

References

- [1] M. Bernstein. Reducing the man-machine barrier: The sequence analysis workbench. *Bioinformatics*, 3(3):229–232, 1987.
- [2] M. Bernstein. Using spreadsheet languages to understand sequence analysis algorithms. *Bioinformatics*, 3(3):217–221, 1987.
- [3] T.N. Bryant. Programs for evaluating and characterising bacterial taxonomic data. *Bioinformatics*, 3(1):45–48, 1987.
- [4] J. Campione-Piccardo. Graphic and dna sequence interface for the pcp123 database system for managing recombinant dna data. *Bioinformatics*, 3(4):359–359, 1987.
- [5] J. Csirik, J. Magyar, and G. Polner. A computer algorithm to determine the recognition site of restriction enzymes. *Bioinformatics*, 3(3):245–246, 1987.
- [6] A. Danckaert, C. Mugnier, P. Dessen, and M. Cohen-Solal. A computer program for the design of optimal synthetic oligonucleotide probes for protein coding genes. *Bioinformatics*, 3(4):303–307, 1987.
- [7] M. Edwards, D.R. Morse, and A.H. Fielding. Expert systems: Frames, rules or logic for species identification? *Bioinformatics*, 3(1):1–7, 1987.
- [8] G. Fichant and C. Gautier. Statistical method for predicting protein coding regions in nucleic acid sequences. *Bioinformatics*, 3(4):287–295, 1987.
- [9] A. Galat and I.H. Goldberg. Analysis of microdensitometric data in terms of probability of cleavage of dna. *Bioinformatics*, 3(4):333–338, 1987.
- [10] P.D. Gershon and P.E. Hammond. A microprocessor-based control unit for plasmodium falciparum culture apparatus. *Bioinformatics*, 3(1):21–24, 1987.
- [11] O. Gotoh. Pattern matching of biological sequences with limited storage. *Bioinformatics*, 3(1):17–20, 1987.

- [12] U. Grob and K. Stuber. Genexpert, a program system for nucleic acid sequence structural interpretation. *Bioinformatics*, 3(3):243–244, 1987.
- [13] K.D. Gruskin and T.F. Smith. Molecular genetics and computer analyses. *Bioinformatics*, 3(3):167–170, 1987.
- [14] D.P. Hader and M. Truss. High resolution scanning of absorbing and fluorescent electrophoresis gels using video image analysis. *Bioinformatics*, 3(4):339–343, 1987.
- [15] R. Henderson, C. Macintyre, H. Macleod, and H. Talbot. An evaluation of some statistics packages for the bbc microcomputer. *Bioinformatics*, 3(4):279–282, 1987.
- [16] D.G. Higgins and M. Gouy. Interfacing similarity search software with the sequence retrieval system acnuc. *Bioinformatics*, 3(3):239–241, 1987.
- [17] H.B. Jenson. Two computer programs for rapid entry of dna sequence data. *Bioinformatics*, 3(4):283–286, 1987.
- [18] A.K Konopka and G.W Smythers. Distan — a program which detects significant distances between short oligonucleotides. *Bioinformatics*, 3(3):193–201, 1987.
- [19] M. Kudo, Y. Iida, and M. Shimbo. Syntactic pattern analysis of 5'-splice site sequences of mrna precursors in higher eukaryote genes. *Bioinformatics*, 3(4):319–324, 1987.
- [20] J.M. Lacroix and M.C. Lavoie. Microcomputer package for statistical analysis of microbial populations. *Bioinformatics*, 3(4):309–312, 1987.
- [21] J.A. Laszlo. Determination of stoichiometric association constants by a non-iterative computational method. *Bioinformatics*, 3(4):351–357, 1987.
- [22] Y. Lida. Dna sequences and multivariate statistical analysis. categorical discrimination approach to 5' splice site signals of mrna precursors in higher eukaryotes' genes. *Bioinformatics*, 3(2):93–98, 1987.
- [23] F.X. Malcata. Computer aided design of pellets for fixed-bed reactors performing michaelis-menten reactions. *Bioinformatics*, 3(4):297–301, 1987.

