A Programming Course in Bioinformatics for Computer and Information Science Students

Appendix I: Course Reading List

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Course reading list . as contained in compiled course reader.

Each reading is numbered in the for N.M were N is the number of the lecture, corresponding to the discussion in Section 1.3, and the numbering of Table IA. M is the sequence of readings for that lecture. All readings were gathered together in a course reader, purchased by students for approximately $50.00. Copyright for all materials was obtained by the producer of the course reader, who also paid fees for copyrights, and added these to the cost of the reader.

1.1. Altman, R. B. (1992). A few basic concepts about DNA, RNA and Proteins. Stanford, CA. Unpublished.

2.1. Gribskov, M. & J. Devereux (1992). Sequence Analysis Primer. UWBC Biotechnical Resource Series. R. R. Burgess. New York, W. H. Freeman & Co.**:** 124-137.

2.2. Needleman, S. B. & C. D. Wunsch (1970). "A General Method Applicable to the Search for Similarities in the Amino Acid Sequence of Two Proteins." J. Mol. Biol. **48**: 443-452.

3.1. Stryer, L. (1988). Biochemistry. New York, W.H. Freeman. pages 15-40 (chapter 2).

3.2. Calladine, C. R. & H. R. Drew (1992). Understanding DNA, Academic Press**:** 1-40.

4.1. Craig, J. J. (1986). Introduction to Robotics Mechanics and Control. Menlo Park, CA, Addison-Wesley. Chapter 2 (p. 15-59).

4.2. Arun, K. S., T. S. Huang & S. D. Blostein (1987). "Least-squares fitting of two 3-D point sets." IEEE Transactions on Pattern Analysis and Machine Intelligence **9**(5): 698-700.

5.1. Hinds, D. A. & M. Levitt (1992). "A lattice model for protein structure prediction at low resolution." Proc Natl Acad Sci U S A **89**(7): 2536-40.

6.1. Stryer, L. (1988). Biochemistry. New York, W.H. Freeman. pages 141-174 (chapter 7).

8.1. Klingler, T. & D. Brutlag (1993). Detection of Correlations in tRNA Sequences with Structural Implications. Proceedings of the First International Conference on Intelligent Systems for Molecular Biology. L. Hunter, D. Searls and J. Shavlik. Menlo Park, AAAI Press**:** 225-233.

8.2. Klingler, T. & D. Brutlag (1994). "Discovering Structural Correlations in alpha-Helices." Protein Science **3**: 1847-1857.

9.1. Daggett, V. & M. Levitt (1992). "A model of the molten globule state from molecular dynamics simulations." Proc Natl Acad Sci U S A **89**(11): 5142-6.

10.1. Altman, R. B. (1995). "A probabilistic approach to determining biological structure: integrating uncertain data sources", Int. J. Human Comp. Studies., in press..

11.1 Koza, J. R. (1994). Evolution of a computer program for classifying protein segments as transmembrane domains using genetic programming. Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology, Stanford, CA. R. Altman, D. Brutlag, P. Karp, R. Lathrop and D. Searls. Menlo Park, AAAI Press**:** 244-252.

11.2 Koza, J. R. (1994). Introduction to genetic programming. Advances in Genetic Programming. J. Kinnear, K E. Cambridge, MA, MIT Press**:** 21-45.

12.1. Rabiner, L. R. (1989). "A tutorial on hidden Markov models and selected applications in speech recognition." Proc IEEE **77**(2): 257-286.

12.2. Krogh, A., M. Brown, I. S. Mian, K. Sjolander & D. Haussler (1994). "Hidden Markov Models in Computational Biology: Applications to Protein Modeling." J. Mol. Biol. **235**: 1501-1531.

13.1. Bagley, S.C. and Altman, R., "Characterizing the microenvironment surrounding protein sites." Protein Science, 4, 622-635, 1995.

13.2. Bagley, S.C., Wei, L., Cheng, C., and Altman, R.B., Characterizing oriented protein structural sites using biochemical properties, Third International Conference on Intelligent Systems in Molecular Biology, Cambridge, London, July, 1995, AAAI Press, Menlo Park, p. 12-20.

14.1. Richards, F. M. (1985). "Calculation of Molecular Volumes and Areas for Structures of Known Geometry." Methods in Enzymology **115**: 440-464.

14.2. Gerstein, M., J. Tsai & M. Levitt (1995). "The Volume of Atoms on the Protein Surface: Calculated from Simulation using Voronoi Polyhedra." J. Mol. Biol., in press.

15.1 Garnier, J. & B. Robson (1990). The GOR method for predicting secondary structure in proteins. Prediction of Protein Structure and the Principles of Protein Conformation. G. R. Fasman. New York, Plenum Press**:** 417-465.

15.2. Prevelige, J., P & G. D. Fasman (1990). Chou-Fasman prediction of the secondary structure of proteins. Prediction of Protein Structure and the Principles of Protein Conformation. G. R. Fasman. New York, Plenum Press**:** 391-416.

16.1. Clark, D. A., C. J. Rawlings & S. Doursenot (1994). Genetic Map Construction with Constraints. Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology. R. Altman, D. Brutlag, P. Karp, R. Lathrop and D. Searls. Menlo Park, AAAI Press**:** 78-86.

16.2 Istvanick, W., A. Kryder, G. Lewandowski, J. Meidanis, A. Rang, S. Wyman & D. Joseph (1993). Dynamic Methods for Fragment Assembly in Large Scale Genome Sequencing Projects. Proceedings of the Twenty-Sixth Hawaii International Conference on System Sciences. L. Hunter. Los Alamitos, CA, IEEE Computer Society Press. **I:** 534-543.

17.1. Milosavljevic, A. (1993). Discovering Sequence Similarity by the Algorithmic Significance Method. Proceedings of the First International Conference on Intelligent Systems for Molecular Biology. R. Altman, D. Brutlag, P. Karp, R. Lathrop and D. Searls. Menlo Park, AAAI Press**:** 284-291.

17.2. Thorne, J. L., H. Kishino & J. Felsenstein (1991). "An evolutionary model for maximum likelihood alignment of DNA sequences [published erratum appears in J Mol Evol 1992 Jan;34(1):91]." J Mol Evol **33**(2): 114-24.

18.1. Letovsky, S. & M. Berlyn (1994). Issues in the Design of Complex Scientific Databases. Hawaii International Conference on Systems Science. L. Hunter. Maui, Hawaii, IEEE Computer Society Press. **V:** 5-14.

18.2. Karp, P. (1992). The design space of frame knowledge representations systems, SRI International.

18.3. Karp, P. & S. Paley (1994). Representations of Metabolic Knowledge: Pathways. Second International Conference on Intelligent Systems for Molecular Biology. R. Altman, Brutlag, D., Karp, P., Lathrop, R., Searls, D. Stanford, CA, AAAI Press**:** 203-211.

19.1 Altman, R. B., B. Weiser & H. Noller (1994). Constraint Satisfaction Techniques for Modeling Large Complexes: Application to the Central Domain of 16S Ribosomal RNA. Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology. R. Altman, D. Brutlag, P. Karp, R. Lathrop and D. Searls. Menlo Park, AAAI Press**:** p. 10-18.