Mao, Shu-Lin Wang, and Wei Zhang. Prediction of potential associations between MicroRNA and disease based on Bayesian probabilistic matrix factorization model. *Journal of Computational Biology*, 26(9):1030–1039, September 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0012; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0012`.

Mao:2019:HDH

[MXJ19] Xiaodan Mao, Yichen Xu, and Zhenran Jiang. HColonDB: a database for human colon cancer research. *Journal of Computational Biology*, 26(3):218–224, March 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0193; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0193`.

Mo:2020:KRE

[MXW+20] Lujiao Mo, Guanhua Xu, Channi Wu, Kanda Pan, Ping Pan, Lingfeng Yu, and Xiaoyuan Shen. Key regulatory effect of activated *HIF-1α /VEGFA* signaling pathway in systemic capillary leak syndrome confirmed by bioinformatics analysis. *Journal of Computational Biology*, 27(6):914–922, June 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0222; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0222`.

Martin:2011:GAA

[MYBK+11] Jeffrey W. Martin, Anthony K. Yan, Chris Bailey-Kellogg, Pei Zhou, and Bruce R. Donald. A geometric arrangement algorithm for structure determination of symmetric protein homo-oligomers from NOEs and RDCs. *Journal of Computational Biology*, 18(11):1507–1523, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0173; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0173`.

Myers:1995:TSA

[Mye95] Eugene W. Myers. Toward simplifying and accurately formulating fragment assembly. *Journal of Computational Biology*, 2(2):275–290, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.275; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.275`.

Myers:1996:AMN

[Mye96] Eugene W. Myers. Approximate matching of network expressions with spacers. *Journal of Computational Biology*, 3(1):33–51, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.33; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.33`.

Myers:2003:SRI

[Mye03] Eugene W. Myers. Special RECOMB 2002 issue. *Journal of Computational Biology*, 10(3–4):237, June 2003. CODEN

JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Mahmud:2020:EDT

[MYS+20] A. K. M. Firoj Mahmud, Doo Yang, Per Stenberg, Ilya Ioshikhes, and Soumyadeep Nandi. Exploring a *Drosophila* transcription factor interaction network to identify cis-regulatory modules. *Journal of Computational Biology*, 27(8):1313–1328, August 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0160; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0160`.

Maximova:2018:SBM

[MZC+18] Tatiana Maximova, Zijing Zhang, Daniel B. Carr, Erion Plaku, and Amarda Shehu. Sample-based models of protein energy landscapes and slow structural rearrangements. *Journal of Computational Biology*, 25(1):33–50, January 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0158; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0158`.

Moskon:2018:GAV

[MZM18] Miha Moškon, Nikolaj Zimic, and Miha Mraz. Grohar: Automated visualization of genome-scale metabolic models and their pathways. *Journal of Computational Biology*, 25(5):505–508, May 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0209; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0209`.

Moulton:2000:MRS

[MZS+00] Vincent Moulton, Michael Zuker, Michael Steel, Robin Pointon, and David Penny. Metrics on RNA secondary structures. *Journal of Computational Biology*, 7(1–2):277–292, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Ma:2017:DCB

[MZS+17] Xiuli Ma, Guangyu Zhou, Jingbo Shang, Jingjing Wang, Jian Peng, and Jiawei Han. Detection of complexes in biological networks through diversified dense subgraph mining. *Journal of Computational Biology*, 24(9):923–941, September

2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0037; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0037.

Naito:2018:HSS

[Nai18] Tatsuhiko Naito. Human splice-site prediction with deep neural networks. *Journal of Computational Biology*, 25(8):954–961, August 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0041; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0041.

Naor:1994:NOA

[NB94] Dalit Naor and Douglas L. Brutlag. On near-optimal alignments of biological sequences. *Journal of Computational Biology*, 1(4):349–366, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.349; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.349.

Nurk:2013:ASC

[NBA+13] Sergey Nurk, Anton Bankevich, Dmitry Antipov, Alexey A. Gurevich, Anton Korobeynikov, Alla Lapidus, Andrey D. Prjibelski, Alexey Pyshkin, Alexander Sirotkin, Yakov Sirotkin, Ramunas Stepanauskas, Scott R. Clingenpeel, Tanja Woyke, Jeffrey S. Mclean, Roger Lasken, Glenn Tesler, Max A. Alekseyev, and Pavel A. Pevzner. Assembling single-cell genomes and mini-metagenomes from chimeric MDA products. *Journal of Computational Biology*, 20(10):714–737, October 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0084; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0084.

Nowicki:2018:MPI

[NBB18] Marek Nowicki, Davit Bzhalava, and Piotr Bała. Massively parallel implementation of sequence alignment with basic local alignment search tool using parallel computing in Java library. *Journal of Computational Biology*, 25(8):871–881, August 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/

abs/10.1089/cmb.2018.0079; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0079.

Newkirk:2011:AAS

[NBC+11] Daniel Newkirk, Jacob Biesinger, Alvin Chon, Kyoko Yokomori, and Xiaohui Xie. AREM: Aligning short reads from ChIP-Sequencing by expectation maximization. *Journal of Computational Biology*, 18(11):1495–1505, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0185; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0185.

Narasimhan:2002:MPS

[NBG+02] Giri Narasimhan, Changsong Bu, Yuan Gao, Xuning Wang, Ning Xu, and Kalai Mathee. Mining protein sequences for motifs. *Journal of Computational Biology*, 9(5):707–720, October 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652702761034145; https://www.liebertpub.com/doi/pdf/10.1089/106652702761034145.

Nguyen:2013:DMD

[NBGA13] Viet-An Nguyen, Jordan Boyd-Graber, and Stephen F. Altschul. Dirichlet mixtures, the Dirichlet process, and the structure of protein space. *Journal of Computational Biology*, 20(1):1–18, January 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0244; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0244.

Nadkarni:1996:DWD

[NCC+96] Prakash Nadkarni, Kei-Hoi Cheung, Carmela Castiglione, Perry Miller, and Kenneth Kidd. DNA workbench: a database package to manage regional physical mapping. *Journal of Computational Biology*, 3(2):319–329, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.319; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.319.

Nation:2021:CAF

[NCMS+21] J. B. Nation, Justin Cabot-Miller, Oren Segal, Robert Lucito, and Kira Adaricheva. Combining algorithms to find signatures that predict risk in early-stage stomach cancer. *Journal of Computational Biology*, 28(10):985–1006, October 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0568; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0568`.

Novinskaya:2017:DLD

[NDMK17] Anastasia Novinskaya, Didier Devaurs, Mark Moll, and Lydia E. Kavraki. Defining low-dimensional projections to guide protein conformational sampling. *Journal of Computational Biology*, 24(1):79–89, January 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0144; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0144`.

Nebel:2002:CPR

[Neb02] Markus E. Nebel. Combinatorial properties of RNA secondary structures. *Journal of Computational Biology*, 9 (3):541–573, June 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652702760138628; https://www.liebertpub.com/doi/pdf/10.1089/106652702760138628`.

Nasser:2022:DUN

[NES22] Rami Nasser, Yonina C. Eldar, and Roded Sharan. Deep unfolding for non-negative matrix factorization with application to mutational signature analysis. *Journal of Computational Biology*, 29(1):45–55, January 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0438; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0438`.

Neuwald:2014:BSO

[Neu14a] Andrew F. Neuwald. A Bayesian sampler for optimization of protein domain hierarchies. *Journal of Computational Biology*, 21(3):269–286, March 2014. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0099; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0099.

Neuwald:2014:ECI

[Neu14b] Andrew F. Neuwald. Evaluating, comparing, and interpreting protein domain hierarchies. *Journal of Computational Biology*, 21(4):287–302, April 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0098; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0098.

Newberg:2008:SGS

[New08] Lee A. Newberg. Significance of gapped sequence alignments. *Journal of Computational Biology*, 15(9):1187–1194, November 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0125; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0125.

Nojgaard:2021:CGS

[NFHM21] Nikolai Nøjgaard, Walter Fontana, Marc Hellmuth, and Daniel Merkle. Cayley graphs of semigroups applied to atom tracking in chemistry. *Journal of Computational Biology*, 28(7):701–715, July 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0548; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0548.

Nov:2013:OSA

[NFJ13] Yuval Nov, Alexander Fulton, and Karl-Erich Jaeger. Optimal scanning of all single-point mutants of a protein. *Journal of Computational Biology*, 20(12):990–997, December 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0026; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0026.

Nigham:2008:PCF

[NH08] Anshul Nigham and David Hsu. Protein conformational flexibility analysis with noisy data. *Journal of Computational*

Biology, 15(7):813–828, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0138; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0138`.

Nguyen:2010:SWP

[NHOV10] Nha Nguyen, Heng Huang, Soontorn Oraintara, and An Vo. Stationary wavelet packet transform and dependent Laplacian bivariate shrinkage estimator for Array-CGH data smoothing. *Journal of Computational Biology*, 17(2):139–152, February 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0013; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0013`.

Nguyen:2015:BPG

[NHZ+15] Ngan Nguyen, Glenn Hickey, Daniel R. Zerbino, Brian Raney, Dent Earl, Joel Armstrong, W. James Kent, David Haussler, and Benedict Paten. Building a Pan-genome reference for a population. *Journal of Computational Biology*, 22(5):387–401, May 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0146; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0146`.

Nicodeme:2001:FAM

[Nic01] Pierre Nicodème. Fast approximate motif statistics. *Journal of Computational Biology*, 8(3):235–248, June 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270152530836; https://www.liebertpub.com/doi/pdf/10.1089/10665270152530836`.

Narayanan:2007:CPI

[NK07] Manikandan Narayanan and Richard M. Karp. Comparing protein interaction networks via a graph match-and-split algorithm. *Journal of Computational Biology*, 14(7):892–907, September 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0025; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0025`.

Ng:2011:ACS

[NK11] Patrick Ng and Uri Keich. Alignment constrained sampling. *Journal of Computational Biology*, 18(2):155–168, February 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0220; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0220`.

Novikov:2021:SRS

[NKG+21] Daniel Novikov, Sergey Knyazev, Mark Grinshpon, Pelin Icer, Pavel Skums, and Alex Zelikovsky. Scalable reconstruction of SARS-CoV-2 phylogeny with recurrent mutations. *Journal of Computational Biology*, 28(11):1130–1141, November 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0306; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0306`.

Newton:2001:DVE

[NKR+01] M. A. Newton, C. M. Kendziorski, C. S. Richmond, F. R. Blattner, and K. W. Tsui. On differential variability of expression ratios: Improving statistical inference about gene expression changes from microarray data. *Journal of Computational Biology*, 8(1):37–52, February 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652701300099074; https://www.liebertpub.com/doi/pdf/10.1089/106652701300099074`.

Newberg:2009:ECD

[NL09] Lee A. Newberg and Charles E. Lawrence. Exact calculation of distributions on integers, with application to sequence alignment. *Journal of Computational Biology*, 16(1):1–18, January 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0137; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0137`.

Nolan:2017:IMS

[NLC17] Bridget E. Nolan, Emily Levenson, and Brian Y. Chen. Influential mutations in the SMAD4 trimer complex can be detected from disruptions of electrostatic complementarity. *Journal of Computational Biology*, 24(1):68–78, January

2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0162; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0162.

Nambiar:2023:TNN

[NLH+23] Ananthan Nambiar, Simon Liu, Maeve Heflin, John Malcolm Forsyth, Sergei Maslov, Mark Hopkins, and Anna Ritz. Transformer neural networks for protein family and interaction prediction tasks. *Journal of Computational Biology*, 30(1):95–111, January 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0132; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0132.

Noe:2014:CCS

[NM14] Laurent Noé and Donald E. K. Martin. A coverage criterion for spaced seeds and its applications to support vector machine string kernels and k-mer distances. *Journal of Computational Biology*, 21(12):947–963, December 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0173; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0173.

Noto:2015:CCS

[NME+15] Keith Noto, Saeed Majidi, Andrea G. Edlow, Heather C. Wick, Diana W. Bianchi, and Donna K. Slonim. CSAX: Characterizing systematic anomalies in eXpression data. *Journal of Computational Biology*, 22(5):402–413, May 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0155; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0155.

Nedelec:2005:PAA

[NMG+05] Elodie Nédélec, Thomas Moncion, Elisabeth Gassiat, Bruno Bossard, Guillemette Duchateau-Nguyen, Alain Denise, and Michel Termier. A pairwise alignment algorithm which favors clusters of blocks. *Journal of Computational Biology*, 12(1):33–47, February 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.33;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.33.

Nettelblad:2013:FAD

[NMH13] Carl Nettelblad, Behrang Mahjani, and Sverker Holmgren. Fast and accurate detection of multiple quantitative trait loci. *Journal of Computational Biology*, 20(9):687–702, September 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0242; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0242.

Nourani:2021:GGO

[Nou21] Esmaeil Nourani. GoVec: Gene ontology representation learning using weighted heterogeneous graph and meta-path. *Journal of Computational Biology*, 28(12):1196–1207, December 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0069; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0069.

Nagarajan:2009:PCS

[NP09] Niranjan Nagarajan and Mihai Pop. Parametric complexity of sequence assembly: Theory and applications to next generation sequencing. *Journal of Computational Biology*, 16(7):897–908, July 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0005; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0005.

Navarro:2003:FSC

[NR03] Gonzalo Navarro and Mathieu Raffinot. Fast and simple character classes and bounded gaps pattern matching, with applications to protein searching. *Journal of Computational Biology*, 10(6):903–923, December 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703322756140; https://www.liebertpub.com/doi/pdf/10.1089/106652703322756140.

Nebel:2011:LCR

[NRW11] Markus E. Nebel, Christian M. Reidys, and Rita R. Wang. Loops in canonical RNA pseudoknot structures. *Journal of Computational Biology*, 18(12):1793–1806, December

2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0022; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0022.

Ng:2018:BBD

[NS18] Albert Ng and Dong Si. Beta-barrel detection for medium resolution cryo-electron microscopy density maps using genetic algorithms and ray tracing. *Journal of Computational Biology*, 25(3):326–336, March 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0155; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0155.

Nakajima:2023:CDR

[NS23] Masaru Nakajima and Andrew D. Smith. Counting distinguishable RNA secondary structures. *Journal of Computational Biology*, 30(10):1089–1097, October 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0501; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0501.

Nicola:2008:NMA

[NSA08] George Nicola, Colin A. Smith, and Ruben Abagyan. New method for the assessment of all drug-like pockets across a structural genome. *Journal of Computational Biology*, 15(3):231–240, April 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0178; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0178.

Niu:2023:SAG

[NSH+23] Puhua Niu, Maria J. Soto, Shuai Huang, Byung jun Yoon, Edward R. Dougherty, Francis J. Alexander, Ian Blaby, and Xiaoning Qian. Sensitivity analysis of genome-scale metabolic flux prediction. *Journal of Computational Biology*, 30(7):751–765, July 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0368; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0368.

Navlakha:2009:RBM

[NSK09] Saket Navlakha, Michael C. Schatz, and Carl Kingsford. Revealing biological modules via graph summarization. *Journal of Computational Biology*, 16(2):253–264, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.11TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.11TT`.

Ness:2018:BAL

[NSMV18] Robert O. Ness, Karen Sachs, Parag Mallick, and Olga Vitek. A Bayesian active learning experimental design for inferring signaling networks. *Journal of Computational Biology*, 25(7):709–725, July 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0247; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0247`.

Nayeem:2023:MFP

[NSRR23] Muhammad Ali Nayeem, Naser Anjum Samudro, M. Saifur Rahman, and M. Sohel Rahman. MAMMLE: a framework for phylogeny estimation based on multiobjective application-aware multiple sequence alignment and maximum likelihood ensemble. *Journal of Computational Biology*, 30(3):245–249, March 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0533; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0533`.

Nayak:1999:SCH

[NSZ99] Ashwin Nayak, Alistair Sinclair, and Uri Zwick. Spatial codes and the hardness of string folding problems. *Journal of Computational Biology*, 6(1):13–36, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.13; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.13`.

Nicolas:2006:RJM

[NTMM06] Pierre Nicolas, Anne-Sophie Tocquet, Vincent Miele, and Florence Muri. A reversible jump Markov chain Monte Carlo algorithm for bacterial promoter motifs discovery. *Journal of Computational Biology*, 13(3):651–667, April 2006. CODEN

JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.651; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.651.

Noy:2011:SBF

[NTWF11] Karin Noy, Fadi Towfic, Gayle M. Wittenberg, and Daniel Fasulo. Shape-based feature matching improves protein identification via LC-MS and tandem MS. *Journal of Computational Biology*, 18(4):547–557, April 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0155; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0155.

Nuel:2004:LSL

[Nue04] G. Nuel. LD-SPatt: Large deviations statistics for patterns on Markov chains. *Journal of Computational Biology*, 11 (6):1023–1033, December 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.1023; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.1023.

Nelson:2009:RCG

[NV09] Craig Nelson and Stéphane Vialette. RECOMB–Comparative genomics special issue. *Journal of Computational Biology*, 16 (10):1285–1286, October 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.002P.

Ni:2012:RNM

[NV12] Shengyu Ni and Martin Vingron. R2KS: a novel measure for comparing gene expression based on ranked gene lists. *Journal of Computational Biology*, 19(6):766–775, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0026; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0026.

Nguyen:2015:SWE

[NVCW15] Nha Nguyen, An Vo, Inchan Choi, and Kyoung-Jae Won. A stationary wavelet entropy-based clustering approach accurately predicts gene expression. *Journal of Computational*

Biology, 22(3):236–249, March 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0221; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0221.

Nguyen:2014:WAD

[NVW14] Nha Nguyen, An Vo, and Kyoung-Jae Won. A wavelet approach to detect enriched regions and explore epigenomic landscapes. *Journal of Computational Biology*, 21(11):846–854, November 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0095; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0095.

Nov:2005:MAP

[NW05] Yuval Nov and Lawrence M. Wein. Modeling and analysis of protein design under resource constraints. *Journal of Computational Biology*, 12(2):247–282, March 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.247; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.247.

Nebel:2012:ACP

[NW12] Markus E. Nebel and Frank Weinberg. Algebraic and combinatorial properties of common RNA pseudoknot classes with applications. *Journal of Computational Biology*, 19 (10):1134–1150, October 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0094; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0094.

Nakhleh:2005:RRE

[NWLS05] Luay Nakhleh, Tandy Warnow, C. Randal Linder, and Katherine St.John. Reconstructing reticulate evolution in species — theory and practice. *Journal of Computational Biology*, 12(6):796–811, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.796; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.796.

Navlakha:2010:FBA

[NWN+10] Saket Navlakha, James White, Niranjan Nagarajan, Mihai Pop, and Carl Kingsford. Finding biologically accurate clusterings in hierarchical tree decompositions using the variation of information. *Journal of Computational Biology*, 17(3):503–516, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0173; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0173`.

Niu:2020:WGC

[NXGL20] Xiaoguang Niu, Yongtao Xu, Ni Gao, and Aiwu Li. Weighted gene coexpression network analysis reveals the critical lncRNAs and mRNAs in development of Hirschsprung's disease. *Journal of Computational Biology*, 27(7):1115–1129, July 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0261; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0261`.

Niu:2015:DTI

[NXL+15] Shu-Yuan Niu, Ming-Yuan Xin, Jian Luo, Ming-Yao Liu, and Zhen-Ran Jiang. DSEP: a tool implementing novel method to predict side effects of drugs. *Journal of Computational Biology*, 22(12):1108–1117, December 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0129; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0129`.

Niyogisubizo:2025:AGR

[NZM+25] Jovial Niyogisubizo, Keliang Zhao, Jintao Meng, Yi Pan, Rosiyadi Didi, and Yanjie Wei. Attention-guided residual U-net with SE connection and ASPP for watershed-based cell segmentation in microscopy images. *Journal of Computational Biology*, 32(2):225–237, February 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0446; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0446`.

Overton:1994:QSQ

[OAHA94] G. Christian Overton, Jeffrey S. Aaronson, Juergen Haas, and Julie Adams. QGB: a system for querying sequence database fields and features. *Journal of Computational Biology*, 1(1):3–14, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.3; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.3`.

Ogurtsov:2024:MGG

[OAR+24] Aleksey Ogurtsov, Gelio Alves, Alex Rubio, Brendan Joyce, Björn Andersson, Roger Karlsson, Edward R. B. Moore, and Yi-Kuo Yu. `MiCId GUI`: The graphical user interface for `MiCId`, a fast microorganism classification and identification workflow with accurate statistics and high recall. *Journal of Computational Biology*, 31(2):175–178, February 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0149; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0149`.

Ouangraoua:2010:CSG

[OB10] Aïda Ouangraoua and Anne Bergeron. Combinatorial structure of genome rearrangements scenarios. *Journal of Computational Biology*, 17(9):1129–1144, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0126; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0126`.

Orenstein:2016:EDC

[OB16] Yaron Orenstein and Bonnie Berger. Efficient design of compact unstructured RNA libraries covering all k-mers. *Journal of Computational Biology*, 23(2):67–79, February 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0179; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0179`.

Ozcelik:2023:FIG

[ÖBA+23] Rıza Özçelik, Alperen Bağ, Berk Atil, Melih Barsbey, Arzucan Özgür, and Elif Ozkirimli. A framework for improving

the generalizability of drug–target affinity prediction models. *Journal of Computational Biology*, 30(11):1226–1239, November 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0208; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0208`.

Oliveira:2019:CSR

[OBDD19a] Andre Rodrigues Oliveira, Klairton Lima Brito, Ulisses Dias, and Zanoni Dias. On the complexity of sorting by reversals and transpositions problems. *Journal of Computational Biology*, 26(11):1223–1229, November 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0078; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0078`.

Oliveira:2019:SWR

[OBDD19b] Andre Rodrigues Oliveira, Klairton Lima Brito, Zanoni Dias, and Ulisses Dias. Sorting by weighted reversals and transpositions. *Journal of Computational Biology*, 26(5):420–431, May 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0257; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0257`.

OReilly:2016:EEO

[OBDV16] Eliza O'Reilly, François Baccelli, Gustavo De Veciana, and Haris Vikalo. End-to-end optimization of high-throughput DNA sequencing. *Journal of Computational Biology*, 23 (10):789–800, October 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0185; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0185`.

Oliveira:2003:CMI

[OBJO+03] Joseph S. Oliveira, Colin G. Bailey, Janet B. Jones-Oliveira, David A. Dixon, Dean W. Gull, and Mary L. Chandler. A computational model for the identification of biochemical pathways in the Krebs cycle. *Journal of Computational Biology*, 10(1):57–82, February 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.`

liebertpub.com/doi/abs/10.1089/106652703763255679; https://www.liebertpub.com/doi/pdf/10.1089/106652703763255679.

Ouangraoua:2011:TPU

[OBS11] Aïda Ouangraoua, Anne Bergeron, and Krister M. Swenson. Theory and practice of ultra-perfection. *Journal of Computational Biology*, 18(9):1219–1230, September 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0086; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0086.

Ohkubo:2000:PEF

[OC00] Y. Zenmei Ohkubo and Gordon M. Crippen. Potential energy function for continuous state models of globular proteins. *Journal of Computational Biology*, 7(3–4):363–379, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Oill:2021:PAR

[ODNW21] Angela M. Taravella Oill, Anagha J. Deshpande, Heini M. Natri, and Melissa A. Wilson. PopInf: an approach for reproducibly visualizing and assigning population affiliation in genomic samples of uncertain origin. *Journal of Computational Biology*, 28(3):296–303, March 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0434; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0434.

Osmankovic:2018:NAD

[ODPB18] Dinko Osmankovic, Semir Doric, Naris Pojskic, and Lada Lukic Bilela. New approach to detect coiled coil and leucine zipper motifs in protein sequences. *Journal of Computational Biology*, 25(11):1278–1283, November 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0104; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0104.

Ovadia:2011:CRP

[OFCLH11] Y. Ovadia, D. Fielder, C. Conow, and R. Libeskind-Hadas. The cophylogeny reconstruction problem is NP-Complete. *Journal of Computational Biology*, 18(1):59–65, January 2011.

CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0240; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0240.

ONeill:2014:IRT

[OFE14] Patrick K. O'Neill, Robert Forder, and Ivan Erill. Informational requirements for transcriptional regulation. *Journal of Computational Biology*, 21(5):373–384, May 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0032; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0032.

Ozery-Flato:2007:SRT

[OFS07] Michal Ozery-Flato and Ron Shamir. Sorting by reciprocal translocations via reversals theory. *Journal of Computational Biology*, 14(4):408–422, May 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.A003; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.A003.

Ozery-Flato:2008:SGC

[OFS08] Michal Ozery-Flato and Ron Shamir. Sorting genomes with centromeres by translocations. *Journal of Computational Biology*, 15(7):793–812, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0136; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0136.

Ozery-Flato:2009:SCK

[OFS09] Michal Ozery-Flato and Ron Shamir. Sorting cancer karyotypes by elementary operations. *Journal of Computational Biology*, 16(10):1445–1460, October 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0083; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0083.

Ott:2003:SAA

[OH03] Jurg Ott and Josephine Hoh. Set association analysis of SNP case-control and microarray data. *Journal of Computational*

Biology, 10(3–4):569–574, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

OHare:2015:IHD

[O'H15] Anthony O'Hare. Inference in high-dimensional parameter space. *Journal of Computational Biology*, 22(11): 997–1004, November 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0086; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0086`.

Ojewole:2018:BBB

[OJFD18] Adegoke A. Ojewole, Jonathan D. Jou, Vance G. Fowler, and Bruce R. Donald. *BBK* (Branch and Bound Over K*)*: a provable and efficient ensemble-based protein design algorithm to optimize stability and binding affinity over large sequence spaces. *Journal of Computational Biology*, 25(7):726–739, July 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0267; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0267`.

Oliveira:2004:HTA

[OJOD+04] Joseph S. Oliveira, Janet B. Jones-Oliveira, David A. Dixon, Colin G. Bailey, and Dean W. Gull. Hyperdigraph-theoretic analysis of the EGFR signaling network: Initial steps leading to GTP:Ras complex formation. *Journal of Computational Biology*, 11(5):812–842, October 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.812; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.812`.

Ohlebusch:2008:SEC

[OK08] Enno Ohlebusch and Stefan Kurtz. Space efficient computation of rare maximal exact matches between multiple sequences. *Journal of Computational Biology*, 15(4):357–377, May 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0105; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0105`.

Orlovich:2021:SFS

[OKKS21] Yury Orlovich, Kirill Kukharenko, Volker Kaibel, and Pavel Skums. Scale-free spanning trees and their application in genomic epidemiology. *Journal of Computational Biology*, 28(10):945–960, October 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0500; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0500`.

Orenstein:2013:RAF

[OMS13] Yaron Orenstein, Eran Mick, and Ron Shamir. RAP: Accurate and fast motif finding based on protein-binding microarray data. *Journal of Computational Biology*, 20(5):375–382, May 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0253; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0253`.

Ouedraogo:2024:OPR

[OO24] Wend Yam D. D. Ouedraogo and Aida Ouangraoua. Orthology and paralogy relationships at transcript level. *Journal of Computational Biology*, 31(4):277–293, April 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0400; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0400`.

Ouangraoua:2014:ICC

[OR14] Aïda Ouangraoua and Mathieu Raffinot. On the identification of conflicting contiguities in ancestral genome reconstruction. *Journal of Computational Biology*, 21(1):64–79, January 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0086; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0086`.

Orenstein:2020:RBU

[Ore20] Yaron Orenstein. Reverse de Bruijn: Utilizing reverse peptide synthesis to cover all amino acid k-mers. *Journal of Computational Biology*, 27(3):376–385, March 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0448;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0448.

Ouangraoua:2011:AMD

[OSC11] Aïda Ouangraoua, Krister M. Swenson, and Cedric Chauve. A 2-approximation for the minimum duplication speciation problem. *Journal of Computational Biology*, 18(9):1041–1053, September 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0108; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0108.

Ong:2015:SMM

[OSK+15] Edison Ong, Anthony Szedlak, Yunyi Kang, Peyton Smith, Nicholas Smith, Madison McBride, Darren Finlay, Kristiina Vuori, James Mason, Edward D. Ball, Carlo Piermarocchi, and Giovanni Paternostro. A scalable method for molecular network reconstruction identifies properties of targets and mutations in acute myeloid leukemia. *Journal of Computational Biology*, 22(4):266–288, April 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0297; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0297.

Orenstein:2018:JBC

[OYB18] Yaron Orenstein, Yun William Yu, and Bonnie Berger. Joker de Bruijn: Covering k-mers using joker characters. *Journal of Computational Biology*, 25(11):1171–1178, November 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0032; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0032.

Onuki:2012:PMB

[OYY+12] Ritsuko Onuki, Ryo Yamada, Rui Yamaguchi, Minoru Kanehisa, and Tetsuo Shibuya. Population model–based inter-diplotype similarity measure for accurate diplotype clustering. *Journal of Computational Biology*, 19(1):55–67, January 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0227; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0227.

Penchovsky:2003:DLD

[PA03] Robert Penchovsky and Jörg Ackermann. DNA library design for molecular computation. *Journal of Computational Biology*, 10(2):215–229, April 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652703321825973; https://www.liebertpub.com/doi/pdf/10.1089/106652703321825973`.

Pattengale:2010:HMB

[PABE+10] Nicholas D. Pattengale, Masoud Alipour, Olaf R. P. Bininda-Emonds, Bernard M. E. Moret, and Alexandros Stamatakis. How many bootstrap replicates are necessary? *Journal of Computational Biology*, 17(3):337–354, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0179; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0179`.

Pachter:2002:AGP

[PAC02] Lior Pachter, Marina Alexandersson, and Simon Cawley. Applications of generalized pair hidden Markov models to alignment and gene finding problems. *Journal of Computational Biology*, 9(2):389–399, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270252935520; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935520`.

Parida:1998:UFO

[Par98] Laxmi Parida. A uniform framework for ordered restriction map problems. *Journal of Computational Biology*, 5 (4):725–739, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.725; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.725`.

Parida:2006:UPS

[Par06] Laxmi Parida. Using PQ structures for genomic rearrangement phylogeny. *Journal of Computational Biology*, 13(10): 1685–1700, December 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1685;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1685.

Parida:2007:DTM

[Par07a] Laxmi Parida. Discovering topological motifs using a compact notation. *Journal of Computational Biology*, 14(3):300–323, April 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0142; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0142.

Parida:2007:GPP

[Par07b] Laxmi Parida. Gapped permutation pattern discovery for gene order comparisons. *Journal of Computational Biology*, 14(1):45–55, January 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0103; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0103.

Parida:2007:SSL

[Par07c] Laxmi Parida. Statistical significance of large gene clusters. *Journal of Computational Biology*, 14(9):1145–1159, November 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0064; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0064.

Parida:2010:ARG

[Par10] Laxmi Parida. Ancestral recombinations graph: a reconstructability perspective using random-graphs framework. *Journal of Computational Biology*, 17(10):1345–1370, October 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0243; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0243.

Park:2024:UGR

[Par24] Heewon Park. Unveiling gene regulatory networks that characterize difference of molecular interplays between gastric cancer drug sensitive and resistance cell lines. *Journal of Computational Biology*, 31(3):257–274, March 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0215; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0215.

Pham:2013:PGN

[PAS+13] Son K. Pham, Dmitry Antipov, Alexander Sirotkin, Glenn Tesler, Pavel A. Pevzner, and Max A. Alekseyev. Path-set graphs: a novel approach for comprehensive utilization of paired reads in genome assembly. *Journal of Computational Biology*, 20(4):359–371, April 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0098; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0098.

Patterson:2024:SIP

[Pat24] Murray Patterson. *Special Issue, Part I* 19th International Symposium on Bioinformatics Research and Applications (ISBRA 2023). *Journal of Computational Biology*, 31(6):473–474, June 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Patterson:2025:SIP

[Pat25] Murray Patterson. *Special Issue, Part 2* 19th International Symposium on Bioinformatics Research and Applications (ISBRA 2023). *Journal of Computational Biology*, 32(2):125–126, February 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0905.

Palkowski:2018:PTC

[PB18] Marek Palkowski and Wlodzimierz Bielecki. Parallel tiled codes implementing the Smith–Waterman alignment algorithm for two and three sequences. *Journal of Computational Biology*, 25(10):1106–1119, October 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0006; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0006.

Paige:2021:RGP

[PBB+21] Brooks Paige, James Bell, Aurélien Bellet, Adrià Gascón, and Daphne Ezer. Reconstructing genotypes in private genomic

databases from genetic risk scores. *Journal of Computational Biology*, 28(5):435–451, May 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Park:2017:PCA

[PBMC17] Byeonghyeok Park, Min-Jeong Baek, Byoungnam Min, and In-Geol Choi. Prokaryotic contig annotation pipeline server: Web application for a prokaryotic genome annotation pipeline based on the `Shiny App` package. *Journal of Computational Biology*, 24(9):917–922, September 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0066; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0066`.

Pachter:1999:DBA

[PBS+99] Lior Pachter, Serafim Batzoglou, Valentin I. Spitkovsky, Eric Banks, Eric S. Lander, Daniel J. Kleitman, and Bonnie Berger. A dictionary-based approach for gene annotation. *Journal of Computational Biology*, 6(3–4):419–430, October 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Pounds:2005:SDE

[PC05] Stan Pounds and Cheng Cheng. Statistical development and evaluation of microarray gene expression data filters. *Journal of Computational Biology*, 12(4):482–495, May 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.482; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.482`.

Polynikis:2011:DCV

[PCC+11] Athanasios Polynikis, Giulia Cuccato, Stefania Criscuolo, Stephen J. Hogan, Mario Di Bernardo, and Diego Di Bernardo. Design and construction of a versatile synthetic network for bistable gene expression in mammalian systems. *Journal of Computational Biology*, 18(2):195–203, February 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0208; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0208`.

Parker:2013:SGD

[PCGBK13] Andrew S. Parker, Yoonjoo Choi, Karl E. Griswold, and Chris Bailey-Kellogg. Structure-guided deimmunization of therapeutic proteins. *Journal of Computational Biology*, 20 (2):152–165, February 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0251; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0251`.

Park:2018:SMB

[PCS18] Joonyeon Park, Myeongji Cho, and Hyeon S. Son. Simulation model of bacterial resistance to antibiotics using individual-based modeling. *Journal of Computational Biology*, 25(9):1059–1070, September 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0064; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0064`.

Pepe:2016:CPP

[PD16] Daniele Pepe and Jin Hwan Do. Comparison of perturbed pathways in two different cell models for Parkinson's disease with structural equation model. *Journal of Computational Biology*, 23(2):90–101, February 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0156; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0156`.

Pala:2020:EME

[PD20a] Elİf Pala and Tuba Denkçeken. Evaluation of miRNA expression profiles in schizophrenia using principal-component analysis-based unsupervised feature extraction method. *Journal of Computational Biology*, 27(8):1253–1263, August 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0412; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0412`.

Pepe:2020:AAM

[PD20b] Daniele Pepe and Jin Hwan Do. Analyzing apomorphine-mediated effects in a cell model for Parkinson's disease with

partial least squares structure equation modeling. *Journal of Computational Biology*, 27(8):1273–1282, August 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0386; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0386`.

Pagliarini:2013:GSM

[PdB13] Roberto Pagliarini and Diego di Bernardo. A genome-scale modeling approach to study inborn errors of liver metabolism: Toward an in silico patient. *Journal of Computational Biology*, 20(5):383–397, May 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0276; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0276`.

Pardo-diaz:2022:EIG

[PdBdP+22] Javier Pardo-diaz, Mariano Beguerisse-díaz, Philip S. Poole, Charlotte M. Deane, and Gesine Reinert. Extracting information from gene coexpression networks of *Rhizobium leguminosarum*. *Journal of Computational Biology*, 29(7):752–768, July 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0600; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0600`.

Porreca:2008:SIP

[PDdJFT08] Riccardo Porreca, Samuel Drulhe, Hidde de Jong, and Giancarlo Ferrari-Trecate. Structural identification of piecewise-linear models of genetic regulatory networks. *Journal of Computational Biology*, 15(10):1365–1380, December 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0109; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0109`.

Paten:2011:CGG

[PDE+11] Benedict Paten, Mark Diekhans, Dent Earl, John St.John, Jian Ma, Bernard Suh, and David Haussler. Cactus graphs for genome comparisons. *Journal of Computational Biology*, 18(3):469–481, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0252;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0252.

