

References

- [1] P. Agarwal. Simulation of aggregation in dictyostelium using the cell programming language. *Bioinformatics*, 10(6):647–655, 1994.
- [2] J. Altimiras, M. Feliu, A. Aissaoui, and L. Tort. Computing heart rate variability using spectral analysis techniques: Hrvuab, a ready-to-use program. *Bioinformatics*, 10(5):559–562, 1994.
- [3] E. Arakawa, H. Yoshikura, and K. Yamamoto. Some features on rna folding structures of cytochrome c oxidase subunit ii and cytochrome p450. *Bioinformatics*, 10(1):7–9, 1994.
- [4] H. Blocker and D.N. Lincoln. The "shortmer" approach to nucleic acid sequence analysis. i: Computer simulation of sequencing projects to find economical primer sets. *Bioinformatics*, 10(2):193–197, 1994.
- [5] D. Bray and S. Lay. Rapid numerical integration algorithm for finding the equilibrium state of a system of coupled binding reactions. *Bioinformatics*, 10(5):471–476, 1994.
- [6] T.N. Bryant. A bacterial identification teaching exercise revisited. *Bioinformatics*, 10(3):329–334, 1994.
- [7] T.N. Bryant. Identifying correct bacteriological vocabulary: Software to look up rkc codes and statements. *Bioinformatics*, 10(6):657–660, 1994.
- [8] T.N. Bryant. A program for reordering coded data. *Bioinformatics*, 10(3):359–360, 1994.
- [9] M.L. Cain and L.W. Murray. Non-linear regression models to estimate the size of dna fragments. *Bioinformatics*, 10(6):677–680, 1994.
- [10] H. Cantalloube, C. Nahum, A. Achour, T. Lehner, I. Callebaut, A. Burny, B. Bizzini, J.P. Mornon, D. Zagury, and J.F. Zagury. Automat: A novel software system for the systematic search for protein (or dna) similarities with a notable application to autoimmune diseases and aids. *Bioinformatics*, 10(2):153–161, 1994.

- [11] C. Caporale, C. Sepe, C. Caruso, P. Petrilli, and V. Buonocore. An algorithm to determine protein sequence alignment by utilizing data obtained from a peptide mixture and individual peptides. *Bioinformatics*, 10(5):489–494, 1994.
- [12] W. Chang, I.N. Shindyalov, C. Pu, and P.E. Bourne. Design and application of pdblib, a c++ macromolecular class library. *Bioinformatics*, 10(6):575–586, 1994.
- [13] M.S. Chapman. Sequence similarity scores and the inference of structure-function relationships. *Bioinformatics*, 10(2):111–119, 1994.
- [14] D.A. Clark and C.J. Rawlings. Intelligent systems for molecular biology: Review of the first international conference. *Bioinformatics*, 10(2):199–205, 1994. see Erratum in *Comput. Appl. Biosci.*, Vol. 10, 1994, No. 3.
- [15] M.G. Claros and G. von Heijne. Toppred ii: An improved software for membrane protein structure predictions. *Bioinformatics*, 10(6):685–686, 1994.
- [16] J. Clotet, J. Cedano, and E. Querol. An excel spreadsheet computer program combining algorithms for prediction of protein structural characteristics. *Bioinformatics*, 10(5):495–500, 1994.
- [17] F. Corpet and B. Michot. Rnalign program: Alignment of rna sequences using both primary and secondary structures. *Bioinformatics*, 10(4):389–399, 1994.
- [18] F. Dardel. Mc-fit: Using monte-carlo methods to get accurate confidence limits on enzyme parameters. *Bioinformatics*, 10(3):273–275, 1994.
- [19] R. Doelz. Hierarchical access system for sequence libraries in europe (hassle): A tool to access sequence databases remotely. *Bioinformatics*, 10(1):31–34, 1994.
- [20] R.G. Duggleby. Calculation of the molecular weight of proteins from electrophoretic and gel exclusion chromatographic experiments. *Bioinformatics*, 10(2):133–135, 1994.

