References

[1] John Aach and George M. Church. Aligning gene expression time series with time warping algorithms. *Bioinformatics*, 17(6):495–508, 2001.

[2] Gonçalo R. Abecasis, Stacey S. Cherny, W.O.C. Cookson, and Lon R. Cardon. Grr: Graphical representation of relationship errors. *Bioinformatics*, 17(8):742–743, 2001.

[3] Frédéric Achard, Guy Vaysseix, and Emmanuel Barillot. Xml, bioinformatics and data integration. *Bioinformatics*, 17(2):115–125, 2001.

[4] Ezekiel F. Adebiyi, Tao Jiang, and Michael Kaufmann. An efficient algorithm for finding short approximate non-tandem repeats. *Bioinformatics*, 17(S1):5–12, 2001.

[5] P.S. Umesh Adiga, A. Bhomra, M.G. Turri, A. Nicod, S.R. Datta, P. Jeavons, R. Mott, and J. Flint. Automatic analysis of agarose gel images. *Bioinformatics*, 17(11):1084–1089, 2001.

[6] D.A. Afonnikov, D.Yu. Oshchepkov, and N.A. Kolchanov. Detection of conserved physico-chemical characteristics of proteins by analyzing clusters of positions with co-ordinated substitutions. *Bioinformatics*, 17(11):1035–1046, 2001.

[7] Jonas S. Almeida, João A. Carriço, António Maretzek, Peter A. Noble, and Madilyn Fletcher. Analysis of genomic sequences by chaos game representation. *Bioinformatics*, 17(5):429–437, 2001.

[8] Cécile André, Pierre Vincens, Jean-François Boisvieux, and Serge Hazout. Mosaic: Segmenting multiple aligned dna sequences. *Bioinformatics*, 17(2):196–197, 2001.

[9] Gordana Apic, Julian Gough, and Sarah A. Teichmann. An insight into domain combinations. *Bioinformatics*, 17(S1):83–89, 2001.

[10] Rolf Apweiler, Paul Kersey, Viv Junker, and Amos Bairoch. Technical comment to "database verification studies of swiss-prot and genbank" by karp et al. *Bioinformatics*, 17(6):533–534, 2001.

[11] Abdullah N. Arslan, Ömer Egecioglu, and Pavel A. Pevzner. A new approach to sequence comparison: Normalized sequence alignment. *Bioinformatics*, 17(4):327–337, 2001.

[12] Prasith Baccam, Robert J. Thompson, Olivier Fedrigo, Susan Carpenter, and James L. Cornette. Paq: Partition analysis of quasispecies. *Bioinformatics*, 17(1):16–22, 2001.

[13] Vineet Bafna and Nathan Edwards. Scope: A probabilistic model for scoring tandem mass spectra against a peptide database. *Bioinformatics*, 17(S1):13–21, 2001.

[14] Pierre-François Baisnée, Pierre Baldi, Søren Brunak, and Anders Gorm Pedersen. Flexibility of the genetic code with respect to dna structure. *Bioinformatics*, 17(3):237–248, 2001.

[15] Pierre Baldi and Anthony D. Long. A bayesian framework for the analysis of microarray expression data: Regularized t -test and statistical inferences of gene changes. *Bioinformatics*, 17(6):509–519, 2001.

[16] Ziv Bar-Joseph, David K. Gifford, and Tommi S. Jaakkola. Fast optimal leaf ordering for hierarchical clustering. *Bioinformatics*, 17(S1):22–29, 2001.

[17] Malay Kumar Basu. Sewer: A customizable and integrated dynamic html interface to bioinformatics services. *Bioinformatics*, 17(6):577–578, 2001.

[18] Michael Baudis and Michael L. Cleary. Progenetix.net: An online repository for molecular cytogenetic aberration data. *Bioinformatics*, 17(12):1228–1229, 2001.

[19] Moritz Y. Becker and Isabel Rojas. A graph layout algorithm for drawing metabolic pathways. *Bioinformatics*, 17(5):461–467, 2001.

[20] Gill Bejerano, Yevgeny Seldin, Hanah Margalit, and Naftali Tishby. Markovian domain fingerprinting: Statistical segmentation of protein sequences. *Bioinformatics*, 17(10):927–934, 2001.

[21] Gill Bejerano and Golan Yona. Variations on probabilistic suffix trees: Statistical modeling and prediction of protein families. *Bioinformatics*, 17(1):23–43, 2001.

[22] Mathieu Blanchette and Saurabh Sinha. Separating real motifs from their artifacts. *Bioinformatics*, 17(S1):30–38, 2001.

[23] J. Blazewicz, P. Formanowicz, M. Kasprzak, M. Jaroszewski, and W.T. Markiewicz. Construction of dna restriction maps based on a simplified experiment. *Bioinformatics*, 17(5):398–404, 2001.

[24] Joel R. Bock and David A. Gough. Predicting protein-protein interactions from primary structure. *Bioinformatics*, 17(5):455–460, 2001.

[25] Michael V. Boland and Robert F. Murphy. A neural network classifier capable of recognizing the patterns of all major subcellular structures in fluorescence microscope images of hela cells. *Bioinformatics*, 17(12):1213–1223, 2001.

[26] Eva Bolten, Alexander Schliep, Sebastian Schneckener, Dietmar Schomburg, and Rainer Schrader. Clustering protein sequences — structure prediction by transitive homology. *Bioinformatics*, 17(10):935–941, 2001.

[27] James Borneman, Marek Chrobak, Gianluca Della Vedova, Andres Figueroa, and Tao Jiang. Probe selection algorithms with applications in the analysis of microbial communities. *Bioinformatics*, 17(S1):39–48, 2001.

[28] Mark Borodovsky, Eugene Koonin, Chris Burge, Jim Fickett, John Logsdon, Andrej Sali, Gary Stormo, and Igor Zhulin. The third georgia tech-emory international conference on bioinformatics: In silico biology; bioinformatics after human genome (november 15-18, 2001, atlanta, georgia, usa). *Bioinformatics*, 17(10):859–861, 2001.

[29] S. Bortoluzzi, F. d'Alessi, C. Romualdi, and G.A. Danieli. Differential expression of genes coding for ribosomal proteins in different human tissues. *Bioinformatics*, 17(12):1152–1157, 2001.

[30] Alvis Brazma. On the importance of standardisation in life sciences. *Bioinformatics*, 17(2):113–114, 2001.