Picard:2008:AEN

[PDK+08] F. Picard, J.-J. Daudin, M. Koskas, S. Schbath, and S. Robin. Assessing the exceptionality of network motifs. *Journal of Computational Biology*, 15(1):1–20, January 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0137; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0137.

Przytycka:2006:GTI

[PDSD06] Teresa Przytycka, George Davis, Nan Song, and Dannie Durand. Graph theoretical insights into evolution of multidomain proteins. *Journal of Computational Biology*, 13 (2):351–363, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.351; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.351.

Pevzner:2000:MTP

[PDT00] Pavel A. Pevzner, Vlado Dančík, and Chris L. Tang. Mutation-tolerant protein identification by mass spectrometry. *Journal of Computational Biology*, 7(6):777–787, December 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270050514927; https://www.liebertpub.com/doi/pdf/10.1089/10665270050514927.

Pan:2016:CCB

[PDZ+16] Yuchao Pan, Yuxi Dong, Jingtian Zhou, Mark Hallen, Bruce R. Donald, Jianyang Zeng, and Wei Xu. cOSPREY: a cloud-based distributed algorithm for large-scale computational protein design. *Journal of Computational Biology*, 23(9):737–749, September 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0234; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0234.

Prajapati:2020:GPP

[PE20] Rutvi Prajapati and Isaac Arnold Emerson. Gene prioritization in Parkinson's disease using human protein–protein

interaction network. *Journal of Computational Biology*, 27 (11):1610–1621, November 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0281; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0281`.

Peer:2022:SIRa

[Pe'22a] Itsik Pe'er. Special issue: RECOMB 2022, part 1. *Journal of Computational Biology*, 29(11):1155, November 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.29075.ip`.

Peer:2022:SIRb

[Pe'22b] Itsik Pe'er. Special issue: RECOMB 2022, part 2. *Journal of Computational Biology*, 29(12):1269, December 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.29076.ip`.

Penner:2020:BFE

[Pen20a] Robert C. Penner. Backbone free energy estimator applied to viral glycoproteins. *Journal of Computational Biology*, 27 (10):1495–1508, October 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0120; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0120`.

Penner:2020:CHF

[Pen20b] Robert C. Penner. Conserved high free energy sites in human coronavirus spike glycoprotein backbones. *Journal of Computational Biology*, 27(11):1622–1630, November 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0193; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0193`.

Peng:2022:RSIa

[Pen22a] Jian Peng. RECOMB 2021 special issue. *Journal of Computational Biology*, 29(1):2, January 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.29050.jp`.

Peng:2022:RSIb

[Pen22b] Jian Peng. RECOMB 2021 special issue. *Journal of Computational Biology*, 29(2):91, February 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.29051.jp`.

Paten:2018:SUC

[PER+18] Benedict Paten, Jordan M. Eizenga, Yohei M. Rosen, Adam M. Novak, Erik Garrison, and Glenn Hickey. Superbubbles, ultrabubbles, and cacti. *Journal of Computational Biology*, 25(7):649–663, July 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0251; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0251`.

Pevzner:1995:CMD

[Pev95] Pavel A. Pevzner. Combinatorial methods for DNA mapping and sequencing. *Journal of Computational Biology*, 2(2):153–158, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.153; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.153`.

Pevzner:1998:P

[Pev98] Pavel A. Pevzner. Preface. *Journal of Computational Biology*, 5(3):367, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.367`.

Pellow:2017:IBF

[PFK17] David Pellow, Darya Filippova, and Carl Kingsford. Improving Bloom filter performance on sequence data using k-mer Bloom filters. *Journal of Computational Biology*, 24(6):547–557, June 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0155; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0155`.

Pradines:2005:APL

[PFRD05] Joël R. Pradines, Victor Farutin, Steve Rowley, and Vlado Dančík. Analyzing protein lists with large networks: Edge-count probabilities in random graphs with given expected degrees. *Journal of Computational Biology*, 12(2):113–128, March 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.113; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.113`.

Piccolboni:2003:CFC

[PG03] Antonio Piccolboni and Dan Gusfield. On the complexity of fundamental computational problems in pedigree analysis. *Journal of Computational Biology*, 10(5):763–773, October 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652703322539088; https://www.liebertpub.com/doi/pdf/10.1089/106652703322539088`.

Perlman:2011:CDG

[PGA+11] Liat Perlman, Assaf Gottlieb, Nir Atias, Eytan Ruppin, and Roded Sharan. Combining drug and gene similarity measures for drug-target elucidation. *Journal of Computational Biology*, 18(2):133–145, February 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0213; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0213`.

Palazoglu:2004:FDP

[PGAE04] Ahmet Palazoglu, Attila Gursoy, Yaman Arkun, and Burak Erman. Folding dynamics of proteins from denatured to native state: Principal component analysis. *Journal of Computational Biology*, 11(6):1149–1168, December 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.1149; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.1149`.

Parker:2011:OCM

[PGBK11] Andrew S. Parker, Karl E. Griswold, and Chris Bailey-Kellogg. Optimization of combinatorial mutagenesis. *Journal of Computational Biology*, 18(11):1743–1756, November

2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0152; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0152.

Pattengale:2007:ECR

[PGM07] Nicholas D. Pattengale, Eric J. Gottlieb, and Bernard M. E. Moret. Efficiently computing the Robinson–Foulds metric. *Journal of Computational Biology*, 14(6):724–735, July 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R012; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R012.

Perez:2016:CPA

[PGV16] Nelson Pérez, Miguel Gutierrez, and Nelson Vera. Computational performance assessment of k-mer counting algorithms. *Journal of Computational Biology*, 23(4):248–255, April 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0199; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0199.

Piau:2002:MRS

[Pia02] Didier Piau. Mutation–replication statistics of polymerase chain reactions. *Journal of Computational Biology*, 9(6):831–847, December 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270260518308; https://www.liebertpub.com/doi/pdf/10.1089/10665270260518308.

Piccolboni:2008:MSA

[Pic08] Antonio Piccolboni. Multivariate segmentation in the analysis of transcription tiling array data. *Journal of Computational Biology*, 15(7):845–856, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0141; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0141.

Park:2023:GRN

[PIM23] Heewon Park, Seiya Imoto, and Satoru Miyano. Gene regulatory network-classifier: Gene regulatory network-based classifier and its applications to gastric cancer drug (5-fluorouracil)

marker identification. *Journal of Computational Biology*, 30(2):223–243, February 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0181; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0181.

Pragman:2015:MDT

[PIWR15] Alexa Pragman, Richard Issacson, Christine Wendt, and Cavan Reilly. A method for determining taxonomical contributions to group differences in microbiomic investigations. *Journal of Computational Biology*, 22(10):930–939, October 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0021; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0021.

Persing:2015:SAC

[PJB+15] Adam Persing, Ajay Jasra, Alexandros Beskos, David Balding, and Maria De Iorio. A simulation approach for change-points on phylogenetic trees. *Journal of Computational Biology*, 22(1):10–24, January 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0218; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0218.

Pan:2020:OOM

[PJL20] Weihua Pan, Tao Jiang, and Stefano Lonardi. OMGS: Optical map-based genome scaffolding. *Journal of Computational Biology*, 27(4):519–533, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0310; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0310.

Pacholczyk:2011:ELP

[PK11] Marcin Pacholczyk and Marek Kimmel. Exploring the landscape of protein-ligand interaction energy using probabilistic approach. *Journal of Computational Biology*, 18(6):843–850, June 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0017; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0017.

Piwowar:2019:DAM

[PK19] Monika Piwowar and Tomasz Kułaga. Directional association measurement in contingency tables: Genomic case. *Journal of Computational Biology*, 26(3):235–240, March 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0202; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0202`.

Ponomarenko:1997:GPP

[PKK97] Michael P. Ponomarenko, Anna N. Kolchanova, and Nikolay A. Kolchanov. Generating programs for predicting the activity of functional sites. *Journal of Computational Biology*, 4(1):83–90, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.83; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.83`.

Popic:2018:FMB

[PKSB18] Victoria Popic, Volodymyr Kuleshov, Michael Snyder, and Serafim Batzoglou. Fast metagenomic binning via hashing and Bayesian clustering. *Journal of Computational Biology*, 25(7):677–688, July 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0250; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0250`.

Petri:2011:ESE

[PKZ11] Tobias Petri, Robert Küffner, and Ralf Zimmer. Experiment specific expression patterns. *Journal of Computational Biology*, 18(11):1423–1435, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0159; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0159`.

Potra:2006:AFT

[PL06] Florian A. Potra and Xing Liu. Aligning families of two-dimensional gels by a combined multiresolution forward-inverse transformation approach. *Journal of Computational Biology*, 13(7):1384–1395, September 2006. CO-

DEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1384; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1384.

Peng:2016:ZIB

[PLL16] Xiaoling Peng, Gang Li, and Zhenqiu Liu. Zero-inflated beta regression for differential abundance analysis with metagenomics data. *Journal of Computational Biology*, 23(2):102–110, February 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0157; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0157.

Pang:2018:CAC

[PLSL18] Fengqian Pang, Heng Li, Yonggang Shi, and Zhiwen Liu. Computational analysis of cell dynamics in videos with hierarchical-pooled deep-convolutional features. *Journal of Computational Biology*, 25(8):934–953, August 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0023; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0023.

Potra:2006:PIA

[PLSM+06] Florian A. Potra, Xing Liu, Françoise Seillier-Moiseiwitsch, Anindya Roy, Yaming Hang, Mark R. Marten, Babu Raman, and Carol Whisnant. Protein image alignment via piecewise affine transformations. *Journal of Computational Biology*, 13(3):614–630, April 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.614; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.614.

Pang:2025:EMD

[PLZX25] Fengqian Pang, Chunyue Lei, Hongfei Zhao, and Zhiqiang Xing. An earth mover's distance-based self-supervised framework for cellular dynamic grading in live-cell imaging. *Journal of Computational Biology*, 32(3):274–297, March 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0672; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0672.

Peris:2014:SSN

[PM14] Guillermo Peris and Andrés Marzal. Statistical significance of normalized global alignment. *Journal of Computational Biology*, 21(3):257–268, March 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0167; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0167`.

Park:2024:NCE

[PM24] Heewon Park and Satoru Miyano. Network-constrained eigen-single-cell profile estimation for uncovering crucial immunogene regulatory systems in human bone marrow. *Journal of Computational Biology*, 31(11):1158–1178, November 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0539; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0539`.

Prabhakara:2013:MUH

[PMAP13] Shruthi Prabhakara, Raunaq Malhotra, Raj Acharya, and Mary Poss. Mutant-Bin: Unsupervised haplotype estimation of viral population diversity without reference genome. *Journal of Computational Biology*, 20(6):453–463, June 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0174; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0174`.

Parida:2008:EAR

[PMCB08] Laxmi Parida, Marta Melé, Francesc Calafell, and Jaume Bertranpetit. Estimating the ancestral recombinations graph (ARG) as compatible networks of SNP patterns. *Journal of Computational Biology*, 15(9):1133–1153, November 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0065; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0065`.

Pisanti:2003:PMP

[PMF+03] N. Pisanti, R. Marangoni, P. Ferragina, A. Frangioni, A. Savona, C. Pisanelli, and F. Luccio. PaTre: a method for paralogy trees construction. *Journal of Computational Biology*,

10(5):791–802, October 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703322539105; https://www.liebertpub.com/doi/pdf/10.1089/106652703322539105.

Pirro:2016:BPE

[PMG+16] Stefano Pirrò, Antonella Minutolo, Andrea Galgani, Marina Potestà, Vittorio Colizzi, and Carla Montesano. Bioinformatics prediction and experimental validation of MicroRNAs involved in cross-kingdom interaction. *Journal of Computational Biology*, 23(12):976–989, December 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0059; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0059.

Paszek:2021:TDL

[PMGE21] Jarosław Paszek, Alexey Markin, Paweł Górecki, and Oliver Eulenstein. Taming the duplication-loss-coalescence model with integer linear programming. *Journal of Computational Biology*, 28(8):758–773, August 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0011; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0011.

Patterson:2015:WWH

[PMP+15] Murray Patterson, Tobias Marschall, Nadia Pisanti, Leo van Iersel, Leen Stougie, Gunnar W. Klau, and Alexander Schönhuth. WhatsHap: Weighted haplotype assembly for future-generation sequencing reads. *Journal of Computational Biology*, 22(6):498–509, June 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0157; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0157.

Park:2017:IBF

[PNIM17] Heewon Park, Atsushi Niida, Seiya Imoto, and Satoru Miyano. Interaction-based feature selection for uncovering cancer driver genes through copy number-driven expression level. *Journal of Computational Biology*, 24(2):138–152, February 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0140; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0140.

Park:2015:SOG

[PNMI15] Heewon Park, Atushi Niida, Satoru Miyano, and Seiya Imoto. Sparse overlapping group lasso for integrative multi-omics analysis. *Journal of Computational Biology*, 22(2):73–84, February 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0197; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0197.

Petrucci:2020:ISS

[PNPC20] Enrico Petrucci, Laurent Noé, Cinzia Pizzi, and Matteo Comin. Iterative spaced seed hashing: Closing the gap between spaced seed hashing and k-mer hashing. *Journal of Computational Biology*, 27(2):223–233, February 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0298; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0298.

Preparata:2004:DSH

[PO04] Franco P. Preparata and John S. Oliver. DNA sequencing by hybridization using semi-degenerate bases. *Journal of Computational Biology*, 11(4):753–765, August 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.753; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.753.

Pal:2023:SMG

[POP23] Soumitra Pal, Brian Oliver, and Teresa M. Przytycka. Stochastic modeling of gene expression evolution uncovers tissue- and sex-specific properties of expression evolution in the *Drosophila* genus. *Journal of Computational Biology*, 30(1):21–40, January 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0121; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0121.

Pacinkova:2023:IBF

[PP23] Anna Pačínková and Vlad Popovici. IntOMICS: a Bayesian framework for reconstructing regulatory networks using multi-omics data. *Journal of Computational Biology*, 30(5):569–574, May 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0149; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0149`.

Pande:2023:PTC

[PPL+23] Akshara Pande, Sumeet Patiyal, Anjali Lathwal, Chakit Arora, Dilraj Kaur, Anjali Dhall, Gaurav Mishra, Harpreet Kaur, Neelam Sharma, Shipra Jain, Salman Sadullah Usmani, Piyush Agrawal, and ... See all authors. Pfeature: a tool for computing wide range of protein features and building prediction models. *Journal of Computational Biology*, 30(2):204–222, February 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0241; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0241`.

Plewczynski:2014:HSA

[PPV+14] Dariusz Plewczynski, Anna Philips, Marcin Von Grotthuss, Leszek Rychlewski, and Krzysztof Ginalski. HarmonyDOCK: The structural analysis of poses in protein-ligand docking. *Journal of Computational Biology*, 21(3):247–256, March 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0111; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0111`.

Pellegrina:2020:FAF

[PPV20] Leonardo Pellegrina, Cinzia Pizzi, and Fabio Vandin. Fast approximation of frequent k-mers and applications to metagenomics. *Journal of Computational Biology*, 27(4):534–549, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0314; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0314`.

Philippakis:2008:DCU

[PQBB08] Anthony A. Philippakis, Aaron M. Qureshi, Michael F. Berger, and Martha L. Bulyk. Design of compact, universal

DNA microarrays for protein binding microarray experiments. *Journal of Computational Biology*, 15(7):655–665, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0114; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0114`.

Poirel:2013:TNA

[PRC+13] Christopher L. Poirel, Richard R. Rodrigues, Katherine C. Chen, John J. Tyson, and T. M. Murali. Top-down network analysis to drive bottom-up modeling of physiological processes. *Journal of Computational Biology*, 20(5):409–418, May 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0274; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0274`.

P:2024:DVW

[PRC+24] Preeti P, Azeen Riyaz, Alakto Choudhury, Priyanka Ray Choudhury, Nischal Pradhan, Abhishek Singh, Mihir Nakul, Chhavi Dudeja, Abhijeet Yadav, and ... See all authors. DNASCANNER v2: a Web-based tool to analyze the characteristic properties of nucleotide sequences. *Journal of Computational Biology*, 31(7):651–669, July 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Preparata:2013:CC

[Pre13] Franco P. Preparata. On contigs and coverage. *Journal of Computational Biology*, 20(6):424–432, June 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0243; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0243`.

Pirogov:2016:RPN

[PRKG16] Sergey Pirogov, Alexander Rybko, Anastasia Kalinina, and Mikhail Gelfand. Recombination processes and nonlinear Markov chains. *Journal of Computational Biology*, 23 (9):711–717, September 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0051; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0051`.

Pape:2008:CPA

[PRSV08] Utz J. Pape, Sven Rahmann, Fengzhu Sun, and Martin Vingron. Compound Poisson approximation of the number of occurrences of a position frequency matrix (PFM) on both strands. *Journal of Computational Biology*, 15(6):547–564, July 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0084; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0084`.

Polyanovsky:2008:RGP

[PRT08] Valery Polyanovsky, Mikhail A. Roytberg, and Vladimir G. Tumanyan. Reconstruction of genuine pair-wise sequence alignment. *Journal of Computational Biology*, 15(4):379–391, May 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0145; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0145`.

Przytycka:1998:TRA

[Prz98] Teresa M. Przytycka. Transforming rooted agreement into unrooted agreement. *Journal of Computational Biology*, 5 (2):335–349, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.335; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.335`.

Przytycka:2007:SCC

[Prz07] Teresa Przytycka. Stability of characters and construction of phylogenetic trees. *Journal of Computational Biology*, 14(5):539–549, June 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R001; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R001`.

Przytycka:2016:P

[Prz16] Teresa Przytycka. Preface. *Journal of Computational Biology*, 23 (5):299, May 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.29001.tp`.

Przytycka:2024:RFS

[Prz24] Teresa M. Przytycka. Rosalind Franklin Society proudly announces the 2023 award recipient for *Journal of Computational Biology*. *Journal of Computational Biology*, 31(9):783, September 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Pevzner:2011:PSM

[PS11] Pavel A. Pevzner and Ron Shamir. Preface: 2^{nd} Satellite Meeting on Bioinformatics Education, Research in Computational Molecular Biology (RECOMB–BE 2010). *Journal of Computational Biology*, 18(7):865, July 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.007p`.

Pei:2012:RBN

[PS12] Baikang Pei and Dong-Guk Shin. Reconstruction of biological networks by incorporating prior knowledge into Bayesian network models. *Journal of Computational Biology*, 19(12): 1324–1334, December 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0194; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0194`.

Picard:2017:LCP

[PSB17] Vincent Picard, Anne Siegel, and Jérémie Bourdon. A logic for checking the probabilistic steady-state properties of reaction networks. *Journal of Computational Biology*, 24(8):734–745, August 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0099; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0099`.

Pisanti:2009:REN

[PSCP09] Nadia Pisanti, Henry Soldano, Mathilde Carpentier, and Joel Pothier. A relational extension of the notion of motifs: Application to the common 3D protein substructures searching problem. *Journal of Computational Biology*, 16(12):1635–1660, December 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0019; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0019`.

Pirro:2020:HPT

[PSG+20] Stefano Pirrò, Filomena Spada, Emanuela Gadaleta, Federica Ferrentino, Graeme J. Thorn, Gianni Cesareni, and Claude Chelala. HiPPO and PANDA: Two bioinformatics tools to support analysis of mass cytometry data. *Journal of Computational Biology*, 27(8):1283–1294, August 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0384; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0384`.

Park:2018:ANI

[PSIM18] Heewon Park, Teppei Shimamura, Seiya Imoto, and Satoru Miyano. Adaptive NetworkProfiler for identifying cancer characteristic-specific gene regulatory networks. *Journal of Computational Biology*, 25(2):130–145, February 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0120; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0120`.

Presson:2006:MMD

[PSLP06] Angela P. Presson, Eric Sobel, Kenneth Lange, and Jeanette C. Papp. Merging microsatellite data. *Journal of Computational Biology*, 13(6):1131–1147, July 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1131; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1131`.

Petrovs:2021:IWA

[PSP21] Rudolfs Petrovs, Egils Stalidzans, and Agris Pentjuss. IMFLer: a Web application for interactive metabolic flux analysis and visualization. *Journal of Computational Biology*, 28 (10):1021–1032, October 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0056; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0056`.

Passos:2009:ODO

[PTWB09] Valéria Lima Passos, Frans E. S. Tan, Bjorn Winkens, and Martijn P. F. Berger. Optimal designs for one- and two-color mi-

croarrays using mixed models: a comparative evaluation of their efficiencies. *Journal of Computational Biology*, 16(1):67–83, January 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0048; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0048`.

Preparata:2000:SHI

[PU00] Franco P. Preparata and Eli Upfal. Sequencing-by-hybridization at the information-theory bound: an optimal algorithm. *Journal of Computational Biology*, 7(3–4):621–630, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Prakash:2017:ECM

[PV17] Celine Prakash and Arndt Von Haeseler. An enumerative combinatorics model for fragmentation patterns in RNA sequencing provides insights into nonuniformity of the expected fragment starting-point and coverage profile. *Journal of Computational Biology*, 24(3):200–212, March 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0096; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0096`.

Pollastri:2006:MDR

[PVFB06] Gianluca Pollastri, Alessandro Vullo, Paolo Frasconi, and Pierre Baldi. Modular DAG–RNN architectures for assembling coarse protein structures. *Journal of Computational Biology*, 13(3):631–650, April 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.631; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.631`.

Pevzner:2022:MWC

[PVR+22] Pavel Pevzner, Martin Vingron, Christian Reidys, Fengzhu Sun, and Sorin Istrail. Michael Waterman's contributions to computational biology and bioinformatics. *Journal of Computational Biology*, 29(7):601–615, July 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.29066.pp; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.29066.pp`.

Pavlidis:2002:LGF

[PWCN02] Paul Pavlidis, Jason Weston, Jinsong Cai, and William Stafford Noble. Learning gene functional classifications from multiple data types. *Journal of Computational Biology*, 9(2):401–411, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270252935539; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935539`.

Pei:2017:GCP

[PWFZ17] Chao Pei, Shu-Lin Wang, Jianwen Fang, and Wei Zhang. GSMC: Combining parallel Gibbs sampling with maximal cliques for hunting DNA motif. *Journal of Computational Biology*, 24(12):1243–1253, December 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0100; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0100`.

Pereira:2016:HFA

[PWKAF16] Mariana Buongermino Pereira, Mikael Wallroth, Erik Kristiansson, and Marina Axelson-Fisk. HattCI: Fast and accurate *attC* site identification using hidden Markov models. *Journal of Computational Biology*, 23(11):891–902, November 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0024; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0024`.

Perez-Wohlfeil:2018:PPP

[PWT18] Esteban Pérez-Wohlfeil and Oswaldo Trelles. Precise and parallel pairwise metagenomic comparisons. *Journal of Computational Biology*, 25(8):841–849, August 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0081; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0081`.

Puniyani:2013:NMU

[PX13] Kriti Puniyani and Eric P. Xing. NP-MuScL: Unsupervised global prediction of interaction networks from multiple data sources. *Journal of Computational Biology*, 20 (11):892–904, November 2013. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0093; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0093.

Pan:2023:IFS

[PXLP23] Liang Pan, Xia Xiao, Shengyun Liu, and Shaoliang Peng. An integration framework of secure multiparty computation and deep neural network for improving drug–drug interaction predictions. *Journal of Computational Biology*, 30(9):1034–1045, September 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0076; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0076.

Petersen:2019:DRL

[PYG+19] Brenden K. Petersen, Jiachen Yang, Will S. Grathwohl, Chase Cockrell, Claudio Santiago, Gary An, and Daniel M. Faissol. Deep reinforcement learning and simulation as a path toward precision medicine. *Journal of Computational Biology*, 26(6):597–604, June 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0168; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0168.

Park:2019:RSS

[PYIM19] Heewon Park, Makoto Yamada, Seiya Imoto, and Satoru Miyano. Robust sample-specific stability selection with effective error control. *Journal of Computational Biology*, 26(3):202–217, March 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0180; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0180.

Park:2022:UMM

[PYIM22] Heewon Park, Rui Yamaguchi, Seiya Imoto, and Satoru Miyano. Uncovering molecular mechanisms of drug resistance via network-constrained common structure identification. *Journal of Computational Biology*, 29(3):257–275, March 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0314; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0314.

Preparata:2005:QPS

[PZC05] Franco P. Preparata, Louxin Zhang, and Kwok Pui Choi. Quick, practical selection of effective seeds for homology search. *Journal of Computational Biology*, 12(9):1137–1152, November 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1137; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1137`.

Pasaniuc:2011:AEE

[PZH11] Bogdan Paşaniuc, Noah Zaitlen, and Eran Halperin. Accurate estimation of expression levels of homologous genes in RNA-seq experiments. *Journal of Computational Biology*, 18(3):459–468, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0259; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0259`.

Petroni:2015:SSA

[PZMM15] Mattia Petroni, Nikolaj Zimic, Miha Mraz, and Miha Moškon. Stochastic simulation algorithm for gene regulatory networks with multiple binding sites. *Journal of Computational Biology*, 22(3):218–226, March 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0064; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0064`.

Pang:2010:MMP

[PZZ+10] Xiaodong Pang, Linxiang Zhou, Mingjun Zhang, Fang Xie, Long Yu, Lili Zhang, Lina Xu, and Xinyi Zhang. A mathematical model for peptide inhibitor design. *Journal of Computational Biology*, 17(8):1081–1093, August 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0272; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0272`.

Pungpapong:2020:IBK

[PZZ20] Vitara Pungpapong, Min Zhang, and Dabao Zhang. Integrating biological knowledge into case–control analysis through iterated conditional Modes/Medians algorithm. *Journal of Computational Biology*, 27(7):1171–1179, July 2020. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0319; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0319.

Qingge:2025:GAM

[QBA+25] Letu Qingge, Kushal Badal, Richard Annan, Jordan Sturtz, Xiaowen Liu, and Binhai Zhu. Generative AI models for the protein scaffold filling problem. *Journal of Computational Biology*, 32(2):127–142, February 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0510; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0510.

Qiu:2019:EDE

[QbMyD+19] Yong Qiu, Ling bing Meng, Chen yi Di, Yu hu Huo, Bo chen Yao, Teng jiao Zhang, and Zhen Hua. Exploration of the differentially expressed long noncoding RNAs and genes of morphine tolerance via bioinformatic analysis. *Journal of Computational Biology*, 26(12):1379–1393, December 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0188; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0188.

Qi:2024:CTU

[QEk24] Yuanyuan Qi and Mohammed El-kebir. Consensus tree under the ancestor–descendant distance is NP-Hard. *Journal of Computational Biology*, 31(1):58–70, January 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0262; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0262.

Qian:2022:SPI

[QFLL22] Kun Qian, Shiwei Fu, Hongwei Li, and Wei Vivian Li. The scINSIGHT package for integrating single-cell RNA-Seq data from different biological conditions. *Journal of Computational Biology*, 29(11):1233–1236, November 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0244; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0244.

Qiu:2010:RCC

[QGP10] Peng Qiu, Andrew J. Gentles, and Sylvia K. Plevritis. Reducing the computational complexity of information theoretic approaches for reconstructing gene regulatory networks. *Journal of Computational Biology*, 17(2):169–176, February 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0052; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0052`.

Qiu:2020:CPE

[QLW20] Yier Qiu, Guowen Lu, and Yingjie Wu. Coexpression of PBX1 and EMP2 as prognostic biomarkers in estrogen receptor-negative breast cancer via data mining. *Journal of Computational Biology*, 27(10):1509–1518, October 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0491; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0491`.

Quo:2011:ACM

[QMMW11] Chang F. Quo, Richard A. Moffitt, Alfred H. Merrill, Jr., and May D. Wang. Adaptive control model reveals systematic feedback and key molecules in metabolic pathway regulation. *Journal of Computational Biology*, 18(2):169–182, February 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0215; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0215`.

Qiu:2009:SCD

[QP09] Peng Qiu and Sylvia K. Plevritis. Simultaneous class discovery and classification of microarray data using spectral analysis. *Journal of Computational Biology*, 16(7):935–944, July 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0227; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0227`.

Qi:2019:BAK

[QQL+19] Yuewen Qi, Haowen Qi, Zeyuan Liu, Peiyuan He, and Bingqing Li. Bioinformatics analysis of key genes and pathways in colorectal cancer. *Journal of Computational Biology*, 26(4):364–375,

April 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0237; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0237.

Qin:2013:TRI

[QR13] Jing Qin and Christian M. Reidys. On topological RNA interaction structures. *Journal of Computational Biology*, 20(7):495–513, July 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0282; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0282.

Qian:2009:QPP

[QSY09] Xiaoning Qian, Sing-Hoi Sze, and Byung-Jun Yoon. Querying pathways in protein interaction networks based on hidden Markov models. *Journal of Computational Biology*, 16 (2):145–157, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.02TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.02TT.

Qiao:2023:MVE

[QsYSxL23] Qian Qiao, Sha sha Yuan, Junliang Shang, and Jin xing Liu. Multi-view enhanced tensor nuclear norm and local constraint model for cancer clustering and feature gene selection. *Journal of Computational Biology*, 30(8):889–899, August 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0107; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0107.

Quesado:2024:HGA

[QTRA24] Pedro Quesado, Luis H. M. Torres, Bernardete Ribeiro, and Joel P. Arrais. A hybrid GNN approach for improved molecular property prediction. *Journal of Computational Biology*, 31(11):1146–1157, November 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0452; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0452.

Raghavan:2006:MGF

[RAC+06] N. Raghavan, D. Amaratunga, J. Cabrera, A. Nie, J. Qin, and M. McMillian. On methods for gene function scoring as a means of facilitating the interpretation of microarray results. *Journal of Computational Biology*, 13(3):798–809, April 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.798; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.798`.

Ramanathan:2010:OAM

[RAKL10] Arvind Ramanathan, Pratul K. Agarwal, Maria Kurnikova, and Christopher J. Langmead. An online approach for mining collective behaviors from molecular dynamics simulations. *Journal of Computational Biology*, 17(3):309–324, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0167; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0167`.

Rodriguez:2013:AIC

[RBEB13] Jesse M. Rodriguez, Sivan Bercovici, Megan Elmore, and Serafim Batzoglou. Ancestry inference in complex admixtures via variable-length Markov chain linkage models. *Journal of Computational Biology*, 20(3):199–211, March 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0088; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0088`.

Rajasekaran:2005:EAP

[RBH05] S. Rajasekaran, S. Balla, and C.-H. Huang. Exact algorithms for planted motif problems. *Journal of Computational Biology*, 12(8):1117–1128, October 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1117; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1117`.

Rosenthal:2019:BET

[RBH+19] Michael Rosenthal, Darshan Bryner, Fred Huffer, Shane Evans, Anuj Srivastava, and Nicola Neretti. Bayesian estimation of three-dimensional chromosomal structure from

single-cell Hi-C data. *Journal of Computational Biology*, 26 (11):1191–1202, November 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0100; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0100.

Rohrer:1994:SPE

[RBK94] G. A. Rohrer, D. W. Behrens, and J. W. Keele. A simplified procedure for entry of raw genotypic data. *Journal of Computational Biology*, 1(2):111–119, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.111; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.111.

Ravi:2019:ENC

[RBKJ19] Guru Raj Rao Ravi, Jayashree Biswal, Sureka Kanagarajan, and Jeyaraman Jeyakanthan. Exploration of N5-CAIR mutase novel inhibitors from *Pyrococcus horikoshii* OT3: a computational study. *Journal of Computational Biology*, 26(5):457–472, May 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0248; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0248.

Reimers:2015:FFM

[RBOS15] Arne C. Reimers, Frank J. Bruggeman, Brett G. Olivier, and Leen Stougie. Fast flux module detection using matroid theory. *Journal of Computational Biology*, 22(5):414–424, May 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0141; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0141.

Reddy:2006:SBB

[RC06] Chandan K. Reddy and Hsiao-Dong Chiang. A stability boundary based method for finding saddle points on potential energy surfaces. *Journal of Computational Biology*, 13(3):745–766, April 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.745; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.745.

Rastegari:2007:PNA

[RC07] Baharak Rastegari and Anne Condon. Parsing nucleic acid pseudoknotted secondary structure: Algorithm and applications. *Journal of Computational Biology*, 14(1):16–32, January 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0108; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0108`.

Radu:2014:NFE

[RC14] Alex Radu and Michael Charleston. Node fingerprinting: an efficient heuristic for aligning biological networks. *Journal of Computational Biology*, 21(10):760–770, October 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0114; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0114`.

Radu:2015:NHS

[RC15] Alex Radu and Michael Charleston. Node handprinting: a scalable and accurate algorithm for aligning multiple biological networks. *Journal of Computational Biology*, 22(7):687–697, July 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0247; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0247`.

Rossignolo:2024:ECM

[RC24] Enrico Rossignolo and Matteo Comin. Enhanced compression of k-mer sets with counters via de Bruijn graphs. *Journal of Computational Biology*, 31(6):524–538, June 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Reyna:2021:NNS

[RCER21] Matthew A. Reyna, Uthsav Chitra, Rebecca Elyanow, and Benjamin J. Raphael. NetMix: a network-structured mixture model for reduced-bias estimation of altered subnetworks. *Journal of Computational Biology*, 28(5):469–484, May 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Roy:2012:SSL

[RCSS12] Rajat S. Roy, Kevin C. Chen, Anirvan M. Sengupta, and Alexander Schliep. SLIQ: Simple linear inequalities for ef-

ficient contig scaffolding. *Journal of Computational Biology*, 19(10):1162–1175, October 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0263; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0263`.

Reinert:2009:AFS

[RCSW09] Gesine Reinert, David Chew, Fengzhu Sun, and Michael S. Waterman. Alignment-free sequence comparison (i): Statistics and power. *Journal of Computational Biology*, 16(12): 1615–1634, December 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0198; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0198`.

Rocke:2001:MME

[RD01] David M. Rocke and Blythe Durbin. A model for measurement error for gene expression arrays. *Journal of Computational Biology*, 8(6):557–569, November 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652701753307485; https://www.liebertpub.com/doi/pdf/10.1089/106652701753307485`.

Russo:2009:HSB

[RD09] G. Russo and M. Di Bernardo. How to synchronize biological clocks. *Journal of Computational Biology*, 16(2):379–393, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.21TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.21TT`.

Roskin:2004:SFD

[RDH04] Krishna M. Roskin, Mark Diekhans, and David Haussler. Score functions for determining regional conservation in two-species local alignments. *Journal of Computational Biology*, 11(2–3):395–411, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Robin:2002:OPS

[RDR+02] S. Robin, J.-J. Daudin, H. Richard, M.-F. Sagot, and S. Schbath. Occurrence probability of structured motifs in random se-

quences. *Journal of Computational Biology*, 9(6):761–773, December 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270260518254; https://www.liebertpub.com/doi/pdf/10.1089/10665270260518254.

Rito:2012:IAH

[RDR12] Tiago Rito, Charlotte M. Deane, and Gesine Reinert. The importance of age and high degree, in protein-protein interaction networks. *Journal of Computational Biology*, 19(6):785–795, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0054; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0054.

Renders:2024:LAP

[RDRF24] Luca Renders, Lore Depuydt, Sven Rahmann, and Jan Fostier. Lossless approximate pattern matching: Automated design of efficient search schemes. *Journal of Computational Biology*, 31(10):975–989, October 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0664; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0664.

Reese:1997:ISS

[REKH97] Martin G. Reese, Frank H. Eeckman, David Kulp, and David Haussler. Improved splice site detection in Genie. *Journal of Computational Biology*, 4(3):311–323, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.311; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.311.

Rondel:2025:EEE

[RFH+25] Filipp Martin Rondel, Hafsa Farooq, Roya Hosseini, Akshay Juyal, Sergey Knyazev, Serghei Mangul, Artem S. Rogovskyy, and Alexander Zelikovsky. Estimating enzyme expression and metabolic pathway activity in *Borreliella*-infected and uninfected mice. *Journal of Computational Biology*, 32(2):188–197, February 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0564;

https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0564.

Rubinov:1995:RSS

[RG95] A. R. Rubinov and M. S. Gelfand. Reconstruction of a string from substring precedence data. *Journal of Computational Biology*, 2(2):371–381, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.371; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.371.

