BT 310 Bioinformatics and Computational Biology Laboratory (0-0-6-6)

Molecular databases and their organization; Analysis of Restriction sites in a known DNA fragment; Design of a specific PCR primer for an amplicon; Homology search algorithm; Multiple sequence alignment and phylogenetic analysis; Gene identification strategies; Identification of structural and functional motifs; Visualization and analysis of protein structure; Homology Modeling of protein.

Texts:

1. Bioinformatics computing: the complete practical guide to bioinformatics for lifescientists, B. Bryan, Prentice Hall, 2000.
2. Bioinformatics: methods and protocols, S. Misener and S. A. Krawetz, Humana Press, 2000.
3. Bioinformatics – A Practical Guide to the Analysis of Genes and Proteins, D. Baxevanis, and B. F. F. Ouellette, 2nd Ed., John Wiley and Sons Inc., 2001.
4. Molecular Modelling: Principles and Applications, A. R. Leach, Addison-Wesley Pub. Co. 1997.
5. Bioinformatics: Sequence and Genome Analysis, David Mount
6. Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids, Richard Durbin, Sean R Eddy, Anders Krogh, Graeme Mitchison

References:

1. Structural Bioinformatics, P. E. Bourne and H. Weissig, WILEY, 2003.
2. Bioinformatics - From Genomes to Drugs, T. Lengauer, Vols 1 and 2, Wiley-VCH, 2002.
3. Introduction to bioinformatics: a theoretical and practical approach, S. A. Krawetz and D. D. Womble, Humana Press, 2003.
4. Bioinformatics: sequence, structure and databanks-a practical Approach, D. Higgins and W. Taylor (ed.), Oxford, 2000.