[31] Fiona S.L. Brinkman, Ivan Wan, Robert E.W. Hancock, Ann M. Rose, and Steven J. Jones. Phyloblast: Facilitating phylogenetic analysis of blast results. *Bioinformatics*, 17(4):385–387, 2001.

[32] Jeremy Buhler. Efficient large-scale sequence comparison by locality-sensitive hashing. *Bioinformatics*, 17(5):419–428, 2001.

[33] Janusz M. Bujnicki, Arne Elofsson, Daniel Fischer, and Leszek Rychlewski. Structure prediction meta server. *Bioinformatics*, 17(8):750–751, 2001.

[34] Yury V. Bukhman and Jeffrey Skolnick. Biomolquest: Integrated database-based retrieval of protein structural and functional information. *Bioinformatics*, 17(5):468–478, 2001. see Erratum in Bioinformatics, Vol. 17, 2001, No. 8, 759-759.

[35] Y.V. Bukhman and J. Skolnick. Erratum to "biomolquest: Integrated database-based retrieval of protein structural and functional information". *Bioinformatics*, 17(8):759–759, 2001. Originally in Bioinformatics, Vol. 17, 2001, No. 5, 468-478.

[36] Pierre R. Bushel, Hisham Hamadeh, Lee Bennett, Stella Sieber, Karla Martin, Emile F. Nuwaysir, Kate Johnson, Kelli Reynolds, Richard S. Paules, and Cynthia A. Afshari. Maps: A microarray project system for gene expression experiment information and data validation. *Bioinformatics*, 17(6):564–565, 2001.

[37] Man-Suen Chan, Martin C.J. Maiden, and Brian G. Spratt. Database-driven multi locus sequence typing (mlst) of bacterial pathogens. *Bioinformatics*, 17(11):1077–1083, 2001.

[38] Tony Y.T. Chan. Unsupervised classification of noisy chromosomes. *Bioinformatics*, 17(5):438–444, 2001.

[39] Derek Y. Chiang, Patrick O. Brown, and Michael B. Eisen. Visualizing associations between genome sequences and gene expression data using genome-mean expression profiles. *Bioinformatics*, 17(S1):49–55, 2001.

[40] Hui-Hsien Chou and Michael H. Holmes. Dna sequence quality trimming and vector removal. *Bioinformatics*, 17(12):1093–1104, 2001.

[41] John S. Chuang and Dan Roth. Gene recognition based on dag shortest paths. *Bioinformatics*, 17(S1):56–64, 2001.

[42] Avril Coghlan, Dónall A. Mac Dónaill, and Nigel H. Buttimore. Representation of amino acids as five-bit or three-bit patterns for filtering protein databases. *Bioinformatics*, 17(8):676–685, 2001.

[43] Jacques Colinge and Georg Feger. Detecting the impact of sequencing errors on sage data. *Bioinformatics*, 17(9):840–842, 2001.

[44] Richard M.R. Coulson, Anton J. Enright, and Christos A. Ouzounis. Transcription-associated protein families are primarily taxon-specific. *Bioinformatics*, 17(1):95–97, 2001.

[45] David G. Cox and Federico Canzian. Genotype transposer: Automated genotype manipulation for linkage disequilibrium analysis. *Bioinformatics*, 17(8):738–739, 2001.

[46] P.I.W. de Bakker, A. Bateman, D.F. Burke, R.N. Miguel, K. Mizuguchi, J. Shi, H. Shirai, and T.L. Blundell. Homstrad: Adding sequence information to structure-based alignments of homologous protein families. *Bioinformatics*, 17(8):748–749, 2001.

[47] Charlotte M. Deane, Quentin Kaas, and Tom L. Blundell. Score: Predicting the core of protein models. *Bioinformatics*, 17(6):541–550, 2001.

[48] Chris H.Q. Ding and Inna Dubchak. Multi-class protein fold recognition using support vector machines and neural networks. *Bioinformatics*, 17(4):349–358, 2001.

[49] Zsuzsanna Dosztányi and Andrew E. Torda. Amino acid similarity matrices based on force fields. *Bioinformatics*, 17(8):686–699, 2001.

[50] Dominique Douguet and Gilles Labesse. Easier threading through web-based comparisons and cross-validations. *Bioinformatics*, 17(8):752–753, 2001.

[51] Alexei Drummond and Korbinian Strimmer. Pal: An object-oriented programming library for molecular evolution and phylogenetics. *Bioinformatics*, 17(7):662–663, 2001.

[52] B. Dysvik and I. Jonassen. J-express: Exploring gene expression data using java. *Bioinformatics*, 17(4):369–370, 2001.

[53] Barbara A. Eckman, Anthony S. Kosky, Laroco, and Jr. Leonardo A. Extending traditional query-based integration approaches for functional characterization of post-genomic data. *Bioinformatics*, 17(7):587–601, 2001.

[54] Anton J. Enright and Christos A. Ouzounis. Biolayout — an automatic graph layout algorithm for similarity visualization. *Bioinformatics*, 17(9):853–854, 2001.

[55] Eleazar Eskin, William N. Grundy, and Yoram Singer. Using mixtures of common ancestors for estimating the probabilities of discrete events in biological sequences. *Bioinformatics*, 17(1):65–73, 2001.

[56] Rob M. Ewing and J. Michael Cherry. Visualization of expression clusters using sammon's non-linear mapping. *Bioinformatics*, 17(7):658–659, 2001.

[57] Eran Eyal, Rafael Najmanovich, Vladimir Sobolev, and Marvin Edelman. Mutaprot: A web interface for structural analysis of point mutations. *Bioinformatics*, 17(4):381–382, 2001.

[58] Volker A. Eyrich, Marc A. Martí-Renom, Dariusz Przybylski, Mallur S. Madhusudhan, András Fiser, Florencio Pazos, Alfonso Valencia, Andrej Sali, and Burkhard Rost. Eva: Continuous automatic evaluation of protein structure prediction servers. *Bioinformatics*, 17(12):1242–1243, 2001.

[59] Rosel Kretschmer-Kazemi Far, Wolfgang Nedbal, and Georg Sczakiel. Concepts to automate the theoretical design of effective antisense oligonucleotides. *Bioinformatics*, 17(11):1058–1061, 2001.

[60] Piero Fariselli and Rita Casadio. Prediction of disulfide connectivity in proteins. *Bioinformatics*, 17(10):957–964, 2001.

[61] Piero Fariselli and Rita Casadio. Rcnpred: Prediction of the residue coordination numbers in proteins. *Bioinformatics*, 17(2):202–204, 2001.