- [24] F.X. Malcata. Hersim: A microcomputer program designed to compute the limits of conversion for real homogeneous isothermal enzymic reactors. *Bioinformatics*, 3(2):105–109, 1987.
- [25] G. Mengeritsky and T.F. Smith. Recognition of characteristic patterns in sets of functionally equivalent dna sequences. *Bioinformatics*, 3(3):223–227, 1987.
- [26] F. Michiels, A.G. Craig, G. Zehetner, G.P. Smith, and H. Lehrach. Molecular approaches to genome analysis: A strategy for the construction of ordered overlapping clone libraries. *Bioinformatics*, 3(3):203–210, 1987.
- [27] J.L. Micol. Two different approaches to computer-aided teaching of microbial genetics. *Bioinformatics*, 3(2):89–92, 1987.
- [28] N.J. Moote, P. Chenier, M. Mikhail, and J. Drouin. A program for the graphic representation and manipulation of dna sequences. *Bioinformatics*, 3(3):189–192, 1987.
- [29] H.B. Nicholas, Y.M. Chen, and W.H. McClain. Comparison of trna sequences. *Bioinformatics*, 3(1):53–53, 1987.
- [30] Jr. Nicholas, H.B. and W.H. McClain. An algorithm for discriminating sequences and its application to yeast transfer rna. *Bioinformatics*, 3(3):177–181, 1987.
- [31] A. Page. A non-linear regression program in basic for estimating km and vmax. *Bioinformatics*, 3(1):49–51, 1987.
- [32] S. Pascarella and F. Bossa. Proteus: A suite of programs for prediction of structural features of proteins using an apple iie. *Bioinformatics*, 3(4):325–331, 1987.
- [33] D. Penny and M.D. Hendy. Turbotree: A fast algorithm for minimal trees. *Bioinformatics*, 3(3):183–187, 1987.
- [34] L.M. Pullan. Automated radioligand receptor binding analysis with templates for lotus. *Bioinformatics*, 3(2):131–131, 1987.
- [35] W.W. Ralph, T. Webster, and T.F. Smith. A modified chou and fasman protein structure algorithm. *Bioinformatics*, 3(3):211–216, 1987.

- [36] J.G Reich and W. Meiske. A simple statistical significance test of window scores in large dot matrices obtained from protein or nucleic acid sequences. *Bioinformatics*, 3(1):25–30, 1987.
- [37] A.H. Reisner and C.A. Bucholtz. Two-dimensional abstract representations (signatures) of proteins. *Bioinformatics*, 3(3):171–175, 1987.
- [38] M. Santibanez and K. Rohde. A multiple alignment program for protein sequences. *Bioinformatics*, 3(2):111–114, 1987.
- [39] W. Saurin. Repetitive palindromic sequences in escherichia coli. detection and characterization with a new computer program. *Bioinformatics*, 3(2):121–127, 1987.
- [40] W. Saurin and P. Marliere. Matching relational patterns in nucleic acid sequences. *Bioinformatics*, 3(2):115–120, 1987.
- [41] W. Sofer and P. Martin. Analysis of densitometric data obtained from electrophoretic analysis. *Bioinformatics*, 3(2):129–129, 1987.
- [42] P.A. Stockwell and G.B. Petersen. Homed: A homologous sequence editor. *Bioinformatics*, 3(1):37–43, 1987.
- [43] G.M. Studnicka. Hyperbolic regression analysis for kinetics, electrophoresis, elisa, ria, bradford, lowry, and other applications. *Bioinformatics*, 3(1):9–16, 1987.
- [44] W.R Taylor. Multiple sequence alignment by a pairwise algorithm. *Bioinformatics*, 3(2):81–87, 1987.
- [45] D. Verotta and L.B. Sheiner. Simultaneous modeling of pharmacokinetics and pharmacodynamics: An improved algorithm. *Bioinformatics*, 3(4):345–349, 1987.
- [46] M.J. Weise. An access interface for the ms-dos diskette format of genbank(r), a gene sequence database. *Bioinformatics*, 3(4):313–317, 1987.
- [47] A.V. Whitmore. Recording waveforms with the acorn bbc microcomputer. *Bioinformatics*, 3(2):130–130, 1987.

- [48] A. Wohlgemuth and D.P. Dubey. Symbolic reinterpretation of hla gene products-impact on interpretation of hla data at the molecular level. *Bioinformatics*, 3(3):233–238, 1987.
- [49] K. Yamamoto, N. Sakurai, and H. Yoshikura. Graphics of rna secondary structure; towards an object-oriented algorithm. *Bioinformatics*, 3(2):99–103, 1987. see Erratum in Computer Applications in the Biosciences, Vol. 3, 1987, No. 3, 277.
- [50] K. Yamamoto and H. Yoshikura. An improved algorithm for the prediction of optimum and suboptimum folding structures of long single-stranded rna. *Bioinformatics*, 3(1):31–35, 1987.