References

[1] C.J. Benham. Computation of dna structural variability — a new predictor of dna regulatory regions. *Bioinformatics*, 12(5):375–381, 1996.

[2] S.M. Bhandarkar, S. Chirravuri, and J. Arnold. Parods — a study of parallel algorithms for ordering dna sequences. *Bioinformatics*, 12(4):269–280, 1996.

[3] A. Bolshoy, I. Ioshikhes, and E.N. Trifonov. Applicability of the multiple alignment algorithm for detection of weak patterns: Periodically distributed dna pattern as a study case. *Bioinformatics*, 12(5):383–389, 1996.

[4] P. Bucher, J.W. Fickett, and A. Hatzigeorgiou. Computational analysis of transcriptional regulatory elements: A field in flux. *Bioinformatics*, 12(5):361–362, 1996.

[5] J.A. Byers. Taxokey: A universal taxonomic key program using dos text files and graphics. *Bioinformatics*, 12(3):185–189, 1996.

[6] C. Caporale, C. Sepe, C. Caruso, A.M. Garzillo, and V. Buonocore. An algorithm to analyse the hydrolysis pathway of peptides and proteins by sequence analyses of unfractionated digestion mixtures. *Bioinformatics*, 12(2):81–88, 1996.

[7] E.S. Carter II and C.S. Tung. Namot2 — a redesigned nucleic acid modeling tool: Construction of non-canonical dna structures. *Bioinformatics*, 12(1):25–30, 1996.

[8] C.C. Chen, R.O. Chen, and R.B. Altman. Constraining volume by matching the moments of a distance distribution. *Bioinformatics*, 12(4):319–326, 1996.

[9] J.M. Claverie and S. Audic. The statistical significance of nucleotide position-weight matrix matches. *Bioinformatics*, 12(5):431–439, 1996.

[10] K.N. Degtyarenko and P. Fabian. The directory of p450-containing systems on worldwide web. *Bioinformatics*, 12(3):237–240, 1996.

[11] L. Duret, E. Gasteiger, and G. Perriere. Lalnview: A graphical viewer for pairwise sequence alignments. *Bioinformatics*, 12(6):507–510, 1996.

[12] F. Eggenberger, N. Redaschi, and R. Doelz. Fastalert — an automatic search system to alert about new entries in biological sequence databanks. *Bioinformatics*, 12(2):129–133, 1996.

[13] P. Fariselli and R. Casadio. Htp: A neural network-based method for predicting the topology of helical transmembrane domains in proteins. *Bioinformatics*, 12(1):41–48, 1996.

[14] C. Fondrat and A. Kalogeropoulos. Approaching the function of new genes by detection of their potential upstream activation sequences in saccharomyces cerevisiae: Application to chromosome iii. *Bioinformatics*, 12(5):363–374, 1996.

[15] N. Galtier, M. Gouy, and C. Gautier. Seaview and phylo_win: Two graphic tools for sequence alignment and molecular phylogeny. *Bioinformatics*, 12(6):543–548, 1996.

[16] J.P. Grillasca, D. Aubert, R. Planells, N. Domingo, and H. Lafont. Little kevin: A program for the estimation of protein homology by analysing the amino acid compositions and sequences. *Bioinformatics*, 12(4):347–351, 1996.

[17] G Grillo, M. Attimonelli, S. Liuni, and G. Pesole. Cleanup: A fast computer program for removing redundancies from nucleotide sequence databases. *Bioinformatics*, 12(1):1–8, 1996.

[18] W.N. Grundy, T.L. Bailey, and C.P. Elkan. Parameme: A parallel implementation and a web interface for a dna and protein motif discovery tool. *Bioinformatics*, 12(4):303–310, 1996.

[19] X. Guan and E.C. Uberbacher. Alignments of dna and protein sequences containing frameshift errors. *Bioinformatics*, 12(1):31–40, 1996.

[20] J. Hanke and J.G. Reich. Kohonen map as a visualization tool for the analysis of protein sequences: Multiple alignments, domains and segments of secondary structures. *Bioinformatics*, 12(6):447–454, 1996.

[21] S. Hannenhalli, W. Feldman, H.F. Lewis, S.S. Skiena, and P.A. Pevzner. Positional sequencing by hybridization. *Bioinformatics*, 12(1):19–24, 1996.

[22] W.J. Heitler. A simple method for the removal of mains interference from pre-recorded electrophysiological data. *Bioinformatics*, 12(6):539–542, 1996.

[23] J.G. Henikoff and S. Henikoff. Using substitution probabilities to improve position-specific scoring matrices. *Bioinformatics*, 12(2):135–143, 1996.

[24] G. Herrmann, A. Schon, R. Brack-Werner, and T. Werner. Conrad: A method for identification of variable and conserved regions within proteins by scale-space filtering. *Bioinformatics*, 12(3):197–203, 1996.

[25] R.W. Hooft, C. Sander, M. Scharf, and G. Vriend. The pdbfinder database: A summary of pdb, dssp and hssp information with added value. *Bioinformatics*, 12(6):525–529, 1996.