[62] Carol Friedman, Pauline Kra, Hong Yu, Michael Krauthammer, and Andrey Rzetsky. Genies: A natural-languange processing system for the extraction of molecular pathways from journal articles. *Bioinformatics*, 17(S1):74–82, 2001.

[63] Dmitrij Frishman, Kaj Albermann, Jean Hani, Klaus Heumann, Agnes Metanomski, Alfred Zollner, and Hans-Werner Mewes. Functional and structural genomics using pedant. *Bioinformatics*, 17(1):44–57, 2001.

[64] Martin C. Frith, Ulla Hansen, and Zhiping Weng. Detection of cis - element clusters in higher eukaryotic dna. *Bioinformatics*, 17(10):878–889, 2001.

[65] Georg Fuellen, Johann-Wolfgang Wägele, and Robert Giegerich. Minimum conflict: A divide-and-conquer approach to phylogeny estimation. *Bioinformatics*, 17(12):1168–1178, 2001.

[66] Ken-ichiro Fukuda and Toshihisa Takagi. Knowledge representation of signal transduction pathways. *Bioinformatics*, 17(9):829–837, 2001.

[67] Robert Garian. Prediction of quaternary structure from primary structure. *Bioinformatics*, 17(6):551–556, 2001.

[68] Brian Gaschen, Carla Kuiken, Bette Korber, and Brian Foley. Retrieval and on-the-fly alignment of sequence fragments from the hiv database. *Bioinformatics*, 17(5):415–418, 2001.

[69] Birgitta Geier, Gabi Kastenmüller, Matthias Fellenberg, Hans-Werner Mewes, and Burkhard Morgenstern. The hib database of annotated unigene clusters. *Bioinformatics*, 17(6):571–572, 2001.

[70] Christoph Gille and Cornelius Frömmel. Strap: Editor for structural alignments of proteins. *Bioinformatics*, 17(4):377–378, 2001.

[71] Leo Goodstadt and Chris P. Ponting. Chroma: Consensus-based colouring of multiple alignments for publication. *Bioinformatics*, 17(9):845–846, 2001.

[72] J. Gorodkin, C. Zwieb, and B. Knudsen. Semi-automated update and cleanup of structural rna alignment databases. *Bioinformatics*, 17(7):642–645, 2001.

[73] Debraj GuhaThakurta and Gary D. Stormo. Identifying target sites for cooperatively binding factors. *Bioinformatics*, 17(7):608–621, 2001.

[74] David Hall, Suchendra M. Bhandarkar, Jonathan Arnold, and Tongzhang Jiang. Physical mapping with automatic capture of hybridization data. *Bioinformatics*, 17(3):205–213, 2001.

[75] Jochen Hampe, Andreas Wollstein, Timothy Lu, Hans-Jürgen Frevel, Marcus Will, Carl Manaster, and Stefan Schreiber. An integrated system for high throughput taqmantexttrademark based snp genotyping. *Bioinformatics*, 17(7):654–655, 2001.

[76] Sridhar Hannenhalli and Samuel Levy. Promoter prediction in the human genome. *Bioinformatics*, 17(S1):90–96, 2001.

[77] Eric Harley, Anthony Bonner, and Nathan Goodman. Uniform integration of genome mapping data using intersection graphs. *Bioinformatics*, 17(6):487–494, 2001.

[78] Artemis G. Hatzigeorgiou, Petko Fiziev, and Martin Reczko. Diana-est: A statistical analysis. *Bioinformatics*, 17(10):913–919, 2001.

[79] Vasileios Hatzivassiloglou, Pablo A. Duboué, and Andrey Rzhetsky. Disambiguating proteins, genes, and rna in text: A machine learning approach. *Bioinformatics*, 17(S1):97–106, 2001.

[80] Yang He, Xiangming Xu, Kenneth R. Tobutt, and Martin S. Ridout. Polylink: To support two-point linkage analysis in autotetraploids. *Bioinformatics*, 17(8):740–741, 2001.

[81] Andreas Heger and Liisa Holm. Picasso: Generating a covering set of protein family profiles. *Bioinformatics*, 17(3):272–279, 2001.

[82] C. Helma, R.D. King, S. Kramer, and A. Srinivasan. The predictive toxicology challenge 2000-2001. *Bioinformatics*, 17(1):107–108, 2001.

[83] Javier Herrero, Alfonso Valencia, and Joaquín Dopazo. A hierarchical unsupervised growing neural network for clustering gene expression patterns. *Bioinformatics*, 17(2):126–136, 2001.

[84] Win Hide. Exscript: An "ex"-centric approach to the description of transcript diversity. *Bioinformatics*, 17(6):485–486, 2001.

[85] Mark Hoebeke, Hélène Chiapello, Philippe Noirot, and Philippe Bessières. Spid: A subtilis protein interaction database. *Bioinformatics*, 17(12):1209–1212, 2001.

[86] Ian Holmes and William J. Bruno. Evolutionary hmms: A bayesian approach to multiple alignment. *Bioinformatics*, 17(9):803–820, 2001.

[87] Katsuhisa Horimoto, Satoshi Fukuchi, and Kentaro Mori. Comprehensive comparison between locations of orthologous genes on archaeal and bacterial genomes. *Bioinformatics*, 17(9):791–802, 2001.

[88] Katsuhisa Horimoto and Hiroyuki Toh. Statistical estimation of cluster boundaries in gene expression profile data. *Bioinformatics*, 17(12):1143–1151, 2001.

[89] Sujun Hua and Zhirong Sun. Support vector machine approach for protein subcellular localization prediction. *Bioinformatics*, 17(8):721–728, 2001.

[90] John P. Huelsenbeck and Fredrik Ronquist. Mrbayes: Bayesian inference of phylogenetic trees. *Bioinformatics*, 17(8):754–755, 2001.

[91] Hubert Hug and Rainer Schuler. Strategies for the development of a peptide computer. *Bioinformatics*, 17(4):364–368, 2001.

[92] Lawrence Hunter, Ronald C. Taylor, Sonia M. Leach, and Richard Simon. Gest: A gene expression search tool based on a novel bayesian similarity metric. *Bioinformatics*, 17(S1):115–122, 2001.

[93] Dirk Husmeier and Frank Wright. Probabilistic devergence measures for detecting interspecies recombination. *Bioinformatics*, 17(S1):123–131, 2001.