Rioux:1994:PSE

[RGL94] Pierre A. Rioux, William A. Gilbert, and Timothy G. Littlejohn. A portable search engine and browser for the entrez database. *Journal of Computational Biology*, 1 (4):293–295, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.293; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.293.

Reyes:2012:AGG

[RGM+12] R. Reyes, D. Gamermann, A. Montagud, D. Fuente, J. Triana, J. F. Urchueguía, and P. Fernández de Córdoba. Automation on the generation of genome-scale metabolic models. *Journal of Computational Biology*, 19(12):1295–1306, December 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0183; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0183.

Rahman:2019:ATH

[RH19] Mohammad S. Rahman and Gholamreza Haffari. Analyzing tumor heterogeneity by incorporating long-range mutational influences and multiple sample data into heterogeneity factorial hidden Markov model. *Journal of Computational Biology*, 26(9):985–1002, September 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0242; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0242.

Rondel:2021:PAA

[RHS+21] Filipp Martin Rondel, Roya Hosseini, Bikram Sahoo, Sergey Knyazev, Igor Mandric, Frank Stewart, Ion I. Măndoiu, Bogdan Pasaniuc, Yuri Porozov, and Alexander Zelikovsky. Pipeline for analyzing activity of metabolic pathways in planktonic communities using metatranscriptomic data. *Journal of Computational Biology*, 28(8):842–855, August 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0053; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0053`.

Roberts:2004:PSA

[RHY+04] Michael Roberts, Brian R. Hunt, James A. Yorke, Randall A. Bolanos, and Arthur L. Delcher. A preprocessor for shotgun assembly of large genomes. *Journal of Computational Biology*, 11(4):734–752, August 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.734; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.734`.

Richardson:2006:FSE

[Ric06] Joel E. Richardson. `fjoin`: Simple and efficient computation of feature overlaps. *Journal of Computational Biology*, 13(8):1457–1464, October 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1457; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1457`.

Ristov:2016:FSP

[Ris16] Strahil Ristov. A fast and simple pattern matching with Hamming distance on large alphabets. *Journal of Computational Biology*, 23(11):874–876, November 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0020; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0020`.

Rajasekaran:2002:ECP

[RJS02] S. Rajasekaran, X. Jin, and J. L. Spouge. The efficient computation of position-specific match scores with the fast Fourier trans-

form. *Journal of Computational Biology*, 9(1):23–33, January 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270252833172; https://www.liebertpub.com/doi/pdf/10.1089/10665270252833172`.

Riis:1996:IPP

[RK96] Søren Kamaric Riis and Anders Krogh. Improving prediction of protein secondary structure using structured neural networks and multiple sequence alignments. *Journal of Computational Biology*, 3(1):163–183, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.163; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.163`.

Ram:2014:SAS

[RKTS14] Hari Ram, Alok Kumar, Lebin Thomas, and Ved Pal Singh. *In silico* approach to study adaptive divergence in nucleotide composition of the 16s rRNA gene among bacteria thriving under different temperature regimes. *Journal of Computational Biology*, 21(10):753–759, October 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0116; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0116`.

Rustici:1994:TDS

[RL94] Mauro Rustici and Arthur M. Lesk. Three-dimensional searching for recurrent structural motifs in data bases of protein structures. *Journal of Computational Biology*, 1 (2):121–132, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.121; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.121`.

Roy:2006:HSM

[RLA+06] Sushmita Roy, Terran Lane, Chris Allen, Anthony D. Aragon, and Margaret Werner-Washburne. A hidden-state Markov model for cell population deconvolution. *Journal of Computational Biology*, 13(10):1749–1774, December 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.`

1089/cmb.2006.13.1749; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1749.

Rubio-Largo:2018:PMM

[RLCVVR18] Álvaro Rubio-Largo, Mauro Castelli, Leonardo Vanneschi, and Miguel A. Vega-Rodríguez. A parallel multiobjective metaheuristic for multiple sequence alignment. *Journal of Computational Biology*, 25(9):1009–1022, September 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0031; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0031.

Rao:2013:NMQ

[RLH13] Xiayu Rao, Dejian Lai, and Xuelin Huang. A new method for quantitative real-time polymerase chain reaction data analysis. *Journal of Computational Biology*, 20(9):703–711, September 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0279; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0279.

Rodin:2009:UWA

[RLK+09] Andrei S. Rodin, Anatoliy Litvinenko, Kathy Klos, Alanna C. Morrison, Trevor Woodage, Josef Coresh, and Eric Boerwinkle. Use of wrapper algorithms coupled with a random forests classifier for variable selection in large-scale genomic association studies. *Journal of Computational Biology*, 16(12):1705–1718, December 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0037; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0037.

Rubio-Largo:2017:RAT

[RLVCVR17] Álvaro Rubio-Largo, Leonardo Vanneschi, Mauro Castelli, and Miguel A. Vega-Rodríguez. Reducing alignment time complexity of ultra-large sets of sequences. *Journal of Computational Biology*, 24(11):1144–1152, November 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0097; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0097.

Rodolphe:2000:TCM

[RM00] François Rodolphe and Catherine Mathé. Translation conditional models for protein coding sequences. *Journal of Computational Biology*, 7(1–2):249–260, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Rajaraman:2018:TRA

[RM18] Ashok Rajaraman and Jian Ma. Toward recovering allele-specific cancer genome graphs. *Journal of Computational Biology*, 25(7):624–636, July 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0022; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0022`.

Rahman:2021:RMS

[RM21] Amatur Rahman and Paul Medevedev. Representation of k-mer sets using spectrum-preserving string sets. *Journal of Computational Biology*, 28(4):381–394, April 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Rodin:2005:MGE

[RMC+05] Andrei Rodin, Thomas H. Mosley, Jr., Andrew G. Clark, Charles F. Sing, and Eric Boerwinkle. Mining genetic epidemiology data with Bayesian networks application to *apoe* gene variation and plasma lipid levels. *Journal of Computational Biology*, 12(1):1–11, February 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1`.

Rozas:2023:PDP

[RMC+23] Gladys M. Cavero Rozas, Jose M. Cisneros Mandujano, Yomali A. Ferreyra Chombo, Daniela V. Moreno Rencoret, Yerko M. Ortiz Mora, Martín E. Gutiérrez Pescarmona, and Alberto J. Donayre Torres. `pyBrick-DNA`: a Python-based environment for automated genetic component assembly. *Journal of Computational Biology*, 30(12):1315–1321, December 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0008; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0008`.

Rosati:2018:EMS

[RMK+18] Elise Rosati, Morgan Madec, Jean-Baptiste Kammerer, Luc Hébrard, Christophe Lallement, and Jacques Haiech. Efficient modeling and simulation of space-dependent biological systems. *Journal of Computational Biology*, 25(8):917–933, August 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0012; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0012`.

Ramensky:2000:DST

[RMRT00] V. E. Ramensky, V. Ju. Makeev, M. A. Roytberg, and V. G. Tumanyan. DNA segmentation through the Bayesian approach. *Journal of Computational Biology*, 7(1–2):215–231, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Radmacher:2002:PCP

[RMS02] Michael D. Radmacher, Lisa M. McShane, and Richard Simon. A paradigm for class prediction using gene expression profiles. *Journal of Computational Biology*, 9(3): 505–511, June 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652702760138592; https://www.liebertpub.com/doi/pdf/10.1089/106652702760138592`.

Rohani:2016:RSW

[RMWC16] Leyla Rohani, Derrick J. Morton, Xiao-Qian Wang, and Jaideep Chaudhary. Relative stability of wild-type and mutant p53 core domain: a molecular dynamic study. *Journal of Computational Biology*, 23(2):80–89, February 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0163; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0163`.

Robben:2023:CSW

[RND+23] Michael Robben, Mohammad Sadegh Nasr, Avishek Das, Jai Prakash Veerla, Manfred Huber, Justyn Jaworski, Jon Weidanz, and Jacob Luber. Comparison of the strengths and weaknesses of machine learning algorithms and feature selection on KEGG database microbial gene pathway

annotation and its effects on reconstructed network topology. *Journal of Computational Biology*, 30(7):766–782, July 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0370; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0370.

Rahman:2018:HNA

[RNH18] Mohammad S. Rahman, Ann E. Nicholson, and Gholamreza Haffari. HetFHMM: a novel approach to infer tumor heterogeneity using factorial hidden Markov models. *Journal of Computational Biology*, 25(2):182–193, February 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0101; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0101.

Ruths:2006:HGS

[RNI+06] Derek A. Ruths, Luay Nakhleh, M. Sriram Iyengar, Shrikanth A. G. Reddy, and Prahlad T. Ram. Hypothesis generation in signaling networks. *Journal of Computational Biology*, 13 (9):1546–1557, November 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1546; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1546.

Robbins:1994:GIC

[Rob94] Robert J. Robbins. Genome informatics i: Community databases. *Journal of Computational Biology*, 1(3):173–190, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.173; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.173.

Robbins:1996:BEI

[Rob96] Robert J. Robbins. Bioinformatics: Essential infrastructure for global biology[1]. *Journal of Computational Biology*, 3(3):465–478, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.465; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.465.

Rossi:2022:FME

[ROB+22] Massimiliano Rossi, Marco Oliva, Paola Bonizzoni, Ben Langmead, Travis Gagie, and Christina Boucher. Finding maximal exact matches using the r-index. *Journal of Computational Biology*, 29(2):188–194, February 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0445; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0445`.

Rodland:2006:PRS

[Rød06] Einar Andreas Rødland. Pseudoknots in RNA secondary structures: Representation, enumeration, and prevalence. *Journal of Computational Biology*, 13(6):1197–1213, July 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1197; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1197`.

Rossi:2022:MPI

[ROL+22] Massimiliano Rossi, Marco Oliva, Ben Langmead, Travis Gagie, and Christina Boucher. MONI: a pangenomic index for finding maximal exact matches. *Journal of Computational Biology*, 29(2):169–187, February 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0290; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0290`.

Rosenberg:2005:ASI

[Ros05] Noah A. Rosenberg. Algorithms for selecting informative marker panels for population assignment. *Journal of Computational Biology*, 12(9):1183–1201, November 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1183; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1183`.

Rosenberg:2007:CCH

[Ros07] Noah A. Rosenberg. Counting coalescent histories. *Journal of Computational Biology*, 14(3):360–377, April 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0109; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0109.

Rothenberg:2019:CGR

[Rot19] Ellen V. Rothenberg. Causal gene regulatory network modeling and genomics: Second-generation challenges. *Journal of Computational Biology*, 26(7):703–718, July 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0098; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0098.

Rao:2015:CSM

[RPR+15] Aditya Rao, Deepthi P., C. H. Renumadhavi, M. Girish Chandra, and Rajgopal Srinivasan. Compressed sensing methods for DNA microarrays, RNA interference, and metagenomics. *Journal of Computational Biology*, 22(2):145–158, February 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0244; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0244.

Raje:2002:DFR

[RPS02] D. V. Raje, H. J. Purohit, and R. N. Singh. Distinguishing features of 16s rDNA gene for five dominating bacterial genus observed in bioremediation. *Journal of Computational Biology*, 9(6):819–829, December 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270260518290; https://www.liebertpub.com/doi/pdf/10.1089/10665270260518290.

Reinharz:2013:USE

[RPW13] Vladimir Reinharz, Yann Ponty, and Jérôme Waldispühl. Using structural and evolutionary information to detect and correct pyrosequencing errors in noncoding RNAs. *Journal of Computational Biology*, 20(11):905–919, November 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0085; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0085.

Reva:1998:OPS

[RRFS98] Boris A. Reva, D. S. Rykunov, Alexei V. Finkelstein, and Jeffrey Skolnick. Optimization of protein structure on lattices using a self-consistent field approach. *Journal of Computational Biology*, 5(3):531–538, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.531; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.531`.

Razgulyaev:1995:SPN

[RRGC95] Oleg Razgulyaev, Anatoly Rubinov, Mikhail Gelfand, and Alexander Chetverin. Sequencing potential of nested Strand hybridization. *Journal of Computational Biology*, 2(2):383–395, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.383; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.383`.

Rempala:2007:VMM

[RRKT07] Grzegorz A. Rempala, Kenneth S. Ramos, Ted Kalbfleisch, and Ivo Teneng. Validation of a mathematical model of gene transcription in aggregated cellular systems: Application to L1 retrotransposition. *Journal of Computational Biology*, 14(3):339–349, April 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0125; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0125`.

Rauf:2013:FMC

[RRNB13] Imran Rauf, Florian Rasche, François Nicolas, and Sebastian Böcker. Finding maximum colorful subtrees in practice. *Journal of Computational Biology*, 20(4):311–321, April 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0083; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0083`.

Reva:1995:CLM

[RROF95] Boris A. Reva, Dmitrii S. Rykunov, Arthur J. Olson, and Alexei V. Finkelstein. Constructing lattice models of protein chains with side groups. *Journal of Computational Biology*, 2(4):527–535, January 1995. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.527; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.527.

Reinert:1998:CPP

[RS98] Gesine Reinert and Sophie Schbath. Compound Poisson and Poisson process approximations for occurrences of multiple words in Markov chains. *Journal of Computational Biology*, 5(2):223–253, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.223; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.223.

Robin:2001:NCS

[RS01] Stéphane Robin and Sophie Schbath. Numerical comparison of several approximations of the word count distribution in random sequences. *Journal of Computational Biology*, 8(4):349–359, September 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701752236179; https://www.liebertpub.com/doi/pdf/10.1089/106652701752236179.

Rabie:2012:SSA

[RS12] Huwaida S. Rabie and Ian W. Saunders. A simulation study to assess a variable selection method for selecting single nucleotide polymorphisms associated with disease. *Journal of Computational Biology*, 19(10):1151–1161, October 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0105; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0105.

Roch:2013:RTT

[RS13] Sebastien Roch and Sagi Snir. Recovering the treelike trend of evolution despite extensive lateral genetic transfer: a probabilistic analysis. *Journal of Computational Biology*, 20(2):93–112, February 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0234; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0234.

Roddur:2024:ETC

[RSEK24] Mrinmoy Saha Roddur, Sagi Snir, and Mohammed El-Kebir. Enforcing temporal consistency in migration history inference. *Journal of Computational Biology*, 31(5):396–415, May 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0352; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0352`.

Rasmussen:2006:EGF

[RSM06] Kim R. Rasmussen, Jens Stoye, and Eugene W. Myers. Efficient q-gram filters for finding all ϵ-matches over a given length. *Journal of Computational Biology*, 13 (2):296–308, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.296; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.296`.

Ribeiro:2009:DSM

[RSR+09] Andre S. Ribeiro, Olli-Pekka Smolander, Tiina Rajala, Antti Häkkinen, and Olli Yli-Harja. Delayed stochastic model of transcription at the single nucleotide level. *Journal of Computational Biology*, 16(4):539–553, April 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0153; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0153`.

Reinert:2000:PSP

[RSW00] Gesine Reinert, Sophie Schbath, and Michael S. Waterman. Probabilistic and statistical properties of words: An overview. *Journal of Computational Biology*, 7(1–2):1–46, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Rangamaran:2018:ETI

[RUGR18] Vijaya Raghavan Rangamaran, Bharathram Uppili, Dharani Gopal, and Kirubagaran Ramalingam. EasyQC: Tool with interactive user interface for efficient next-generation sequencing data quality control. *Journal of Computational Biology*, 25(12):1301–1311, December 2018. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0186; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0186.

Raphael:2015:SIC

[RV15] Benjamin J. Raphael and Fabio Vandin. Simultaneous inference of cancer pathways and tumor progression from cross-sectional mutation data. *Journal of Computational Biology*, 22(6):510–527, June 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0161; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0161.

Roweis:1999:RED

[RW99] Sam Roweis and Erik Winfree. On the reduction of errors in DNA computation. *Journal of Computational Biology*, 6(1):65–75, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.65; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.65.

Reidys:2010:SRP

[RW10] Christian M. Reidys and Rita R. Wang. Shapes of RNA pseudoknot structures. *Journal of Computational Biology*, 17 (11):1575–1590, November 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0006; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0006.

Roweis:1998:SBM

[RWB+98] Sam Roweis, Erik Winfree, Richard Burgoyne, Nickolas V. Chelyapov, Myron F. Goodman, Paul W. K. Rothemund, and Leonard M. Adleman. A sticker-based model for DNA computation. *Journal of Computational Biology*, 5 (4):615–629, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.615; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.615.

Ruan:2020:IPG

[RXH+20] Sha-Sha Ruan, Yi-Chen Xiao, Pei-Cheng He, Yi Wang, and Tao Ma. Identification of potential gene signatures related to sleep deprivation. *Journal of Computational Biology*, 27(6):904–913, June 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0177; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0177`.

Ren:2022:KNM

[RYY22] Ruohan Ren, Changchuan Yin, and Stephen S.-T. Yau. `kmer2vec`: a novel method for comparing DNA sequences by `word2vec` embedding. *Journal of Computational Biology*, 29(9):1001–1021, September 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0536; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0536`.

Ren:2023:PPT

[RYZ23] Jie Ren, Huaimin Yuan, and Qimin Zhang. Positivity preserving truncated Euler–Maruyama scheme for the stochastic age-structured HIV/AIDS model. *Journal of Computational Biology*, 30(3):293–322, March 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0032; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0032`.

Ribeiro:2006:GMS

[RZK06] Andre Ribeiro, Rui Zhu, and Stuart A. Kauffman. A general modeling strategy for gene regulatory networks with stochastic dynamics. *Journal of Computational Biology*, 13(9):1630–1639, November 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1630; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1630`.

Sahinalp:2018:PSA

[Sah18] Cenk Sahinalp. Preface: Selected articles from RECOMB 2017. *Journal of Computational Biology*, 25(7):623, July 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-

8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.29017.cs.

Salzberg:1995:LPC

[Sal95] Steven Salzberg. Locating protein coding regions in human DNA using a decision tree algorithm. *Journal of Computational Biology*, 2(3):473–485, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.473; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.473.

Sehl:2009:ASS

[SAL09] Mary Sehl, Alexander V. Alekseyenko, and Kenneth L. Lange. Accurate stochastic simulation via the step anticipation τ-leaping (SAL) algorithm. *Journal of Computational Biology*, 16(9):1195–1208, September 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0249; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0249.

Sitharam:2006:MVS

[SAM06] Meera Sitharam and Mavis Agbandje-Mckenna. Modeling virus self-assembly pathways: Avoiding dynamics using geometric constraint decomposition. *Journal of Computational Biology*, 13(6):1232–1265, July 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1232; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1232.

Sammeth:2009:CAS

[Sam09] Michael Sammeth. Complete alternative splicing events are bubbles in splicing graphs. *Journal of Computational Biology*, 16(8):1117–1140, August 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0108; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0108.

Sankoff:1998:MGR

[SB98] David Sankoff and Mathieu Blanchette. Multiple genome rearrangement and breakpoint phylogeny. *Journal of Computa-*

tional Biology, 5(3):555–570, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.555; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.555`.

Sankoff:1999:PIG

[SB99] David Sankoff and Mathieu Blanchette. Phylogenetic invariants for genome rearrangements. *Journal of Computational Biology*, 6(3–4):431–445, October 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Sun:2005:DMS

[SB05] Yanni Sun and Jeremy Buhler. Designing multiple simultaneous seeds for DNA similarity search. *Journal of Computational Biology*, 12(6):847–861, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.847; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.847`.

Siebert:2007:DPA

[SB07] Sven Siebert and Rolf Backofen. A dynamic programming approach for finding common patterns in RNAs. *Journal of Computational Biology*, 14(1):33–44, January 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0089; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0089`.

Shahinuzzaman:2017:MAS

[SB17] Md Shahinuzzaman and Dipak Barua. A multiscale algorithm for spatiotemporal modeling of multivalent protein–protein interaction. *Journal of Computational Biology*, 24 (12):1275–1283, December 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0178; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0178`.

Sharma:2021:ISI

[SB21] Vishnu Kumar Sharma and Prasad V. Bharatam. Identification of selective inhibitors of *Ld* DHFR enzyme using pharmacoinformatic methods. *Journal of Computational Biol-*

ogy, 28(1):43–59, January 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0332; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0332`.

Sun:1997:PSE

[SBAW97] Fengzhu Sun, Gary Benson, Norm Arnheim, and Michael Waterman. Pooling strategies for establishing physical genome maps using FISH. *Journal of Computational Biology*, 4 (4):467–486, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.467; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.467`.

Sharon:2005:CBV

[SBC+05] Itai Sharon, Aaron Birkland, Kuan Chang, Ran El-Yaniv, and Golan Yona. Correcting BLAST *e*-values for low-complexity segments. *Journal of Computational Biology*, 12 (7):980–1003, September 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.980; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.980`.

Sankoff:2000:EEE

[SBD+00] David Sankoff, David Bryant, Mélanie Deneault, B. Franz Lang, and Gertraud Burger. Early eukaryote evolution based on mitochondrial gene order breakpoints. *Journal of Computational Biology*, 7(3–4):521–535, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Shibuya:2022:SMS

[SBK22] Yoshihiro Shibuya, Djamal Belazzougui, and Gregory Kucherov. Set-min sketch: a probabilistic map for power-law distributions with application to k-mer annotation. *Journal of Computational Biology*, 29(2):140–154, February 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0429; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0429`.

Soto:2021:TTD

[SBNS21] Carlos Soto, Darshan Bryner, Nicola Neretti, and Anuj Srivastava. Toward a three-dimensional chromosome shape alphabet. *Journal of Computational Biology*, 28(6):601–618, June 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0383; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0383`.

Safonova:2015:DAH

[SBP15] Yana Safonova, Anton Bankevich, and Pavel A. Pevzner. dipSPAdes: Assembler for highly polymorphic diploid genomes. *Journal of Computational Biology*, 22(6):528–545, June 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0153; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0153`.

Sharon:2011:PBF

[SBPS11] Itai Sharon, Sivan Bercovici, Ron Y. Pinter, and Tomer Shlomi. Pathway-based functional analysis of metagenomes. *Journal of Computational Biology*, 18(3):495–505, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0260; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0260`.

Subramanian:2020:RTR

[SBRG20] Sai H. Sankara Subramanian, Karpaga Raja Sundari Balachandran, Vijaya Raghavan Rangamaran, and Dharani Gopal. RemeDB: Tool for rapid prediction of enzymes involved in bioremediation from high-throughput metagenome data sets. *Journal of Computational Biology*, 27(7):1020–1029, July 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0345; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0345`.

Schbath:2000:ENC

[SBT00] Sophie Schbath, Nathalie Bossard, and Simon Tavaré. The effect of nonhomogeneous clone length distribution on the progress of an STS mapping project. *Journal of Computational Biology*, 7

(1–2):47–57, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Szczurek:2010:IKD

[SBTV10] Ewa Szczurek, Przemysław Biecek, Jerzy Tiuryn, and Martin Vingron. Introducing knowledge into differential expression analysis. *Journal of Computational Biology*, 17(8):953–967, August 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0034; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0034`.

Senter:2015:FAK

[SC15] Evan Senter and Peter Clote. Fast, approximate kinetics of RNA folding. *Journal of Computational Biology*, 22 (2):124–144, February 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0193; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0193`.

Saravanaraman:2014:NRN

[SCB14] Ponne Saravanaraman, Raj Kumar Chinnadurai, and Rathanam Boopathy. A new role for the nonpathogenic nonsynonymous single-nucleotide polymorphisms of acetylcholinesterase in the treatment of Alzheimer's disease: a computational study. *Journal of Computational Biology*, 21(8):632–647, August 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0005; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0005`.

Smith:1998:SBA

[SCC+98] Lloyd M. Smith, Robert M. Corn, Anne E. Condon, Max G. Lagally, Anthony G. Frutos, Qinghua Liu, and Andrew J. Thiel. A surface-based approach to DNA computation. *Journal of Computational Biology*, 5(2):255–267, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.255; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.255`.

Shan:2022:DSM

[SCD+22] Xu Shan, Jinyu Chen, Kangning Dong, Wei Zhou, and Shihua Zhang. Deciphering the spatial modular patterns of tissues by integrating spatial and single-cell transcriptomic data. *Journal of Computational Biology*, 29(7):650–663, July 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0617; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0617`.

Schbath:1997:CPP

[Sch97a] Sophie Schbath. Coverage processes in physical mapping by anchoring random clones. *Journal of Computational Biology*, 4(1):61–82, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.61; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.61`.

Schbath:1997:ESD

[Sch97b] Sophie Schbath. An efficient statistic to detect over- and under-represented words in DNA sequences. *Journal of Computational Biology*, 4(2):189–192, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.189; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.189`.

Schbath:2000:ODW

[Sch00] Sophie Schbath. An overview on the distribution of word counts in Markov chains. *Journal of Computational Biology*, 7(1–2):193–201, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Schrider:2009:AHS

[SCH09] Daniel R. Schrider, James C. Costello, and Matthew W. Hahn. All human-specific gene losses are present in the genome as pseudogenes. *Journal of Computational Biology*, 16(10):1419–1427, October 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0085; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0085`.

Schwartz:2021:RSIa

[Sch21a] Russell Schwartz. RECOMB 2020 special issue. *Journal of Computational Biology*, 28(4):345, April 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Schwartz:2021:RSIb

[Sch21b] Russell Schwartz. RECOMB 2020 special issue. *Journal of Computational Biology*, 28(5):433–434, May 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Smoly:2016:ART

[SCSA+16] Ilan Smoly, Amir Carmel, Yonat Shemer-Avni, Esti Yeger-Lotem, and Michal Ziv-Ukelson. Algorithms for regular tree grammar network search and their application to mining human–viral infection patterns. *Journal of Computational Biology*, 23(3):165–179, March 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0168; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0168`.

Sewell:1995:MCP

[SD95] Roger F. Sewell and Richard Durbin. Method for calculation of probability of matching a bounded regular expression in a random data string. *Journal of Computational Biology*, 2(1):25–31, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.25; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.25`.

Segal:2003:RAM

[SDC03] Mark R. Segal, Kam D. Dahlquist, and Bruce R. Conklin. Regression approaches for microarray data analysis. *Journal of Computational Biology*, 10(6):961–980, December 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652703322756177; https://www.liebertpub.com/doi/pdf/10.1089/106652703322756177`.

Stegle:2010:RBT

[SDC+10] Oliver Stegle, Katherine J. Denby, Emma J. Cooke, David L. Wild, Zoubin Ghahramani, and Karsten M. Borgwardt. A ro-

bust Bayesian two-sample test for detecting intervals of differential gene expression in microarray time series. *Journal of Computational Biology*, 17(3):355–367, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0175; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0175`.

Spouge:2024:SPS

[SDCF24] John L. Spouge, Pijush Das, Ye Chen, and Martin Frith. The statistics of parametrized syncmers in a simple mutation process without spurious matches. *Journal of Computational Biology*, 31(12):1195–1210, December 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0508; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0508`.

Schneidman-Duhovny:2008:DPD

[SDDI+08] Dina Schneidman-Duhovny, Oranit Dror, Yuval Inbar, Ruth Nussinov, and Haim J. Wolfson. Deterministic pharmacophore detection via multiple flexible alignment of drug-like molecules. *Journal of Computational Biology*, 15(7):737–754, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0130; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0130`.

Salzberg:1998:DTS

[SDFH98] Steven Salzberg, Arthur L. Delcher, Kenneth H. Fasman, and John Henderson. A decision tree system for finding genes in DNA. *Journal of Computational Biology*, 5 (4):667–680, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.667; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.667`.

Sarr:2016:VAR

[SDFR16] Abdoulaye Sarr, Anya Désilles, Alexandra Fronville, and Vincent Rodin. A viability approach for robustness measurement, organizational autopoiesis, and cell turnover in a multicellular system. *Journal of Computational Biology*, 23(4):256–269,

April 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0187; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0187.

Song:2007:ADR

[SDG+07] Yun S. Song, Zhihong Ding, Dan Gusfield, Charles H. Langley, and Yufeng Wu. Algorithms to distinguish the role of gene-conversion from single-crossover recombination in the derivation of SNP sequences in populations. *Journal of Computational Biology*, 14(10):1273–1286, December 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0096; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0096.

Sefer:2016:DEC

[SDK16] Emre Sefer, Geet Duggal, and Carl Kingsford. Deconvolution of ensemble chromatin interaction data reveals the latent mixing structures in cell subpopulations. *Journal of Computational Biology*, 23(6):425–438, June 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0210; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0210.

Saidi:2019:EMR

[SDMN19] Rabie Saidi, Wajdi Dhifli, Mondher Maddouri, and Engelbert Mephu Nguifo. Efficiently mining recurrent substructures from protein three-dimensional structure graphs. *Journal of Computational Biology*, 26(6):561–571, June 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0171; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0171.

Sun:2020:NMB

[SDP+20] Nan Sun, Rui Dong, Shaojun Pei, Changchuan Yin, and Stephen S.-T. Yau. A new method based on coding sequence density to cluster bacteria. *Journal of Computational Biology*, 27(12):1688–1698, December 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0509;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0509.

Searls:2001:JGL

[Sea01] David B. Searls. From *jabberwocky* to genome: Lewis Carroll and computational biology. *Journal of Computational Biology*, 8(3):339–348, June 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270152530881; https://www.liebertpub.com/doi/pdf/10.1089/10665270152530881.

Sefer:2025:DPD

[Sef25] Emre Sefer. DRGAT: Predicting drug responses via diffusion-based graph attention network. *Journal of Computational Biology*, 32(3):330–350, March 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0807; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0807.

Seligmann:2013:TDR

[Sel13] Hervé Seligmann. Triplex DNA:RNA, 3'-to-5' inverted RNA and protein coding in mitochondrial genomes. *Journal of Computational Biology*, 20(9):660–671, September 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0134; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0134.

Serang:2015:FNM

[Ser15] Oliver Serang. A fast numerical method for max-convolution and the application to efficient max-product inference in Bayesian networks. *Journal of Computational Biology*, 22(8):770–783, August 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0013; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0013.

Silverbush:2011:OOP

[SES11] Dana Silverbush, Michael Elberfeld, and Roded Sharan. Optimally orienting physical networks. *Journal of Computational Biology*, 18(11):1437–1448, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0163;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0163.

Seok:2009:FAC

[SEV09] Sang-Cheol Seok, Michael Evans, and Veronica J. Vieland. Fast and accurate calculation of a computationally intensive statistic for mapping disease genes. *Journal of Computational Biology*, 16(5):659–676, May 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0175; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0175.

Steel:1995:CCL

[SF95] M. A. Steel and Y. X. Fu. Classifying and counting linear phylogenetic invariants for the jukes–Cantor model. *Journal of Computational Biology*, 2(1):39–47, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.39; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.39.

Shatkay:2003:MBL

[SF03] Hagit Shatkay and Ronen Feldman. Mining the biomedical literature in the genomic era: An overview. *Journal of Computational Biology*, 10(6):821–855, December 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703322756104; https://www.liebertpub.com/doi/pdf/10.1089/106652703322756104.

Schindler:2012:SAV

[SF12] Christina Schindler and Wolfgang B. Fischer. Sequence alignment of viral channel proteins with cellular ion channels. *Journal of Computational Biology*, 19(9):1060–1072, September 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0297; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0297.

Sahlin:2017:SVD

[SFA17] Kristoffer Sahlin, Mattias Frånberg, and Lars Arvestad. Structural variation detection with read pair information: an im-

proved null hypothesis reduces bias. *Journal of Computational Biology*, 24(6):581–589, June 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0124; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0124`.

Souaiaia:2011:CSC

[SFC11] Tade Souaiaia, Zach Frazier, and Ting Chen. ComB: SNP calling and mapping analysis for color and nucleotide space platforms. *Journal of Computational Biology*, 18(6):795–807, June 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0027; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0027`.

Sankoff:1997:CSI

[SFN97] David Sankoff, Vincent Ferretti, and Joseph H. Nadeau. Conserved segment identification. *Journal of Computational Biology*, 4(4):559–565, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.559; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.559`.

Schweiger:2018:USA

[SFR+18] Regev Schweiger, Eyal Fisher, Elior Rahmani, Liat Shenhav, Saharon Rosset, and Eran Halperin. Using stochastic approximation techniques to efficiently construct confidence intervals for heritability. *Journal of Computational Biology*, 25(7):794–808, July 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0047; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0047`.

States:1994:QCU

[SG94] David J. States and Warren Gish. QGB: Combined use of sequence similarity and codon bias for coding region identification. *Journal of Computational Biology*, 1(1):39–50, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.39; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.39`.

Sakhanenko:2010:MLN

[SG10] Nikita A. Sakhanenko and David J. Galas. Markov logic networks in the analysis of genetic data. *Journal of Computational Biology*, 17(11):1491–1508, November 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0044; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0044`.

Sakhanenko:2012:PLM

[SG12] Nikita A. Sakhanenko and David J. Galas. Probabilistic logic methods and some applications to biology and medicine. *Journal of Computational Biology*, 19(3):316–336, March 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0234; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0234`.

Sakhanenko:2015:BDA

[SG15] Nikita A. Sakhanenko and David J. Galas. Biological data analysis as an information theory problem: Multivariable dependence measures and the shadows algorithm. *Journal of Computational Biology*, 22(11):1005–1024, November 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0051; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0051`.

Savard:2011:GHD

[SGBEM11] Olivier Tremblay Savard, Yves Gagnon, Denis Bertrand, and Nadia El-Mabrouk. Genome halving and double distance with losses. *Journal of Computational Biology*, 18 (9):1185–1199, September 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0136; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0136`.

Sun:2019:BAS

[SGCD19] Chao Sun, Yifan Gu, Guoqing Chen, and Yibao Du. Bioinformatics analysis of stromal molecular signatures associated with breast and prostate cancer. *Journal of Computational Biology*, 26(10):1130–1139, October 2019. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0045; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0045.

Saffarian:2012:RLO

[SGdMT12] Azadeh Saffarian, Mathieu Giraud, Antoine de Monte, and Hélène Touzet. RNA locally optimal secondary structures. *Journal of Computational Biology*, 19(10):1120–1133, October 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0178; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0178.

Silberberg:2012:LSE

[SGK+12] Yael Silberberg, Assaf Gottlieb, Martin Kupiec, Eytan Ruppin, and Roded Sharan. Large-scale elucidation of drug response pathways in humans. *Journal of Computational Biology*, 19(2):163–174, February 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0264; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0264.

Setty:2011:HTI

[SGP11] Manu N. Setty, Alexander Gusev, and Itsik Pe'er. HLA type inference via haplotypes identical by descent. *Journal of Computational Biology*, 18(3):483–493, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0258; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0258.

Sarkar:2012:SSO

[SGSN12] Deepayan Sarkar, Steve Goldstein, David C. Schwartz, and Michael A. Newton. Statistical significance of optical map alignments. *Journal of Computational Biology*, 19(5):478–492, May 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0221; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0221.

Saffarian:2015:MAR

[SGT15] Azadeh Saffarian, Mathieu Giraud, and Hélène Touzet. Modeling alternate RNA structures in genomic sequences. *Journal of Computational Biology*, 22(3):190–204, March 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0272; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0272`.

Sharan:2005:MSG

[SGYBD05] Roded Sharan, Jens Gramm, Zohar Yakhini, and Amir Ben-Dor. Multiplexing schemes for generic SNP genotyping assays. *Journal of Computational Biology*, 12(5):514–533, June 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.514; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.514`.

Siepel:2004:CPH

[SH04a] Adam Siepel and David Haussler. Combining phylogenetic and hidden Markov models in biosequence analysis. *Journal of Computational Biology*, 11(2–3):413–428, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Smith:2004:TQC

[SH04b] Kaleigh Smith and Mike Hallett. Towards quality control for DNA microarrays. *Journal of Computational Biology*, 11(5):945–970, October 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.945; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.945`.

Song:2005:CMA

[SH05] Yun S. Song and Jotun Hein. Constructing minimal ancestral recombination graphs. *Journal of Computational Biology*, 12(2):147–169, March 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.147; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.147`.

Sankoff:2006:DGD

[SH06] David Sankoff and Lani Haque. The distribution of genomic distance between random genomes. *Journal of Computational Biology*, 13(5):1005–1012, June 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1005; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1005`.

Shi:2017:ICS

[SH17] Funan Shi and Haiyan Huang. Identifying cell subpopulations and their genetic drivers from single-cell RNA-Seq data using a biclustering approach. *Journal of Computational Biology*, 24(7):663–674, July 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0049; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0049`.

