BIO-INFORMATICS : ALGORITHMS AND APPLICATIONS

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TYPE OF COURSE   : Rerun | Core | UG/PG

COURSE DURATION   : 12 weeks (24 Jan' 22 - 15 Apr' 22)

EXAM DATE   : 24 Apr 2022

PRE-REQUISITES : Basic knowledge of Biology and any computer language would be helpful

INTENDED AUDIENCE : Students, PhD scholars, teachers, industry

INDUSTRIES APPLICABLE TO : Cognizant, TCS

COURSE OUTLINE :
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.

ABOUT INSTRUCTOR :
Prof. 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. He has published over 200 research articles, 40 reviews, 5 editorials and a book on Protein Bioinformatics: From Sequence to Function by Elsevier/Academic Press. His papers received more than 9000 citations and h-index is 52.

COURSE PLAN :

Week 1 **:** Introduction, DNA sequence analysis, DNA Databases

Week 2 **:** Protein structure and function, protein sequence databases, sequence alignment

Week 3 **:** PAM matrix, Global and local alignment, BLAST: features and scores

Week 4 **:** Multiple sequence alignment, Conservation score, phylogenetic trees

Week 5 **:** Protein sequence analysis, hydrophobicity profiles, non-redundant datasets

Week 6 **:** Protein secondary structures, Ramachandran plot, propensity, secondary structure prediction

Week 7 **:** Protein tertiary structure, Protein Data Bank, visualization tools, structural classification

Week 8 **:** Protein structural analysis, protein structure prediction

Week 9 **:** Protein stability, energetic contributions, database, stabilizing residues

Week 10 **:** Protein folding rates, proteins interactions, binding site residues

Week 11 **:** Computer aided drug design, docking, screening, QSAR

Week 12 **:** Development of algorithms, awk programming, machine learning techniques, applications using WEKA