BT 301 Bioinformatics and Computational Biology (2-0-0-4)

Introduction to bioinformatics; Gene bank sequence database; submitting sequences to database; Analysis of genome content and organization; Analysis of protein content and organization; Analysis of protein structures; Identification of signature motifs in proteins; Comparative genomics and proteomics.

Basics of aligning nucleic acid and protein sequences; Phylogenetic analysis using internet; Secondary structure prediction; protein structure-function relationships; computational analysis of protein-ligand binding; enzyme catalysis and protein folding.

Texts:

1. 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.
2. Molecular Modelling: Principles and Applications, A. R. Leach, Addison-Wesley Pub. Co. 1997.
3. Bioinformatics: Principles and Applications, Zhumur Ghosh and Bibekanand Mallick
4. Bioinformatics: Sequence and Genome Analysis, David Mount
5. 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.