Shamir:2000:PSR

[Sha00] Ron Shamir. Preface: Special RECOMB 2000 issue. *Journal of Computational Biology*, 7(3–4):329–330, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Sharan:2015:P

[Sha15] Roded Sharan. Preface. *Journal of Computational Biology*, 22 (5):335, May 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.030P`.

Schwartz:2003:RIH

[SHB+03] Russell Schwartz, Bjarni V. Halldórsson, Vineet Bafna, Andrew G. Clark, and Sorin Istrail. Robustness of inference of haplotype block structure. *Journal of Computational Biology*, 10(1):13–19, February 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652703763255642; https://www.liebertpub.com/doi/pdf/10.1089/106652703763255642`.

Sun:2018:ASB

[SHCM18] Chen Sun, Robert S. Harris, Rayan Chikhi, and Paul Medvedev. AllSome sequence Bloom trees. *Journal of Computational Biology*, 25(5):467–479, May 2018. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0258; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0258.

Sul:2011:IPG

[SHE11] Jae Hoon Sul, Buhm Han, and Eleazar Eskin. Increasing power of groupwise association test with likelihood ratio test. *Journal of Computational Biology*, 18(11):1611–1624, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0161; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0161.

Sorenson:2000:MSE

[SHG00] Jon M. Sorenson and Teresa Head-Gordon. Matching simulation and experiment: a new simplified model for simulating protein folding. *Journal of Computational Biology*, 7(3–4):469–481, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Sorenson:2002:PES

[SHG02] Jon M. Sorenson and Teresa Head-Gordon. Protein engineering study of protein L by simulation. *Journal of Computational Biology*, 9(1):35–54, January 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/10665270252833181; https://www.liebertpub.com/doi/pdf/10.1089/10665270252833181.

Sverchkov:2020:CSN

[ShHGC20] Yuriy Sverchkov, Yi hsuan Ho, Audrey Gasch, and Mark Craven. Context-specific nested effects models. *Journal of Computational Biology*, 27(3):403–417, March 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0459; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0459.

Shibuya:2007:ESR

[Shi07] Tetsuo Shibuya. Efficient substructure RMSD query algorithms. *Journal of Computational Biology*, 14(9):1201–1207, November 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0079; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0079.

Shibuya:2010:SPD

[Shi10a] Tetsuo Shibuya. Searching protein 3-D structures in linear time. *Journal of Computational Biology*, 17(3):203–219, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0148; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0148.

Shibuya:2010:SPT

[Shi10b] Tetsuo Shibuya. Searching protein three-dimensional structures in faster than linear time. *Journal of Computational Biology*, 17(4):593–602, April 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0217; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0217.

Stolte:2008:MCE

[SHMS08] Thomas Stolte, Volker Hösel, Johannes Müller, and Michael Speicher. Modeling clonal expansion from M-FISH experiments. *Journal of Computational Biology*, 15(2):221–230, March 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0076; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0076.

Scheubert:2011:CFT

[SHRB11] Kerstin Scheubert, Franziska Hufsky, Florian Rasche, and Sebastian Böcker. Computing fragmentation trees from metabolite multiple mass spectrometry data. *Journal of Computational Biology*, 18(11):1383–1397, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0168; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0168.

Sun:2024:HHO

[SHZ+24] Xiao-Yan Sun, Zhen-Jie Hou, Wen-Guang Zhang, Yan Chen, and Hai-Bin Yao. HTFSMMA: Higher-order topological guided

small molecule–MicroRNA associations prediction. *Journal of Computational Biology*, 31(9):886–906, September 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Shibuya:1997:NFA

[SI97] Tetsuo Shibuya and Hiroshi Imai. New flexible approaches for multiple sequence alignment. *Journal of Computational Biology*, 4(3):385–413, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.385; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.385`.

Sachs:2009:LSN

[SIC+09] Karen Sachs, Solomon Itani, Jennifer Carlisle, Garry P. Nolan, Dana Pe'er, and Douglas A. Lauffenburger. Learning signaling network structures with sparsely distributed data. *Journal of Computational Biology*, 16(2):201–212, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.07TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.07TT`.

Siepel:2003:AES

[Sie03] Adam C. Siepel. An algorithm to enumerate sorting reversals for signed permutations. *Journal of Computational Biology*, 10 (3–4):575–597, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Sharan:2005:IPC

[SIK+05] Roded Sharan, Trey Ideker, Brian Kelley, Ron Shamir, and Richard M. Karp. Identification of protein complexes by comparative analysis of yeast and bacterial protein interaction data. *Journal of Computational Biology*, 12(6):835–846, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.835; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.835`.

Scott:2006:EAD

[SIKS06] Jacob Scott, Trey Ideker, Richard M. Karp, and Roded Sharan. Efficient algorithms for detecting signaling pathways

in protein interaction networks. *Journal of Computational Biology*, 13(2):133–144, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.133; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.133.

Sinha:2003:DM

[Sin03] Saurabh Sinha. Discriminative motifs. *Journal of Computational Biology*, 10(3–4):599–615, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Sperrin:2012:RIA

[SJ12] Matthew Sperrin and Thomas Jaki. Recovering independent associations in genetics: a comparison. *Journal of Computational Biology*, 19(8):978–987, August 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0141; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0141.

Siderius:2018:MSM

[SJ18] Michael Siderius and Filip Jagodzinski. Mutation sensitivity maps: Identifying residue substitutions that impact protein structure via a rigidity analysis in silico mutation approach. *Journal of Computational Biology*, 25(1):89–102, January 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0165; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0165.

Sharan:2013:RBM

[SK13] Roded Sharan and Richard M. Karp. Reconstructing Boolean models of signaling. *Journal of Computational Biology*, 20(3):249–257, March 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0241; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0241.

Sagiroglu:2017:SAE

[SK17] Mahmut Şamil Sağiroğlu and M. Oğuzhan Külekci. A system architecture for efficient transmission of massive DNA sequencing data. *Journal of Computational Biology*, 24(11):

1081–1088, November 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0016; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0016`.

Solomon:2018:ISL

[SK18] Brad Solomon and Carl Kingsford. Improved search of large transcriptomic sequencing databases using split sequence Bloom trees. *Journal of Computational Biology*, 25(7):755–765, July 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0265; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0265`.

Suvorova:2019:NMP

[SK19] Yulia M. Suvorova and Eugene V. Korotkov. New method for potential fusions detection in protein-coding sequences. *Journal of Computational Biology*, 26(11):1253–1261, November 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0122; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0122`.

Sefer:2021:MLS

[SK21] Emre Sefer and Carl Kingsford. Metric labeling and semimetric embedding for protein annotation prediction. *Journal of Computational Biology*, 28(5):514–525, May 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Son:2023:EOD

[SK23] Donghui Son and Jaejik Kim. Estimation of ordinary differential equation models for gene regulatory networks through data cloning. *Journal of Computational Biology*, 30(5):609–618, May 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0201; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0201`.

Sapra:2021:PDM

[SKDR21] Dikscha Sapra, Harpreet Kaur, Anjali Dhall, and Gajendra P. S. Raghava. ProCanBio: a database of manually curated biomarkers for prostate cancer. *Journal of*

Computational Biology, 28(12):1248–1257, December 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0348; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0348.

Stoyanov:2000:GIC

[SKG+00] Ognyan Stoyanov, Alexander Kister, Israel Gelfand, Casimir Kulikowski, and Cyrus Chothia. Geometric invariant core for the C_L and C_{H1} domains of immunoglobulin molecules. *Journal of Computational Biology*, 7(5):673–684, October 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701446143; https://www.liebertpub.com/doi/pdf/10.1089/106652701446143.

Sakhanenko:2017:ICD

[SKGG17] Nikita A. Sakhanenko, James Kunert-Graf, and David J. Galas. The information content of discrete functions and their application in genetic data analysis. *Journal of Computational Biology*, 24(12):1153–1178, December 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0143; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0143.

Schill:2024:COB

[SKL+24] Rudolf Schill, Maren Klever, Andreas Lösch, Y. Linda Hu, Stefan Vocht, Kevin Rupp, Lars Grasedyck, Rainer Spang, and Niko Beerenwinkel. Correcting for observation bias in cancer progression modeling. *Journal of Computational Biology*, 31(10):927–945, October 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0666; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0666.

Schuemie:2005:WSD

[SKM05] Martijn J. Schuemie, Jan A. Kors, and Barend Mons. Word sense disambiguation in the biomedical domain: An overview. *Journal of Computational Biology*, 12(5):554–565, June 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.

1089/cmb.2005.12.554; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.554.

Southworth:2009:PBP

[SKO09] Lucinda K. Southworth, Stuart K. Kim, and Art B. Owen. Properties of balanced permutations. *Journal of Computational Biology*, 16(4):625–638, April 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0144; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0144.

Sakoparnig:2012:BPC

[SKP+12] Thomas Sakoparnig, Tobias Kockmann, Renato Paro, Christian Beisel, and Niko Beerenwinkel. Binding profiles of chromatin-modifying proteins are predictive for transcriptional activity and promoter-proximal pausing. *Journal of Computational Biology*, 19(2):126–138, February 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0258; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0258.

Shi:2009:CEI

[SKS+09] Yanxin Shi, Michael Klutstein, Itamar Simon, Tom Mitchell, and Ziv Bar-Joseph. A combined expression-interaction model for inferring the temporal activity of transcription factors. *Journal of Computational Biology*, 16(8):1035–1049, August 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0024; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0024.

Slonim:1997:BHG

[SKSL97] Donna Slonim, Leonid Kruglyak, Lincoln Stein, and Eric Lander. Building human genome maps with radiation hybrids. *Journal of Computational Biology*, 4(4):487–504, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.487; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.487.

Swanson:2008:IMQ

[SKT08] Rosemarie Swanson, Ioannis Kagiampakis, and Jerry W. Tsai. An information measure of the quality of protein secondary structure prediction. *Journal of Computational Biology*, 15(1):65–79, January 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0199; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0199`.

Silva:2023:BFA

[SKW23] Luiz A. G. Silva, Luis A. B. Kowada, and Maria E. M. T. Walter. A barrier for further approximating sorting by transpositions. *Journal of Computational Biology*, 30(12):1277–1288, December 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0138; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0138`.

Stojmirovic:2012:IFI

[SkY12] Aleksandar Stojmirović and Yi kuo Yu. Information flow in interaction networks II: Channels, path lengths, and potentials. *Journal of Computational Biology*, 19(4):379–403, April 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0228; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0228`.

Scornavacca:2012:FST

[SLA12] Celine Scornavacca, Simone Linz, and Benjamin Albrecht. A first step toward computing all hybridization networks for two rooted binary phylogenetic trees. *Journal of Computational Biology*, 19(11):1227–1242, November 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0192; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0192`.

Smith:1997:CLP

[SLB+97] Temple F. Smith, Loredana Lo Conte, Jadwiga Bienkowska, Chrysanthe Gaitatzes, Robert G. Rogers, Jr., and Richard Lathrop. Current limitations to protein threading approaches. *Journal of Computational Biology*, 4(3):217–225, January 1997. CO-

DEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.217; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.217.

Schmidler:2000:BSP

[SLB00] Scott C. Schmidler, Jun S. Liu, and Douglas L. Brutlag. Bayesian segmentation of protein secondary structure. *Journal of Computational Biology*, 7(1–2):233–248, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Shen:2023:IDA

[SlGW+23] Yi Shen, Ying lian Gao, Juan Wang, Bo xin Guan, and Jin xing Liu. Identification of disease-associated MicroRNAs via locality-constrained linear coding-based ensemble learning. *Journal of Computational Biology*, 30(8):926–936, August 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0084; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0084.

Santafe:2008:IPS

[SLL08] Guzmán Santafé, Jose A. Lozano, and Pedro Larrañaga. Inference of population structure using genetic markers and a Bayesian model averaging approach for clustering. *Journal of Computational Biology*, 15(2):207–220, March 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0051; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0051.

Su:2017:MSA

[SLL+17] Wenhe Su, Xiangke Liao, Yutong Lu, Quan Zou, and Shaoliang Peng. Multiple sequence alignment based on a suffix tree and center-star strategy: a linear method for multiple nucleotide sequence alignment on spark parallel framework. *Journal of Computational Biology*, 24(12):1230–1242, December 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0040; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0040.

Shao:2023:CGM

[SLL+23] Jian Shao, Ziqing Liu, Shaoyun Li, Benrui Wu, Zedong Nie, Yuefei Li, and Kaixin Zhou. Continuous glucose monitoring time series data analysis: a time series analysis package for continuous glucose monitoring data. *Journal of Computational Biology*, 30(1):112–116, January 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0100; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0100`.

Shao:2015:EAC

[SLM15] Mingfu Shao, Yu Lin, and Bernard M. E. Moret. An exact algorithm to compute the double-cut-and-join distance for genomes with duplicate genes. *Journal of Computational Biology*, 22(5):425–435, May 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0096; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0096`.

Schmidler:2007:SES

[SLO07] Scott C. Schmidler, Joseph E. Lucas, and Terrence G. Oas. Statistical estimation of statistical mechanical models: Helix-coil theory and peptide helicity prediction. *Journal of Computational Biology*, 14(10):1287–1310, December 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0008; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0008`.

Swenson:2009:HSI

[SLRM09] Krister M. Swenson, Yu Lin, Vaibhav Rajan, and Bernard M. E. Moret. Hurdles and sorting by inversions: Combinatorial, statistical, and experimental results. *Journal of Computational Biology*, 16(10):1339–1351, October 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0156; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0156`.

Srivatsa:2023:CES

[SLS23] Arjun Srivatsa, Haoyun Lei, and Russell Schwartz. A clonal evolution simulator for planning somatic evolution studies. *Journal of Computational Biology*, 30(8):831–847, August 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0086; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0086`.

Sukpol:2024:CSC

[SLT24] Wimonnat Sukpol, Teeraphan Laomettachit, and Anuwat Tangthanawatsakul. A cancer subpopulation competition model reveals optimal levels of immune response that minimize tumor size. *Journal of Computational Biology*, 31 (11):1179–1194, November 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0618; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0618`.

Sze:2006:PTS

[SLY06] Sing-Hoi Sze, Yue Lu, and Qingwu Yang. A polynomial time solvable formulation of multiple sequence alignment. *Journal of Computational Biology*, 13(2):309–319, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.309; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.309`.

Su:2009:CHD

[SLYC09] Ming-Wei Su, Hsiu-Man Lin, Hanna S. Yuan, and Woei-Chyn Chu. Categorizing host-dependent RNA viruses by principal component analysis of their codon usage preferences. *Journal of Computational Biology*, 16(11):1539–1547, November 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0046; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0046`.

Sun:2015:MSM

[SLZH15] Miao Sun, Dejian Lai, Li Zhang, and Xuelin Huang. Modified SuperCurve method for analysis of reverse-phase protein array

data. *Journal of Computational Biology*, 22(8):765–769, August 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0007; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0007.

Sagot:1998:ISP

[SM98] Marie-France Sagot and Eugene W. Myers. Identifying satellites and periodic repetitions in biological sequences. *Journal of Computational Biology*, 5(3):539–553, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.539; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.539.

Spiro:2004:LAM

[SM04] Peter A. Spiro and Natasa Macura. A local alignment metric for accelerating biosequence database search. *Journal of Computational Biology*, 11(1):61–82, January 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652704773416894; https://www.liebertpub.com/doi/pdf/10.1089/106652704773416894.

Shojaie:2009:AGS

[SM09] Ali Shojaie and George Michailidis. Analysis of gene sets based on the underlying regulatory network. *Journal of Computational Biology*, 16(3):407–426, March 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0081; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0081.

Shao:2016:FEA

[SM16] Mingfu Shao and Bernard M. E. Moret. A fast and exact algorithm for the exemplar breakpoint distance. *Journal of Computational Biology*, 23(5):337–346, May 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0193; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0193.

Shao:2017:CBD

[SM17] Mingfu Shao and Bernard M. E. Moret. On computing breakpoint distances for genomes with duplicate genes. *Journal of Computational Biology*, 24(6):571–580, June 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0149; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0149`.

Sahlin:2020:NCL

[SM20] Kristoffer Sahlin and Paul Medvedev. De Novo clustering of long-read transcriptome data using a greedy, quality value-based algorithm. *Journal of Computational Biology*, 27(4):472–484, April 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0299; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0299`.

Soliman:2015:DMM

[SMC+15] Ahmed T. Soliman, Tao Meng, Shu-Ching Chen, S. S. Iyengar, Puneeth Iyengar, John Yordy, and Mei-Ling Shyu. Driver missense mutation identification using feature selection and model fusion. *Journal of Computational Biology*, 22(12): 1075–1085, December 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0110; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0110`.

Shi:2007:QMB

[SMD+07] Yi Y. Shi, Gerald A. Miller, Oleg Denisenko, Hong Qian, and Karol Bomsztyk. Quantitative model for binary measurements of protein-protein interactions. *Journal of Computational Biology*, 14(7):1011–1023, September 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0024; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0024`.

Schierwater:1996:ENP

[SMKS96] Bernd Schierwater, Dirk Metzler, Katja Krüger, and Bruno Streit. The effects of nested primer binding sites on the

reproducibility of PCR: Mathematical modeling and computer simulation studies. *Journal of Computational Biology*, 3(2):235–251, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.235; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.235`.

Shatkay:2004:TEA

[SMM+04] Hagit Shatkay, Jason Miller, Clark Mobarry, Michael Flanigan, Shibu Yooseph, and Granger Sutton. ThurGood: Evaluating assembly-to-assembly mapping. *Journal of Computational Biology*, 11(5):800–811, October 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.800; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.800`.

Souza:2024:BBA

[SMML24] Michael Souza, Nilton Maia, Rômulo S. Marques, and Carlile Lavor. A branch-and-bound algorithm for the molecular ordered covering problem. *Journal of Computational Biology*, 31(6):475–485, June 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Sadeh:2013:CUU

[SMS13] Mohammad J. Sadeh, Giusi Moffa, and Rainer Spang. Considering unknown unknowns: Reconstruction of nonconfoundable causal relations in biological networks. *Journal of Computational Biology*, 20(11):920–932, November 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0119; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0119`.

Schbath:2012:MRG

[SMZ+12] Sophie Schbath, Véronique Martin, Matthias Zytnicki, Julien Fayolle, Valentin Loux, and Jean-François Gibrat. Mapping reads on a genomic sequence: an algorithmic overview and a practical comparative analysis. *Journal of Computational Biology*, 19(6):796–813, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0022;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0022.

Shi:2020:CDM

[SnGqC20] Ke Shi, Meng na Ge, and Xiao qiao Chen. Coordinated DNA methylation and gene expression data for identification of the critical genes associated with childhood atopic asthma. *Journal of Computational Biology*, 27(1):109–120, January 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0194; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0194.

Snir:2019:BIG

[Sni19] Sagi Snir. Bounds on identification of genome evolution pacemakers. *Journal of Computational Biology*, 26(8):806–821, August 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0178; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0178.

Sharov:2014:CPR

[SNQ+14] Alexei A. Sharov, Akira Nishiyama, Yong Qian, Dawood B. Dudekula, Dan L. Longo, David Schlessinger, and Minoru S. H. Ko. Chromatin properties of regulatory DNA probed by manipulation of transcription factors. *Journal of Computational Biology*, 21(8):569–577, August 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0126; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0126.

Sandak:1998:MBS

[SNW98] Bilha Sandak, Ruth Nussinov, and Haim J. Wolfson. A method for biomolecular structural recognition and docking allowing conformational flexibility. *Journal of Computational Biology*, 5(4):631–654, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.631; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.631.

Shatsky:2004:FAF

[SNW04] Maxim Shatsky, Ruth Nussinov, and Haim J. Wolfson. FlexProt: Alignment of flexible protein structures without a predefinition of hinge regions. *Journal of Computational Biology*, 11(1):83–106, January 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652704773416902; https://www.liebertpub.com/doi/pdf/10.1089/106652704773416902`.

Shenker:2011:ETB

[SOD+11] Solomon Shenker, Charles W. O'Donnell, Srinivas Devadas, Bonnie Berger, and Jérôme Waldispühl. Efficient traversal of beta-sheet protein folding pathways using ensemble models. *Journal of Computational Biology*, 18(11):1635–1647, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0176; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0176`.

Soloveichik:2009:RSC

[Sol09] David Soloveichik. Robust stochastic chemical reaction networks and bounded Tau-leaping. *Journal of Computational Biology*, 16(3):501–522, March 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0063; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0063`.

Sze:1997:VAG

[SP97] Sing-Hoi Sze and Pavel A. Pevzner. Las Vegas algorithms for gene recognition: Suboptimal and error-tolerant spliced alignment. *Journal of Computational Biology*, 4 (3):297–309, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.297; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.297`.

Snir:2011:TMP

[SP11] Sagi Snir and Lior Pachter. Tracing the most parsimonious indel history. *Journal of Computational Biology*, 18(8):967–986, August 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/`

abs/10.1089/cmb.2010.0325; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0325.

Simmons:2015:DWD

[SPBB15] Sean Simmons, Jian Peng, Jadwiga Bienkowska, and Bonnie Berger. Discovering what dimensionality reduction really tells us about RNA-Seq data. *Journal of Computational Biology*, 22(8):715–728, August 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0085; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0085.

Surujon:2019:SWN

[SPC19] Defne Surujon, Yann Ponty, and Peter Clote. Small-world networks and RNA secondary structures. *Journal of Computational Biology*, 26(1):16–26, January 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0125; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0125.

Schbath:1995:EMD

[SPD95] Sophie Schbath, Bernard Prum, and Elisabeth De Turckheim. Exceptional motifs in different Markov chain models for a statistical analysis of DNA sequences. *Journal of Computational Biology*, 2(3):417–437, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.417; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.417.

Santiago:2018:HDU

[SPD18] Caio Santiago, Vivian Pereira, and Luciano Digiampietri. Homology detection using multilayer maximum clustering coefficient. *Journal of Computational Biology*, 25(12):1328–1338, December 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0266; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0266.

Speed:2008:P

[Spe08] Terry Speed. Preface. *Journal of Computational Biology*, 15 (7):653, September 2008. CODEN JCOBEM. ISSN 1066-

5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.P001.

Sahoo:2023:IBU

[SPSZ23] Bikram Sahoo, Zandra Pinnix, Seth Sims, and Alex Zelikovsky. Identifying biomarkers using support vector machine to understand the racial disparity in triple-negative breast cancer. *Journal of Computational Biology*, 30(4):502–517, April 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0422; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0422.

Shen:2022:WIM

[SPW22] Chengze Shen, Minhyuk Park, and Tandy Warnow. WITCH: Improved multiple sequence alignment through weighted consensus hidden Markov model alignment. *Journal of Computational Biology*, 29(8):782–801, August 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0585; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0585.

Sindi:2010:IFE

[SR10] Suzanne S. Sindi and Benjamin J. Raphael. Identification and frequency estimation of inversion polymorphisms from haplotype data. *Journal of Computational Biology*, 17(3):517–531, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0185; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0185.

Sanchez:2025:TGI

[SRB+25] Juan Felipe Sánchez, Salah Ramtani, Abdelkader Boucetta, Marco Antonio Velasco, Juan Jairo Vaca-González, Carlos A. Duque-Daza, and Diego A. Garzón-Alvarado. Is tumor growth influenced by the bone remodeling process? *Journal of Computational Biology*, 32(1):104–124, January 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0390; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0390.

Serra:2016:SMB

[SRF16] Fabrizio Serra, Chiara Romualdi, and Federico Fogolari. Similarity measures based on the overlap of ranked genes are effective for comparison and classification of microarray data. *Journal of Computational Biology*, 23(7):603–614, July 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0057; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0057`.

Swenson:2010:SSP

[SRLM10] Krister M. Swenson, Vaibhav Rajan, Yu Lin, and Bernard M. E. Moret. Sorting signed permutations by inversions in $O(n \log n)$ time. *Journal of Computational Biology*, 17(3):489–501, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0184; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0184`.

Siegel:1998:ORF

[SRM+98] Andrew F. Siegel, Jared C. Roach, Charles Magness, Ed Thayer, and Ger Van Den Engh. Optimization of restriction fragment DNA mapping. *Journal of Computational Biology*, 5(1):113–126, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.113; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.113`.

Spang:2002:NAR

[SRS02] Rainer Spang, Marc Rehmsmeier, and Jens Stoye. A novel approach to remote homology detection: Jumping alignments. *Journal of Computational Biology*, 9(5):747–760, October 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652702761034172; https://www.liebertpub.com/doi/pdf/10.1089/106652702761034172`.

Saule:2011:CRP

[SRSD11] Cédric Saule, Mireille Régnier, Jean-Marc Steyaert, and Alain Denise. Counting RNA pseudoknotted structures. *Journal of Computational Biology*, 18(10):1339–1351, October

2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0086; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0086.

Siegel:1998:EVT

[SRV98] Andrew F. Siegel, Jared C. Roach, and Ger Van Den Engh. Expectation and variance of true and false fragment matches in DNA restriction mapping. *Journal of Computational Biology*, 5(1):101–111, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.101; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.101.

Song:2013:AFS

[SRZ+13] Kai Song, Jie Ren, Zhiyuan Zhai, Xuemei Liu, Minghua Deng, and Fengzhu Sun. Alignment-free sequence comparison based on next-generation sequencing reads. *Journal of Computational Biology*, 20(2):64–79, February 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0228; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0228.

Skiena:1995:RSS

[SS95] Steven S. Skiena and Gopalakrishnan Sundaram. Reconstructing strings from substrings. *Journal of Computational Biology*, 2(2):333–353, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.333; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.333.

Storey:2001:AVL

[SS01] John D. Storey and David Siegmund. Approximate P-values for local sequence alignments: Numerical studies. *Journal of Computational Biology*, 8(5):549–556, October 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701753216530; https://www.liebertpub.com/doi/pdf/10.1089/106652701753216530.

Sung:2004:GCE

[SS04] Myong-Hee Sung and Richard Simon. Genomewide conserved epitope profiles of HIV-1 predicted by biophysical properties of MHC binding peptides. *Journal of Computational Biology*, 11(1):125–145, January 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652704773416920; https://www.liebertpub.com/doi/pdf/10.1089/106652704773416920`.

Segal:2005:DMI

[SS05a] Eran Segal and Roded Sharan. A discriminative model for identifying spatial *cis*-regulatory modules. *Journal of Computational Biology*, 12(6):822–834, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.822; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.822`.

Sturmfels:2005:TIPa

[SS05b] Bernd Sturmfels and Seth Sullivant. Toric ideals of phylogenetic invariants. *Journal of Computational Biology*, 12(2):204–228, March 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.204; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.204`.

Sturmfels:2005:TIPb

[SS05c] Bernd Sturmfels and Seth Sullivant. Toric ideals of phylogenetic invariants. *Journal of Computational Biology*, 12(4):457–481, May 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.457; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.457`.

Scheid:2007:CUC

[SS07] Stefanie Scheid and Rainer Spang. Compensating for unknown confounders in microarray data analysis using filtered permutations. *Journal of Computational Biology*, 14(5):669–681, June 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/`

10.1089/cmb.2007.R009; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R009.

Senchyna:2023:DEN

[SS23] Fiona Senchyna and Rahul Singh. Dynamic epidemiological networks: a data representation framework for modeling and tracking of SARS-CoV-2 variants. *Journal of Computational Biology*, 30(4):446–468, April 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0469; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0469.

Sterner:2007:PAC

[SSB07] Beckett Sterner, Rohit Singh, and Bonnie Berger. Predicting and annotating catalytic residues: An information theoretic approach. *Journal of Computational Biology*, 14(8):1058–1073, October 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0042; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0042.

Sedaghat:2023:SSA

[SSC23] Nafiseh Sedaghat, Tamon Stephen, and Leonid Chindelevitch. Speeding up the structural analysis of metabolic network models using the Fredman–Khachiyan algorithm B. *Journal of Computational Biology*, 30(6):678–694, June 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0319; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0319.

Song:2007:DAC

[SSD07] N. Song, R. D. Sedgewick, and D. Durand. Domain architecture comparison for multidomain homology identification. *Journal of Computational Biology*, 14(4):496–516, May 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.A009; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.A009.

Steel:1994:RTW

[SSH94] M. A. Steel, L. A. Székely, and M. D. Hendy. Reconstructing trees when sequence sites evolve at variable rates. *Journal of*

Computational Biology, 1(2):153–163, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.153; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.153.

Schonhuth:2010:TIA

[SSH+10] Alexander Schönhuth, Raheleh Salari, Fereydoun Hormozdiari, Artem Cherkasov, and S. Cenk Sahinalp. Towards improved assessment of functional similarity in large-scale screens: a study on indel length. *Journal of Computational Biology*, 17(1):1–20, January 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0031; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0031.

Schon:2020:DRP

[SSH+20] Marian Schön, Jakob Simeth, Paul Heinrich, Franziska Görtler, Stefan Solbrig, Tilo Wettig, Peter J. Oefner, Michael Altenbuchinger, and Rainer Spang. DTD: an R package for digital tissue deconvolution. *Journal of Computational Biology*, 27(3):386–389, March 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0469; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0469.

Solar:2019:SOP

[SSIP+19] Roberto Solar, Victor Sepulveda, Alonso Inostrosa-Psijas, Oscar Rojas, Veronica Gil-Costa, and Mauricio Marin. A service-oriented platform for approximate Bayesian computation in population genetics. *Journal of Computational Biology*, 26(3):266–279, March 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0217; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0217.

Salari:2013:ITP

[SSKH+13] Raheleh Salari, Syed Shayon Saleh, Dorna Kashef-Haghighi, David Khavari, Daniel E. Newburger, Robert B. West, Arend Sidow, and Serafim Batzoglou. Inference of tumor phylogenies with improved somatic mutation discovery. *Journal*

of Computational Biology, 20(11):933–944, November 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0106; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0106.

Sun:2022:SSC

[SSLL22] Tianyi Sun, Dongyuan Song, Wei Vivian Li, and Jingyi Jessica Li. Simulating single-cell gene expression count data with preserved gene correlations by scDesign2. *Journal of Computational Biology*, 29(1):23–26, January 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0440; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0440.

Shi:2010:PAE

[SSLMW10] Haixiang Shi, Bertil Schmidt, Weiguo Liu, and Wolfgang Müller-Wittig. A parallel algorithm for error correction in high-throughput short-read data on CUDA-Enabled graphics hardware. *Journal of Computational Biology*, 17(4):603–615, April 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0062; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0062.

Salmela:2016:GFE

[SSMT16] Leena Salmela, Kristoffer Sahlin, Veli Mäkinen, and Alexandru I. Tomescu. Gap filling as exact path length problem. *Journal of Computational Biology*, 23(5):347–361, May 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0197; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0197.

Shatsky:2006:MCP

[SSPNW06] Maxim Shatsky, Alexandra Shulman-Peleg, Ruth Nussinov, and Haim J. Wolfson. The multiple common point set problem and its application to molecule binding pattern detection. *Journal of Computational Biology*, 13 (2):407–428, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.407;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.407.

Saha:2021:NPN

[SSR21] Subrata Saha, Ahmed Soliman, and Sanguthevar Rajasekaran. A novel pathway network analytics method based on graph theory. *Journal of Computational Biology*, 28(11):1104–1112, November 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0257; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0257.

Saurabh:2020:SIC

[SSS20] Kumar Saurabh, Maxim Solovchuk, and Tony Wen Hann Sheu. Solution of ion channel flow using immersed boundary–lattice Boltzmann methods. *Journal of Computational Biology*, 27(7):1144–1156, July 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0265; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0265.

Syed:2021:MLM

[SSS+21] Khajamoinuddin Syed, William Sleeman, Payal Soni, Michael Hagan, Jatinder Palta, Rishabh Kapoor, and Preetam Ghosh. Machine-learning models for multicenter prostate cancer treatment plans. *Journal of Computational Biology*, 28 (2):166–184, February 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0188; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0188.

Silva:2019:UMF

[SSTM19] Gabriel H. G. Silva, Edans F. O. Sandes, George Teodoro, and Alba C. M. A. Melo. Using multiple Fickett bands to accelerate biological sequence comparisons. *Journal of Computational Biology*, 26(9):908–922, September 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0031; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0031.

Sharma:2019:SBA

[SSV19] B. Sharan Sharma, Prabodha K. Swain, and Ramtej J. Verma. A systematic bioinformatics approach to Motif-based analysis of human locus control regions. *Journal of Computational Biology*, 26(12):1427–1437, December 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0155; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0155`.

Soule:2020:NLC

[SSW20] Antoine Soulé, Jean-Marc Steyaert, and Jérôme Waldispühl. A nested 2-level cross-validation ensemble learning pipeline suggests a negative pressure against crosstalk snoRNA-mRNA interactions in *Saccharomyces cerevisiae*. *Journal of Computational Biology*, 27(3):390–402, March 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0464; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0464`.

Saeedi:2022:GTM

[SSY+22] Seyran Saeedi, Myrna Serrano, Dennis G. Yang, J. Paul Brooks, Gregory A. Buck, and Tomasz Arodz. Group testing matrix design for PCR screening with real-valued measurements. *Journal of Computational Biology*, 29(12):1397–1411, December 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0413; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0413`.

Sun:1995:ATG

[SSZC95] Jian Sun, Wen-Yuan Song, Li-Huang Zhu, and Run-Sheng Chen. Analysis of tRNA gene sequences by neural network. *Journal of Computational Biology*, 2(3):409–416, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.409; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.409`.

Song:2024:PPI

[SSZG24] Junrong Song, Zhiming Song, Jinpeng Zhang, and Yuanli Gong. Privacy-preserving identification of cancer subtype-

specific driver genes based on multigenomics data with privatedriver. *Journal of Computational Biology*, 31(2):99–116, February 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0115; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0115`.

Sengupta:2002:QCM

[ST02a] Rimli Sengupta and Martin Tompa. Quality control in manufacturing oligo arrays: a combinatorial design approach. *Journal of Computational Biology*, 9(1):1–22, January 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270252833163; https://www.liebertpub.com/doi/pdf/10.1089/10665270252833163`.

Shamir:2002:LSS

[ST02b] Ron Shamir and Dekel Tsur. Large scale sequencing by hybridization. *Journal of Computational Biology*, 9(2):413–428, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270252935548; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935548`.

Sankoff:2005:CBR

[ST05] David Sankoff and Phil Trinh. Chromosomal breakpoint reuse in genome sequence rearrangement. *Journal of Computational Biology*, 12(6):812–821, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.812; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.812`.

Snir:2010:NTD

[ST10] Sagi Snir and Edward Trifonov. A novel technique for detecting putative horizontal gene transfer in the sequence space. *Journal of Computational Biology*, 17(11):1535–1548, November 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0095; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0095`.

Sverdlov:2017:CME

[ST17] Serge Sverdlov and Elizabeth Thompson. Combinatorial methods for epistasis and dominance. *Journal of Computational Biology*, 24(4):267–279, April 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0112; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0112`.

Stepancic:2014:EGS

[Ste14] Živa Stepančič. Enhancing Gibbs sampling method for motif finding in DNA with initial graph representation of sequences. *Journal of Computational Biology*, 21(10):741–752, October 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0106; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0106`.

Schulz-Trieglaff:2008:CQP

[STHG+08] Ole Schulz-Trieglaff, Rene Hussong, Clemens Gröpl, Andreas Leinenbach, Andreas Hildebrandt, Christian Huber, and Knut Reinert. Computational quantification of peptides from LC-MS data. *Journal of Computational Biology*, 15(7):685–704, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0117; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0117`.

Sorooshyari:2018:PMP

[STP18] Siamak K. Sorooshyari, Matthew P. Taylor, and H. Vincent Poor. Probabilistic modeling of pseudorabies virus infection in a neural circuit. *Journal of Computational Biology*, 25(11):1231–1246, November 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0131; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0131`.

Salamon:1996:DUC

[STRT96] Hugh Salamon, Jorma Tarhio, Kjersti Rønningen, and Glenys Thomson. On distinguishing unique combinations in biological sequences. *Journal of Computational Biology*, 3 (3):407–423, January 1996. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.407; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.407`.

Singh:1996:DTP

[STV96] Raj K. Singh, Alexander Tropsha, and Iosif I. Vaisman. Delaunay tessellation of proteins: Four body nearest-neighbor propensities of amino acid residues. *Journal of Computational Biology*, 3(2):213–221, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.213; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.213`.