[26] F. Hospital, C. Dillmann, and A.E. Melchinger. A general algorithm to compute multilocus genotype frequencies under various mating systems. *Bioinformatics*, 12(6):455–462, 1996.

[27] L. Hu, E.F. Saulinskas, P. Johnson, and P.B. Harrington. Development of an expert system for amino acid sequence identification. *Bioinformatics*, 12(4):311–318, 1996.

[28] X. Huang and J. Zhang. Methods for comparing a dna sequence with a protein sequence. *Bioinformatics*, 12(6):497–506, 1996.

[29] R. Hughey. Parallel hardware for sequence comparison and alignment. *Bioinformatics*, 12(6):473–479, 1996.

[30] R. Hughey and A. Krogh. Hidden markov models for sequence analysis: Extension and analysis of the basic method. *Bioinformatics*, 12(2):95–107, 1996.

[31] G.B. Hutchinson. The prediction of vertebrate promoter regions using differential hexamer frequency analysis. *Bioinformatics*, 12(5):391–398, 1996.

[32] I.B. Jakobsen and S. Easteal. A program for calculating and displaying compatibility matrices as an aid in determining reticulate evolution in molecular sequences. *Bioinformatics*, 12(4):291–295, 1996.

[33] D.C. Jamison, B. Mills, and B. Schatz. An extensible network query unification system for biological databases. *Bioinformatics*, 12(2):145–150, 1996.

[34] S. Kanaya, Y. Kudo, Y. Nakamura, and T. Ikemura. Detection of genes in escherichia coli sequences determined by genome projects and prediction of protein production levels, based on multivariate diversity in codon usage. *Bioinformatics*, 12(3):213–225, 1996.

[35] H. Karas, R. Knuppel, W. Schulz, H. Sklenar, and E. Wingender. Combining structural analysis of dna with search routines for the detection of transcription regulatory elements. *Bioinformatics*, 12(5):441–446, 1996.

[36] J. Kim, J.R. Cole, and S. Pramanik. Alignment of possible secondary structures in multiple rna sequences using simulated annealing. *Bioinformatics*, 12(4):259–267, 1996.

[37] R.D. King and C.G. Angus. Pm — protein music. *Bioinformatics*, 12(3):251–252, 1996.

[38] I. Kuznetsov and P. Morozov. Geometry: A software package for nucleotide sequence analysis using statistical geometry in sequence space. *Bioinformatics*, 12(4):297–301, 1996.

[39] G. Labesse. Mulblast 1.0: A multiple alignment of blast output to boost protein sequence similarity analysis. *Bioinformatics*, 12(6):463–467, 1996.

[40] S. Lanzavecchia, L. Tosoni, and P.L. Bellon. Fast sinogram computation and the sinogram-based alignment of images. *Bioinformatics*, 12(6):531–537, 1996.

[41] A.S. Law and D.W. Burt. qvalue — a program to calculate comparative measures of genomic reorganisation from cytogenetic and/or linkage information. *Bioinformatics*, 12(3):181–183, 1996.

[42] J. Lazovic. Selection of amino acid parameters for fourier transform-based analysis of proteins. *Bioinformatics*, 12(6):553–562, 1996.

[43] K. Lindauer, C. Bendic, and J. Suhnel. Hbexplore — a new tool for identifying and analysing hydrogen bonding patterns in biological macromolecules. *Bioinformatics*, 12(4):281–289, 1996.

[44] V.Ju. Makeev and V.G. Tumanyan. Search of periodicities in primary structure of biopolymers: A general fourier approach. *Bioinformatics*, 12(1):49–54, 1996.

[45] M.P. Maradona. Software for microbial fingerprinting by means of the infrared spectra. *Bioinformatics*, 12(4):353–356, 1996.

[46] O. Matzura and A. Wennborg. Rnadraw: An integrated program for rna secondary structure calculation and analysis under 32-bit microsoft windows. *Bioinformatics*, 12(3):247–249, 1996.

[47] L. Milanesi, M. Muselli, and P. Arrigo. Hamming-clustering method for signals prediction in 5' and 3' regions of eukaryotic genes. *Bioinformatics*, 12(5):399–404, 1996.

[48] U.S. Murty, K. Jamil, D. Krishna, and P.J. Reddy. Rule-based system for the fast identification of species of indian anopheline mosquitoes. *Bioinformatics*, 12(6):491–495, 1996.

[49] A. Nakaya, K. Taura, K. Yamamoto, and A. Yonezawa. Visualization of rna secondary structures using highly parallel computers. *Bioinformatics*, 12(3):205–211, 1996.

[50] A. Nandy. Two-dimensional graphical representation of dna sequences and intron- exon discrimination in intron-rich sequences. *Bioinformatics*, 12(1):55–62, 1996.

[51] B.I. Osborne. Three sets of macintosh applescripts for the automatic submission of sequence data to the internet blast server. *Bioinformatics*, 12(3):257–258, 1996.