- [21] E.M. el Mansi, G.C. Dawson, and C.F. Bryce. Steady-state modelling of metabolic flux between the tricarboxylic acid cycle and the glyoxylate bypass in escherichia coli. *Bioinformatics*, 10(3):295–299, 1994.
- [22] Y. Elkind, B. Nir, and J.I. Weller. Maximum likelihood estimation of quantitative trait loci parameters with the aid of genetic markers using a standard statistical package. *Bioinformatics*, 10(5):513–517, 1994.
- [23] L.B. Ellis and R.P. Milius. Valid and invalid implementations of gor secondary structure predictions. *Bioinformatics*, 10(3):341–348, 1994.
- [24] M.L. Engle and C. Burks. Genfrag 2.1: New features for more robust fragment assembly benchmarks. *Bioinformatics*, 10(5):567–568, 1994.
- [25] M. Farza and A. Cheruy. Bioestim: Software for automatic design of estimators in bioprocess engineering. *Bioinformatics*, 10(5):477–488, 1994.
- [26] V.B. Fedoseyeva, S.A. Otenko, and A.A. Alexandrov. Nucleotide sequence statistical analysis of pauses in rna elongation by escherichia coli rna polymerase. *Bioinformatics*, 10(1):13–17, 1994.
- [27] A. Fire. A four-dimensional digital image archiving system for cell lineage tracing and retrospective embryology. *Bioinformatics*, 10(4):443–447, 1994.
- [28] K.U. Frohlich. Sequence similarity presenter: A tool for the graphic display of similarities of long sequences for use in presentations. *Bioinformatics*, 10(2):179–183, 1994.
- [29] R. Fuchs. Fast protein block searches. *Bioinformatics*, 10(1):79–80, 1994.
- [30] R. Fuchs. Predicting protein function: A versatile tool for the apple macintosh. *Bioinformatics*, 10(2):171–178, 1994.
- [31] R. Fuchs. Sequence analysis by electronic mail: A tool for accessing internet e-mail servers. *Bioinformatics*, 10(4):413–417, 1994.
- [32] R. Gambari, S. Volinia, C. Nesti, C. Scapoli, and I. Barrai. A set of alu-free frequent decamers from mammalian genomes enriched in transcription factor signals. *Bioinformatics*, 10(5):501–508, 1994.

- [33] F.U. Gast. A macintosh program for the versatile generation of random nucleic acid sequences and their structural analysis. *Bioinformatics*, 10(1):49–51, 1994.
- [34] O. Gefeller and T. Bregenzler. Computer programs for exact nonparametric inference. *Bioinformatics*, 10(2):213–214, 1994.
- [35] W.A. Gilbert. Farfetch — an internet-based sequence entry server. *Bioinformatics*, 10(2):207–208, 1994.
- [36] A. Gleizes and A. Henaut. A global approach for contig construction. *Bioinformatics*, 10(4):401–408, 1994.
- [37] A. Godzik and J. Skolnick. Flexible algorithm for direct multiple alignment of protein structures and sequences. *Bioinformatics*, 10(6):587–596, 1994.
- [38] B. Golding. Exploratory analysis of multiple sequence alignments using phylogenies. *Bioinformatics*, 10(3):243–247, 1994.
- [39] O. Gotoh. Further improvement in methods of group-to-group sequence alignment with generalized profile operations. *Bioinformatics*, 10(4):379–387, 1994.
- [40] J.M. Hancock and J.S. Armstrong. Simple34: An improved and enhanced implementation for vax and sun computers of the simple algorithm for analysis of clustered repetitive motifs in nucleotide sequences. *Bioinformatics*, 10(1):67–70, 1994.
- [41] K.W. Hart, D.B. Searls, and G.C. Overton. Sortez: A relational translator for ncbi’s asn.1 database. *Bioinformatics*, 10(4):369–378, 1994.
- [42] K. Heumann, D. George, and H.W. Mewes. A new concept of sequence data distribution on wide area networks. *Bioinformatics*, 10(5):519–526, 1994.
- [43] W.G. Hoeck. Infotrac tfd: A microcomputer implementation of the transcription factor database tfd with a graphical user interface. *Bioinformatics*, 10(3):323–327, 1994.
- [44] X. Huang. An algorithm for identifying regions of a dna sequence that satisfy a content requirement. *Bioinformatics*, 10(3):219–225, 1994.