[94] Daniel H. Huson, Knut Reinert, Saul A. Kravitz, Karin A. Remington, Art L. Delcher, Ian M. Dew, Mike Flanigan, Aaron L. Halpern, Zhongwu Lai, Clark M. Mobarry, Granger G. Sutton, and Eugene W. Myers. Design of a compartmentalized shotgun assembler for the human genome. *Bioinformatics*, 17(S1):132–139, 2001.

[95] Kazuhisa Ichikawa. A-cell: Graphical user interface for the construction of biochemical reaction models. *Bioinformatics*, 17(5):483–484, 2001.

[96] Ingrid B. Jakobsen, Jennifer A. Saleeba, Michael Poidinger, and Timothy G. Littlejohn. Treegenebrowser: Phylogenetic data mining of gene sequences from public databases. *Bioinformatics*, 17(6):535–540, 2001.

[97] Neema Jamshidi, Jeremy S. Edwards, Tom Fahland, George M. Church, and Bernhard O. Palsson. Dynamic simulation of the human red blood cell metabolic network. *Bioinformatics*, 17(3):286–287, 2001.

[98] Kimberly F. Johnson and Simon M. Lin. Critical assessment of microarray data analysis: The 2001 challenge. *Bioinformatics*, 17(9):857–858, 2001.

[99] K.A. Jolley, E.J. Feil, M.-S. Chan, and M.C.J. Maiden. Sequence type analysis and recombinational tests (start). *Bioinformatics*, 17(12):1230–1231, 2001.

[100] I. King Jordan, G. Reid Bishop, and Daniel S. Gonzalez. Sequence and structural aspects of functional diversification in class i α-mannosidase evolution. *Bioinformatics*, 17(10):965–976, 2001.

[101] Thomas Junier, Marco Pagni, and Philipp Bucher. mmsearch: A motif arrangement language and search program. *Bioinformatics*, 17(12):1234–1235, 2001.

[102] Thomas Kämpke, Markus Kieninger, and Michael Mecklenburg. Efficient primer design algorithms. *Bioinformatics*, 17(3):214–225, 2001.

[103] Peter D. Karp, Suzanne Paley, and Jingchun Zhu. Database verification studies of swiss-prot and genbank. *Bioinformatics*, 17(6):526–532, 2001.

[104] Kevin Karplus and Birong Hu. Evaluation of protein multiple alignments by sam-t99 using the balibase multiple alignment test set. *Bioinformatics*, 17(8):713–720, 2001.

[105] Xiayi Ke, Andrew Collins, and Shu Ye. Pira pcr designer for restriction analysis of single nucleotide polymorphisms. *Bioinformatics*, 17(9):838–839, 2001.

[106] Xiayi Ke, William Tapper, and Andrew Collins. Ldb2000: Sequence-based integrated maps of the human genome. *Bioinformatics*, 17(7):581–586, 2001.

[107] Szymon M. Kielbasa, Jan O. Korbel, Dieter Beule, Johannes Schuchhardt, and Hanspeter Herzel. Combining frequency and positional information to predict transcription factor binding sites. *Bioinformatics*, 17(11):1019–1026, 2001.

[108] Ross D. King, Andreas Karwath, Amanda Clare, and Luc Dehaspe. The utility of different representations of protein sequence for predicting functional class. *Bioinformatics*, 17(5):445–454, 2001.

[109] Nikolay Kolchanov and Charlie Hodgman. The 2nd international conference on the bioinformatics of genome regulation and structure (bgrs-2000), novosibirsk, august 2000. *Bioinformatics*, 17(11):997–997, 2001.

[110] Ian Korf, Paul Flicek, Daniel Duan, and Michael R. Brent. Integrating genomic homology into gene structure prediction. *Bioinformatics*, 17(S1):140–148, 2001.

[111] Frank Kose, Wolfram Weckwerth, Thomas Linke, and Oliver Fiehn. Visualizing plant metabolomic correlation networks using clique-metabolite matrices. *Bioinformatics*, 17(12):1198–1208, 2001.

[112] Jeanne Kowalski. A non-parametric approach to translating gene region heterogeneity associated with phenotype into location heterogeneity. *Bioinformatics*, 17(9):775–790, 2001.

[113] Eileen Kraemer, Jian Wang, Jinhua Guo, Samuel Hopkins, and Jonathan Arnold. An analysis of gene-finding programs for neurospora crassa. *Bioinformatics*, 17(10):901–912, 2001.

[114] Ernst Kretschmann, Wolfgang Fleischmann, and Rolf Apweiler. Automatic rule generation for protein annotation with the c4.5 data mining algorithm applied on swiss-prot. *Bioinformatics*, 17(10):920–926, 2001.

[115] Sudhir Kumar, Koichiro Tamura, Ingrid B. Jakobsen, and Masatoshi Nei. Mega2: Molecular evolutionary genetics analysis software. *Bioinformatics*, 17(12):1244–1245, 2001.

[116] Salvatore Lanzavecchia, Francesca Cantele, and Pier Luigi Bellon. Alignment of 3d structures of macromolecular assemblies. *Bioinformatics*, 17(1):58–62, 2001.

[117] Michael Lappe, Jong Park, Oliver Niggemann, and Liisa Holm. Generating protein interaction maps from incomplete data: Application to fold assignment. *Bioinformatics*, 17(S1):149–156, 2001.

[118] Nicolas Le Novère. Melting, computing the melting temperature of nucleic acid duplex. *Bioinformatics*, 17(12):1226–1227, 2001.

[119] Nicolas Le Novère and Thomas Simon Shimizu. Stochsim: Modelling of stochastic biomolecular processes. *Bioinformatics*, 17(6):575–576, 2001.

[120] J.L. Lessem and S.S. Cherny. Defries-fulker multiple regression analysis of sibship qtl data: A sas® macro. *Bioinformatics*, 17(4):371–372, 2001. see Erratum in Bioinformatics, Vol. 18, 2002, No. 6, 896-896.

[121] Catherine Letondal. A web interface generator for molecular biology programs in unix. *Bioinformatics*, 17(1):73–82, 2001.

[122] Siu-wai Leung, Chris Mellish, and Dave Robertson. Basic gene grammars and dna-chartparser for language processing of escherichia coli promoter dna sequences. *Bioinformatics*, 17(3):226–236, 2001.

[123] Victor G. Levitsky, Olga A. Podkolodnaya, Nikolay A. Kolchanov, and Nikolay L. Podkolodny. Nucleosome formation potential of eukaryotic dna: Calculation and promoters analysis. *Bioinformatics*, 17(11):998–1010, 2001.