Sun:1995:PCR

[Sun95] Fengzhu Sun. The polymerase chain reaction and branching processes. *Journal of Computational Biology*, 2(1):63–86, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.63; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.63`.

Sun:1999:MDS

[Sun99] Fengzhu Sun. Modeling DNA shuffling. *Journal of Computational Biology*, 6(1):77–90, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.77; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.77`.

Sun:2013:PRC

[Sun13] Fengzhu Sun. Preface: Research in Computational Molecular Biology (RECOMB 2013). *Journal of Computational Biology*, 20(10):713, October 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.020p`.

Sun:2018:RBL

[Sun18] Weitao Sun. The relationship between low-frequency motions and community structure of residue network in protein molecules. *Journal of Computational Biology*, 25 (1):103–113, January 2018. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0171; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0171.

Schwikowski:1997:DPH

[SV97] Benno Schwikowski and Martin Vingron. The deferred path heuristic for the generalized tree alignment problem. *Journal of Computational Biology*, 4(3):415–431, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.415; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.415.

Stefankovic:2007:PMM

[ŠV07] Daniel Štefankovič and Eric Vigoda. Phylogeny of mixture models: Robustness of maximum likelihood and non-identifiable distributions. *Journal of Computational Biology*, 14(2):156–189, March 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0126; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0126.

Samykannu:2019:SCB

[SVA+19] Gopinath Samykannu, Princy Vijayababu, Christian Bharathi Antonyraj, Perumal Perumal, Sundarabaalaji Narayanan, Syed Ibrahim Basheer Ahamed, and Jeyakumar Natarajan. In silico characterization of B cell and T cell epitopes for subunit vaccine design of *Salmonella typhi* PgtE: a molecular dynamics simulation approach. *Journal of Computational Biology*, 26(2):105–116, February 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0010; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0010.

Shrestha:2017:GED

[SVCA17] Samana Shrestha, Adam Vanasse, Leon N. Cooper, and Michael P. Antosh. Gene expression as a dosimeter in irradiated *Drosophila melanogaster*. *Journal of Computational Biology*, 24(12):1265–1274, December 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0170;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0170.

Santos:2014:EPF

[SVD14] José Santos, Pablo Villot, and Martin Diéguez. Emergent protein folding modeled with evolved neural cellular automata using the 3D HP model. *Journal of Computational Biology*, 21(11):823–845, November 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0077; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0077.

Samaga:2010:CCI

[SVK10] Regina Samaga, Axel Von Kamp, and Steffen Klamt. Computing combinatorial intervention strategies and failure modes in signaling networks. *Journal of Computational Biology*, 17(1):39–53, January 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0121; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0121.

Steijaert:2010:CSD

[SVL+10] M. N. Steijaert, J. H. K. Van Den Brink, A. M. L. Liekens, P. A. J. Hilbers, and H. M. M. Ten Eikelder. Computing the stochastic dynamics of phosphorylation networks. *Journal of Computational Biology*, 17(2):189–199, February 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0059; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0059.

Solodskikh:2019:PER

[SVP19] Sergey A. Solodskikh, Alexey S. Velikorondy, and Vasily N. Popov. Predictive estimates of risks associated with type 2 diabetes mellitus on the basis of biochemical biomarkers and derived time-dependent parameters. *Journal of Computational Biology*, 26(10):1041–1049, October 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0028; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0028.

Sul:2011:BCP

[SW11] Seung-Jin Sul and Tiffani L. Williams. Big cat phylogenies, consensus trees, and computational thinking. *Journal of Computational Biology*, 18(7):895–906, July 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0199; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0199`.

Saha:2007:VEP

[SWK+07] Nilanjan Saha, Layne T. Watson, Karen Kafadar, Naren Ramakrishnan, Alexey Onufriev, Shrinivasrao Mane, and Cecilia Vasquez-Robinet. Validation and estimation of parameters for a general probabilistic model of the PCR process. *Journal of Computational Biology*, 14(1):97–112, January 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0123; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0123`.

Snir:2008:SQP

[SWR08] Sagi Snir, Tandy Warnow, and Satish Rao. Short quartet puzzling: a new quartet-based phylogeny reconstruction algorithm. *Journal of Computational Biology*, 15(1):91–103, January 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0103; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0103`.

Shu:2020:TMB

[SWS+20] Yongqian Shu, Xiaohong Wu, Jia Shen, Dongdong Luo, Xiang Li, Hailong Wang, and Yuanhua Tom Tang. Tumor mutation burden computation in two pan-cancer precision medicine next-generation sequencing panels. *Journal of Computational Biology*, 27(10):1553–1560, October 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0055; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0055`.

Stojmirovic:2007:IFI

[SY07] Aleksandar Stojmirović and Yi-Kuo Yu. Information flow in interaction networks. *Journal of Computational Biology*,

14(8):1115–1143, October 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0069; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0069`.

Stojmirovic:2009:GAB

[SY09] Aleksandar Stojmirović and Yi-Kuo Yu. Geometric aspects of biological sequence comparison. *Journal of Computational Biology*, 16(4):579–610, April 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0100; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0100`.

Shaw:2022:FEF

[SY22] Jim Shaw and Yun William Yu. `flopp`: Extremely fast long-read polyploid haplotype phasing by uniform tree partitioning. *Journal of Computational Biology*, 29(2):195–211, February 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0436; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0436`.

Shen:2002:SPA

[SYYH02] Shi-Yi Shen, Jun Yang, Adam Yao, and Pei-Ing Hwang. Super pairwise alignment (SPA): an efficient approach to global alignment for homologous sequences. *Journal of Computational Biology*, 9(3):477–486, June 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652702760138574; https://www.liebertpub.com/doi/pdf/10.1089/106652702760138574`.

Su:2023:EGE

[SZL+23] Rui Su, Jujuan Zhuang, Shuhan Liu, Di Liu, and Kexin Feng. EnILs: a general ensemble computational approach for predicting inducing peptides of multiple interleukins. *Journal of Computational Biology*, 30(12):1289–1304, December 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0002; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0002`.

Sung:2002:CEP

[SZMS02] Myong-Hee Sung, Yingdong Zhao, Roland Martin, and Richard Simon. T-cell epitope prediction with combinatorial peptide libraries. *Journal of Computational Biology*, 9 (3):527–539, June 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652702760138619; https://www.liebertpub.com/doi/pdf/10.1089/106652702760138619`.

Shen:2019:MMD

[SZMZ19] Kexin Shen, Shujuan Zhang, Shurong Ma, and Haishan Zhang. Molecular markers and diagnostic model specific for Barrett's esophagus. *Journal of Computational Biology*, 26 (12):1367–1378, December 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0064; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0064`.

Shrivastava:2022:GDL

[SZSA22] Harsh Shrivastava, Xiuwei Zhang, Le Song, and Srinivas Aluru. GRNUlar: a deep learning framework for recovering single-cell gene regulatory networks. *Journal of Computational Biology*, 29(1):27–44, January 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0437; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0437`.

Sui:2009:BAD

[SZSW09] Yunxia Sui, Xiaoyue Zhao, Terence P. Speed, and Zhijin Wu. Background adjustment for DNA microarrays using a database of microarray experiments. *Journal of Computational Biology*, 16(11):1501–1515, November 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0063; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0063`.

Song:2012:CAF

[SZTW12] Kai Song, Ze Zhang, Tuo-Peng Tong, and Fang Wu. Classifier assessment and feature selection for recognizing short coding sequences of human genes. *Journal of Computational*

Biology, 19(3):251–260, March 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0078; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0078.

Swidan:2006:RAP

[SZUP06] Firas Swidan, Michal Ziv-Ukelson, and Ron Y. Pinter. On the repeat-annotated phylogenetic tree reconstruction problem. *Journal of Computational Biology*, 13(8):1397–1418, October 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1397; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1397.

Song:2010:CCA

[SZVM10] Giltae Song, Louxin Zhang, Tomas Vinar, and Webb Miller. CAGE: Combinatorial analysis of gene-cluster evolution. *Journal of Computational Biology*, 17(9):1227–1242, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0094; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0094.

Sankoff:2009:TIR

[SZW+09] David Sankoff, Chunfang Zheng, P. Kerr Wall, Claude dePamphilis, Jim Leebens-Mack, and Victor A. Albert. Towards improved reconstruction of ancestral gene order in angiosperm phylogeny. *Journal of Computational Biology*, 16 (10):1353–1367, October 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0103; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0103.

Shi:2020:IPM

[SZY+20] Yu Shi, Shan Zhu, Jianxin Yang, Minghai Shao, Wenxiu Ding, Wanrong Jiang, Xinchen Sun, and Ninghua Yao. Investigation of potential mechanisms associated with non-small cell lung cancer. *Journal of Computational Biology*, 27(9):1433–1442, September 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0081; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0081.

Tanushev:1997:CLT

[TA97] Miroslav S. Tanushev and Richard Arratia. Central limit theorem for renewal theory for several patterns. *Journal of Computational Biology*, 4(1):35–44, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.35; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.35`.

Thapa:2021:MGD

[TA21] Ishwor Thapa and Hesham Ali. A multiomics graph database system for biological data integration and cancer informatics. *Journal of Computational Biology*, 28(2):209–219, February 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0231; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0231`.

Thankachan:2016:PEA

[TAA16] Sharma V. Thankachan, Alberto Apostolico, and Srinivas Aluru. A provably efficient algorithm for the k-mismatch average common substring problem. *Journal of Computational Biology*, 23(6):472–482, June 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0235; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0235`.

Tozzo:2022:WDW

[TaAF+22] Veronica Tozzo, Chloé agathe Azencott, Samuele Fiorini, Emanuele Fava, Andrea Trucco, and Annalisa Barla. Where do we stand in regularization for life science studies? *Journal of Computational Biology*, 29(3):213–232, March 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0371; https://www.liebertpub.com/doi/reader/10.1089/cmb.2019.0371`.

Tithi:2023:FNR

[TAJZ23] Saima Sultana Tithi, Frank O. Aylward, Roderick V. Jensen, and Liqing Zhang. FastViromeExplorer-Novel: Recovering draft genomes of novel viruses and phages in metagenomic data. *Journal of Computational Biology*, 30(4):391–408, April

2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0397; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0397.

Takahashi:1996:MSN

[Tak96] Yoshikane Takahashi. A mathematical solution to a network designing problem. *Journal of Computational Biology*, 3(1):97–141, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.97; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.97.

Telles:2013:LP

[TAMW13] Guilherme P. Telles, Nalvo F. Almeida, Rosane Minghim, and Maria Emilia M. T. Walter. Live phylogeny. *Journal of Computational Biology*, 20(1):30–37, January 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0219; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0219.

Taneri:2011:TRE

[Tan11] Bahar Taneri. Is there room for ethics within bioinformatics education? *Journal of Computational Biology*, 18(7):907–916, July 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0187; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0187.

Tang:2023:PRS

[Tan23] Haixu Tang. Preface: RECOMB 2023 special issue. *Journal of Computational Biology*, 30(11):1145, November 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.29101.ht.

Taylor:1994:MBP

[Tay94] William R. Taylor. Motif-biased protein sequence alignment. *Journal of Computational Biology*, 1(4):297–310, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.

1089/cmb.1994.1.297; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.297.

Traykov:2016:NHA

[TAY16] Metodi Traykov, Slav Angelov, and Nicola Yanev. A new heuristic algorithm for protein folding in the HP model. *Journal of Computational Biology*, 23(8):662–668, August 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0015; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0015.

Thayer:2000:DPC

[TBB00] Edward C. Thayer, Chris Bystroff, and David Baker. Detection of protein coding sequences using a mixture model for local protein amino acid sequence. *Journal of Computational Biology*, 7(1–2):317–327, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Theilhaber:2001:BEF

[TBJF01] Joachim Theilhaber, Steven Bushnell, Amanda Jackson, and Rainer Fuchs. Bayesian estimation of fold-changes in the analysis of gene expression: The PFOLD algorithm. *Journal of Computational Biology*, 8(6):585–614, November 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701753307502; https://www.liebertpub.com/doi/pdf/10.1089/106652701753307502.

Tuller:2010:RAG

[TBKR10] Tamir Tuller, Hadas Birin, Martin Kupiec, and Eytan Ruppin. Reconstructing ancestral genomic sequences by coevolution: Formal definitions, computational issues, and biological examples. *Journal of Computational Biology*, 17 (9):1327–1344, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0112; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0112.

Tambonis:2018:DEA

[TBL18] Tiago Tambonis, Marcelo Boareto, and Vitor B. P. Leite. Differential expression analysis in RNA-seq data using a geometric approach. *Journal of Computational Biology*, 25

(11):1257–1265, November 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0244; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0244.

Tuncbag:2013:SRM

[TBP+13] Nurcan Tuncbag, Alfredo Braunstein, Andrea Pagnani, Shao-Shan Carol Huang, Jennifer Chayes, Christian Borgs, Riccardo Zecchina, and Ernest Fraenkel. Simultaneous reconstruction of multiple signaling pathways via the prize-collecting Steiner forest problem. *Journal of Computational Biology*, 20(2):124–136, February 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0092; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0092.

Tresch:2007:DDI

[TBS+07] Achim Tresch, T. Beissbarth, H. Sültmann, R. Kuner, A. Poustka, and A. Buness. Discrimination of direct and indirect interactions in a network of regulatory effects. *Journal of Computational Biology*, 14(9):1217–1228, November 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0085; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0085.

Thankachan:2016:APM

[TCL+16] Sharma V. Thankachan, Sriram P. Chockalingam, Yongchao Liu, Alberto Apostolico, and Srinivas Aluru. ALFRED: a practical method for alignment-free distance computation. *Journal of Computational Biology*, 23(6):452–460, June 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0217; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0217.

Tesler:2008:P

[TD08] Glenn Tesler and Dannie Durand. Preface. *Journal of Computational Biology*, 15(8):943–946, October 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/

10.1089/cmb.2008.P002; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.P002.

Tinh:2024:QEP

[TDV24] Nguyen Huy Tinh, Cuong Cao Dang, and Le Sy Vinh. QMix: an efficient program to automatically estimate multi-matrix mixture models for amino acid substitution process. *Journal of Computational Biology*, 31(8):703–707, August 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0403; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0403.

Teitelman:1996:PCA

[TE96] Michael Teitelman and Frank H. Eeckman. Principal component analysis and large-scale correlations in non-coding sequences of human DNA. *Journal of Computational Biology*, 3(4):573–576, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.573; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.573.

Tvedebrink:2012:ICD

[TEMM12] Torben Tvedebrink, Poul Svante Eriksen, Helle Smidt Mogensen, and Niels Morling. Identifying contributors of DNA mixtures by means of quantitative information of STR typing. *Journal of Computational Biology*, 19(7):887–902, July 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0055; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0055.

Tavakoli:2024:GPR

[TGA24] Neda Tavakoli, Daniel Gibney, and Srinivas Aluru. GraphSlimmer: Preserving read mappability with the minimum number of variants. *Journal of Computational Biology*, 31(7):616–637, July 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Tcheremenskaia:2008:PAI

[TGT08] Olga Tcheremenskaia, Alessandro Giuliani, and Maurizio Tomasi. PROFALIGN algorithm identifies the regions containing folding determinants by scoring pairs of hydrophobic

profiles of remotely related proteins. *Journal of Computational Biology*, 15(4):445–455, May 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0100; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0100`.

Tarraga:2019:PIA

[TGTG19] Wilson Alberto Tárraga, Horacio Alberto Garda, Juan Domingo Toledo, and Marina Cecilia Gonzalez. Potential inhibitors of the activity of the cholesterol-ester transfer protein. *Journal of Computational Biology*, 26(12):1458–1469, December 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0227; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0227`.

Tran:2017:CBM

[TH17a] Ngoc Tam L. Tran and Chun-Hsi Huang. Cloud-based MOTIFSIM: Detecting similarity in large DNA motif data sets. *Journal of Computational Biology*, 24(5):450–459, May 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0080; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0080`.

Tran:2017:MES

[TH17b] Ngoc Tam L. Tran and Chun-Hsi Huang. MOTIFSIM 2.1: an enhanced software platform for detecting similarity in multiple DNA motif data sets. *Journal of Computational Biology*, 24(9):895–905, September 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0005; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0005`.

Thomas:2021:MNT

[Tho21] Sunil Thomas. Mapping the nonstructural transmembrane proteins of severe acute respiratory syndrome coronavirus 2. *Journal of Computational Biology*, 28(9):909–921, September 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0627; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0627`.

Takai-Igarashi:1998:DCS

[TINK98] Takako Takai-Igarashi, Yoko Nadaoka, and Tsuguchika Kaminuma. A database for cell signaling networks. *Journal of Computational Biology*, 5(4):747–754, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.747; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.747`.

Thanh:2021:CKF

[TKO21] Vo Hong Thanh, Dani Korpela, and Pekka Orponen. Co-transcriptional kinetic folding of RNA secondary structures including pseudoknots. *Journal of Computational Biology*, 28(9):892–908, September 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0606; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0606`.

Tamilarasi:2024:DSG

[TKSA24] M. Tamilarasi, S. Kumarganesh, K. Martin Sagayam, and J. Andrew. Detection and segmentation of glioma tumors utilizing a UNet convolutional neural network approach with non-subsampled shearlet transform. *Journal of Computational Biology*, 31(8):757–768, August 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0339; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0339`.

Tang:2005:UMP

[TKT+05] Xinyu Tang, Bonnie Kirkpatrick, Shawna Thomas, Guang Song, and Nancy M. Amato. Using motion planning to study RNA folding kinetics. *Journal of Computational Biology*, 12(6):862–881, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.862; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.862`.

Tang:2008:BFB

[TKW08] Man-Hung Eric Tang, Anders Krogh, and Ole Winther. BayesMD: Flexible biological modeling for motif discovery.

Journal of Computational Biology, 15(10):1347–1363, December 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0176; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0176.

Tavori:2023:CER

[TL23] Jhonatan Tavori and Hanoch Levy. On the convexity of the effective reproduction number. *Journal of Computational Biology*, 30(7):783–795, July 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0371; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0371.

Turutina:2006:IAA

[TLK+06] Vera P. Turutina, Andrew A. Laskin, Nikolay A. Kudryashov, Konstantin G. Skryabin, and Eugene V. Korotkov. Identification of amino acid latent periodicity within 94 protein families. *Journal of Computational Biology*, 13(4):946–964, May 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.946; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.946.

Tzou:2014:SSN

[TLP+14] Wen-Shyong Tzou, Ying-Tsang Lo, Tun-Wen Pai, Chin-Hwa Hu, and Chung-Hao Li. Stochastic simulation of notch signaling reveals novel factors that mediate the differentiation of neural stem cells. *Journal of Computational Biology*, 21(7):548–567, July 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0022; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0022.

Tomescu:2017:SCC

[TM17] Alexandru I. Tomescu and Paul Medvedev. Safe and complete contig assembly through omnitigs. *Journal of Computational Biology*, 24(6):590–602, June 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0141; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0141.

Thornton:2022:UDD

[TM22] Micah Thornton and Monnie Mcgee. Use of DFT distance metrics for classification of SARS-CoV-2 genomes. *Journal of Computational Biology*, 29(5):453–464, May 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0229; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0229`.

Teixeira:2018:LSS

[TMC+18] Andreia Sofia Teixeira, Pedro T. Monteiro, João A. Carriço, Francisco C. Santos, and Alexandre P. Francisco. Large-scale simulations of bacterial populations over complex networks. *Journal of Computational Biology*, 25(8):850–861, August 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0083; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0083`.

Tamura:2023:GDA

[TMfTK23] Takeyuki Tamura, Ai Muto-fujita, Yukako Tohsato, and Tomoyuki Kosaka. Gene deletion algorithms for minimum reaction network design by mixed-integer linear programming for metabolite production in constraint-based models: gDel_minRN. *Journal of Computational Biology*, 30(5):553–568, May 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0352; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0352`.

Trong:2020:SGA

[TMG+20] Trung Ngo Trong, Juha Mehtonen, Gerardo González, Roger Kramer, Ville Hautamäki, and Merja Heinäniemi. Semisupervised generative autoencoder for single-cell data. *Journal of Computational Biology*, 27(8):1190–1203, August 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0337; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0337`.

Tang:2021:SCF

[TMH+21] Wan Tang, Degong Mu, Ling Han, Xianmin Guo, Bing Han, and Dong Song. Screening of clinical factors related to prog-

nosis of breast cancer based on the Cox proportional risk model. *Journal of Computational Biology*, 28(1):89–98, January 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0110; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0110`. See retraction notice [Ano22b].

Thijs:2002:GSM

[TML+02] Gert Thijs, Kathleen Marchal, Magali Lescot, Stephane Rombauts, Bart De Moor, Pierre Rouzé, and Yves Moreau. A Gibbs sampling method to detect overrepresented motifs in the upstream regions of coexpressed genes. *Journal of Computational Biology*, 9(2):447–464, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270252935566; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935566`.

Tjarnberg:2013:OSC

[TNSS13] Andreas Tjärnberg, Torbjörn E. M. Nordling, Matthew Studham, and Erik L. L. Sonnhammer. Optimal sparsity criteria for network inference. *Journal of Computational Biology*, 20(5):398–408, May 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0268; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0268`.

Tosatto:2005:VFF

[Tos05] Silvio C. E. Tosatto. The Victor/FRST function for model quality estimation. *Journal of Computational Biology*, 12 (10):1316–1327, December 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1316; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1316`.

Tan:2011:OCF

[TP11] Frans E. S. Tan and Valéria Lima Passos. On the *A*-optimality criterion for finding two-color microarray optimal designs. *Journal of Computational Biology*, 18(6):835–841, June 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0009; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0009.

Tembe:2009:SCF

[TPH+09] Waibhav D. Tembe, John V. Pearson, Nils Homer, James Lowey, Edward Suh, and David W. Craig. Statistical comparison framework and visualization scheme for ranking-based algorithms in high-throughput genome-wide studies. *Journal of Computational Biology*, 16(4):565–577, April 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0151; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0151.

Teodoro:2003:UPF

[TPK03] Miguel L. Teodoro, George N. Phillips, Jr., and Lydia E. Kavraki. Understanding protein flexibility through dimensionality reduction. *Journal of Computational Biology*, 10(3–4):617–634, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Toubiana:2019:GAO

[TPSB19] David Toubiana, Rami Puzis, Avi Sadka, and Eduardo Blumwald. A genetic algorithm to optimize weighted gene co-expression network analysis. *Journal of Computational Biology*, 26(12):1349–1366, December 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0221; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0221.

Than:2011:CPS

[TR11] Cuong V. Than and Noah A. Rosenberg. Consistency properties of species tree inference by minimizing deep coalescences. *Journal of Computational Biology*, 18(1):1–15, January 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0102; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0102.

Tran:1998:ECS

[Tra98] Nicholas Tran. An easy case of sorting by reversals. *Journal of Computational Biology*, 5(4):741–746, January 1998. CODEN

JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.741; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.741.

Travis:2019:CMP

[Tra19] Anthony S. Travis. Chemical modeling: From Paul Ehrlich's dyes to β-blockers — a brief history. *Journal of Computational Biology*, 26(7):726–734, July 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0092; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0092.

Tuller:2009:HOG

[TRB+09] Tamir Tuller, Udi Rubinstein, Dani Bar, Michael Gurevitch, Eytan Ruppin, and Martin Kupiec. Higher-order genomic organization of cellular functions in yeast. *Journal of Computational Biology*, 16(2):303–316, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.15TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.15TT.

Than:2007:CFH

[TRIN07] Cuong Than, Derek Ruths, Hideki Innan, and Luay Nakhleh. Confounding factors in HGT detection: Statistical error, coalescent effects, and multiple solutions. *Journal of Computational Biology*, 14(4):517–535, May 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.A010; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.A010.

Thomas:2017:ERT

[TRS17] Lebin Thomas, Hari Ram, and Ved Pal Singh. Evolutionary relationships and taxa-specific conserved signature indels among cellulases of archaea, bacteria, and eukarya. *Journal of Computational Biology*, 24(10):1029–1042, October 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0161; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0161.

Tabatabaee:2023:QSP

[TRW23] Yasamin Tabatabaee, Sebastien Roch, and Tandy Warnow. QR-STAR: a polynomial-time statistically consistent method for rooting species trees under the coalescent. *Journal of Computational Biology*, 30(11):1146–1181, November 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0185; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0185`.

Tsang:1996:SFP

[TS96] Simon Tsang and Milton H. Saier, Jr. A simple flexible program for the computational analysis of amino acyl residue distribution in proteins: Application to the distribution of aromatic versus aliphatic hydrophobic amino acids in transmembrane α-helical spanners of integral membrane transport proteins. *Journal of Computational Biology*, 3(1):185–190, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.185; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.185`.

Tanay:2004:MMI

[TS04] Amos Tanay and Ron Shamir. Multilevel modeling and inference of transcription regulation. *Journal of Computational Biology*, 11(2–3):357–375, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Terashi:2012:LPT

[TSTS12] Genki Terashi, Tetsuo Shibuya, and Mayuko Takeda-Shitaka. LB3D: a protein three-dimensional substructure search program based on the lower bound of a root mean square deviation value. *Journal of Computational Biology*, 19(5):493–503, May 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0230; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0230`.

Toyoizumi:2012:END

[TT12] Hiroshi Toyoizumi and Hideo Tsubouchi. Estimating the number of double-Strand breaks formed during meiosis from partial observation. *Journal of Computational Biology*, 19 (12):1277–1283, December 2012. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0209; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0209.

Thomas:2007:SPM

[TTTA07] Shawna Thomas, Xinyu Tang, Lydia Tapia, and Nancy M. Amato. Simulating protein motions with rigidity analysis. *Journal of Computational Biology*, 14(6):839–855, July 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R019; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R019.

Tsai:2017:ESM

[TTTL17] Shin-Fu Tsai, Chih-Wei Tung, Chen-An Tsai, and Chen-Tuo Liao. An exhaustive scan method for SNP main effects and SNP $\times$ SNP interactions over highly homozygous genomes. *Journal of Computational Biology*, 24(12):1254–1264, December 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0140; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0140.

Tran:2015:NMP

[TVNP15] Tuan-Anh Tran, Nam Tri Vo, Hoang Duc Nguyen, and Bao The Pham. A novel method to predict highly expressed genes based on radius clustering and relative synonymous codon usage. *Journal of Computational Biology*, 22(12):1086–1096, December 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0121; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0121.

Tichy:2005:EPT

[TW05] Robert F. Tichy and Stephan Wagner. Extremal problems for topological indices in combinatorial chemistry. *Journal of Computational Biology*, 12(7):1004–1013, September 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1004; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1004.

Tang:2002:ZFG

[TWY02] Mengxiang Tang, Michael Waterman, and Shibu Yooseph. Zinc finger gene clusters and tandem gene duplication. *Journal of Computational Biology*, 9(2):429–446, April 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270252935557; https://www.liebertpub.com/doi/pdf/10.1089/10665270252935557`.

Tian:2017:IGI

[TXL+17] Xin Tian, Mingyuan Xin, Jian Luo, Mingyao Liu, and Zhenran Jiang. Identification of genes involved in breast cancer metastasis by integrating protein–protein interaction information with expression data. *Journal of Computational Biology*, 24(2):172–182, February 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0206; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0206`.

Tian:2020:DPM

[TYS+20] Yingxuan Tian, Min Yu, Li Sun, Linghua Liu, Jun Wang, Ke Hui, Qiaofeng Nan, Xinyu Nie, Yajuan Ren, and Xiaoping Ren. Distinct patterns of mRNA and lncRNA expression differences between lung squamous cell carcinoma and adenocarcinoma. *Journal of Computational Biology*, 27(7):1067–1078, July 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0164; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0164`.

Ta:2019:WIV

[TYSX19] Michael Ta, Changchuan Yin, Gary Lee Smith, and Wenbo Xu. A workflow to improve variant calling accuracy in molecular barcoded sequencing reads. *Journal of Computational Biology*, 26(1):96–103, January 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0110; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0110`.

Tan:2023:NNM

[TZB+23] Jiahui Tan, Yutong Zhao, Cara C. Burns, Dechao Tian, and Kun Zhao. Novel network method major minor variation clustering enables identification of poliovirus clusters with high-resolution linkages. *Journal of Computational Biology*, 30(4):409–419, April 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0292; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0292`.

Tabb:2014:CED

[TZHR14] Loni Philip Tabb, Wei Zhao, Jingyu Huang, and Gail L. Rosen. Characterizing the empirical distribution of prokaryotic genome n-mers in the presence of nullomers. *Journal of Computational Biology*, 21(10):732–740, October 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0108; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0108`.

Topfer:2013:PIV

[TZP+13] Armin Töpfer, Osvaldo Zagordi, Sandhya Prabhakaran, Volker Roth, Eran Halperin, and Niko Beerenwinkel. Probabilistic inference of viral quasispecies subject to recombination. *Journal of Computational Biology*, 20(2):113–123, February 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0232; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0232`.

Tang:2020:IBR

[TZZY20] Yiyang Tang, Lihuang Zha, Xiaofang Zeng, and Zaixin Yu. Identification of biomarkers related to systemic sclerosis with or without pulmonary hypertension using co-expression analysis. *Journal of Computational Biology*, 27(10):1519–1531, October 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0492; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0492`.

Urrutia-Baca:2019:IAD

[UBGFD+19] Victor Hugo Urrutia-Baca, Ricardo Gomez-Flores, Myriam Angélica De La Garza-Ramos, Patricia Tamez-Guerra,

Daniela Guadalupe Lucio-Sauceda, and María Cristina Rodríguez-Padilla. Immunoinformatics approach to design a novel epitope-based oral vaccine against *Helicobacter pylori*. *Journal of Computational Biology*, 26(10):1177–1190, October 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0062; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0062`.

Ulitsky:2006:ACS

[UBTC06] Igor Ulitsky, David Burstein, Tamir Tuller, and Benny Chor. The average common substring approach to phylogenomic reconstruction. *Journal of Computational Biology*, 13(2):336–350, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.336; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.336`.

Uechi:2019:MAD

[UGS19] Lisa Uechi, David J. Galas, and Nikita A. Sakhanenko. Multivariate analysis of data sets with missing values: an information theory-based reliability function. *Journal of Computational Biology*, 26(2):152–171, February 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0179; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0179`.

Uricaru:2011:NDA

[UMR11] Raluca Uricaru, Alban Mancheron, and Eric Rivals. Novel definition and algorithm for chaining fragments with proportional overlaps. *Journal of Computational Biology*, 18 (9):1141–1154, September 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0126; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0126`.

Urban:2019:DST

[URB+19] Paulina Urban, Vahid Rezaei, Grzegorz Bokota, Michał Denkiewicz, Subhadip Basu, and Dariusz Plewczyński. Dendritic spines taxonomy: The functional and structural classification • time-dependent probabilistic model of neuronal activa-

tion. *Journal of Computational Biology*, 26(4):322–335, April 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0155; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0155`.

Urban:2020:MAH

[UTD+20] Paulina Urban, Vahid Rezaei Tabar, Michał Denkiewicz, Grzegorz Bokota, Nirmal Das, Subhadip Basu, and Dariusz Plewczynski. The mixture of autoregressive hidden Markov models of morphology for dentritic spines during activation process. *Journal of Computational Biology*, 27(9): 1471–1485, September 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0383; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0383`.

Vasiljeva:2017:DPE

[VA17] Ieva Vasiljeva and Ognjen Arandjelović. Diagnosis prediction from electronic health records using the binary diagnosis history vector representation. *Journal of Computational Biology*, 24(8):767–786, August 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0023; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0023`.

Vilaplana:2018:MED

[VAS+18] Jordi Vilaplana, Rui Alves, Francesc Solsona, Jordi Mateo, Ivan Teixidó, and Marc Pifarré. MetReS, an efficient database for genomic applications. *Journal of Computational Biology*, 25(2):200–213, February 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0103; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0103`.

Veeramani:2009:MFC

[VB09] Balaji Veeramani and Joel S. Bader. Metabolic flux correlations, genetic interactions, and disease. *Journal of Computational Biology*, 16(2):291–302, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.14TT;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.14TT.

Vinar:2010:RHC

[VBSS10] Tomáš Vinař, Broňa Brejová, Giltae Song, and Adam Siepel. Reconstructing histories of complex gene clusters on a phylogeny. *Journal of Computational Biology*, 17(9): 1267–1279, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0090; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0090.

Veliz-Cuba:2011:BMC

[VCS11] Alan Veliz-Cuba and Brandilyn Stigler. Boolean models can explain bistability in the *lac* operon. *Journal of Computational Biology*, 18(6):783–794, June 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0031; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0031.

Vexler:2014:ECT

[VCY14] Albert Vexler, Xiwei Chen, and Jihnhee Yu. Evaluations and comparisons of treatment effects based on best combinations of biomarkers with applications to biomedical studies. *Journal of Computational Biology*, 21(9):709–721, September 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0097; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0097.

Veselsky:2012:OPA

[Ves12] M. Veselsky. Order of precedence and age of Y-DNA haplotypes. *Journal of Computational Biology*, 19(11):1243–1250, November 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0193; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0193.

Voges:2018:TLS

[VFOK18] Jan Voges, Ali Fotouhi, Jörn Ostermann, and Muhammed Oğuzhan Külekci. A two-level scheme for quality score compression. *Journal of Computational Biology*, 25(10):1141–1151, October

2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0065; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0065.

Vijayakumar:2022:HFR

[Vij22] Saravanan Vijayakumar. Harnessing fuzzy rule based system for screening major histocompatibility complex class I peptide epitopes from the whole proteome: an implementation on the proteome of *Leishmania donovani*. *Journal of Computational Biology*, 29(9):1045–1058, September 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0464; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0464.

Vacic:2010:GKP

[VILR10] Vladimir Vacic, Lilia M. Iakoucheva, Stefano Lonardi, and Predrag Radivojac. Graphlet kernels for prediction of functional residues in protein structures. *Journal of Computational Biology*, 17(1):55–72, January 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0029; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0029.

Lehmann:2022:RIQ

[vLKMR22] Kjong van Lehmann, Andre Kahles, Magdalena Murr, and Gunnar Rätsch. RNA instant quality check: Alignment-free RNA-degradation detection. *Journal of Computational Biology*, 29(8):857–866, August 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0603; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0603.

Valouev:2006:AOM

[VLL+06] Anton Valouev, Lei Li, Yu-Chi Liu, David C. Schwartz, Yi Yang, Yu Zhang, and Michael S. Waterman. Alignment of optical maps. *Journal of Computational Biology*, 13(2):442–462, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.442;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.442.

vonLohneysen:2024:PCP

[vLSV+24] Sarah von Löhneysen, Thomas Spicher, Yuliia Varenyk, Hua-Ting Yao, Ronny Lorenz, Ivo Hofacker, and Peter F. Stadler. Phylogenetic and chemical probing information as soft constraints in RNA secondary structure prediction. *Journal of Computational Biology*, 31(6):549–563, June 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Veksler-Lublinsky:2007:SBF

[VLZUBK07] Isana Veksler-Lublinsky, Michal Ziv-Ukelson, Danny Barash, and Klara Kedem. A structure-based flexible search method for motifs in RNA. *Journal of Computational Biology*, 14 (7):908–926, September 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0061; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0061.

Vijayasatya:2006:OAP

[VM06] Ravi Vijayasatya and Amar Mukherjee. An optimal algorithm for perfect phylogeny haplotyping. *Journal of Computational Biology*, 13(4):897–928, May 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.897; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.897.

Venkat:2017:BNB

[VND17] Priya S. Venkat, Krishna R. Narayanan, and Aniruddha Datta. A Bayesian network-based approach to selection of intervention points in the mitogen-activated protein kinase plant defense response pathway. *Journal of Computational Biology*, 24(4):327–339, April 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0089; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0089.

Voorkamp:2014:MAA

[Voo14] Josh Voorkamp. Maximal acyclic agreement forests. *Journal of Computational Biology*, 21(10):723–731, October 2014.

CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0093; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0093.

Vega-Rodriguez:2018:PSI

[VRGC18] Miguel A. Vega-Rodríguez and José M. Granado-Criado. *Preface to the Special Issue*: Parallel computing in computational biology: a technological point of view. *Journal of Computational Biology*, 25(8):837–840, August 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.29018.mavr; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.29018.mavr.

