



Course Title: Basic Bioinformatics

Course Code: BIOF202

Units: 04

L	T	P/ S	SW/F W	TOTAL CREDIT UNITS
3	0	2	0	4

Course Objectives:

Theory: The basic objective is to give students an introduction to the basic practical techniques of bioinformatics. Emphasis will be given to the application of bioinformatics and biological databases to problem solving in real research problems. The students will become familiar with the use of a wide variety of internet applications, biological database and will be able to apply these methods to research problems.

Practical: The aim is to provide practical training in bioinformatics methods including accessing the major public sequence databases, use of the different computational tools to find sequences, analysis of protein and nucleic acid sequences by various software packages. It also provides a step by step, theoretical and practical introduction to the development of useful tools for automation of complex computer jobs, and making these tools accessible on the network from a Web browser.

Pre-requisites: Basic knowledge of Biology, Mathematics and Computer.

Student Learning Outcomes:

- The students will be able to describe the contents and properties of the most important bioinformatics databases, perform text- and sequence-based searches, and analyze and discuss the results in light of molecular biological knowledge
- The students will be able to explain the major steps in pairwise and multiple sequence alignment, explain the principle for, and execute pairwise sequence alignment by dynamic programming
- The students will be able to predict the secondary and tertiary structures of protein sequences.

Course Contents/Syllabus- Theory:

	Weightage (%)
Module I	25%

<p>Introduction to Bioinformatics Definition and History and Applications of Bioinformatics, Internet resources, various databases and bioinformatics tools, organization of databases</p>	
<p>Module II</p>	25%
<p>Biological Databases</p> <p>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</p>	
<p>Module III</p>	25%
<p>Sequence Analysis</p> <p>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</p>	
<p>Module IV</p>	25%
<p>Structure Prediction</p> <p>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. Use of modeller</p>	

Pedagogy for Course Delivery:

Theory

Lectures : 41
Presentation : 3
Class Test : 1
Total : 45

Practical

Practical : 28

Lab internal : 2
 Total : 30

List of Experiments:

1. Referencing in Scientific literature and their practical usage, PubMed
2. Sequence retrieval
3. Biological Databases: Study of different Biological databases (esp. the ones given below), Format.
4. Pair wise sequence alignment
5. Local and Global alignment – Algorithms
6. DOT matrix analysis
7. Databases search for homologous sequence using (BLAST) and (FASTA)
8. MSA: (Clustal W, Clustal X, PILE UP), Algorithms-MSA, Progressive alignment etc, Problems with MSA method, Statistics behind MSA
9. Protein structure prediction tools

Assessment/ Examination Scheme:

Theory L/T (%)	Lab/Practical/Studio (%)	Total
75%	25%	100%

Theory Assessment (L&T):

Components (Drop down)	Class Test 1	Home Assignment	Presentation/ Seminar	Attendance	End Term Examination
Weight age (%)	15	5	5	5	70

Lab/ Practical/ Studio Assessment:

Components (Drop down)	Continuous Assessment/Internal Assessment				End Term Examination			
	Class Test (Practical based)	Lab record	viva	Attendance	Lab record	Performance	Viva	Total
Weight age (%)	15	5	5	5	10	40	20	70

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TEXT BOOKS

- Bioinformatics: Sequence, Structure and Databanks: A Practical Approach (The Practical Approach Series, 236), Des Higgins (Editor), Willie Taylor. 1st edition, October 2000, Oxford University Press. ISBN: 978-0199637904.
- Bioinformatics: Sequence and Genome Analysis, David W. Mount. 2nd edition, June 2004, Cold spring harbor laboratory press. ISBN: 978-0879697129

REFERENCES

- Introduction to Bioinformatics, Teresa Attwood, David Parry-Smith, 1st edition, May 2001, Pearson Education. ISBN: 978-8178085074
- Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, Second Edition, Andreas D. Baxevanis, B. F. Francis Ouellette. 3rd edition, October 2004, A John Wiley & Sons, Inc., Publication. ISBN: 978-0471478782.

Any other Study Material:

- Online tutorials