[52] R.D. Page. Treeview: An application to display phylogenetic trees on personal computers. *Bioinformatics*, 12(4):357–358, 1996.

[53] D.N Perkins and T.K. Attwood. Xfinger: A tool for searching and visualising protein fingerprints and patterns. *Bioinformatics*, 12(2):89–94, 1996.

[54] G. Perriere, J.R. Lobry, and J. Thioulouse. Correspondence discriminant analysis: A multivariate method for comparing classes of protein and nucleic acid sequences. *Bioinformatics*, 12(6):519–524, 1996.

[55] G. Perriere and J. Thioulouse. On-line tools for sequence retrieval and multivariate statistics in molecular biology. *Bioinformatics*, 12(1):63–69, 1996.

[56] D.S. Prestridge. Signal scan 4.0: Additional databases and sequence formats. *Bioinformatics*, 12(2):157–160, 1996.

[57] V. Proutski and E.C. Holmes. Primer master: A new program for the design and analysis of pcr primers. *Bioinformatics*, 12(3):253–255, 1996.

[58] K. Quandt, K. Grote, and T. Werner. Genomeinspector: A new approach to detect correlation patterns of elements on genomic sequences. *Bioinformatics*, 12(5):405–413, 1996.

[59] A. Rambaut, N.C. Grassly, S. Nee, and P.H. Harvey. Bi-de: An application for simulating phylogenetic processes. *Bioinformatics*, 12(6):469–471, 1996.

[60] I.B. Rogozin, L. Milanesi, and N.A. Kolchanov. Gene structure prediction using information on homologous protein sequence. *Bioinformatics*, 12(3):161–170, 1996.

[61] J.P. Rolland, M.J. Fliflа, M. Garreau, and D. Thomas. Ibis version 3: An osf/motif-based interface for ibis-integrated biological imaging system. *Bioinformatics*, 12(3):241–245, 1996.

[62] D.A .and D. Thieffry Rosenblueth, A.M. Huerta, H. Salgado, and J. Collado-Vides. Syntactic recognition of regulatory regions in escherichia coli. *Bioinformatics*, 12(5):415–422, 1996.

[63] G. Schaftenaar, K. Cuelenaere, J.H. Noordik, and T. Etzold. A tcl-based srs v. 4 interface. *Bioinformatics*, 12(2):151–155, 1996.

[64] B.A. Shapiro and J.C. Wu. An annealing mutation operator in the genetic algorithms for rna folding. *Bioinformatics*, 12(3):171–180, 1996.

[65] R.K. Singh, D.L. Hoffman, S.G. Tell, and C.T. White. Bioscan: A network sharable computational resource for searching biosequence databases. *Bioinformatics*, 12(3):191–196, 1996.

[66] K. Sjolander, K. Karplus, M. Brown, R. Hughey, A. Krogh, I.S. Mian, and D. Haussler. Dirichlet mixtures: A method for improved detection of weak but significant protein sequence homology. *Bioinformatics*, 12(4):327–345, 1996.

[67] J. Suhnel. Image library of biological macromolecules. *Bioinformatics*, 12(3):227–229, 1996.

[68] L. Tosoni, S. Lanzavecchia, and P.L. Bellon. Image and volume data rotation with 1- and 3-pass algorithms. *Bioinformatics*, 12(6):549–552, 1996.

[69] E.N. Trifonov. Interfering contexts of regulatory sequence elements. *Bioinformatics*, 12(5):423–429, 1996.

[70] W. Vahrson, K. Hermann, J. Kleffe, and B. Wittig. Object-oriented sequence analysis: Scl — a c++ class library. *Bioinformatics*, 12(2):119–127, 1996.

[71] Y. Wada and H. Yasue. Development of an animal genome database and its search system. *Bioinformatics*, 12(3):231–235, 1996.

[72] J. Wallman, G.A. Hoelzer, and D.J. Melnick. The effects of social structure, geographical structure, and population size on the evolution of mitochondrial dna: I. a simulation model. *Bioinformatics*, 12(6):481–489, 1996.

[73] M.F. Wilkins, L. Boddy, C.W. Morris, and R. Jonker. A comparison of some neural and non-neural methods for identification of phytoplankton from flow cytometry data. *Bioinformatics*, 12(1):9–18, 1996.

[74] F. Wolfertstetter, K. Frech, G. Herrmann, and T. Werner. Identification of functional elements in unaligned nucleic acid sequences by a novel tuple search algorithm. *Bioinformatics*, 12(1):71–80, 1996.

[75] C.H. Wu, S. Zhao, H.L. Chen, C.J. Lo, and J. McLarty. Motif identification neural design for rapid and sensitive protein family search. *Bioinformatics*, 12(2):109–118, 1996.

[76] Y. Xu and E.C. Uberbacher. A polynomial-time algorithm for a class of protein threading problems. *Bioinformatics*, 12(6):511–517, 1996.