Vardi:2012:LCB

[VRS12] Liram Vardi, Eytan Ruppin, and Roded Sharan. A linearized constraint-based approach for modeling signaling networks. *Journal of Computational Biology*, 19(2):232–240, February 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0277; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0277.

Vandin:2016:SCC

[VRU16] Fabio Vandin, Benjamin J. Raphael, and Eli Upfal. On the sample complexity of cancer pathways identification. *Journal of Computational Biology*, 23(1):30–41, January 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0100; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0100.

VonHaeseler:1998:EDA

[VS98] Arndt Von Haeseler and Michael Schöniger. Evolution of DNA or amino acid sequences with dependent sites. *Journal of Computational Biology*, 5(1):149–163, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.149; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.149.

Vernot:2008:RNB

[VSGD08] Benjamin Vernot, Maureen Stolzer, Aiton Goldman, and Dannie Durand. Reconciliation with non-binary species trees. *Journal of Computational Biology*, 15(8):981–1006, October 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0092; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0092`.

Veerassamy:2003:TPM

[VST03] Shalini Veerassamy, Andrew Smith, and Elisabeth R. M. Tillier. A transition probability model for amino acid substitutions from blocks. *Journal of Computational Biology*, 10(6):997–1010, December 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652703322756195; https://www.liebertpub.com/doi/pdf/10.1089/106652703322756195`.

Vesterstrom:2006:FSS

[VT06] Jakob Vesterstrøm and William R. Taylor. Flexible secondary structure based protein structure comparison applied to the detection of circular permutation. *Journal of Computational Biology*, 13(1):43–63, January 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.43; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.43`.

vanUitert:2008:BSB

[vUMW08] Miranda van Uitert, Wouter Meuleman, and Lodewyk Wessels. Biclustering sparse binary genomic data. *Journal of Computational Biology*, 15(10):1329–1345, December 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0066; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0066`.

Vandin:2011:ADS

[VUR11] Fabio Vandin, Eli Upfal, and Benjamin J. Raphael. Algorithms for detecting significantly mutated pathways in cancer. *Journal of Computational Biology*, 18(3):507–522, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0265; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0265.

Vingron:1997:TIM

[VV97] Martin Vingron and Arndt Von Haeseler. Towards integration of multiple alignment and phylogenetic tree construction. *Journal of Computational Biology*, 4(1):23–34, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.23; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.23.

Vexler:2018:TTV

[VY18] Albert Vexler and Jihnhee Yu. To t-test or not to t-test? A p-values-based point of view in the receiver operating characteristic curve framework. *Journal of Computational Biology*, 25(6):541–550, June 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0216; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0216.

Wu:2010:SQN

[WA10] Zhijin Wu and Martin J. Aryee. Subset quantile normalization using negative control features. *Journal of Computational Biology*, 17(10):1385–1395, October 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0049; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0049.

Wong:2008:DHO

[WAC08] Andrew K. C. Wong, Wai-Ho Au, and Keith C. C. Chan. Discovering high-order patterns of gene expression levels. *Journal of Computational Biology*, 15(6):625–637, July 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0147; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0147.

Wagner:2004:RPL

[Wag04] Andreas Wagner. Reconstructing pathways in large genetic networks from genetic perturbations. *Journal of Computational*

Biology, 11(1):53–60, January 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652704773416885; https://www.liebertpub.com/doi/pdf/10.1089/106652704773416885.

Wang:2020:CPR

[WAM20] Feiqi Wang, Tatsuya Akutsu, and Tomoya Mori. Comparison of pseudoknotted RNA secondary structures by topological centroid identification and tree edit distance. *Journal of Computational Biology*, 27(9):1443–1451, September 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0512; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0512.

Wang:1994:SPR

[Wan94] Chi Wang. A subgraph problem from restriction maps of DNA. *Journal of Computational Biology*, 1(3):227–234, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.227; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.227.

Wagner:2005:LRM

[WAPM05] Michael Wagner, Rafał Adamczak, Aleksey Porollo, and Jarosław Meller. Linear regression models for solvent accessibility prediction in proteins. *Journal of Computational Biology*, 12(3):355–369, April 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.355; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.355.

Wareham:1995:SPN

[War95] H. Todd Wareham. A simplified proof of the NP- and MAX SNP-hardness of multiple sequence tree alignment. *Journal of Computational Biology*, 2(4):509–514, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.509; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.509.

Wang:2022:TOL

[WAX22] Haohan Wang, Bryon Aragam, and Eric P. Xing. Trade-offs of linear mixed models in genome-wide association studies. *Journal of Computational Biology*, 29(3):233–242, March 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0157; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0157`.

Wise:2015:CID

[WBJ15] Aaron Wise and Ziv Bar-Joseph. cDREM: Inferring dynamic combinatorial gene regulation. *Journal of Computational Biology*, 22(4):324–333, April 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0010; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0010`.

Wang:2004:SSI

[WC04] Sue-Jane Wang and James J. Chen. Sample size for identifying differentially expressed genes in microarray experiments. *Journal of Computational Biology*, 11(4):714–726, August 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.714; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.714`.

Waldispuhl:2007:CPF

[WC07] J. Waldispühl and P. Clote. Computing the partition function and sampling for saturated secondary structures of RNA, with respect to the Turner energy model. *Journal of Computational Biology*, 14(2):190–215, March 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0012; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0012`.

Wang:2016:IMN

[WC16] Yuandi Wang and Jinyu Cong. An improved model of nonuniform coleochaete cell division. *Journal of Computational Biology*, 23(8):693–709, August 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0021;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0021.

Wong:1998:TRB

[WCC98] Wing Hung Wong, Yan Cui, and Run Sheng Chen. Torsional relaxation for biopolymers. *Journal of Computational Biology*, 5(4):655–665, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.655; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.655.

Wu:2006:RET

[WCC+06] Kun-Pin Wu, Jia-Ming Chang, Jun-Bo Chen, Chi-Fon Chang, Wen-Jin Wu, Tai-Huang Huang, Ting-Yi Sung, and Wen-Lian Hsu. RIBRA — an error-tolerant algorithm for the NMR backbone assignment problem. *Journal of Computational Biology*, 13(2):229–244, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.229; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.229.

Wang:2018:SFS

[WCL18a] Hong Wang, Xiaolin Chen, and Gang Li. Survival forests with R-squared splitting rules. *Journal of Computational Biology*, 25(4):388–395, April 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0107; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0107.

Wang:2018:MLB

[WCL+18b] Hsin-Yao Wang, Shih-Cheng Chang, Wan-Ying Lin, Chun-Hsien Chen, Szu-Hsien Chiang, Kai-Yao Huang, Bo-Yu Chu, Jang-Jih Lu, and Tzong-Yi Lee. Machine learning-based method for obesity risk evaluation using single-nucleotide polymorphisms derived from next-generation sequencing. *Journal of Computational Biology*, 25(12):1347–1360, December 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0002; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0002.

Wang:2008:EGW

[WCM+08] Wenyi Wang, Benilton Carvalho, Nathaniel D. Miller, Jonathan Pevsner, Aravinda Chakravarti, and Rafael A. Irizarry. Estimating genome-wide copy number using allele-specific mixture models. *Journal of Computational Biology*, 15(7):857–866, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0148; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0148`.

Wang:2018:IMI

[WCZ+18] Zihao Wang, Yu Chen, Jingrong Zhang, Lun Li, Xiaohua Wan, Zhiyong Liu, Fei Sun, and Fa Zhang. ICON-MIC: Implementing a CPU/MIC collaboration parallel framework for ICON on Tianhe-2 supercomputer. *Journal of Computational Biology*, 25(3):270–281, March 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0151; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0151`.

Williams:2001:CGO

[WDA01] Glenn A. Williams, Jonathan M. Dugan, and Russ B. Altman. Constrained global optimization for estimating molecular structure from atomic distances. *Journal of Computational Biology*, 8(5):523–547, October 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652701753216521; https://www.liebertpub.com/doi/pdf/10.1089/106652701753216521`.

Wang:2024:EHS

[WDF24] Yuexuan Wang, Ritabrata Dutta, and Andreas Futschik. Estimating haplotype structure and frequencies: a Bayesian approach to unknown design in pooled genomic data. *Journal of Computational Biology*, 31(8):708–726, August 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0211; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0211`.

Wang:2020:SCG

[WDZ20] Ruike Wang, Xia Du, and Yaqin Zhi. Screening of critical genes involved in metastasis and prognosis of high-grade serous ovar-

ian cancer by gene expression profile data. *Journal of Computational Biology*, 27(7):1104–1114, July 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0235; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0235.

Wendl:2005:PAC

[Wen05] Michael C. Wendl. Probabilistic assessment of clone overlaps in DNA fingerprint mapping via a priori models. *Journal of Computational Biology*, 12(3):283–297, April 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.283; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.283.

Wendl:2006:GCT

[Wen06] Michael C. Wendl. A general coverage theory for shotgun DNA sequencing. *Journal of Computational Biology*, 13(6):1177–1196, July 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1177; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1177.

Wu:2020:UFI

[WES20] Yue Wu, Eleazar Eskin, and Sriram Sankararaman. A unifying framework for imputing summary statistics in genome-wide association studies. *Journal of Computational Biology*, 27(3):418–428, March 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0449; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0449.

Winter:2012:ACT

[WF12] Paweł Winter and Rasmus Fonseca. Adjustable chain trees for proteins. *Journal of Computational Biology*, 19(1):83–99, January 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0320; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0320.

Wang:2025:BDD

[WFC25] GuiShen Wang, Hui Feng, and Chen Cao. BiRNN-DDI: a drug-drug interaction event type prediction model based on bidirectional recurrent neural network and Graph2Seq representation. *Journal of Computational Biology*, 32(2):198–211, February 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0476; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0476`.

Werner:2018:LDP

[WFH18] Matthias Werner, Pascal Fieth, and Alexander Hartmann. Large-deviation properties of sequence alignment of correlated sequences. *Journal of Computational Biology*, 25(12): 1339–1346, December 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0269; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0269`.

Wang:2020:MAD

[WFL+20] Rong Wang, Lei Fu, Jinbin Li, Di Zhao, Yulan Zhao, and Ling Yin. Microarray analysis for differentially expressed genes between stromal and epithelial cells in development and metastasis of invasive breast cancer. *Journal of Computational Biology*, 27(12):1631–1643, December 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0154; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0154`.

Wang:1998:CAT

[WG98] Lusheng Wang and Dan Gusfield. Constructing additive trees when the error is small. *Journal of Computational Biology*, 5(1):127–133, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.127; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.127`.

Wexler:2008:VUL

[WG08a] Ydo Wexler and Dan Geiger. Variational upper and lower bounds for probabilistic graphical models. *Journal*

of Computational Biology, 15(7):721–735, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0129; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0129.

Wrabl:2008:SRP

[WG08b] James O. Wrabl and Nick V. Grishin. Statistics of random protein superpositions: p-values for pairwise structure alignment. *Journal of Computational Biology*, 15(3):317–355, April 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0161; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0161.

Wang:2021:EGS

[WGC+21] Shijia Wang, Shufei Ge, Caroline Colijn, Priscila Biller, Liangliang Wang, and Lloyd T. Elliott. Estimating genetic similarity matrices using phylogenies. *Journal of Computational Biology*, 28(6):587–600, June 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0375; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0375.

Walker:1998:ACD

[WGL98] Wynn L. Walker, David S. Goodsell, and Elliot M. Landaw. An analysis of a class of DNA sequence reading molecules. *Journal of Computational Biology*, 5(3):571–583, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.571; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.571.

Wang:2023:GWA

[WGS+23] Shijia Wang, Shufei Ge, Benjamin Sobkowiak, Liangliang Wang, Louis Grandjean, Caroline Colijn, and Lloyd T. Elliott. Genome-wide association with uncertainty in the genetic similarity matrix. *Journal of Computational Biology*, 30(2):189–203, February 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0067; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0067.

Wolfinger:2001:AGS

[WGW+01] Russell D. Wolfinger, Greg Gibson, Elizabeth D. Wolfinger, Lee Bennett, Hisham Hamadeh, Pierre Bushel, Cynthia Afshari, and Richard S. Paules. Assessing gene significance from cDNA microarray expression data via mixed models. *Journal of Computational Biology*, 8(6):625–637, November 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652701753307520; https://www.liebertpub.com/doi/pdf/10.1089/106652701753307520`.

Wahde:2001:MGR

[WH01] Mattias Wahde and John Hertz. Modeling genetic regulatory dynamics in neural development. *Journal of Computational Biology*, 8(4):429–442, September 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652701752236223; https://www.liebertpub.com/doi/pdf/10.1089/106652701752236223`.

Wu:2006:CED

[WH06] Jing Wu and David Haussler. Coding exon detection using comparative sequences. *Journal of Computational Biology*, 13(6):1148–1164, July 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1148; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1148`.

Wimberley:2020:PAC

[WH20] Charles E. Wimberley and Steffen Heber. PeakPass: Automating ChIP-Seq blacklist creation. *Journal of Computational Biology*, 27(2):259–268, February 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0295; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0295`.

Wu:2009:CIA

[WHC09] Li-Ching Wu, Jorng-Tzong Horng, and Yong-An Chen. A computation to integrate the analysis of genetic variations occurring within regulatory elements and their possible effects. *Journal of Computational Biology*, 16(12):1731–1747, December 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-

8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0247; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0247.

Wang:2013:FFC

[WHD13] Hua Wang, Heng Huang, and Chris Ding. Function–function correlated multi-label protein function prediction over interaction networks. *Journal of Computational Biology*, 20(4):322–343, April 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0272; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0272.

Wang:2015:CPF

[WHD15] Hua Wang, Heng Huang, and Chris Ding. Correlated protein function prediction via maximization of data-knowledge consistency. *Journal of Computational Biology*, 22(6):546–562, June 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0172; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0172.

Wang:2013:PPP

[WHDN13] Hua Wang, Heng Huang, Chris Ding, and Feiping Nie. Predicting protein–protein interactions from multimodal biological data sources via nonnegative matrix tri-factorization. *Journal of Computational Biology*, 20(4):344–358, April 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0273; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0273.

Wu:2019:IIA

[WHJE19] Yue Wu, Farhad Hormozdiari, Jong Wha J. Joo, and Eleazar Eskin. Improving imputation accuracy by inferring causal variants in genetic studies. *Journal of Computational Biology*, 26(11):1203–1213, November 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0139; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0139.

Wang:2021:GRP

[WHK21] Xiao Wang, Dan Hao, and Haja N. Kadarmideen. `GeneDMRs`: an R package for gene-based differentially methylated regions analysis. *Journal of Computational Biology*, 28(3):304–316, March 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0081; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0081`.

Wang:2017:RFA

[WHL17] Ying Wang, Haiyan Hu, and Xiaoman Li. rRNAFilter: a fast approach for ribosomal RNA read removal without a reference database. *Journal of Computational Biology*, 24(4):368–375, April 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0113; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0113`.

Wu:2020:DMM

[WHLR20] Xihai Wu, Yunhui Han, Fangmei Liu, and Lihong Ruan. Downregulations of miR-449a and miR-145-5p act as prognostic biomarkers for endometrial cancer. *Journal of Computational Biology*, 27(5):834–844, May 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0215; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0215`.

West:2006:VPS

[WHW+06] Joseph West, John Healy, Michael Wigler, William Casey, and Bud Mishra. Validation of *S. Pombe* sequence assembly by microarray hybridization. *Journal of Computational Biology*, 13(1):1–20, January 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1`.

Wang:2013:CCN

[WHY+13] Zhanyong Wang, Farhad Hormozdiari, Wen-Yun Yang, Eran Halperin, and Eleazar Eskin. CNVeM: Copy number variation detection using uncertainty of read mapping. *Journal of Computational Biology*, 20(3):224–236, March 2013.

CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0258; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0258.

Wu:2005:SMI

[WI05] Zhijin Wu and Rafael A. Irizarry. Stochastic models inspired by hybridization theory for short oligonucleotide arrays. *Journal of Computational Biology*, 12(6):882–893, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.882; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.882.

Willett:1999:DBA

[Wil99] Peter Willett. Dissimilarity-based algorithms for selecting structurally diverse sets of compounds. *Journal of Computational Biology*, 6(3–4):447–457, October 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Waterman:1997:PSR

[WIP97] Michael S. Waterman, Sorin Istrail, and Pavel A. Pevzner. Preface: Special RECOMB'97 issues. *Journal of Computational Biology*, 4(3):215, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.215.

Wang:1994:CMS

[WJ94] Lusheng Wang and Tao Jiang. On the complexity of multiple sequence alignment. *Journal of Computational Biology*, 1(4):337–348, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.337; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.337.

Wang:2014:CMC

[WJD14] Junshan Wang, Ajay Jasra, and Maria De Iorio. Computational methods for a class of network models. *Journal of Computational Biology*, 21(2):141–161, February 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0082; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0082.

Wauthier:2011:NCS

[WJJ11] Fabian L. Wauthier, Michael I. Jordan, and Nebojsa Jojic. Nonparametric combinatorial sequence models. *Journal of Computational Biology*, 18(11):1649–1660, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0175; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0175`.

Worley:1995:INM

[WKC+95] K. C. Worley, K. Y. King, S. Chua, E. R. B. Mccabe, and R. F. Smith. Identification of new members of a carbohydrate kinase-encoding gene family. *Journal of Computational Biology*, 2(3):451–458, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.451; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.451`.

Wu:2018:RRE

[WLA+18] Shuangyang Wu, Wanfei Liu, Hasan Awad Aljohi, Sarah A. Alromaih, Ibrahim O. Alanazi, Qiang Lin, Jun Yu, and Songnian Hu. REDO: RNA editing detection in plant organelles based on variant calling results. *Journal of Computational Biology*, 25(5):509–516, May 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0214; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0214`.

Wen:2018:SGI

[WLC18] Jian-Xin Wen, Xiao-Qin Li, and Yu Chang. Signature gene identification of cancer occurrence and pattern recognition. *Journal of Computational Biology*, 25(8):907–916, August 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0261; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0261`.

Wen:2013:CGW

[WLF13] Yalu Wen, Ming Li, and Wenjiang J. Fu. Catching the genomic wave in oligonucleotide single-nucleotide polymorphism

arrays by modeling sequence binding. *Journal of Computational Biology*, 20(7):514–523, July 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0102; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0102.

Wang:2023:SNS

[WLF+23] Zhichao Wang, Xuelei Li, Jianping Fan, Jintao Meng, Zhenli Lin, Yi Pan, and Yanjie Wei. SWsnn: a novel simulator for spiking neural networks. *Journal of Computational Biology*, 30(9):951–960, September 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0098; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0098.

Wan:2003:DSR

[WLFW03] Honghui Wan, Lugang Li, Scott Federhen, and John C. Wootton. Discovering simple regions in biological sequences associated with scoring schemes. *Journal of Computational Biology*, 10(2):171–185, April 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703321825955; https://www.liebertpub.com/doi/pdf/10.1089/106652703321825955.

Wu:2012:DPC

[WlLK+12] Min Wu, Xiao li Li, Chee-Keong Kwoh, See-Kiong Ng, and Limsoon Wong. Discovery of protein complexes with core-attachment structures from tandem affinity purification (TAP) data. *Journal of Computational Biology*, 19 (9):1027–1042, September 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0293; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0293.

Wekesa:2021:PPF

[WLM21] Jael Sanyanda Wekesa, Yushi Luan, and Jun Meng. Predicting protein functions based on differential co-expression and neighborhood analysis. *Journal of Computational Biology*, 28(1):1–18, January 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0120;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0120.

Wong:2011:SAR

[WLS+11] Thomas K. F. Wong, T. W. Lam, Wing-Kin Sung, Brenda W. Y. Cheung, and S. M. Yiu. Structural alignment of RNA with complex pseudoknot structure. *Journal of Computational Biology*, 18(1):97–108, January 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0275; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0275.

Wang:2022:KMM

[WLXW22] Haohan Wang, Oscar Lopez, Eric P. Xing, and Wei Wu. Kernel mixed model for transcriptome association study. *Journal of Computational Biology*, 29(12):1353–1356, December 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0280; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0280.

Wang:2012:MNB

[WLYC12] Yi Wang, Henry C. M. Leung, S. M. Yiu, and Francis Y. L. Chin. MetaCluster 4.0: a novel binning algorithm for NGS reads and huge number of species. *Journal of Computational Biology*, 19(2):241–249, February 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0276; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0276.

Wu:2004:MPM

[WMC04] Rongling Wu, Chang-Xing Ma, and George Casella. A mixed polyploid model for linkage analysis in outcrossing tetraploids using a pseudo-test backcross design. *Journal of Computational Biology*, 11(4):562–580, August 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.562; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.562.

Wang:2014:FMD

[WMC14] Xun Wang, Ying Miao, and Minquan Cheng. Finding motifs in DNA sequences using low-dispersion sequences. *Journal of Computational Biology*, 21(4):320–329, April 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0054; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0054`.

Wang:2006:PTA

[WMD06] Lincong Wang, Ramgopal R. Mettu, and Bruce Randall Donald. A polynomial-time algorithm for *De Novo* protein backbone structure determination from nuclear magnetic resonance data. *Journal of Computational Biology*, 13(7):1267–1288, September 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1267; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1267`.

Wagle:2024:ACB

[WMG+24] Sanket Wagle, Alexey Markin, Paweł Górecki, Tavis K. Anderson, and Oliver Eulenstein. Asymmetric cluster-based measures for comparative phylogenetics. *Journal of Computational Biology*, 31(4):312–327, April 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0338; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0338`.

Wang:2017:ARR

[WMK17] Hao Wang, Joel McManus, and Carl Kingsford. Accurate recovery of ribosome positions reveals slow translation of wobble-pairing codons in yeast. *Journal of Computational Biology*, 24(6):486–500, June 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0147; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0147`.

Wang:2020:MM

[WMP+20] Yue Wang, Andrey Minarsky, Robert Penner, Christophe Soulé, and Nadya Morozova. Model of morphogenesis. *Journal of Computational Biology*, 27(9):1373–1383, September

2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0414; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0414.

Wittler:2011:CSB

[WMPS11] Roland Wittler, Ján Maňuch, Murray Patterson, and Jens Stoye. Consistency of sequence-based gene clusters. *Journal of Computational Biology*, 18(9):1023–1039, September 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0083; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0083.

Wu:1999:MRS

[WNMB99] Thomas D. Wu, Craig G. Nevill-Manning, and Douglas L. Brutlag. Minimal-risk scoring matrices for sequence analysis. *Journal of Computational Biology*, 6(2):219–235, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.219; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.219.

Wang:2003:RTI

[WOG03] Yonghong Wang, Hongyu Ou, and Fengbiao Guo. Recognition of translation initiation sites of eukaryotic genes based on an EM algorithm. *Journal of Computational Biology*, 10 (5):699–708, October 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703322539042; https://www.liebertpub.com/doi/pdf/10.1089/106652703322539042.

Wooley:1999:TCB

[Woo99] John C. Wooley. Trends in computational biology: a summary based on a RECOMB plenary lecture, 1999. *Journal of Computational Biology*, 6(3–4):459–474, October 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Waldispuhl:2014:SAF

[WOW+14] Jérôme Waldispühl, Charles W. O'Donnell, Sebastian Will, Srinivas Devadas, Rolf Backofen, and Bonnie Berger. Simultaneous alignment and folding of protein sequences. *Journal of Computational Biology*, 21(7):477–491, July 2014.

CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0163; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0163.

Waldispuhl:2011:UAS

[WP11] Jérôme Waldispühl and Yann Ponty. An unbiased adaptive sampling algorithm for the exploration of RNA mutational landscapes under evolutionary pressure. *Journal of Computational Biology*, 18(11):1465–1479, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0181; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0181.

Wang:2019:DMM

[WPL+19] Liang Wang, Yuquan Pei, Shaolei Li, Shanyuan Zhang, and Yue Yang. Distinct molecular mechanisms analysis of three lung cancer subtypes based on gene expression profiles. *Journal of Computational Biology*, 26(10):1140–1155, October 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0046; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0046.

Wu:2025:GBM

[WPS+25] Ziqian Wu, Jiyoon Park, Paul R. Steiner, Bo Zhu, and John X. J. Zhang. A graph-based machine-learning approach combined with optical measurements to understand beating dynamics of cardiomyocytes. *Journal of Computational Biology*, 32(3):239–252, March 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0491; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0491.

Wen:2019:ENB

[WQZ+19] Mingxiang Wen, Xiang Qu, Yanyan Zhu, Lingfang Tian, Zhongqin Shen, Xiulin Yang, and Xianqing Shi. Exploration of novel biomarkers in vasculitis by integrated bioinfomatic approaches. *Journal of Computational Biology*, 26 (12):1448–1457, December 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0176;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0176.

Wilson:2023:ECB

[WR23] Deangelo Wilson and John D. Rogers. Evaluating compression-based phylogeny estimation in the presence of incomplete lineage sorting. *Journal of Computational Biology*, 30(3):250–260, March 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0197; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0197.

Wang:1999:NTD

[WRS+99] Jason T. L. Wang, Steve Rozen, Bruce A. Shapiro, Dennis Shasha, Zhiyuan Wang, and Maisheng Yin. New techniques for DNA sequence classification. *Journal of Computational Biology*, 6(2):209–218, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.209; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.209.

Wan:2010:AFS

[WRSW10] Lin Wan, Gesine Reinert, Fengzhu Sun, and Michael S. Waterman. Alignment-free sequence comparison (II): Theoretical power of comparison statistics. *Journal of Computational Biology*, 17(11):1467–1490, November 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0056; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0056.

Wistrand:2004:TPP

[WS04] Markus Wistrand and Erik L. L. Sonnhammer. Transition priors for protein hidden Markov models: An empirical study towards maximum discrimination. *Journal of Computational Biology*, 11(1):181–193, January 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652704773416957; https://www.liebertpub.com/doi/pdf/10.1089/106652704773416957.

Warren:2011:GAR

[WS11] Robert Warren and David Sankoff. Genome aliquoting revisited. *Journal of Computational Biology*, 18(9):1065–1075, Septem-

ber 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0087; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0087.

Wang:2018:MSG

[WSCL18] Xuedong Wang, Wenhui Shang, Yu Chang, and Xiaoqin Li. Methylation signature genes identification of the lung squamous cell carcinoma occurrence and recognition research. *Journal of Computational Biology*, 25(10):1161–1169, October 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0069; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0069.

Wu:1998:RAM

[WSHB98] Thomas D. Wu, Scott C. Schmidler, Trevor Hastie, and Douglas L. Brutlag. Regression analysis of multiple protein structures. *Journal of Computational Biology*, 5(3):585–595, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.585; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.585.

Wildenberg:2003:DSV

[WSS03] Andy Wildenberg, Steven Skiena, and Pavel Sumazin. Deconvolving sequence variation in mixed DNA populations. *Journal of Computational Biology*, 10(3–4):635–652, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Wang:2015:GGI

[WSS+15] Zhanyong Wang, Jae Hoon Sul, Sagi Snir, Jose A. Lozano, and Eleazar Eskin. Gene–gene interactions detection using a two-stage model. *Journal of Computational Biology*, 22(6):563–576, June 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0163; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0163.

Wallace:2015:ASC

[WSW15] Tim Wallace, Ali Sekmen, and Xiaofei Wang. Application of subspace clustering in DNA sequence analysis. *Journal of Computational Biology*, 22(10):940–952, October 2015.

CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0084; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0084.

Wojtowicz:2007:EGF

[WT07] Damian Wójtowicz and Jerzy Tiuryn. Evolution of gene families based on gene duplication, loss, accumulated change, and innovation. *Journal of Computational Biology*, 14(4):479–495, May 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.A008; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.A008.

Wilczynski:2017:FIT

[WT17] Bartek Wilczynski and Jerzy Tiuryn. FastBill: an improved tool for prediction of *Cis*-regulatory modules. *Journal of Computational Biology*, 24(3):193–199, March 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0108; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0108.

Wu:2007:HPI

[WTE07] Xue Wu, Chau-Wen Tseng, and Nathan Edwards. HMMatch: Peptide identification by spectral matching of tandem mass spectra using hidden Markov models. *Journal of Computational Biology*, 14(8):1025–1043, October 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0071; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0071.

Warnow:2025:AEL

[WTE25] Tandy Warnow, Yasamin Tabatabaee, and Steven N. Evans. Advances in estimating level-1 phylogenetic networks from unrooted SNPs. *Journal of Computational Biology*, 32(1):3–27, January 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0710; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0710.

Weng:2011:MPS

[WTM11] J. F. Weng, D. A. Thomas, and I. Mareels. Maximum parsimony, substitution model, and probability phylogenetic trees. *Journal of Computational Biology*, 18(1):67–80, January 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0232; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0232`.

Wang:2019:PSC

[WTY19] Yi Wang, Kun Tian, and Stephen S.-T. Yau. Protein sequence classification using natural vector and convex hull method. *Journal of Computational Biology*, 26(4):315–321, April 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0216; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0216`.

Wu:1996:SBD

[Wu96] Thomas D. Wu. A segment-based dynamic programming algorithm for predicting gene structure. *Journal of Computational Biology*, 3(3):375–394, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.375; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.375`.

Wu:2008:AMC

[Wu08] Yufeng Wu. Association mapping of complex diseases with ancestral recombination graphs: Models and efficient algorithms. *Journal of Computational Biology*, 15(7):667–684, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0116; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0116`.

Wu:2013:ACP

[Wu13] Yufeng Wu. An algorithm for constructing parsimonious hybridization networks with multiple phylogenetic trees. *Journal of Computational Biology*, 20(10):792–804, October 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/`

10.1089/cmb.2013.0072; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0072.

Weiss:1995:MPC

[WV95] Gunter Weiss and Arndt Von Haeseler. Modeling the polymerase chain reaction. *Journal of Computational Biology*, 2(1):49–61, January 1995. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1995.2.49; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1995.2.49.

Wieringen:2011:EFA

[WV11] Wessel N. Van Wieringen and Mark A. Van De Wiel. Exploratory factor analysis of pathway copy number data with an application towards the integration with gene expression data. *Journal of Computational Biology*, 18(5):729–741, May 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0209; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0209.

Wilson:2023:ISC

[WVT23] Tom Wilson, Duong H. T. Vo, and Thomas Thorne. Identifying subpopulations of cells in single-cell transcriptomic data: a Bayesian mixture modeling approach to zero inflation of counts. *Journal of Computational Biology*, 30(10):1059–1074, October 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0273; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0273.

Wang:2018:SLS

[WW18] Xiaodong Wang and Lei Wang. A simple linear space algorithm for computing nonoverlapping inversion and transposition distance in quadratic average time. *Journal of Computational Biology*, 25(6):563–575, June 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0257; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0257.

Wang:2019:CNI

[WW19] Xiaodong Wang and Lei Wang. Computing nonoverlapping inversion distance between two strings in linear average time. *Journal of Computational Biology*, 26(3):193–201, March 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0136; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0136`.

Wang:2020:PLS

[WWC+20] Weiqing Wang, Shaohua Wang, Xiao Chu, Hui Liu, and Ming Xiang. Predicting the lung squamous cell carcinoma diagnosis and prognosis markers by unique DNA methylation and gene expression profiles. *Journal of Computational Biology*, 27(7):1041–1054, July 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0138; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0138`.

White:2017:AIA

[WWH17] Daniel J. White, Jing Wang, and Richard J. Hall. Assessing the impact of assemblers on virus detection in a De Novo metagenomic analysis pipeline. *Journal of Computational Biology*, 24(9):874–881, September 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0008; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0008`.

Wang:2020:ISC

[WWLC20] Xuedong Wang, Xiaoxi Wang, Xiaoqin Li, and Yu Chang. Identification of specific candidate diagnostic biomarkers for lung squamous cell carcinoma based on methylation. *Journal of Computational Biology*, 27(5):825–833, May 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0213; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0213`.

Wang:2016:CWB

[WWZ+16] Yi Wang, Shuangshuang Wang, Dongjie Zhou, Shuai Yang, Yongchao Xu, Chao Yang, and Long Yang. CsSNP: a

Web-based tool for the detecting of comparative segments SNPs. *Journal of Computational Biology*, 23(7):597–602, July 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0215; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0215`.

Wang:2019:ECL

[WWZ19] Xiaodong Wang, Lei Wang, and Daxin Zhu. Efficient computation of longest common subsequences with multiple substring inclusive constraints. *Journal of Computational Biology*, 26(9):938–947, September 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0008; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0008`.

Wang:2019:CMB

[WWZY19] Yuandi Wang, Qingmei Wen, Zhigang Zhou, and Nanjun Yan. Cell modeling based on bubbles with weighted membranes. *Journal of Computational Biology*, 26(3):241–265, March 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0205; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0205`.

Wu:2008:CBD

[WX08] Jing Wu and Jun Xie. Computation-based discovery of *Cis*-regulatory modules by hidden Markov model. *Journal of Computational Biology*, 15(3):279–290, April 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0024; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0024`.

Wang:2023:GRA

[WxLW+23] Ying Wang, Jin xing Liu, Juan Wang, Junliang Shang, and Ying lian Gao. A graph representation approach based on light gradient boosting machine for predicting drug–disease associations. *Journal of Computational Biology*, 30(8):937–947, August 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0078; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0078`.

Wang:2014:FAE

[WXS14] Zhiyong Wang, Jinbo Xu, and Xinghua Shi. Finding alternative expression quantitative trait loci by exploring sparse model space. *Journal of Computational Biology*, 21(5):385–393, May 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0026; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0026`.

Wang:2013:BMA

[WXY+13] Cong-Jun Wang, Rong-Hua Xu, Qiong-Ying Yuan, Yong-Kun Wang, Dong-Wei Shen, Xu-Jing Wang, Wei Gao, Hui Zhang, and Hua Jiang. Bioinformatics method to analyze the mechanism of pancreatic cancer disorder. *Journal of Computational Biology*, 20(6):444–452, June 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0281; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0281`.

Wang:2024:CPT

[WXY+24] Zihan Wang, Mengxia Xu, Zonglin Yang, Yu Jin, and Yong Zhang. Comparing the performance of three computational methods for estimating the effective reproduction number. *Journal of Computational Biology*, 31(2):128–146, February 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0065; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0065`.

Wu:2011:NAB

[WY11] Yu-Wei Wu and Yuzhen Ye. A novel abundance-based algorithm for binning metagenomic sequences using l-tuples. *Journal of Computational Biology*, 18(3):523–534, March 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0245; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0245`.

Wong:2012:SAR

[WY12] Thomas K. F. Wong and S. M. Yiu. Structural alignment of RNA with triple helix structure. *Journal of Computational Biology*, 19(4):365–378, April 2012. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0052; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0052.

Wang:2021:FAC

[WY21] Jiasong Wang and Changchuan Yin. A fast algorithm for computing the Fourier spectrum of a fractional period. *Journal of Computational Biology*, 28(3):269–282, March 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0269; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0269.

Wang:2018:CBM

[WYC+18] Lei Wang, Zhu-Hong You, Xing Chen, Shi-Xiong Xia, Feng Liu, Xin Yan, Yong Zhou, and Ke-Jian Song. A computational-based method for predicting drug-target interactions by using stacked autoencoder deep neural network. *Journal of Computational Biology*, 25(3):361–373, March 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0135; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0135.

Wexler:2005:FAT

[WYKG05] Ydo Wexler, Zohar Yakhini, Yechezkel Kashi, and Dan Geiger. Finding approximate tandem repeats in genomic sequences. *Journal of Computational Biology*, 12(7):928–942, September 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.928; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.928.

Wu:2021:NPD

[WYLW21] Gaoyan Wu, Mengyun Yang, Yaohang Li, and Jianxin Wang. De Novo prediction of drug–target interactions using Laplacian regularized Schatten p-norm minimization. *Journal of Computational Biology*, 28(7):660–673, July 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0538; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0538.

Wang:2012:BGA

[WYT12] Mingjie Wang, Yuzhen Ye, and Haixu Tang. A *de Bruijn* graph approach to the quantification of closely-related genomes in a microbial community. *Journal of Computational Biology*, 19(6):814–825, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0058; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0058`.

Wang:2018:LGP

[WYY+18] Xiaoqian Wang, Jingwen Yan, Xiaohui Yao, Sungeun Kim, Kwangsik Nho, Shannon L. Risacher, Andrew J. Saykin, Li Shen, and Heng Huang. Longitudinal genotype–phenotype association study through temporal structure auto-learning predictive model. *Journal of Computational Biology*, 25(7):809–824, July 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0008; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0008`.