[124] Victor G. Levitsky, Olga A. Podkolodnaya, Nikolay A. Kolchanov, and Nikolay L. Podkolodny. Nucleosome formation potential of exons, introns, and alu repeats. *Bioinformatics*, 17(11):1062–1064, 2001.

[125] Samuel Levy, Sridhar Hannenhalli, and Christopher Workman. Enrichment of regulatory signals in conserved non-coding genomic sequence. *Bioinformatics*, 17(10):871–877, 2001.

[126] M. Lexa, J. Horak, and B. Brzobohaty. Virtual pcr. *Bioinformatics*, 17(2):192–193, 2001.

[127] Fugen Li and Gary D. Stormo. Selection of optimal dna oligos for gene expression arrays. *Bioinformatics*, 17(11):1067–1076, 2001.

[128] Leping Li, Clarice R. Weinberg, Thomas A. Darden, and Lee G. Pedersen. Gene selection for sample classification based on gene expression data: Study of sensitivity to choice of parameters of the ga/knn method. *Bioinformatics*, 17(12):1131–1142, 2001.

[129] Ming Li, Jonathan H. Badger, Xin Chen, Sam Kwong, Paul Kearney, and Haoyong Zhang. An information-based sequence distance and its application to whole mitochondrial genome phylogeny. *Bioinformatics*, 17(2):149–154, 2001.

[130] Weizhong Li, Lukasz Jaroszewski, and Adam Godzik. Clustering of highly homologous sequences to reduce the size of large protein databases. *Bioinformatics*, 17(3):282–283, 2001.

[131] Rongxiang Liu, Thomas W. Blackwell, and David J. States. Conformational model for binding site recognition by the e.colimetj transcription factor. *Bioinformatics*, 17(7):622–633, 2001.

[132] A. Löytynoja and M.C. Milinkovitch. Soap, cleaning multiple alignments from unstable blocks. *Bioinformatics*, 17(6):573–574, 2001.

[133] Alexander V. Lukashin and Rainer Fuchs. Analysis of temporal gene expression profiles: Clustering by simulated annealing and determining the optimal number of clusters. *Bioinformatics*, 17(5):405–414, 2001.

[134] Izabela Makalowska, Joseph F. Ryan, and Andreas D. Baxevanis. Genemachine: Gene prediction and sequence annotation. *Bioinformatics*, 17(9):843–844, 2001.

[135] Vladimir Makarenkov. T-rex: Reconstructing and visualizing phylogenetic trees and reticulation networks. *Bioinformatics*, 17(7):664–668, 2001.

[136] R.R. Mallios. Predicting class ii mhc/peptide multi-level binding with an iterative stepwise discriminant analysis meta-algorithm. *Bioinformatics*, 17(10):942–948, 2001.

[137] Edward M. Marcotte, Ioannis Xenarios, and David Eisenberg. Mining literature for protein-protein interactions. *Bioinformatics*, 17(4):359–363, 2001.

[138] Marc A. Martí-Renom, Valentin A. Ilyin, and Andrej Sali. Dbali: A database of protein structure alignments. *Bioinformatics*, 17(8):746–747, 2001.

[139] Daniel R. Masys, John B. Welsh, J. Lynn Fink, Michael Gribskov, Igor Klacansky, and Jacques Corbeil. Use of keyword hierarchies to interpret gene expression patterns. *Bioinformatics*, 17(4):319–326, 2001.

[140] Raja Mazumder, Ashok Kolaskar, and Donald Seto. Geneorder: Comparing the order of genes in small genomes. *Bioinformatics*, 17(2):162–166, 2001.

[141] Liam J. McGuffin, Kevin Bryson, and David T. Jones. What are the baselines for protein fold recognition? *Bioinformatics*, 17(1):63–72, 2001.

[142] Gráinne McGuire, Michael C. Denham, and David J. Balding. Mac5: Bayesian inference of phylogenetic trees from dna sequences incorporating gaps. *Bioinformatics*, 17(5):479–480, 2001.

[143] Pedro Mendes and Douglas B. Kell. Meg (model extender for gepasi): A program for the modelling of complex, heterogeneous, cellular systems. *Bioinformatics*, 17(3):288–289, 2001.

[144] Kevin P. Micallef, Mark Cooper, and Dean W. Podlich. Using clusters of computers for large qu-gene simulation experiments. *Bioinformatics*, 17(2):194–195, 2001.

[145] Eugenia Migliavacca, Alexei A. Adzhubei, and Manuel C. Peitsch. Mdb: A database system utilizing automatic construction of modules and star-derived universal language. *Bioinformatics*, 17(11):1047–1052, 2001.

[146] Webb Miller. Comparison of genomic dna sequences: Solved and unsolved problems. *Bioinformatics*, 17(5):391–397, 2001.

[147] Andrey A. Mironov, Pavel S. Novichkov, and Mikhail S. Gelfand. Pro-frame: Similarity-based gene recognition in eukaryotic dna sequences with errors. *Bioinformatics*, 17(1):13–15, 2001.

[148] Hideaki Mizuno, Yoshimasa Tanaka, Kenta Nakai, and Akinori Sarai. Ori-gene: Gene classification based on the evolutionary tree. *Bioinformatics*, 17(2):167–173, 2001.

[149] Fabian Model, Péter Adorján, Alexander Olek, and Christian Piepenbrock. Feature selection for dna methylation based cancer classification. *Bioinformatics*, 17(S1):157–164, 2001.

[150] Steffen Möller, Michael D.R. Croning, and Rolf Apweiler. Evaluation of methods for the prediction of membrane spanning regions. *Bioinformatics*, 17(7):646–653, 2001. see Erratum in Bioinformatics, Vol. 18, 2002, No. 1, 218-218.

[151] Steffen Möller, Jaak Vilo, and Michael D.R. Croning. Prediction of the coupling specificity of g protein coupled receptors to their g proteins. *Bioinformatics*, 17(S1):174–181, 2001.

[152] Bernard M.E. Moret, Li-San Wang, Tandy Warnow, and Stacia K. Wyman. New approaches for reconstructing phylogenies from gene order data. *Bioinformatics*, 17(S1):165–173, 2001.

[153] Ralf Mrowka. A java applet for visualizing protein-protein interaction. *Bioinformatics*, 17(7):669–671, 2001.