- [45] X. Huang. On global sequence alignment. *Bioinformatics*, 10(3):227–235, 1994.
- [46] Y. Ina. Oden: A program package for molecular evolutionary analysis and database search of dna and amino acid sequences. *Bioinformatics*, 10(1):11–12, 1994.
- [47] J. Inglehart and P.C. Nelson. On the limitations of automated restriction mapping. *Bioinformatics*, 10(3):249–261, 1994.
- [48] J. Jursa. Dna modeller: An interactive program for modelling stacks of dna base pairs on a microcomputer. *Bioinformatics*, 10(1):61–65, 1994.
- [49] M. Kamimura and Y. Takahashi. Phi-psi conformational pattern clustering of protein amino acid residues using the potential function method. *Bioinformatics*, 10(2):163–169, 1994.
- [50] J. Kim, S. Pramanik, and M.J. Chung. Multiple sequence alignment using simulated annealing. *Bioinformatics*, 10(4):419–426, 1994.
- [51] Yu.V. Kondrakhin, V.V. Shamin, and N.A. Kolchanov. Construction of a generalized consensus matrix for recognition of vertebrate pre-mrna 3'-terminal processing sites. *Bioinformatics*, 10(6):597–603, 1994.
- [52] S. Kumar, K. Tamura, and M. Nei. Mega: Molecular evolutionary genetics analysis software for microcomputers. *Bioinformatics*, 10(2):189–191, 1994.
- [53] J.M. Lacroix. Dna fragment size determination on agarose gel by using the application gel. *Bioinformatics*, 10(2):185–187, 1994.
- [54] A. Laferriere, D. Gautheret, and R. Cedergren. An rna pattern matching program with enhanced performance and portability. *Bioinformatics*, 10(2):211–212, 1994.
- [55] G.A. Lambert. Software-controlled testing for antidromic activation of single neurones. *Bioinformatics*, 10(3):237–241, 1994.
- [56] C. Landes and J.L. Risler. Fast databank searching with a reduced amino-acid alphabet. *Bioinformatics*, 10(4):453–454, 1994.

- [57] M. Levin. A julia set model of field-directed morphogenesis: Developmental biology and artificial life. *Bioinformatics*, 10(2):85–103, 1994.
- [58] M.P. Maradona. Integrated software for probabilistic identification of microorganisms. *Bioinformatics*, 10(1):71–73, 1994.
- [59] M.R. Mautino. A computer program for construction of circular restriction maps. *Bioinformatics*, 10(4):449–452, 1994.
- [60] W. Miller and M. Boguski. A note about computing all local alignments. *Bioinformatics*, 10(4):455–456, 1994.
- [61] P.J. Monardo, T. Boutell, J.I. Garrels, and G.I. Latter. A distributed system for two-dimensional gel analysis. *Bioinformatics*, 10(2):137–143, 1994.
- [62] P.M. Nadkarni, S.T. Reeders, and J. Zhou. A modification of the align program to assist visual interpretation of mutated sequences. *Bioinformatics*, 10(3):361–362, 1994.
- [63] K. Nakai, T. Tokimori, A. Ogiwara, I. Uchiyama, and T. Niiyama. Gnome — an internet-based sequence analysis tool. *Bioinformatics*, 10(5):547–550, 1994.
- [64] J.T. Niemi and P. Mantsala. Tractor, a program to locate subclones in a nucleotide sequence using only one sequencing reaction. *Bioinformatics*, 10(5):563–566, 1994.
- [65] G.J. Olsen, H. Matsuda, R. Hagstrom, and R. Overbeek. fastdnaml: A tool for construction of phylogenetic trees of dna sequences using maximum likelihood. *Bioinformatics*, 10(1):41–48, 1994.
- [66] L.A. Parodi, C.A. Granatir, and G.M. Maggiora. A consensus procedure for predicting the location of alpha-helical transmembrane segments in proteins. *Bioinformatics*, 10(5):527–535, 1994.
- [67] F.E. Penotti. A distributed system for dna/protein database similarity searches. *Bioinformatics*, 10(3):277–280, 1994.
- [68] J. Posfai, Z. Szaraz, and R.J. Roberts. Visa: Visual sequence analysis for the comparison of multiple amino acid sequences. *Bioinformatics*, 10(5):537–544, 1994.