Wang:2010:TMS

[WZ10] Lusheng Wang and Binhai Zhu. On the tractability of maximal strip recovery. *Journal of Computational Biology*, 17(7):907–914, July 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0084; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0084`.

Wang:2023:PPN

[WZ23] Zong Wang and Qimin Zhang. Positivity-preserving numerical method and relaxed control for stochastic susceptible–infected–vaccinated epidemic model with Markov switching. *Journal of Computational Biology*, 30(6):695–725, June 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0388; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0388`.

Wu:2024:CBN

[WZ24] Yufeng Wu and Louxin Zhang. Computing the bounds of the number of reticulations in a tree–child network that displays a set of trees. *Journal of Computational Biology*, 31(4):345–359,

April 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0309; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0309.

Wu:1996:PCD

[WZC96] Cathy H. Wu, Sheng Zhao, and Hsi-Lien Chen. A protein class database organized with ProSite protein groups and PIR superfamilies. *Journal of Computational Biology*, 3(4):547–561, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.547; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.547.

Wang:2000:EMR

[WZCS00] Dai Wang, Cheng Zhao, Rong Cheng, and Fengzhu Sun. Estimation of the mutation rate during error-prone polymerase chain reaction. *Journal of Computational Biology*, 7(1–2):143–158, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Wang:2021:EVP

[WZCY21] Shisheng Wang, Yi Zhong, Jingqiu Cheng, and Hao Yang. EnrichVisBox: a versatile and powerful Web toolbox for visualizing complex functional enrichment results of omics data. *Journal of Computational Biology*, 28(9):922–930, September 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0564; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0564.

Wang:2020:CRT

[WZG+20a] Xiaojie Wang, Yiyi Zhang, Waleed M. Ghareeb, Shuangming Lin, Xingrong Lu, Ying Huang, Shenghui Huang, Zongbin Xu, and Pan Chi. A comprehensive repertoire of transfer RNA-derived fragments and their regulatory networks in colorectal cancer. *Journal of Computational Biology*, 27 (12):1644–1655, December 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0305; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0305.

Wang:2020:CFD

[WZG+20b] Zihao Wang, Jingrong Zhang, Weifang Gao, Zhiyong Liu, Xiaohua Wan, and Fa Zhang. A consensus framework of distributed multiple-tilt reconstruction in electron tomography. *Journal of Computational Biology*, 27(2):212–222, February 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0287; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0287`.

Wang:2018:MPC

[WZH+18] Shisheng Wang, Wen Zheng, Liqiang Hu, Meng Gong, and Hao Yang. MixProTool: a powerful and comprehensive Web tool for analyzing and visualizing multigroup proteomics data. *Journal of Computational Biology*, 25(10):1123–1127, October 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0050; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0050`.

Wu:2019:IMM

[WZL19] Jie Wu, Yijian Zhang, and Maolan Li. Identification of methylation markers and differentially expressed genes with prognostic value in breast cancer. *Journal of Computational Biology*, 26(12):1394–1408, December 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0179; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0179`.

Wang:2021:EPP

[WZL+21] Nian Wang, Min Zeng, Yiming Li, Fang xiang Wu, and Min Li. Essential protein prediction based on node2vec and XGBoost. *Journal of Computational Biology*, 28(7):687–700, July 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0543; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0543`.

Wu:2010:KSA

[WZW10] Gang Wu, Ying Zhang, and Yimin Wei. Krylov subspace algorithms for computing GeneRank for the analysis of microarray

data mining. *Journal of Computational Biology*, 17(4):631–646, April 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0004; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0004.

Wei:2015:DPA

[WZW15] Zhexue Wei, Daming Zhu, and Lusheng Wang. A dynamic programming algorithm for (1,2)-exemplar breakpoint distance. *Journal of Computational Biology*, 22(7):666–676, July 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0200; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0200.

Wang:2001:PPN

[WZZ01] Lusheng Wang, Kaizhong Zhang, and Louxin Zhang. Perfect phylogenetic networks with recombination. *Journal of Computational Biology*, 8(1):69–78, February 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652701300099119; https://www.liebertpub.com/doi/pdf/10.1089/106652701300099119.

Wexler:2007:SAM

[WZZU07] Ydo Wexler, Chaya Zilberstein, and Michal Ziv-Ukelson. A study of accessible motifs and RNA folding complexity. *Journal of Computational Biology*, 14(6):856–872, July 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R020; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R020.

Xie:2015:DGP

[XAB+15] Bingqing Xie, Gady Agam, Sandhya Balasubramanian, Jinbo Xu, T. Conrad Gilliam, Natalia Maltsev, and Daniela Börnigen. Disease gene prioritization using network and feature. *Journal of Computational Biology*, 22(4):313–323, April 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0001; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0001.

Xu:2006:OMS

[XBLM06] Jinbo Xu, Daniel Brown, Ming Li, and Bin Ma. Optimizing multiple spaced seeds for homology search. *Journal of Computational Biology*, 13(7):1355–1368, September 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1355; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1355`.

Xiang:2024:DDL

[XGD24] Xiaoyang Xiang, Jiaxuan Gao, and Yanrui Ding. DeepPPThermo: a deep learning framework for predicting protein thermostability combining protein-level and amino acid-level features. *Journal of Computational Biology*, 31(2):147–160, February 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0097; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0097`.

Xu:2007:PAP

[XJB07] Jinbo Xu, Feng Jiao, and Bonnie Berger. A parameterized algorithm for protein structure alignment. *Journal of Computational Biology*, 14(5):564–577, June 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R003; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R003`.

Xia:2022:STS

[XJL+22] Yixiao Xia, Minchao Jiang, Yizhang Luo, Guanwen Feng, Gangyong Jia, Hua Zhang, Pu Wang, and Ruiquan Ge. SuccSPred2.0: a two-step model to predict succinylation sites based on multifeature fusion and selection algorithm. *Journal of Computational Biology*, 29(10):1085–1094, October 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0109; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0109`.

Xing:2007:BHI

[XJS07] Eric P. Xing, Michael I. Jordan, and Roded Sharan. Bayesian haplotype inference via the Dirichlet process. *Journal of Computational Biology*, 14(3):267–284, April 2007. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0102; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0102.

Xu:2021:AFP

[XJZ+21] Qiaoji Xu, Lingling Jin, Yue Zhang, Xiaomeng Zhang, Chunfang Zheng, James H. Leebens-mack, and David Sankoff. Ancestral flowering plant chromosomes and gene orders based on generalized adjacencies and chromosomal gene co-occurrences. *Journal of Computational Biology*, 28(11):1156–1179, November 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0340; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0340.

Xie:2005:BMM

[XK05] Jun Xie and Nak-Kyeong Kim. Bayesian models and Markov chain Monte Carlo methods for protein motifs with the secondary characteristics. *Journal of Computational Biology*, 12(7):952–970, September 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.952; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.952.

Xu:2018:PPP

[XL18] Yang Xu and Xiao-Chun Luo. PyPathway: Python package for biological network analysis and visualization. *Journal of Computational Biology*, 25(5):499–504, May 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0199; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0199.

Xu:2020:PEP

[XLLS20] Chunling Xu, Huayi Lu, Fuqiang Li, and Guanfang Su. Protein expression profile on differentiation of bone marrow Mesenchymal stem cells into retinal ganglion-like cells. *Journal of Computational Biology*, 27(8):1329–1336, August 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0024; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0024.

Xu:2013:PDC

[XLZ13] Dong Xu, Hua Li, and Yang Zhang. Protein depth calculation and the use for improving accuracy of protein fold recognition. *Journal of Computational Biology*, 20(10):805–816, October 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0071; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0071`.

Xia:2018:MSP

[XLZ+18a] Ruofan Xia, Yu Lin, Jun Zhou, Bing Feng, and Jijun Tang. A median solver and phylogenetic inference based on double-cut-and-join sorting. *Journal of Computational Biology*, 25(3):302–312, March 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0157; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0157`.

Xiao:2018:OMB

[XLZ+18b] Xiuchun Xiao, Bing Liu, Jing Zhang, Xueli Xiao, and Yi Pan. An optimized method for Bayesian connectivity change point model. *Journal of Computational Biology*, 25(3):337–347, March 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0154; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0154`.

Xia:2024:BCP

[XLZ+24] Juan Xia, Yuxia Li, Haotian Zhu, Feiyang Xue, Feng Shi, and Nana Li. A Bayesian change point model for dynamic alternative transcription start site usage during cellular differentiation. *Journal of Computational Biology*, 31(5):445–457, May 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0174; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0174`.

Xu:1996:IAC

[XMU96] Ying Xu, Richard J. Mural, and Edward C. Uberbacher. An iterative algorithm for correcting sequencing errors in DNA coding regions. *Journal of Computational Biology*,

3(3):333–344, January 1996. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1996.3.333; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1996.3.333.

Xu:2020:DAM

[XMWZ20] Yangchun Xu, Yan Mu, Ling Wang, and Xuan Zhang. Detailed analysis of molecular mechanisms in primary and metastatic melanoma. *Journal of Computational Biology*, 27(1):9–19, January 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0197; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0197.

Xie:2007:RBE

[XS07] Wei Xie and Nikolaos V. Sahinidis. A reduction-based exact algorithm for the contact map overlap problem. *Journal of Computational Biology*, 14(5):637–654, June 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R007; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R007.

Xu:2022:TTF

[XSH+22] Siwei Xu, Mario Skarica, Ahyeon Hwang, Yi Dai, Cheyu Lee, Matthew J. Girgenti, and Jing Zhang. Translator: a *Trans*fer *L*earning approach to facilitate single-cell *AT*AC-Seq data analysis fr*o*m *R*eference dataset. *Journal of Computational Biology*, 29(7):619–633, July 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0596; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0596.

Xia:2008:RAA

[XSS08] Ai Xia, Maria V. Sharakhova, and Igor V. Sharakhov. Reconstructing ancestral autosomal arrangements in the *Anopheles gambiae* complex. *Journal of Computational Biology*, 15(8):965–980, October 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0076; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0076.

Xu:1997:AGI

[XU97] Ying Xu and Edward C. Uberbacher. Automated gene identification in large-scale genomic sequences[1]. *Journal of Computational Biology*, 4(3):325–338, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.325; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.325`.

Xu:2009:FEA

[Xu09] Andrew Wei Xu. A fast and exact algorithm for the median of three problem: a graph decomposition approach. *Journal of Computational Biology*, 16(10):1369–1381, October 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0087; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0087`.

Xu:2010:MPL

[Xu10] Andrew Wei Xu. The median problems on linear multichromosomal genomes: Graph representation and fast exact solutions. *Journal of Computational Biology*, 17(9):1195–1211, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0106; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0106`.

Xing:2005:SMC

[XvdL05] Biao Xing and Mark J. van der Laan. A statistical method for constructing transcriptional regulatory networks using gene expression and sequence data. *Journal of Computational Biology*, 12(2):229–246, March 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.229; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.229`.

Xu:2020:NMB

[XWJZ20] Yangchun Xu, Ling Wang, Lanxiang Jiang, and Xuan Zhang. Novel MicroRNA biomarkers, *miR-142-5p*, *miR-550a*, *miR-1826*, and *miR-1201*, were identified for primary melanoma. *Journal of Computational Biology*, 27(5):815–824, May 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0198; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0198.

Xiao:2008:EVA

[XWLJ08] Jing Xiao, Lusheng Wang, Xiaowen Liu, and Tao Jiang. An efficient voting algorithm for finding additive biclusters with random background. *Journal of Computational Biology*, 15(10):1275–1293, December 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0219; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0219.

Xu:2000:CMN

[XXCE00] Ying Xu, Dong Xu, Oakley H. Crawford, and J. Ralph Einstein. A computational method for NMR-Constrained protein threading. *Journal of Computational Biology*, 7(3–4):449–467, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Xu:1998:ECM

[XXU98] Ying Xu, Dong Xu, and Edward C. Uberbacher. An efficient computational method for globally optimal threading1. *Journal of Computational Biology*, 5(3):597–614, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.597; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.597.

Xia:2021:SIK

[XXZ+21] Yijun Xia, Juan Xie, Jun Zhao, Yin Lou, and Dongsheng Cao. Screening and identification of key biomarkers in melanoma: Evidence from bioinformatic analyses. *Journal of Computational Biology*, 28(3):317–329, March 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0400; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0400.

Xin:2022:DCN

[XYX+22] Bin Xin, Yaning Yang, Xiaolan Xie, Jiandong Shang, Zhengyu Liu, and Shaoliang Peng. Detecting and classifying nu-

clei using multi-scale fully convolutional network. *Journal of Computational Biology*, 29(10):1095–1103, October 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0111; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0111.

Xu:2012:GLM

[XZ12] Jialin Xu and Yu Zhang. A generalized linear model for peak calling in ChIP-Seq data. *Journal of Computational Biology*, 19(6):826–838, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0023; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0023.

Xu:2007:PCB

[XZS07] Wei Xu, Chunfang Zheng, and David Sankoff. Paths and cycles in breakpoint graph of random multichromosomal genomes. *Journal of Computational Biology*, 14(4):423–435, May 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.A004; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.A004.

Xia:2015:MTS

[XZW15a] Kelin Xia, Zhixiong Zhao, and Guo-Wei Wei. Multiresolution topological simplification. *Journal of Computational Biology*, 22(9):887–891, September 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0104; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0104.

Xu:2015:GCA

[XZW15b] Shutan Xu, Shuxue Zou, and Lincong Wang. A geometric clustering algorithm with applications to structural data. *Journal of Computational Biology*, 22(5):436–450, May 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0162; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0162.

Yu:2011:CDM

[YA11] Yi-Kuo Yu and Stephen F. Altschul. The complexity of the Dirichlet model for multiple alignment data. *Journal of Computational Biology*, 18(8):925–939, August 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0039; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0039`.

Yang:2009:PCH

[Yan09] Zheng Rong Yang. Predict collagen hydroxyproline sites using support vector machines. *Journal of Computational Biology*, 16(5):691–702, May 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0167; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0167`.

Yourdkhani:2021:PIP

[YAR21] Samaneh Yourdkhani, Elizabeth S. Allman, and John A. Rhodes. Parameter identifiability for a profile mixture model of protein evolution. *Journal of Computational Biology*, 28(6):570–586, June 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0315; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0315`.

Yeo:2004:MEM

[YB04] Gene Yeo and Christopher B. Burge. Maximum entropy modeling of short sequence motifs with applications to RNA splicing signals. *Journal of Computational Biology*, 11(2–3):377–394, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Ye:2019:OMM

[YBF19] Yan Ye, Chunde Bao, and Wei Fan. Overexpression of miR-101 May target DUSP1 to promote the cartilage degradation in rheumatoid arthritis. *Journal of Computational Biology*, 26(10):1067–1079, October 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0021;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0021.

Yang:2018:CTL

[YCCL18] Cheng-Hong Yang, Yi-Cheng Chiang, Li-Yeh Chuang, and Yu-Da Lin. A CpGCluster-Teaching–Learning-Based optimization for prediction of CpG islands in the human genome. *Journal of Computational Biology*, 25(2):158–169, February 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0178; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0178.

Yang:2016:RRI

[YCP16] Shuo Yang, Shai Carmi, and Itsik Pe'er. Rapidly registering identity-by-descent across ancestral recombination graphs. *Journal of Computational Biology*, 23(6):495–507, June 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0016; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0016.

Yang:2021:IAL

[YcXyW+21] Jie Yang, Qing chun Xu, Zhen yu Wang, Xun Lu, Liu kui Pan, Jun Wu, and Chen Wang. Integrated analysis of an lncRNA-associated ceRNA network reveals potential biomarkers for hepatocellular carcinoma. *Journal of Computational Biology*, 28(3):330–344, March 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0250; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0250.

Yang:2020:IKB

[YDG+20] Bao Yang, Keqin Dong, Peiyuan Guo, Peng Guo, Guo Jie, Guanhua Zhang, and Tianke Li. Identification of key biomarkers and potential molecular mechanisms in oral squamous cell carcinoma by bioinformatics analysis. *Journal of Computational Biology*, 27(1):40–54, January 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0211; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0211.

York:2002:BEN

[YDN02] Thomas L. York, Richard Durrett, and Rasmus Nielsen. Bayesian estimation of the number of inversions in the history of two chromosomes. *Journal of Computational Biology*, 9(6):805–818, December 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/10665270260518281; https://www.liebertpub.com/doi/pdf/10.1089/10665270260518281`.

Yang:2012:SPE

[YDN12] Xinyi Yang, Jennifer E. Dent, and Christine Nardini. An *S*-System Parameter Estimation Method (SPEM) for biological networks. *Journal of Computational Biology*, 19 (2):175–187, February 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0269; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0269`.

Yang:2025:PPD

[YDZ+25] Wanyi Yang, Qingsong Du, Xunyu Zhou, Chuanfang Wu, and Jinku Bao. PDFll: Predictors of disorder and function of proteins from the language of life. *Journal of Computational Biology*, 32(2):143–155, February 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0506; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0506`.

Yanikoglu:2002:MEC

[YE02] Berrin Yanikoglu and Burak Erman. Minimum energy configurations of the 2-dimensional HP-Model of proteins by self-organizing networks. *Journal of Computational Biology*, 9 (4):613–620, August 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652702760277345; https://www.liebertpub.com/doi/pdf/10.1089/106652702760277345`.

Yancopoulos:2009:DPF

[YF09] Sophia Yancopoulos and Richard Friedberg. DCJ path formulation for genome transformations which include insertions, deletions, and duplications. *Journal of Computational Biology*, 16(10):1311–1338, October 2009. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0092; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0092.

Ye:2007:HMM

[YFBK07] Xiaoduan Ye, Alan M. Friedman, and Chris Bailey-Kellogg. Hypergraph model of multi-residue interactions in proteins: Sequentially-constrained partitioning algorithms for optimization of site-directed protein recombination. *Journal of Computational Biology*, 14(6):777–790, July 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.R016; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.R016.

Yin:2021:IPH

[YfZX+21] Yang Yin, Yang fan Zou, Yu Xiao, Tian xi Wang, Ya ni Wang, Zhi cheng Dong, Yu hu Huo, Bo chen Yao, Ling bing Meng, and Shuang xia Du. Identification of potential hub genes of atherosclerosis through bioinformatic analysis. *Journal of Computational Biology*, 28(1):60–78, January 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0334; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0334.

Yang:2005:GCU

[YGP05] Albert C.-C. Yang, Ary L. Goldberger, and C.-K. Peng. Genomic classification using an information-based similarity index: Application to the SARS coronavirus. *Journal of Computational Biology*, 12(8):1103–1116, October 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1103; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1103.

Yu:2001:SSP

[YH01] Yi-Kuo Yu and Terence Hwa. Statistical significance of probabilistic sequence alignment and related local hidden Markov models. *Journal of Computational Biology*, 8(3):249–282, June 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/

10.1089/10665270152530845; https://www.liebertpub.com/doi/pdf/10.1089/10665270152530845.

Yang:2003:SMA

[YHB+03] Yaning Yang, Josephine Hoh, Clemens Broger, Martin Neeb, Joanne Edington, Klaus Lindpaintner, and Jurg Ott. Statistical methods for analyzing microarray feature data with replications. *Journal of Computational Biology*, 10(2): 157–169, April 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652703321825946; https://www.liebertpub.com/doi/pdf/10.1089/106652703321825946.

Yang:2005:EED

[YHC05] Chu-Wen Yang, Chin-Fu Hsiao, and Chen-Kung Chou. Evaluation of experimental designs for two-color cDNA microarrays. *Journal of Computational Biology*, 12(9):1202–1220, November 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1202; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1202.

Yang:2019:TDE

[YHC19] Sihai Yang, Xianhua Han, and Yenwei Chen. Three-dimensional embryonic image segmentation and registration based on shape index and ellipsoid-fitting method. *Journal of Computational Biology*, 26(2):128–142, February 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0165; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0165.

Yang:2015:SHC

[YHEP15] Wen-Yun Yang, Farhad Hormozdiari, Eleazar Eskin, and Bogdan Pasaniuc. A spatial haplotype copying model with applications to genotype imputation. *Journal of Computational Biology*, 22(5):451–462, May 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0151; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0151.

Yang:2017:PAM

[YHT+17] Sihai Yang, Xianhua Han, Yukako Tohsato, Koji Kyoda, Shuichi Onami, Ikuko Nishikawa, and Yenwei Chen. Phenotype analysis method for identification of gene functions involved in asymmetric division of *Caenorhabditis elegans*. *Journal of Computational Biology*, 24(5):436–446, May 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0210; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0210`.

Yan:2018:ICT

[YHW18] Xiaoping Yan, Yu Huang, and Jiabin Wu. Identify cross talk between circadian rhythm and coronary heart disease by multiple correlation analysis. *Journal of Computational Biology*, 25(12):1312–1327, December 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0254; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0254`.

Yang:2017:DHH

[YI17] Doo Yang and Ilya Ioshikhes. *Drosophila* H2A and H2A.Z nucleosome sequences reveal different nucleosome positioning sequence patterns. *Journal of Computational Biology*, 24(4):289–298, April 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0173; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0173`.

Yeang:2004:PNM

[YIJ04] Chen-Hsiang Yeang, Trey Ideker, and Tommi Jaakkola. Physical network models. *Journal of Computational Biology*, 11(2–3):243–262, March 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Yin:2019:EDD

[Yin19] Changchuan Yin. Encoding and decoding DNA sequences by integer chaos game representation. *Journal of Computational Biology*, 26(2):143–151, February 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0173;`

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0173.

Ye:2004:AMP

[YJ04] Jieping Ye and Ravi Janardan. Approximate multiple protein structure alignment using the sum-of-pairs distance. *Journal of Computational Biology*, 11(5):986–1000, October 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.986; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.986.

Yeang:2006:MCF

[YJ06] Chen-Hsiang Yeang and Tommi Jaakkola. Modeling the combinatorial functions of multiple transcription factors. *Journal of Computational Biology*, 13(2):463–480, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.463; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.463.

Yousefian-Jazi:2018:SIF

[YJC18] Ali Yousefian-Jazi and Jinwook Choi. Sequential integration of fuzzy clustering and expectation maximization for transcription factor binding site identification. *Journal of Computational Biology*, 25(11):1247–1256, November 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0230; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0230.

Yordanov:2023:RES

[YjDG+23] Boyan Yordanov, Sara jane Dunn, Colin Gravill, Himanshu Arora, Hillel Kugler, and Christoph M. Wintersteiger. The reasoning engine: a satisfiability modulo theories-based framework for reasoning about discrete biological models. *Journal of Computational Biology*, 30(9):1046–1058, September 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0117; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0117.

Yu:2008:SVT

[YJEP08] Chun-Nam John Yu, Thorsten Joachims, Ron Elber, and Jaroslaw Pillardy. Support vector training of protein alignment models. *Journal of Computational Biology*, 15(7): 867–880, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0152; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0152`.

Yona:2005:URH

[YK05] Golan Yona and Klara Kedem. The URMS-RMS hybrid algorithm for fast and sensitive local protein structure alignment. *Journal of Computational Biology*, 12 (1):12–32, February 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.12; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.12`.

Yildiz:2019:MDS

[YK19] Muslum Yildiz and Abdulkadir Kocak. Molecular dynamics studies of histo-blood group antigen blocking human immunoglobulin A antibody and escape mechanism in noroviruses upon mutation. *Journal of Computational Biology*, 26 (9):962–974, September 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0163; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0163`.

Yamada:2020:CMI

[YKPM20] Naomi Yamada, Prashant Kumar Kuntala, B. Franklin Pugh, and Shaun Mahony. ChExMix: a method for identifying and classifying Protein–DNA interaction subtypes. *Journal of Computational Biology*, 27(3):429–435, March 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0466; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0466`.

Yang:2017:SCA

[YL17] Hu Yang and Xiaoqin Liu. Studies on the clustering algorithm for analyzing gene expression data with a bidirectional penalty. *Journal of Computational Biology*, 24(7):689–698, July 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0051; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0051`.

Yang:2017:JAS

[YLC+17] Cheng-Hong Yang, Yu-Da Lin, Li-Yeh Chuang, Jin-Bor Chen, and Hsueh-Wei Chang. Joint analysis of SNP–SNP-Environment interactions for chronic dialysis by an improved branch and bound algorithm. *Journal of Computational Biology*, 24(12):1212–1225, December 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0090; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0090`.

Yu:2020:IBI

[YLC+20] Fan Yu, Zhong-Sen Le, Li-Hua Chen, Hong Qian, Bo Yu, and Wen-Hua Chen. Identification of biomolecular information in rotenone-induced cellular model of Parkinson's disease by public microarray data analysis. *Journal of Computational Biology*, 27(6):888–903, June 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0151; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0151`.

Yang:2017:PSO

[YLCC17] Cheng-Hong Yang, Yu-Shiun Lin, Li-Yeh Chuang, and Hsueh-Wei Chang. A particle swarm optimization-based approach with local search for predicting protein folding. *Journal of Computational Biology*, 24(10):981–994, October 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0104; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0104`.

Yang:2018:ISB

[YLD+18] Hui Yang, Hao Lv, Hui Ding, Wei Chen, and Hao Lin. iRNA-2OM: a sequence-based predictor for identifying 2'-O-methylation sites in *Homo sapiens*. *Journal of Computational Biology*, 25(11):1266–1277, November 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0004; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0004`.

Yeh:2015:DDI

[YLW+15] Hsin-Yi (Cindy) Yeh, Aaron Lindsey, Chih-Peng Wu, Shawna Thomas, and Nancy M. Amato. Decoy database improvement for protein folding. *Journal of Computational Biology*, 22(9):823–836, September 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0116; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0116`.

Yang:2024:IDC

[YLZ+24] Zhidong Yang, Hongjia Li, Dawei Zang, Renmin Han, and Fa Zhang. Improved denoising of cryo-electron microscopy micrographs with simulation-aware pretraining. *Journal of Computational Biology*, 31(6):564–575, June 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Yeh:2006:PMP

[YM06] Joanne I. Yeh and Lisong Mao. Prediction of membrane proteins in *Mycobacterium tuberculosis* using a support vector machine algorithm. *Journal of Computational Biology*, 13(1):126–129, January 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.126; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.126`.

Yang:2024:SAD

[YMM+24] Jing Yang, Shaojuan Ma, Juan Ma, Jinhua Ran, and Xinyu Bai. Stochastic analysis for the dual virus parallel transmission model with immunity delay. *Journal of Computational Biology*, 31(12):1291–1304, December 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0662; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0662.

Yin:2021:DAS

[YMxW21] Wutao Yin, Sakib Mostafa, and Fang xiang Wu. Diagnosis of autism spectrum disorder based on functional brain networks with deep learning. *Journal of Computational Biology*, 28(2):146–165, February 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0252; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2020.0252.

Yuan:2012:OPG

[YMZ+12] Xiguo Yuan, David J. Miller, Junying Zhang, David Herrington, and Yue Wang. An overview of population genetic data simulation. *Journal of Computational Biology*, 19(1):42–54, January 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0188; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0188.

Yu:2023:MLP

[YQDW23] Ying Yu, Tian Qiu, Junwen Duan, and Jianxin Wang. Multigranularity label prediction model for automatic international classification of diseases coding in clinical text. *Journal of Computational Biology*, 30(8):900–911, August 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0096; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0096.

Yang:2019:MMC

[YRG+19] Yanshen Yang, Jeffrey A. Robertson, Zhen Guo, Jake Martinez, Christy Coghlan, and Lenwood S. Heath. MCAT: Motif combining and association tool. *Journal of Computational Biology*, 26(1):1–15, January 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0113; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0113.

Yu:1999:PSS

[YS99] Lihua Yu and Temple F. Smith. Positional statistical significance in sequence alignment. *Journal of Computational Biology*, 6(2):253–259, January 1999. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1999.6.253; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1999.6.253`.

Yang:2007:PMG

[YS07] Qingwu Yang and Sing-Hoi Sze. Path matching and graph matching in biological networks. *Journal of Computational Biology*, 14(1):56–67, January 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0076; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0076`.

Yang:2010:NPV

[YS10] Zhenyu Yang and David Sankoff. Natural parameter values for generalized gene adjacency. *Journal of Computational Biology*, 17(9):1113–1128, September 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0099; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0099`.

Yohay:2019:EEM

[YS19] Ben Yohay and Sagi Snir. Extending the evolvability model to the prokaryotic world: Simulations and results on real data. *Journal of Computational Biology*, 26(8):794–805, August 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0189; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0189`.

Yamamoto:2023:PPS

[YS23] Akito Yamamoto and Tetsuo Shibuya. Privacy-preserving statistical analysis of genomic data using compressive mechanism with Haar wavelet transform. *Journal of Computational Biology*, 30(2):176–188, February 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0246;`

https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0246.

Yadav:2015:TPR

[YSC15] Sunita Yadav, D. Swati, and Hariharan Chandrasekharan. Thiamine pyrophosphate riboswitch in some representative plant species: a bioinformatics study. *Journal of Computational Biology*, 22(1):1–9, January 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0169; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0169.

Yanover:2008:MLE

[YSFW08] Chen Yanover, Ora Schueler-Furman, and Yair Weiss. Minimizing and learning energy functions for side-chain prediction. *Journal of Computational Biology*, 15(7):899–911, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0158; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0158.

Yooseph:2022:VAB

[YT22] Shibu Yooseph and Sahar Tavakoli. Variational approximation-based model selection for microbial network inference. *Journal of Computational Biology*, 29(7):724–737, July 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0595; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0595.

Yanev:2017:PFP

[YTMY17] Nicola Yanev, Metodi Traykov, Peter Milanov, and Borislav Yurukov. Protein folding prediction in a cubic lattice in hydrophobic-polar model. *Journal of Computational Biology*, 24(5):412–421, May 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0181; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0181.

Yi:2012:SPF

[YTS12] Gangman Yi, Michael R. Thon, and Sing-Hoi Sze. Supervised protein family classification and new family construc-

tion. *Journal of Computational Biology*, 19(8):957–967, August 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0044; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0044.

Yu:2024:MCF

[Yu24] Yun William Yu. On minimizers and convolutional filters: Theoretical connections and applications to genome analysis. *Journal of Computational Biology*, 31(5):381–395, May 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0483; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0483.

Yuan:2009:TRH

[Yua09] Guo-Cheng Yuan. Targeted recruitment of histone modifications in humans predicted by genomic sequences. *Journal of Computational Biology*, 16(2):341–355, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.18TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.18TT.

Yang:2021:FAA

[YW21] Wen Yang and Lusheng Wang. Fast and accurate algorithms for mapping and aligning long reads. *Journal of Computational Biology*, 28(8):789–803, August 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0603; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0603.

Wang:2006:EIA

[yWCF06] Lu yong Wang, Dorin Comaniciu, and Daniel Fasulo. Exploiting interactions among polymorphisms contributing to complex disease traits with boosted generative modeling. *Journal of Computational Biology*, 13(10):1673–1684, December 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.1673; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.1673.

Yu:2011:AMB

[YWN11] Yun Yu, Tandy Warnow, and Luay Nakhleh. Algorithms for MDC-Based multi-locus phylogeny inference: Beyond rooted binary gene trees on single alleles. *Journal of Computational Biology*, 18(11):1543–1559, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0174; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0174`.

Yan:2019:BND

[YWZ+19] Chao-Kun Yan, Wen-Xiu Wang, Ge Zhang, Jian-Lin Wang, and Ashutosh Patel. BiRWDDA: a novel drug repositioning method based on multisimilarity fusion. *Journal of Computational Biology*, 26(11):1230–1242, November 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0063; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0063`.

Yin:2005:FCC

[YY05] Changchuan Yin and Stephen S.-T. Yau. A Fourier characteristic of coding sequences: Origins and a non-Fourier approximation. *Journal of Computational Biology*, 12(9):1153–1165, November 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1153; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1153`.

Yang:2018:DRR

[YY18] Ming Yang and Louis Z. Yang. Determining a reasonable range of relative numerical tolerance values for simulating deterministic models of biochemical reactions. *Journal of Computational Biology*, 25(12):1361–1364, December 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0026; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0026`.

Yang:2019:MBO

[YY19] Louis Z. Yang and Ming Yang. Modeling biological oscillations: Integration of short reaction pauses into a stationary model of a negative feedback loop generates sustained long oscillations.

Journal of Computational Biology, 26(10):1050–1066, October 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0017; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0017`.

Ye:2010:CAD

[YYA10] Xugang Ye, Yi-Kuo Yu, and Stephen F. Altschul. Compositional adjustment of Dirichlet mixture priors. *Journal of Computational Biology*, 17(12):1607–1620, December 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0117; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0117`.

Ye:2011:IDM

[YYA11] Xugang Ye, Yi-Kuo Yu, and Stephen F. Altschul. On the inference of Dirichlet mixture priors for protein sequence comparison. *Journal of Computational Biology*, 18(8):941–954, August 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0040; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0040`.

Yang:2019:RLN

[YYJ19] Yushuang Yang, Wei Yang, and Ling Jin. The role of long non-coding RNA prostate cancer-associated transcript 1 in prostate cancer. *Journal of Computational Biology*, 26 (9):975–984, September 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0240; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0240`.

Ye:2019:STS

[YYL19] Yusong Ye, Zhuoqin Yang, and Jinzhi Lei. Stochastic telomere shortening and the route to limitless replicative potential. *Journal of Computational Biology*, 26(4):350–363, April 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0234; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0234`.

Ye:2020:DMH

[YYL20] Yusong Ye, Zhuoqin Yang, and Jinzhi Lei. DNA methylation heterogeneity induced by collaborations between enhancers. *Journal of Computational Biology*, 27(12):1668–1677, December 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0413; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0413`.

Yan:2023:MSG

[YYM+23] Chaochao Yan, Jinyu Yang, Hehuan Ma, Sheng Wang, and Junzhou Huang. Molecule sequence generation with rebalanced variational autoencoder loss. *Journal of Computational Biology*, 30(1):82–94, January 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0063; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0063`.

Yin:2014:NMC

[YYW14] Changchuan Yin, Xuemeng E. Yin, and Jiasong Wang. A novel method for comparative analysis of DNA sequences by Ramanujan-Fourier transform. *Journal of Computational Biology*, 21(12):867–879, December 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0120; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0120`.

Yeo:2009:ITF

[YYY+09] Zhen Xuan Yeo, Hock Chuan Yeo, Joan Keng Suan Yeo, Ai Li Yeo, Ye Li, and Neil D. Clarke. Inferring transcription factor targets from gene expression changes and predicted promoter occupancy. *Journal of Computational Biology*, 16(2):357–368, February 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.19TT; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.19TT`.

Yang:2010:IGC

[YYZ+10] Qingwu Yang, Gangman Yi, Fenghui Zhang, Michael R. Thon, and Sing-Hoi Sze. Identifying gene clusters within localized regions in multiple genomes. *Journal of Computa-*

tional Biology, 17(5):657–668, May 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0116; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0116.

Yang:2023:NAS

[YYZ23] Xiaochen Yang, Zhanwen Yang, and Chiping Zhang. Numerical analysis of split-step backward Euler method with truncated Wiener process for a stochastic susceptible-infected-susceptible model. *Journal of Computational Biology*, 30 (10):1098–1111, October 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0462; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0462.

Yang:2008:RPS

[YZ08] Jialiang Yang and Louxin Zhang. Run probabilities of seed-like patterns and identifying good transition seeds. *Journal of Computational Biology*, 15(10):1295–1313, December 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0209; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0209.

Yang:2017:MGR

[YZ17] Lianping Yang and Weilin Zhang. A multiresolution graphical representation for similarity relationship and multiresolution clustering for biological sequences. *Journal of Computational Biology*, 24(4):299–310, April 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0030; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0030.

Yamada:2020:IPA

[YzCW20] Kohei Yamada, Zhi zhong Chen, and Lusheng Wang. Improved practical algorithms for rooted subtree prune and regraft (rSPR) distance and hybridization number. *Journal of Computational Biology*, 27(9):1422–1432, September 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0432;

https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0432.

Yu:2024:MRG

[YZPC24] Boyuan Yu, Hao Zhang, Cong Pian, and Yuanyuan Chen. MMG4: Recognition of G4-forming sequences based on Markov model. *Journal of Computational Biology*, 31(12): 1211–1223, December 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0523; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0523.