[154] Tobias Müller, Sven Rahmann, and Marc Rehmsmeier. Non-symmetric score matrices and the detection of homologous transmembrane proteins. *Bioinformatics*, 17(S1):182–189, 2001.

[155] Ekaterina Myasnikova, Anastassia Samsonova, Konstantin Kozlov, Maria Samsonova, and John Reinitz. Registration of the expression patterns of drosophila segmentation genes by two independent methods. *Bioinformatics*, 17(1):3–12, 2001.

[156] Luay Nakhleh, Usman Roshan, Katherine St. John, Jerry Sun, and Tandy Warnow. Designing fast converging phylogenetic methods. *Bioinformatics*, 17(S1):190–198, 2001.

[157] P.C. Ng, J.G. Henikoff, and S. Henikoff. Erratum to "phat: A transmembrane-specific substitution matrix". *Bioinformatics*, 17(3):290–290, 2001. Originally in Bioinformatics, Vol. 16, 2000, No. 9, 760-766.

[158] Hiromi Nishida. Distribution of genes for lysine biosynthesis through the aminoadipate pathway among prokaryotic genomes. *Bioinformatics*, 17(2):189–191, 2001.

[159] Hiromi Nishida. Evolution of amino acid biosynthesis and enzymes with broad substrate specificity. *Bioinformatics*, 17(12):1224–1225, 2001.

[160] T. Nishikawa, T. Ota, and T. Isogai. Erratum to "prediction whether a human cdna sequence contains initiation codon by combining statistical information and similarity with protein sequences". *Bioinformatics*, 17(3):290–290, 2001. Originally in Bioinformatics, Vol. 16, 2000, No. 11, 960-967.

[161] Cédric Notredame. Mocca: Semi-automatic method for domain hunting. *Bioinformatics*, 17(4):373–374, 2001.

[162] P.S. Novichkov, M.S. Gelfand, and A.A. Mironov. Gene recognition in eukaryotic dna by comparison of genomic sequences. *Bioinformatics*, 17(11):1011–1018, 2001.

[163] Uwe Ohler, Heinrich Niemann, Guo-chun Liao, and Gerald M. Rubin. Joint modeling of dna sequence and physical properties to improve eukaryotic promoter recognition. *Bioinformatics*, 17(S1):199–206, 2001.

[164] Toshihide Ono, Haretsugu Hishigaki, Akira Tanigami, and Toshihisa Takagi. Automated extraction of information on protein-protein interactions from the biological literature. *Bioinformatics*, 17(2):155–161, 2001.

[165] Giulio Pavesi, Giancarlo Mauri, and Graziano Pesole. An algorithm for finding signals of unknown length in dna sequences. *Bioinformatics*, 17(S1):207–214, 2001.

[166] William R. Pearson. Training for bioinformatics and computational biology. *Bioinformatics*, 17(9):761–762, 2001.

[167] Dana Pe'er, Aviv Regev, Gal Elidan, and Nir Friedman. Inferring subnetworks from perturbed expression profiles. *Bioinformatics*, 17(1):215–224, 2001.

[168] Jimin Pei and Nick V. Grishin. Al2co: Calculation of positional conservation in a protein sequence alignment. *Bioinformatics*, 17(8):700–712, 2001.

[169] Pavel A. Pevzner and Haixu Tang. Fragment assembly with double-barreled data. *Bioinformatics*, 17(S1):225–233, 2001.

[170] Vinhthuy T. Phan and Steven S. Skiena. Dealing with errors in interactive sequencing by hybridization. *Bioinformatics*, 17(10):862–870, 2001.

[171] W.R. Pitt, M.A. Williams, M. Steven, B. Sweeney, A.J. Bleasby, and D.S. Moss. The bioinformatics template library — generic components for biocomputing. *Bioinformatics*, 17(8):729–737, 2001.

[172] Raf M. Podowski and Erik L.L. Sonnhammer. Medusa: Large scale automatic selection and visual assessment of pcr primer pairs. *Bioinformatics*, 17(7):656–657, 2001.

[173] Gianluca Pollastri, Pierre Baldi, Pietro Fariselli, and Rita Casadio. Improved predication of the number of residue contacts in proteins by recurrent neural networks. *Bioinformatics*, 17(S1):234–242, 2001.

[174] Ponraj Prabakaran, Jianghong An, M. Michael Gromiha, Samuel Selvaraj, Hatsuho Uedaira, Hidetoshi Kono, and Akinori Sarai. Thermodynamic database for protein-nucleic acid interactions (pronit). *Bioinformatics*, 17(11):1027–1034, 2001.

[175] Dong Qi and A. Jamie Cuticchia. Compositional symmetries in complete genomes. *Bioinformatics*, 17(6):557–559, 2001. see Erratum in Bioinformatics, Vol. 18, 2002, No. 4, 648-648.

[176] Günter Raddatz, Michaela Dehio, Thomas F. Meyer, and Christoph Dehio. Primearray: Genome-scale primer design for dna-microarray construction. *Bioinformatics*, 17(1):98–99, 2001.

[177] Vasily E. Ramensky, Vsevolod Ju. Makeev, Mikhail A. Roytberg, and Vladimir G. Tumanyan. Segmentation of long genomic sequences into domains with homogeneous composition with basio software. *Bioinformatics*, 17(11):1065–1066, 2001.

[178] Chenna Ramu. Sir: A simple indexing and retrieval system for biological flat file databases. *Bioinformatics*, 17(8):756–758, 2001.

[179] William C. Ray and Charles J. Daniels. The pacrat system: An extensible www-based system for correlated sequence retrieval, storage and analysis. *Bioinformatics*, 17(1):100–104, 2001.

[180] William C. Ray, Jr. Munson, Robert S., and Charles J. Daniels. Tricross: Using dot-plots in sequence-id space to detect uncataloged intergenic features. *Bioinformatics*, 17(12):1105–1112, 2001.

[181] Pentti Riikonen, Jorma Boberg, Tapio Salakoski, and Mauno Vihinen. Biowap, mobile internet service for bioinformatics. *Bioinformatics*, 17(9):855–856, 2001.

[182] Igor B. Rogozin, Alexey V. Kochetov, Fyodor A. Kondrashov, Eugene V. Koonin, and Luciano Milanesi. Presence of atg triplets in 5' untranslated regions of eukaryotic cdnas correlates with a "weak" context of the start codon. *Bioinformatics*, 17(10):890–900, 2001.