- [69] P.R. Reeves, L. Farnell, and R. Lan. Multicomp: A program for preparing sequence data for phylogenetic analysis. *Bioinformatics*, 10(3):281–284, 1994.
- [70] F. Rodriguez, A. Altibelli, and A. Lopez. Build: A program generator for modelling experimental biological data. *Bioinformatics*, 10(2):145–151, 1994.
- [71] L. Rosenthaler and R. Doelz. Simplified user poll and experience report language (super): Implementation and application. *Bioinformatics*, 10(2):105–109, 1994.
- [72] L. Rosenthaler, R. Doelz, and L. Tosoni. Simplified user poll and experience report language (super): Implementation and application. *Bioinformatics*, 10(1):35–39, 1994.
- [73] B. Rost, C. Sander, and R. Schneider. Phd — an automatic mail server for protein secondary structure prediction. *Bioinformatics*, 10(1):53–60, 1994.
- [74] A. Rzhetsky and M. Nei. Metree: A program package for inferring and testing minimum-evolution trees. *Bioinformatics*, 10(4):409–412, 1994.
- [75] S.A. Sammons and D.P. Dykes. Olgcg: An open look interface to the gcg sequence analysis package. *Bioinformatics*, 10(3):335–339, 1994.
- [76] M.A. Saqi and R. Sayle. Pdbmotif — a tool for the automatic identification and display of motifs in protein structures. *Bioinformatics*, 10(5):545–546, 1994.
- [77] C. Scapoli, A. Rodriguez-Larralde, S. Volinia, M. Beretta, and I. Barrai. Identification of a set of frequent decanucleotides in plants and in animals. *Bioinformatics*, 10(5):465–470, 1994.
- [78] G. Schneider, J. Schuchhardt, and P. Wrede. Artificial neural networks and simulated molecular evolution are potential tools for sequence-oriented protein design. *Bioinformatics*, 10(6):635–645, 1994.
- [79] G. Schneider, T. Todt, and P. Wrede. De novo design of peptides and proteins: Machine-generated sequences by the prosa program. *Bioinformatics*, 10(1):75–77, 1994.

