

Approval: 6th Senate Meeting

Course Name : Bioinformatics Applications for Systems Analysis
Course Number : BY606 & BY606P
Credit : 2-0-2-3
Prerequisites : Knowledge of pattern recognition and artificial intelligence
Students intended for : B. Tech. 3rd & 4th year, M.S. and Ph.D.
Elective or Compulsory : Elective
Semester : Even

Course Outline:

Objective: The course is aimed at providing a basic understanding to the students about bioinformatics methods and their in-depth applications for solving biological problems. The course will include practical sessions for the students to help them master some of the bioinformatics techniques from hands-on experience. The course may also involve a project/term-paper development towards important biological problems within the purview of the course.

Part I: Basic Bioinformatics (5 Lectures)

Introduction to Bioinformatics: What is Bioinformatics? What are the applications of Bioinformatics?

Introduction to Basic Biology: Introduction to basic biological processes to which bioinformatics methods will be mainly applied in this course.

Introduction to Basic Programming: Introduction to basic scripting in Linux/Unix environment and programming (Perl Language) routinely used for bioinformatics analysis.

Sequence and Molecular File formats: Introduction to different file formats used for biological data including GenBank, FASTA, EMBL, Clustal, Phylip, SwissProt. Sequence and molecular file conversion tools (ReadSeq, SeqVerter, etc.).

Databases in Bioinformatics: Introduction to different biological databases (NCBI, EMBL, DDBJ, PIR, SwissProt, etc.), their classification schemes, and biological database retrieval systems.

Part II: Bio-algorithms and Tools (23 Lectures)

Sequence Alignments: Introduction to concept of alignment, Scoring matrices (BLOSUM, PAM), Alignment algorithms for pairs of sequences (Dot Matrix method, Global vs. Local alignment, Dynamic Programming algorithm, Needleman-Wunsch algorithm, Smith Waterman algorithm), Heuristic methods (FASTA, BLAST) Multiple sequence alignment (DPA, Heuristic methods, Genetic Algorithm, Simulated annealing, Profile HMMs).

Gene Prediction Methods: What is gene prediction? Computational methods of gene prediction. Extrinsic vs. Intrinsic methods, Prokaryotic and Eukaryotic gene prediction methods and tools.

Molecular Phylogeny: Introduction to phenotypic and molecular phylogeny. Representation of phylogeny, Molecular clocks, Methods of phylogenetic construction, Evolutionary models (Jukes-Cantor one-parameter model, Kimura two-parameter model), Maximum Parsimony method, Maximum Likelihood method, Distance methods, UPGMA, Neighbor-Joining Method, Fitch-Margoliash method, Minimum Evolution, statistical evaluation of the obtained phylogenetic trees (bootstrapping, Jackknifing), software for phylogenetic analyses (PHYLIP, PAML, PAUP), Tree viewing.

Pathways and Systems Biology: Introduction to pathways and systems biology, Analysis of Pathways, Metabolic network properties, Metabolic control analysis, Simulation of cellular activities.

The lab **BY606P** will expose the students to basic tools and methods used to perform the above bioinformatics analysis on real biological data. The students will learn the effect of parameters and thresholds used for some of the analysis on the results obtained.

Text Book:

Bioinformatics: Methods and Applications Genomics, Proteomics, and Drug Discovery S.C. Rastogi, N. Mendiratta, P. Rastogi (3rd Edition) PHI Learning Private Limited New Delhi (2011)
Bioinformatics Principles and Applications. Z. Ghosh and B. Mallick Oxford University Press.

Other References:

1. Introduction to Bioinformatics. Arthur M. Lesk (3rd Edition) Oxford University Press.
2. Genes IX - 9th ed. Benjamin Lewin.

Articles:

Latest research articles will be advised related to the topic being taught.