[183] T. Andrew Ronneberg, Stephen J. Freeland, and Laura F. Landweber. Genview and gencode: A pair of programs to test theories of genetic code evolution. *Bioinformatics*, 17(3):280–281, 2001.

[184] Leszek Rychlewski. Toolshop: Prerelease inspections for protein structure prediction servers. *Bioinformatics*, 17(12):1240–1241, 2001.

[185] Andrey Rzhetsky and Shawn M. Gomez. Birth of scale-free molecular networks and the number of distinct dna and protein domains per genome. *Bioinformatics*, 17(10):988–996, 2001.

[186] Meena K. Sakharkar, Tin Wee Tan, and Sandro J. de Souza. Generation of a database containing discordant intron positions in eukaryotic genes (midb). *Bioinformatics*, 17(8):671–675, 2001.

[187] John J. Salama, Howard J. Feldman, and Christopher W.V. Hogue. Vistraj: Exploring protein conformational space. *Bioinformatics*, 17(9):851–852, 2001.

[188] Chris Sander. Bioinformatics — challenges in 2001. *Bioinformatics*, 17(1):1–2, 2001.

[189] Frank Schacherer, Claudia Choi, Ulrike Götze, Mathias Krull, Susanne Pistor, and Edgar Wingender. The transpath signal transduction database: A knowledge base on signal transduction networks. *Bioinformatics*, 17(11):1053–1057, 2001.

[190] David B. Searls. Reading the book of life. *Bioinformatics*, 17(7):579–580, 2001.

[191] Eran Segal, Ben Taskar, Audrey Gasch, Nir Friedman, and Daphne Koller. Rich probabilistic models for gene expression. *Bioinformatics*, 17(1):243–252, 2001.

[192] J.N. Selley, J. Swift, and T.K. Attwood. Easy — an expert analysis system for interpreting database search outputs. *Bioinformatics*, 17(1):105–106, 2001.

[193] Bruce A. Shapiro, Jin Chu Wu, David Bengali, and Mark J. Potts. The massively parallel genetic algorithm for rna folding: Mimd implementation and population variation. *Bioinformatics*, 17(2):137–148, 2001.

[194] Hidetoshi Shimodaira and Masami Hasegawa. Consel: For assessing the confidence of phylogenetic tree selection. *Bioinformatics*, 17(12):1246–1247, 2001.

[195] Elizabeth Shoop, Kevin A.T. Silverstein, James E. Johnson, and Ernest F. Retzel. Metafam: A unified classification of protein families. ii. schema and query capabilities. *Bioinformatics*, 17(3):262–271, 2001.

[196] Asim S. Siddiqui, Uwe Dengler, and Geoffrey J. Barton. 3dee: A database of protein structural domains. *Bioinformatics*, 17(2):200–201, 2001.

[197] A. Siepel, A. Farmer, A. Tolopko, M. Zhuang, P. Mendes, W. Beavis, and B. Sobral. Isys: A decentralized, component-based approach to the integration of heterogeneous bioinformatics resources. *Bioinformatics*, 17(1):83–94, 2001.

[198] Kevin A.T. Silverstein, Elizabeth Shoop, James E. Johnson, and Ernest F. Retzel. Metafam: A unified classification of protein families. i. overview and statistics. *Bioinformatics*, 17(3):249–261, 2001.

[199] Kim Lan Sim, Tomoyuki Uchida, and Satoru Miyano. Proddo: A database of disordered proteins from the protein data bank (pdb). *Bioinformatics*, 17(4):379–380, 2001.

[200] Harpreet Singh and G.P.S. Raghava. Propred: Prediction of hla-dr binding sites. *Bioinformatics*, 17(12):1236–1237, 2001.

[201] Steven S. Skiena. Designing better phages. *Bioinformatics*, 17(S1):253–261, 2001.

[202] Rainer Spang and Martin Vingron. Limits of homology detection by pairwise sequence comparison. *Bioinformatics*, 17(4):338–342, 2001.

[203] David States. Time to defend what we have won. *Bioinformatics*, 17(4):299–299, 2001.

[204] David J. States, Volker Nowotny, and Thomas W. Blackwell. Probabilistic approaches to the use of higher order clone relationships in physical map assembly. *Bioinformatics*, 17(S1):262–269, 2001.

[205] Matthias Steinfath, Wasco Wruck, Henrik Seidel, Hans Lehrach, Uwe Radelof, and John O'Brien. Automated image analysis for array hybridization experiments. *Bioinformatics*, 17(7):634–641, 2001.

[206] Robert Stevens, Carole Goble, Patricia Baker, and Andy Brass. A classification of tasks in bioinformatics. *Bioinformatics*, 17(2):180–188, 2001.

[207] C. Stoeckert, A. Pizarro, E. Manduchi, M. Gibson, B. Brunk, J. Crabtree, J. Schug, S. Shen-Orr, and G.C. Overton. A relational schema for both array-based and sage gene expression experiments. *Bioinformatics*, 17(4):300–308, 2001.

[208] Christian E.V. Storm and Erik L.L. Sonnhammer. Nifas: Visual analysis of domain evolution in proteins. *Bioinformatics*, 17(4):343–348, 2001.

[209] P.M. Stothard. Combosa3d: Combining sequence alignments with three-dimensional structures. *Bioinformatics*, 17(2):198–199, 2001.

[210] Shih-Chieh Su, C.-C. Jay Kuo, and Ting Chen. Inference of missing snps and information quantity measurements for haplotype blocks. *Bioinformatics*, 21(9):2001–2007, 2005.

[211] S. Sujatha, S. Balaji, and N. Srinivasan. Pali: A database of alignments and phylogeny of homologous protein structures. *Bioinformatics*, 17(4):375–376, 2001.

[212] Baris E. Suzek, Maria D. Ermolaeva, Mark Schreiber, and Steven L. Salzberg. A probabilistic method for identifying start codons in bacterial genomes. *Bioinformatics*, 17(12):1123–1130, 2001.

[213] Yoshiyuki Suzuki, Takashi Gojobori, and Masatoshi Nei. Adaptsite: Detecting natural selection at single amino acid sites. *Bioinformatics*, 17(7):660–661, 2001.

[214] Jack E. Tabaska, Ramana V. Davuluri, and Michael Q. Zhang. Identifying the 3'-terminal exon in human dna. *Bioinformatics*, 17(7):602–607, 2001.

[215] Amos Tanay and Ron Shamir. Cmputational expansion of genetic networks. *Bioinformatics*, 17(S1):270–278, 2001.

