



Bioinformatics: Algorithms and Applications

Biotechnology

Instructor Name: Prof. M. Michael Gromiha

Institute: IIT Madras

Department: Biotechnology

About Instructor: M Michael Gromiha received his Ph.D in Physics from Bharathidasan University, India and served as STA fellow, RIKEN Researcher, Research Scientist and Senior Scientist at Computational Biology Research Center, AIST, Japan till 2010. Currently, he is working as an Associate Professor at Indian Institute of Technology (IIT) Madras, India. He is teaching courses on bioinformatics, protein structure and function, protein interactions: computational techniques, big data analysis and handling computational biology lab. His main research interests are structural analysis, prediction, folding and stability of globular and membrane proteins, protein interactions and development of bioinformatics databases and tools.

Pre Requisites: : Nil; Basic knowledge on Biology and any computer language would be helpful

Core/Elective: : Core

UG/PG: : Both

Industry Support : Cognizant, TCS

Course Intro: : Bioinformatics is an interdisciplinary field of science for analyzing and interpreting vast biological data using computational techniques. In this course, we aim to give a walkthrough of the major aspects of bioinformatics such as the development of databases, computationally derived hypothesis, algorithms, and computer-aided drug design. During the first section of the course, we will focus on DNA and protein sequence databases and analysis, secondary structures and 3D structural analysis. The second section will be devoted to applications such as prediction of protein structure, folding rates, stability upon mutation, and intermolecular interactions. Further, we will cover computer-aided drug design using docking and QSAR studies. This course is designed to nurture skills and knowledge required for aspiring students, young biologists and research scholars to develop algorithms and tools in bioinformatics.

COURSE PLAN

SL.NO	Week	Module Name
1	1	Introduction, DNA sequence analysis, DNA Databases
2	2	Protein structure and function, protein sequence databases, sequence alignment
3	3	PAM matrix, Global and local alignment, BLAST: features and scores
4	4	Multiple sequence alignment, Conservation score, phylogenetic trees
5	5	Protein sequence analysis, hydrophobicity profiles, non-redundant datasets
6	6	Protein secondary structures, Ramachandran plot, propensity, secondary structure prediction
7	7	Protein tertiary structure, Protein Data Bank, visualization tools, structural classification, contact maps



8	8	Protein structural analysis, protein structure prediction
9	9	Protein stability, energetic contributions, database, stabilizing residues, stability upon mutations
10	10	Protein folding rates, proteins interactions, binding site residues
11	11	Computer aided drug design, docking, screening, QSAR
12	12	Development of algorithms, awk programming, machine learning techniques, applications using WEKA