- [80] V.A. Shepelev and N.V. Yanishevsky. Multidimensional dot-matrices. *Bioinformatics*, 10(6):605–611, 1994.
- [81] S.W. Smith, R. Overbeek, C.R. Woese, W. Gilbert, and P.M. Gillevet. The genetic data environment an expandable gui for multiple sequence analysis. *Bioinformatics*, 10(6):671–675, 1994.
- [82] C. Soderlund and C. Burks. Gram and genfragii: Solving and testing the single-digest, partially ordered restriction map problem. *Bioinformatics*, 10(3):349–358, 1994.
- [83] V.V. Solovyev and A.A. Salamov. Predicting alpha-helix and beta-strand segments of globular proteins. *Bioinformatics*, 10(6):661–669, 1994.
- [84] E.L. Sonnhammer and R. Durbin. A workbench for large-scale sequence homology analysis. *Bioinformatics*, 10(3):301–307, 1994.
- [85] V.B. Strelets, A.A. Ptitsyn, L. Milanesi, and H.A. Lim. Data bank homology search algorithm with linear computation complexity. *Bioinformatics*, 10(3):319–322, 1994.
- [86] R.L. Tatusov and E.V. Koonin. A simple tool to search for sequence motifs that are conserved in blast outputs. *Bioinformatics*, 10(4):457–459, 1994.
- [87] J.D. Thompson, D.G. Higgins, and T.J. Gibson. Improved sensitivity of profile searches through the use of sequence weights and gap excision. *Bioinformatics*, 10(1):19–29, 1994.
- [88] B.K. Tizard, J.A. Stanton, and N.G. Laing. Diffscreen: The merging of image subtraction and molecular genetics for the rapid analysis of differentially screened cdna libraries. *Bioinformatics*, 10(2):209–210, 1994.
- [89] A. Torelli and C.A. Robotti. Advance and adam: Two algorithms for the analysis of global similarity between homologous informational sequences. *Bioinformatics*, 10(1):3–5, 1994.
- [90] O. Trelles-Salazar, E.L. Zapata, and J.M. Carazo. On an efficient parallelization of exhaustive sequence comparison algorithms on message passing architectures. *Bioinformatics*, 10(5):509–511, 1994.

- [91] C.S. Tung and E.S. Carter II. Nucleic acid modeling tool (namot): An interactive graphic tool for modeling nucleic acid structures. *Bioinformatics*, 10(4):427–433, 1994.
- [92] Y. Van de Peer and R. De Wachter. Treecon for windows: A software package for the construction and drawing of evolutionary trees for the microsoft windows environment. *Bioinformatics*, 10(5):569–570, 1994.
- [93] L.L. Walsh. Navigating the brookhaven protein data bank. *Bioinformatics*, 10(5):551–557, 1994.
- [94] Y. Wang, R.A. Prade, J. Griffith, W.E. Timberlake, and J. Arnold. Ods_bootstrap: Assessing the statistical reliability of physical maps by bootstrap resampling. *Bioinformatics*, 10(6):625–634, 1994.
- [95] M.F. Wilkins, C.W. Morris, and L. Boddy. A comparison of radial basis function and backpropagation neural networks for identification of marine phytoplankton from multivariate flow cytometry data. *Bioinformatics*, 10(3):285–294, 1994.
- [96] S.R. Wilson and P.J. Solomon. Estimates for different stages of hiv/aids disease. *Bioinformatics*, 10(6):681–683, 1994.
- [97] D.S. Wishart, R.F. Boyko, and B.D. Sykes. Constrained multiple sequence alignment using xalign. *Bioinformatics*, 10(6):687–688, 1994.
- [98] D.S. Wishart, R.F. Boyko, L. Willard, F.M. Richards, and B.D. Sykes. Seqsee: A comprehensive program suite for protein sequence analysis. *Bioinformatics*, 10(2):121–132, 1994.
- [99] L.W. Wright, J.B. Lichter, J. Reinitz, M.A. Shifman, K.K. Kidd, and P.L. Miller. Computer-assisted restriction mapping: An integrated approach to handling experimental uncertainty. *Bioinformatics*, 10(4):435–442, 1994.
- [100] Y. Xu, R.J. Mural, and E.C. Uberbacher. Constructing gene models from accurately predicted exons: An application of dynamic programming. *Bioinformatics*, 10(6):613–623, 1994.
- [101] P. Zhang, E.A. Schon, S.G. Fischer, E. Cayanis, J. Weiss, S. Kistler, and P.E. Bourne. An algorithm based on graph theory for the assembly

of contigs in physical mapping of dna. *Bioinformatics*, 10(3):309–317, 1994.

- [102] E. Zintzaras, N.P. Brown, and A. Kowald. Growing a classification tree using the apparent misclassification rate. *Bioinformatics*, 10(3):263–271, 1994.