Yang:2013:LLA

[YZWZ13] Lianping Yang, Xiangde Zhang, Tianming Wang, and Hegui Zhu. Large local analysis of the unaligned genome and its application. *Journal of Computational Biology*, 20(1):19–29, January 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0052; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0052.

Zhou:2018:EDB

[ZAG+18] Xinrui Zhou, Amihood Amir, Concettina Guerra, Gadi Landau, and Jarek Rossignac. EDoP distance between sets of incomplete permutations: Application to bacteria classification based on gene order. *Journal of Computational Biology*, 25(11):1193–1202, November 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0063; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0063.

Zakov:2015:RBF

[ZB15] Shay Zakov and Vineet Bafna. Reconstructing breakage fusion bridge architectures using noisy copy numbers. *Journal of Computational Biology*, 22(6):577–594, June 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0166; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0166.

Zhang:1998:ALS

[ZBM98] Zheng Zhang, Piotr Berman, and Webb Miller. Alignments without low-scoring regions. *Journal of Computational Biology*, 5(2):197–210, January 1998. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1998.5.197; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1998.5.197`.

Zhang:2013:SLD

[ZCH+13] ZhiZhuo Zhang, Cheng Wei Chang, Willy Hugo, Edwin Cheung, and Wing-Kin Sung. Simultaneously learning DNA motif along with its position and sequence rank preferences through expectation maximization algorithm. *Journal of Computational Biology*, 20(3):237–248, March 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0233; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0233`.

Zuo:2017:MBA

[ZCK17] Chandler Zuo, Kailei Chen, and Sündüz Keleş. A MAD-Bayes algorithm for state-space inference and clustering with application to querying large collections of ChIP-Seq data sets. *Journal of Computational Biology*, 24(6):472–485, June 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0138; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0138`.

Chen:2020:CCP

[zCULW20] Zhi zhong Chen, Shohei Ueta, Jingyu Li, and Lusheng Wang. Computing a consensus phylogeny via leaf removal. *Journal of Computational Biology*, 27(2):175–188, February 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0269; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0269`.

Zeng:2020:PRR

[ZCY+20] Tian Zeng, Can Chen, Pan Yang, Wenwei Zuo, Xiaoqing Liu, and Yanling Zhang. A protective role for RHOJ in NonSmall cell lung cancer based on integrated bioinformatics anal-

ysis. *Journal of Computational Biology*, 27(7):1092–1103, July 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0209; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0209.

Zhong:2023:DGC

[ZCZ+23] Jiancheng Zhong, Pan Cui, Yihong Zhu, Qiu Xiao, and Zuohang Qu. DAHNGC: a graph convolution model for drug–disease association prediction by using heterogeneous network. *Journal of Computational Biology*, 30(9):1019–1033, September 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0135; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0135.

Zhang:2020:SIK

[ZDG+20] Meng Zhang, Chen-Yi Di, Peng Guo, Ling-Bing Meng, Meng-Jie Shan, Yong Qiu, Pei-Yuan Guo, Ke-Qin Dong, Qi Xie, and Qiang Wang. Screening and identification of key biomarkers in pancreatic cancer: Evidence from bioinformatic analysis. *Journal of Computational Biology*, 27(7):1079–1091, July 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0189; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0189.

Zou:2020:TSC

[ZDZ+20] Pan Zou, Lijin Duan, Shasha Zhang, Xue Bai, Zhenghui Liu, Fengmei Jin, Haibo Sun, Wentao Xu, and Rui Chen. Target specificity of the CRISPR-Cas9 system in *Arabidopsis thaliana*, *Oryza sativa*, and *Glycine max* genomes. *Journal of Computational Biology*, 27(10):1544–1552, October 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0453; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0453.

Zaccaria:2018:PCN

[ZEKKR18] Simone Zaccaria, Mohammed El-Kebir, Gunnar W. Klau, and Benjamin J. Raphael. Phylogenetic copy-number factorization of multiple tumor samples. *Journal of Computational Biology*, 25(7):689–708, July 2018. CODEN JCOBEM.

ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0253; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0253.

Zhao:2005:CAQ

[ZF05] Sheng Zhao and Russell D. Fernald. Comprehensive algorithm for quantitative real-time polymerase chain reaction. *Journal of Computational Biology*, 12(8):1047–1064, October 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1047; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1047.

Zhou:2007:DSS

[ZF07] Leming Zhou and Liliana Florea. Designing sensitive and specific spaced seeds for cross-species mRNA-to-Genome alignment. *Journal of Computational Biology*, 14(2):113–130, March 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0130; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0130.

Zhao:2008:FAW

[ZFAS08] Zhiyu Zhao, Bin Fu, Francisco J. Alanis, and Christopher M. Summa. Feedback algorithm and Web-server for protein structure alignment. *Journal of Computational Biology*, 15(5):505–524, June 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0075; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0075.

Zheng:2009:AJO

[ZFBK09] Wei Zheng, Alan M. Friedman, and Chris Bailey-Kellogg. Algorithms for joint optimization of stability and diversity in planning combinatorial libraries of chimeric proteins. *Journal of Computational Biology*, 16(8):1151–1168, August 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0090; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0090.

Zien:2003:MHM

[ZFZL03] Alexander Zien, Juliane Fluck, Ralf Zimmer, and Thomas Lengauer. Microarrays: How many do you need? *Journal of Computational Biology*, 10(3–4):653–667, June 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Zheng:2010:PFS

[ZGBK10] Wei Zheng, Karl E. Griswold, and Chris Bailey-Kellogg. Protein fragment swapping: a method for asymmetric, selective site-directed recombination. *Journal of Computational Biology*, 17(3):459–475, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0189; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0189`.

Zakov:2011:RPI

[ZGEZu11] Shay Zakov, Yoav Goldberg, Michael Elhadad, and Michal Ziv-ukelson. Rich parameterization improves RNA structure prediction. *Journal of Computational Biology*, 18(11):1525–1542, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0184; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0184`.

Zagordi:2010:DSG

[ZGRB10] Osvaldo Zagordi, Lukas Geyrhofer, Volker Roth, and Niko Beerenwinkel. Deep sequencing of a genetically heterogeneous sample: Local haplotype reconstruction and read error correction. *Journal of Computational Biology*, 17(3):417–428, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0164; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0164`.

Zaharias:2022:RED

[ZGW22] Paul Zaharias, Martin Grosshauser, and Tandy Warnow. Re-evaluating deep neural networks for phylogeny estimation: The issue of taxon sampling. *Journal of Computational Biology*, 29(1):74–89, January 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0383;`

https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0383.

Zhu:2007:BHM

[ZH07] Dongxiao Zhu and Alfred O. Hero III. Bayesian hierarchical model for large-scale covariance matrix estimation. *Journal of Computational Biology*, 14(10):1311–1326, December 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.0151; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.0151.

Zhu:2014:ASB

[ZH14] Peican Zhu and Jie Han. Asynchronous stochastic Boolean networks as gene network models. *Journal of Computational Biology*, 21(10):771–783, October 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0057; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0057.

Zhang:1994:EEP

[Zha94] Zheng Zhang. An exponential example for a partial digest mapping algorithm. *Journal of Computational Biology*, 1(3):235–239, January 1994. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.235; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.235.

Zhang:1997:MMS

[Zha97] Louxin Zhang. On a Mirkin–Muchnik–Smith conjecture for comparing molecular phylogenies. *Journal of Computational Biology*, 4(2):177–187, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.177; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.177.

Zhang:2002:AIC

[Zha02] Jian Zhang. Analysis of information content for biological sequences. *Journal of Computational Biology*, 9(3):487–503, June 2002. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.

liebertpub.com/doi/abs/10.1089/106652702760138583; https://www.liebertpub.com/doi/pdf/10.1089/106652702760138583.

Zhang:2016:TBP

[Zha16] Louxin Zhang. On tree-based phylogenetic networks. *Journal of Computational Biology*, 23(7):553–565, July 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0228; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0228.

Zhou:2010:WMF

[Zho10] Qing Zhou. On weight matrix and free energy models for sequence motif detection. *Journal of Computational Biology*, 17(12):1621–1638, December 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0142; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0142.

Zhou:2017:EPR

[Zho17] Jie Zhou. Effect of protein repetitiveness on protein–protein interaction prediction results using support vector machines. *Journal of Computational Biology*, 24(2):183–192, February 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0233; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0233.

Zhu:2005:HTS

[ZHQS05] Dongxiao Zhu, Alfred O. Hero, Zhaohui S. Qin, and Anand Swaroop. High throughput screening of co-expressed gene pairs with controlled false discovery rate (FDR) and minimum acceptable strength (MAS). *Journal of Computational Biology*, 12(7):1029–1045, September 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.1029; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.1029.

Zhao:2005:FSD

[ZHS05] Xiaoyue Zhao, Haiyan Huang, and Terence P. Speed. Finding short DNA motifs using permuted Markov models. *Journal*

of Computational Biology, 12(6):894–906, July 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.894; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.894.

Zhu:2007:PLS

[Zhu07] Binhai Zhu. Protein local structure alignment under the discrete Fréchet distance. *Journal of Computational Biology*, 14(10):1343–1351, December 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0156; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0156.

Zhang:2020:AAK

[ZHY+20] Tongchuan Zhang, Guodong Hu, Yuedong Yang, Jihua Wang, and Yaoqi Zhou. All-atom knowledge-based potential for RNA structure discrimination based on the distance-scaled finite ideal-gas reference state. *Journal of Computational Biology*, 27(6):856–867, June 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0251; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0251.

Zhao:2016:GTM

[ZHZ+16] Shufang Zhao, Yichao He, Xinlu Zhang, Wen Xu, Weili Wu, and Suogang Gao. Group testing with multiple inhibitor sets and error-tolerant and its decoding algorithms. *Journal of Computational Biology*, 23(10):821–829, October 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0202; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0202.

Zhang:2012:VVE

[ZKC12] Jing Zhang, C.-C. Jay Kuo, and Liang Chen. VERSE: a varying effect regression for splicing elements discovery. *Journal of Computational Biology*, 19(6):855–865, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0063; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0063.

Zhai:2010:PDE

[ZKL+10] Zhiyuan Zhai, Shih-Yen Ku, Yihui Luan, Gesine Reinert, Michael S. Waterman, and Fengzhu Sun. The power of detecting enriched patterns: an HMM approach. *Journal of Computational Biology*, 17(4):581–592, April 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0218; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0218`.

Zheng:2021:LDS

[ZKM21] Hongyu Zheng, Carl Kingsford, and Guillaume Marçais. Lower density selection schemes via small universal hitting sets with short remaining path length. *Journal of Computational Biology*, 28(4):395–409, April 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Zheng:2014:JII

[ZKT14] Chaozhi Zheng, Mary K. Kuhner, and Elizabeth A. Thompson. Joint inference of identity by descent along multiple chromosomes from population samples. *Journal of Computational Biology*, 21(3):185–200, March 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0140; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0140`.

Zeil:2017:CAM

[ZKWH17] Stephanie Zeil, Julio Kovacs, Willy Wriggers, and Jing He. Comparing an atomic model or structure to a corresponding cryo-electron microscopy image at the central axis of a helix. *Journal of Computational Biology*, 24(1):52–67, January 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0145; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0145`.

Zhao:2001:RIU

[ZL01] Hongyu Zhao and Feng Liang. On relationship inference using gamete identity by descent data. *Journal of Computational Biology*, 8(2):191–200, April 2001. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.`

liebertpub.com/doi/abs/10.1089/106652701300312940; https://www.liebertpub.com/doi/pdf/10.1089/106652701300312940.

Zhang:2009:GTT

[ZL09] Melvin Zhang and Hon Wai Leong. Gene team tree: a hierarchical representation of gene teams for all gap lengths. *Journal of Computational Biology*, 16(10):1383–1398, October 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0093; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0093.

Zhu:2022:IAM

[ZL22] Mengqiu Zhu and Yinglei Lai. Improvements achieved by multiple imputation for single-cell RNA-Seq data in clustering analysis and differential expression analysis. *Journal of Computational Biology*, 29(7):634–649, July 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0597; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0597.

Zhang:2020:IHG

[ZLB+20] Rupeng Zhang, Leifeng Lv, Wenrui Ban, Xiaoqian Dang, and Chen Zhang. Identification of hub genes in Duchenne muscular dystrophy: Evidence from bioinformatic analysis. *Journal of Computational Biology*, 27(1):1–8, January 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0167; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0167.

Zhang:2020:ISM

[ZLL+20] Shusen Zhang, Yuanyuan Lu, Zhongxin Liu, Xiaopeng Li, Zhihua Wang, and Zhigang Cai. Identification six metabolic genes as potential biomarkers for lung adenocarcinoma. *Journal of Computational Biology*, 27(10):1532–1543, October 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0454; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0454.

Zhu:2022:DRS

[ZLL+22] Xiaoshu Zhu, Jian Li, Yongchang Lin, Liquan Zhao, Jianxin Wang, and Xiaoqing Peng. Dimensionality reduction of single-cell RNA sequencing data by combining entropy and denoising AutoEncoder. *Journal of Computational Biology*, 29 (10):1074–1084, October 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0118; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0118`.

Zheng:2017:ICA

[ZLM+17] Yu Zheng, Xiaoyang Li, Lydia C. Manor, Hongbao Cao, and Qiusheng Chen. An integrative computational approach to evaluate genetic markers for chronic lymphocytic leukemia. *Journal of Computational Biology*, 24(9):942–952, September 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0041; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0041`.

Zhao:2022:PPE

[ZLP22] Jiajia Zhao, Nancy Lynch, and Stephen C. Pratt. The power of population effect in *Temnothorax* ant house-hunting: a computational modeling approach. *Journal of Computational Biology*, 29(4):382–408, April 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0369; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0369`.

Zhang:2020:SBA

[ZLSY20] Guochang Zhang, Juan Li, Hong Sun, and Guanzheng Yang. Screening for the biomarkers associated with myocardial infarction by bioinformatics analysis. *Journal of Computational Biology*, 27(5):779–785, May 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0180; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0180`.

Zhang:2013:CMS

[ZLTS13] ZhiZhuo Zhang, Guoliang Li, Kim-Chuan Toh, and Wing-Kin Sung. 3D chromosome modeling with semi-definite programming and Hi-C data. *Journal of Computational Biology*, 20(11):831–846, November 2013. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0076; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0076`.

Zhang:2025:AAF

[ZLTZ25] Yan Zhang, Xin Liu, Panrui Tang, and Zuping Zhang. AFMDD: Analyzing functional connectivity feature of major depressive disorder by graph neural network-based model. *Journal of Computational Biology*, 32(2):156–163, February 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0505; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0505`.

Zeng:2022:SDT

[ZLU+22] Xiangrui Zeng, Ziqian Lin, Mostofa Rafid Uddin, Bo Zhou, Chao Cheng, Jing Zhang, Zachary Freyberg, and Min Xu. Structure detection in three-dimensional cellular cryoelectron tomograms by reconstructing two-dimensional annotated tilt series. *Journal of Computational Biology*, 29(8):932–941, August 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0606; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0606`.

Zhang:2020:IDE

[ZLW+20] Zhenan Zhang, Yuqin Liu, Wei Wang, Yue Xing, Nanyang Jiang, Hongrui Zhang, Hanwen Zhang, Lei He, Wei Yue, Lianju Jiang, and Kaili Wang. Identification of differentially expressed genes associated with lymph node tuberculosis by the bioinformatic analysis based on a microarray. *Journal of Computational Biology*, 27(1):121–130, January 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0161; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0161`.

Zhang:2021:ICD

[ZlWL21] Wei Zhang, Shu lin Wang, and Yue Liu. Identification of cancer driver modules based on graph clustering from multiomics data. *Journal of Computational Biology*, 28(10):1007–1020, October 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0052; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0052`.

Zhu:2016:MCU

[ZM16] Xiujun (Sylvia) Zhu and Monnie McGee. Metagenomic classification using an abstraction augmented Markov model. *Journal of Computational Biology*, 23(2):111–122, February 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0141; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0141`.

Zabel:2023:BIW

[ZMGN23] Susanne Zabel, Jennifer Müller, Friedrich Götz, and Kay Nieselt. BLASTphylo: an interactive Web tool for taxonomic and phylogenetic analysis of prokaryotic genes. *Journal of Computational Biology*, 30(9):999–1008, September 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0156; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0156`.

Zheng:2022:DRO

[ZMK22] Hongyu Zheng, Cong Ma, and Carl Kingsford. Deriving ranges of optimal estimated transcript expression due to nonidentifiability. *Journal of Computational Biology*, 29(2):121–139, February 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0444; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0444`.

Zheng:2023:CUM

[ZMK23] Hongyu Zheng, Guillaume Marçais, and Carl Kingsford. Creating and using minimizer sketches in computational genomics. *Journal of Computational Biology*, 30(12):1251–1276, December 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/`

abs/10.1089/cmb.2023.0094; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0094.

Zeiser:2007:MHO

[ZML07] Stefan Zeiser, Johannes Müller, and Volkmar Liebscher. Modeling the Hes1 oscillator. *Journal of Computational Biology*, 14(7):984–1000, September 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0029; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0029.

Zhang:2022:MSC

[ZMppVN22] Ran Zhang, Laetitia Meng-papaxanthos, Jean philippe Vert, and William Stafford Noble. Multimodal single-cell translation and alignment with semi-supervised learning. *Journal of Computational Biology*, 29(11):1198–1212, November 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0264; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0264.

Zornig:2015:RSI

[Zör15] Peter Zörnig. Reduced-size integer linear programming models for string selection problems: Application to the farthest string problem. *Journal of Computational Biology*, 22(8):729–742, August 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0265; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0265.

Zhao:2010:EEE

[ZPB+10] Xiaohong Zhao, Lance E. Palmer, Randall Bolanos, Cristian Mircean, Dan Fasulo, and Gayle M. Wittenberg. EDAR: an efficient error detection and removal algorithm for next generation sequencing data. *Journal of Computational Biology*, 17(11):1549–1560, November 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0127; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0127.

Zeng:2018:GWA

[ZPC+18] Lu Zeng, Stephen M. Pederson, Danfeng Cao, Zhipeng Qu, Zhiqiang Hu, David L. Adelson, and Chaochun Wei. Genome-wide analysis of the association of transposable elements with gene regulation suggests that *Alu* elements have the largest overall regulatory impact. *Journal of Computational Biology*, 25(6):551–562, June 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0228; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0228`.

Zhao:2010:PCM

[ZPD+10] Feng Zhao, Jian Peng, Joe Debartolo, Karl F. Freed, Tobin R. Sosnick, and Jinbo Xu. A probabilistic and continuous model of protein conformational space for template-free modeling. *Journal of Computational Biology*, 17(6):783–798, June 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0235; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0235`.

Zhu:2023:GCM

[ZPD+23] Xiaoshu Zhu, Liyuan Pang, Xiaojun Ding, Wei Lan, Shuang Meng, and Xiaoqing Peng. A gene correlation measurement method for spatial transcriptome data based on partitioning and distribution. *Journal of Computational Biology*, 30(8):877–888, August 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0108; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0108`.

Zhang:2024:HAP

[ZPG+24] Lin Zhang, Jigen Peng, Yongbin Ge, Haiyang Li, and Yuchao Tang. High-accuracy positivity-preserving finite difference approximations of the chemotaxis model for tumor invasion. *Journal of Computational Biology*, 31(12):1224–1258, December 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0316; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0316`.

Zhang:1997:ADS

[ZPM97] Zheng Zhang, William R. Pearson, and Webb Miller. Aligning a DNA sequence with a protein sequence. *Journal of Computational Biology*, 4(3):339–349, January 1997. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.1997.4.339; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1997.4.339`.

Zhang:2010:CGA

[ZPX+10] Xiang Zhang, Feng Pan, Yuying Xie, Fei Zou, and Wei Wang. COE: a general approach for efficient genome-wide two-locus epistasis test in disease association study. *Journal of Computational Biology*, 17(3):401–415, March 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0155; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0155`.

Zhao:2020:HEF

[ZQZ20] Teng Zhao, Kun Qian, and Yi Zhang. High expression of *FGF5* is an independent prognostic factor for poor overall survival and relapse-free survival in lung adenocarcinoma. *Journal of Computational Biology*, 27(6):948–957, June 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0241; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0241`.

Zaitlen:2008:SIA

[ZRGHJ08] Noah Zaitlen, Manuel Reyes-Gomez, David Heckerman, and Nebojsa Jojic. Shift-invariant adaptive double threading: Learning MHC II–Peptide binding. *Journal of Computational Biology*, 15(7):927–942, September 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0183; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0183`.

Zhang:1994:CMA

[ZRHM94] Zheng Zhang, Balaji Raghavachari, Ross C. Hardison, and Webb Miller. Chaining multiple-alignment blocks. *Journal of Computational Biology*, 1(3):217–226, January 1994. CODEN

JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.1994.1.217; https://www.liebertpub.com/doi/pdf/10.1089/cmb.1994.1.217.

Zhang:2020:BNB

[ZRNA20] Lixia Zhang, Leonardo O. Rodrigues, Niven R. Narain, and Viatcheslav R. Akmaev. *bAIcis*: a novel Bayesian network structural learning algorithm and its comprehensive performance evaluation against open-source software. *Journal of Computational Biology*, 27(5):698–708, May 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0210; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0210.

Zhai:2012:NCP

[ZRS+12] Zhiyuan Zhai, Gesine Reinert, Kai Song, Michael S. Waterman, Yihui Luan, and Fengzhu Sun. Normal and compound Poisson approximations for pattern occurrences in NGS reads. *Journal of Computational Biology*, 19(6):839–854, June 2012. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2012.0029; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2012.0029.

Zeng:2011:BAD

[ZRZD11] Jianyang Zeng, Kyle E. Roberts, Pei Zhou, and Bruce Randall Donald. A Bayesian approach for determining protein side-chain rotamer conformations using unassigned NOE data. *Journal of Computational Biology*, 18(11):1661–1679, November 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2011.0172; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2011.0172.

Zhao:2011:MFD

[ZS11] Xiaoyan Zhao and Sing-Hoi Sze. Motif finding in DNA sequences based on skipping nonconserved positions in background Markov chains. *Journal of Computational Biology*, 18(5):759–770, May 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2010.0197; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2010.0197.

Zhukova:2014:KBG

[ZS14] Anna Zhukova and David James Sherman. Knowledge-based generalization of metabolic models. *Journal of Computational Biology*, 21(7):534–547, July 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0143; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0143`.

Zeira:2017:SCJ

[ZS17] Ron Zeira and Ron Shamir. Sorting by cuts, joins, and whole chromosome duplications. *Journal of Computational Biology*, 24(2):127–137, February 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2016.0045; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2016.0045`.

Zhu:2024:NKD

[ZS24] Hao Zhu and Donna Slonim. From noise to knowledge: Diffusion probabilistic model-based neural inference of gene regulatory networks. *Journal of Computational Biology*, 31 (11):1087–1103, November 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0607; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0607`.

Zaman:2023:VVR

[ZSB+23] Sumaira Zaman, Samuel Sledzieski, Bonnie Berger, Yi-Chieh Wu, and Mukul S. Bansal. virDTL: Viral recombination analysis through phylogenetic reconciliation and its application to sarbecoviruses and SARS-CoV-2. *Journal of Computational Biology*, 30(1):3–20, January 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0507; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0507`.

Zhang:2009:EHR

[ZSV+09] Yu Zhang, Giltae Song, Tomáš Vinař, Eric D. Green, Adam Siepel, and Webb Miller. Evolutionary history reconstruction for mammalian complex gene clusters. *Journal of Computational*

Biology, 16(8):1051–1070, August 2009. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0040; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0040`.

Zhang:2000:GAA

[ZSWM00] Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller. A greedy algorithm for aligning DNA sequences. *Journal of Computational Biology*, 7(1–2):203–214, February 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Zhao:2022:SRU

[ZTD+22] Minglu Zhao, Ning Tang, Annya L. Dahmani, Yixin Zhu, Federico Rossano, and Tao Gao. Sharing rewards undermines coordinated hunting. *Journal of Computational Biology*, 29(9):1022–1030, September 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0549; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0549`.

Zwolak:2005:PEM

[ZTW05] Jason W. Zwolak, John J. Tyson, and Layne T. Watson. Parameter estimation for a mathematical model of the cell cycle in frog eggs. *Journal of Computational Biology*, 12(1):48–63, February 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.48; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.48`.

Ziv-Ukelson:2010:FAS

[ZUGVWS10] Michal Ziv-Ukelson, Irit Gat-Viks, Ydo Wexler, and Ron Shamir. A faster algorithm for simultaneous alignment and folding of RNA. *Journal of Computational Biology*, 17 (8):1051–1065, August 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0197; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0197`.

Zhang:2003:EPA

[ZW03] Yu Zhang and Michael S. Waterman. An Eulerian path approach to global multiple alignment for DNA sequences. *Journal of Computational Biology*, 10(6):803–819, December 2003. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/106652703322756096; https://www.liebertpub.com/doi/pdf/10.1089/106652703322756096`.

Zhang:2007:NCC

[ZW07] Liqing Zhang and Layne T. Watson. Note on the computation of critical effective population sizes. *Journal of Computational Biology*, 14(7):950–960, September 2007. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2007.0007; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2007.0007`.

Zaborowski:2019:BEM

[ZW19] Rafał Zaborowski and Bartek Wilczyński. BPscore: an effective metric for meaningful comparisons of structural chromosome segmentations. *Journal of Computational Biology*, 26(4):305–314, April 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2018.0162; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2018.0162`.

Zhang:2023:ADW

[ZW23] Shilong Zhang and Sufang Wang. ATAC-DEA: a Web-based ATAC-Seq data differential peak and annotation analysis application. *Journal of Computational Biology*, 30(3):337–345, March 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0033; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0033`.

Zhou:2004:GCB

[ZWD+04] Xiaobo Zhou, Xiaodong Wang, Edward R. Dougherty, Daniel Russ, and Edward Suh. Gene clustering based on cluster-wide mutual information. *Journal of Computational Biology*, 11(1):147–161, January 2004. CODEN JCOBEM. ISSN

1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/106652704773416939; https://www.liebertpub.com/doi/pdf/10.1089/106652704773416939.

Zhu:2025:CHN

[ZWD25] Rong Zhu, Yong Wang, and Ling-Yun Dai. CLHGNNMDA: Hypergraph neural network model enhanced by contrastive learning for miRNA–disease association prediction. *Journal of Computational Biology*, 32(1):47–63, January 2025. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2024.0720; https://www.liebertpub.com/doi/reader/10.1089/cmb.2024.0720.

Zhao:2018:DPE

[ZWJ18] Jian Zhao, Jiasong Wang, and Hongmei Jiang. Detecting periodicities in eukaryotic genomes by Ramanujan Fourier transform. *Journal of Computational Biology*, 25(9):963–975, September 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0252; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0252.

Zhao:2020:CND

[ZWK+20] Jingwei Zhao, Le Wang, Daliang Kong, Guozhang Hu, and Bo Wei. Construction of novel DNA methylation-based prognostic model to predict survival in glioblastoma. *Journal of Computational Biology*, 27(5):718–728, May 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0125; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0125.

Zhang:2019:IAG

[ZWQ19] Yudong Zhang, Wenxiang Wu, and Hao Qu. Integrated analysis of the gene expression changes during colorectal cancer progression by bioinformatic methods. *Journal of Computational Biology*, 26(10):1168–1176, October 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0056; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0056.

Zhang:2005:BNI

[ZWSF05] Dabao Zhang, Martin T. Wells, Christine D. Smart, and William E. Fry. Bayesian normalization and identification for differential gene expression data. *Journal of Computational Biology*, 12(4):391–406, May 2005. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2005.12.391; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2005.12.391`.

Zhao:2018:SAA

[ZWT18] Yongan Zhao, Xiaofeng Wang, and Haixu Tang. A secure alignment algorithm for mapping short reads to human genome. *Journal of Computational Biology*, 25(6):529–540, June 2018. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0094; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0094`.

Zhang:2017:OOM

[ZWY+17] Li Zhang, Han Wang, Lun Yan, Lingtao Su, and Dong Xu. OMPcontact: an outer membrane protein inter-barrel residue contact prediction method. *Journal of Computational Biology*, 24(3):217–228, March 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0236; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0236`.

Zhou:2016:CPD

[ZWZ16] Yichao Zhou, Yuexin Wu, and Jianyang Zeng. Computational protein design using AND/OR branch-and-bound search. *Journal of Computational Biology*, 23(6):439–451, June 2016. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0212; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0212`.

Zhao:2021:IDE

[ZXZ21] Enfa Zhao, Hang Xie, and Yushun Zhang. Identification of differentially expressed genes associated with idiopathic pulmonary arterial hypertension by integrated bioinformatics approaches. *Journal of Computational Biology*, 28(1):79–88, Jan-

uary 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0433; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0433.

Zou:2023:ILO

[ZY23] Hongliang Zou and Wanting Yu. Integrating low-order and high-order correlation information for identifying phage virion proteins. *Journal of Computational Biology*, 30(10):1131–1143, October 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2022.0237; https://www.liebertpub.com/doi/reader/10.1089/cmb.2022.0237.

Zhihua:2004:TQP

[ZYB+04] Lin Zhihua, Wu Yuzhang, Zhu Bo, Ni Bing, and Wang Li. Toward the quantitative prediction of T-cell epitopes: QSAR studies on peptides having affinity with the class I MHC molecular HLA-A*0201. *Journal of Computational Biology*, 11(4):683–694, August 2004. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2004.11.683; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2004.11.683.

Zheng:2019:SSA

[ZYD+19] Shunxin Zheng, Liuhong Yang, Yisong Dai, Lifang Jiang, Yi Wei, Hongwei Wen, and Yingfang Xu. Screening and survival analysis of hub genes in gastric cancer based on bioinformatics. *Journal of Computational Biology*, 26(11):1316–1325, November 2019. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0119; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0119.

Zhu:2021:PVR

[ZYD21] Lingzhi Zhu, Cheng Yan, and Guihua Duan. Prediction of virus–receptor interactions based on improving similarities. *Journal of Computational Biology*, 28(7):650–659, July 2021. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2020.0544; https://www.liebertpub.com/doi/reader/10.1089/cmb.2020.0544.

Zhao:2020:MLP

[ZYH20] Jing Zhao, Linlin Yin, and Ling He. The MicroRNA landscapes profiling reveals potential signatures of necrotizing enterocolitis in infants. *Journal of Computational Biology*, 27(1):30–39, January 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0183; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0183`.

Zhang:2010:MIS

[ZZ10] Haiying Zhang and Bing Zhou. On the maximal interval subgraph of a tree. *Journal of Computational Biology*, 17 (10):1425–1433, October 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0039; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0039`.

Zheng:2014:DCR

[ZZ14a] Yu Zheng and Louxin Zhang. Are the duplication cost and Robinson–Foulds distance equivalent? *Journal of Computational Biology*, 21(8):578–590, August 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0021; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0021`.

Zhong:2014:SFA

[ZZ14b] Cuncong Zhong and Shaojie Zhang. Simultaneous folding of alternative RNA structures with mutual constraints: an application to next-generation sequencing-based RNA structure probing. *Journal of Computational Biology*, 21(8):609–621, August 2014. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2013.0044; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2013.0044`.

Zitnik:2015:DIE

[ŽZ15] Marinka Žitnik and Blaž Zupan. Data imputation in epistatic MAPs by network-guided matrix completion. *Journal of Computational Biology*, 22(6):595–608, June 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2014.0158; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2014.0158.

Zhang:2020:ISA

[ZZ20] Weina Zhang and Yilun Zhang. Integrated survival analysis of mRNA and microRNA signature of patients with breast cancer based on Cox model. *Journal of Computational Biology*, 27(9):1486–1494, September 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0495; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0495.

Zhang:2024:NDA

[ZZC+24] Xin Zhang, Liangwei Zhao, Ziyi Chai, Hao Wu, Wei Yang, Chen Li, Yu Jiang, and Quanzhong Liu. NPI-DCGNN: an accurate tool for identifying ncRNA-Protein interactions using a dual-channel graph neural network. *Journal of Computational Biology*, 31(8):742–756, August 2024. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0449; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0449.

Zhang:2011:PIB

[ZZHL11] Shu-Bo Zhang, Song-Yu Zhou, Jian-Guo He, and Jian-Huang Lai. Phylogeny inference based on spectral graph clustering. *Journal of Computational Biology*, 18(4):627–637, April 2011. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0028; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0028.

Zien:2000:SIA

[ZZL00] Alexander Zien, Ralf Zimmer, and Thomas Lengauer. A simple iterative approach to parameter optimization. *Journal of Computational Biology*, 7(3–4):483–501, August 2000. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic).

Zhou:2017:GRN

[ZZL+17] Yan Zhou, Baoxue Zhang, Gaorong Li, Tiejun Tong, and Xiang Wan. GD-RDA: a new regularized discriminant analy-

sis for high-dimensional data. *Journal of Computational Biology*, 24(11):1099–1111, November 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0029; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0029`.

Zhang:2022:ULB

[ZZL22] Emily Zhang, Jiajia Zhao, and Nancy Lynch. An upper and lower bound for the convergence time of house-hunting in *Temnothorax* ant colonies. *Journal of Computational Biology*, 29(4):344–357, April 2022. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2021.0364; https://www.liebertpub.com/doi/reader/10.1089/cmb.2021.0364`.

Zhang:2023:PPI

[ZZL23a] Chihao Zhang, Shihua Zhang, and Jingyi Jessica Li. A Python package `itca` for information-theoretic classification accuracy: a criterion that guides data-driven combination of ambiguous outcome labels in multiclass classification. *Journal of Computational Biology*, 30(11):1246–1249, November 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0191; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0191`.

Zhou:2023:PCI

[ZZL+23b] Peixuan Zhou, Yijia Zhang, Zeqian Li, Kuo Pang, and Di Zhao. Protein complex identification based on heterogeneous protein information network. *Journal of Computational Biology*, 30(9):985–998, September 2023. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2023.0081; https://www.liebertpub.com/doi/reader/10.1089/cmb.2023.0081`.

Zhang:2010:PIV

[ZZN10] Xinan Zhang, Yingdong Zhao, and Avidan U. Neumann. Partial immunity and vaccination for influenza. *Journal of Computational Biology*, 17(12):1689–1696, December 2010. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666

(electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2009.0003; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2009.0003.

Zhou:2015:DDA

[ZZNM15] Ping Zhou, Ning Zhang, Ruth Nussinov, and Buyong Ma. Defining the domain arrangement of the mammalian target of Rapamycin complex component Rictor protein. *Journal of Computational Biology*, 22(9):876–886, September 2015. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2015.0103; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2015.0103.

Zheng:2008:DWG

[ZZS08] Chunfang Zheng, Qian Zhu, and David Sankoff. Descendants of whole genome duplication within gene order phylogeny. *Journal of Computational Biology*, 15(8):947–964, October 2008. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2008.0118; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2008.0118.

Zeira:2017:LTA

[ZZS17] Ron Zeira, Meirav Zehavi, and Ron Shamir. A linear-time algorithm for the copy number transformation problem. *Journal of Computational Biology*, 24(12):1179–1194, December 2017. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2017.0060; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2017.0060.

Zilberstein:2006:HTA

[ZZUPY06] Chaya Ben-Zaken Zilberstein, Michal Ziv-Ukelson, Ron Y. Pinter, and Zohar Yakhini. A high-throughput approach for associating MicroRNAs with their activity conditions. *Journal of Computational Biology*, 13(2):245–266, March 2006. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL https://www.liebertpub.com/doi/abs/10.1089/cmb.2006.13.245; https://www.liebertpub.com/doi/pdf/10.1089/cmb.2006.13.245.

Zoller:2020:NPI

[ZZZU20] Roni Zoller, Meirav Zehavi, and Michal Ziv-Ukelson. A new paradigm for identifying reconciliation-scenario altering mutations conferring environmental adaptation. *Journal of Computational Biology*, 27(11):1561–1580, November 2020. CODEN JCOBEM. ISSN 1066-5277 (print), 1557-8666 (electronic). URL `https://www.liebertpub.com/doi/abs/10.1089/cmb.2019.0472`; `https://www.liebertpub.com/doi/pdf/10.1089/cmb.2019.0472`.