[216] Gert Thijs, Magali Lescot, Kathleen Marchal, Stephane Rombauts, Bart de Moor, Pierre Rouzé, and Yves Moreau. A higher-order background model improves the detection of promoter regulatory elements by gibbs sampling. *Bioinformatics*, 17(12):1113–1122, 2001.

[217] Kurt S. Thorn and Andrew A. Bogan. Asedb: A database of alanine mutations and their effects on the free energy of binding in protein interactions. *Bioinformatics*, 17(3):284–285, 2001.

[218] R.C. Togawa, J.F. Antoniw, and J.G.L. Mullins. Tmcompare: Transmembrane region sequence and structure. *Bioinformatics*, 17(12):1238–1239, 2001.

[219] Masaru Tomita. Towards computer aided design (cad) of useful microorganisms. *Bioinformatics*, 17(12):1091–1092, 2001.

[220] Frédéric Tores and Emmanuel Barillot. The art of pedigree drawing: Algorithmic aspects. *Bioinformatics*, 17(2):174–179, 2001.

[221] Olga Troyanskaya, Michael Cantor, Gavin Sherlock, Pat Brown, Trevor Hastie, Robert Tibshirani, David Botstein, and Russ B. Altman. Missing value estimation methods for dna microarrays. *Bioinformatics*, 17(6):520–525, 2001.

[222] Jerry Tsai, Neil Voss, and Mark Gerstein. Determining the minimum number of types necessary to represent the sizes of protein atoms. *Bioinformatics*, 17(10):949–956, 2001.

[223] Gábor E. Tusnády and István Simon. The hmmtop transmembrane topology prediction server. *Bioinformatics*, 17(9):849–850, 2001.

[224] D. Venet, F. Pecasse, C. Maenhaut, and H. Bersini. Separation of samples into their constituents using gene expression data. *Bioinformatics*, 17(S1):279–287, 2001.

[225] Martin Vingron. Bioinformatics needs to adopt statistical thinking. *Bioinformatics*, 17(5):389–390, 2001.

[226] Anja von Heydebreck, Wolfgang Huber, Annemarie Poustka, and Martin Vingron. Identifying splits with clear separation: A new class discovery method for gene expression data. *Bioinformatics*, 17(S1):107–114, 2001.

[227] Andreas Wagner. How to reconstruct a large genetic network from n gene perturbations in fewer than n^2 easy steps. *Bioinformatics*, 17(12):1183–1197, 2001.

[228] Michael E. Wall, Patricia A. Dyck, and Thomas S. Brettin. Svdman — singular value decomposition analysis of microarray data. *Bioinformatics*, 17(6):566–568, 2001.

[229] John M. Ward. Identification of novel families of membrane proteins from the model plant arabidopsis thaliana. *Bioinformatics*, 17(6):560–563, 2001.

[230] Caleb Webber and Geoffrey J. Barton. Estimation of p-values for global alignments of protein sequences. *Bioinformatics*, 17(12):1158–1167, 2001.

[231] Michael Wildpaner, Georg Schneider, Alexander Schleiffer, and Frank Eisenhaber. Taxonomy workbench. *Bioinformatics*, 17(12):1179–1182, 2001.

[232] Michael J. Wise. Oj.py: A software tool for low complexity proteins and protein domains. *Bioinformatics*, 17(S1):288–295, 2001.

[233] Jérôme Wojcik and Vincent Schächter. Protein-protein interaction map inference using interacting domain profile pairs. *Bioinformatics*, 17(S1):296–305, 2001.

[234] Xuhua Xia and Zheng Xie. Amada: Analysis of microarray data. *Bioinformatics*, 17(6):569–570, 2001.

[235] Eric P. Xing and Richard M. Karp. Cliff: Clustering of high-dimensional microarray data via iterative feature filtering using normalized cuts. *Bioinformatics*, 17(S1):306–315, 2001.

[236] Liqun Xing and Volker Brendel. Multi-query sequence blast output examination with museqbox. *Bioinformatics*, 17(8):744–745, 2001.

[237] Y. Xu, D. Xu, and H.N. Gabow. Erratum to "protein domain decomposition using a graph-theoretic approach". *Bioinformatics*, 17(3):290–290, 2001. Originally in Bioinformatics, Vol. 16, 2000, No. 12, 1091-1104.

[238] Chen-Hsiang Yeang, Sridhar Ramaswamy, Pablo Tamayo, Sayan Mukherjee, Ryan M. Rifkin, Michael Angelo, Michael Reich, Eric Lander, Jill Mesirov, and Todd Golub. Molecular classification of multiple tumor types. *Bioinformatics*, 17(S1):316–322, 2001.

[239] K.Y. Yeung, C. Fraley, A. Murua, A.E. Raftery, and W.L. Ruzzo. Model-based clustering and data transformations for gene expression data. *Bioinformatics*, 17(10):977–987, 2001.

[240] K.Y. Yeung, D.R. Haynor, and W.L. Ruzzo. Validating clustering for gene expression data. *Bioinformatics*, 17(4):309–318, 2001.

[241] K.Y. Yeung and W.L. Ruzzo. Principal component analysis for clustering gene expression data. *Bioinformatics*, 17(9):763–774, 2001.

[242] Evgeni M. Zdobnov and Rolf Apweiler. Interproscan — an integration platform for the signature-recognition methods in interpro. *Bioinformatics*, 17(9):847–848, 2001.

[243] Louxin Zhang, Chew-Kiat Heng, and Tin Wee Tan. Cladogramer: Incorporating haplotype frequency into cladogram analysis. *Bioinformatics*, 17(5):481–482, 2001.

[244] Theresa Zhang and Michael Zhang. Promoter extraction from genbank (peg): Automatic extraction of eukaryotic promoter sequences in large sets of genes. *Bioinformatics*, 17(12):1232–1233, 2001.

[245] Alexander Zien, Thomas Aigner, Ralf Zimmer, and Thomas Lengauer. Centralization: A new method for the normalization of gene expression data. *Bioinformatics*, 17(S1):323–331, 2001.

[246] Christian M. Zmasek and Sean R. Eddy. Atv: Display and manipulation of annotated phylogenetic trees. *Bioinformatics*, 17(4):383–384, 2001.

[247] Christian M. Zmasek and Sean R. Eddy. A simple algorithm to infer gene duplication and speciation events on a gene tree. *Bioinformatics*, 17(9):821–828, 2001.