BIOINFORMATICS

Department : **Botany**

Course Directors : **Dr. Lokesh Ravi** & **Dr Jayarama Reddy**

Duration of the Course : **90** hrs (Credits: **3**)

Fees : Rs.4,500/-

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Course Objectives :

- To provide understanding of biological databases and their relevance in research and literature review, and the significance and individuality of key databases with applications.
- To provide deeper understanding to students in regards to the structural and functional properties of biomolecules.
- To bestow on skill set to perform sequence alignment, phylogenetic correlation and structure prediction of biomolecules using bioinformatic tools.

Syllabus (Course Content) :

A. Theory Classes

Unit-1: Introduction to Bioinformatics Definition and History and Applications of Bioinformatics, Internet resources, various databases and bioinformatics tools, organization of databases.

Unit-2: Biological Databases Nucleic acid sequence databases, Protein sequence databases, Repositories for high throughput genomic sequences, Genome Databases, 3D Structure Database, Chemical Structure database, Gene Expression database, Derived Databases, Structure classification database, Protein-Protein interaction database and Pathway database.

Unit-3: Sequence Analysis File formats, Basic concepts of sequence analysis, Scoring matrices, Pair wise sequence alignments, multiple sequence alignment, Database Searches: Keyword-based searches and Sequence-based searches, Profile-based searches, Markov chains and applications.

Unit-4: Structure Prediction Overview and Introduction to Protein Structure, Sequence-Sequence Alignment Methods, Sequence Based Secondary Structure Prediction. Visualization of structures using Rasmol or SPDBV. Fundamentals of the methods for 3D structure prediction, Homology/comparative Modeling, fold recognition, threading approaches, and *ab initio* structure prediction methods.

B. Web interactive online practicals

List of Experiments:

1. Referencing in Scientific literature and their practical usage, PubMed
2. Sequence retrieval
3. Biological Databases: Study of different Biological databases, Sequence formats.
4. Pair wise sequence alignment
5. Local and Global alignment methods
6. Databases search for homologous sequence using (BLAST) and (FASTA)
7. MSA: (Clustal W and Clustal X)
9. Protein structure prediction tools: JPred
10. Molecular Visualization using RasWin

C. Project Work

Based on the web interactive online practicals conducted