



**FORMAT FOR COURSE CURRICULUM**

**Course Title: Bioinformatics & Computational Biology**

**Course Code: BIOF611**

**Credit Units: 04**

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

**Course Objectives:**

Theory: This course will enable the students to achieve skills in Bioinformatics & Computational Biology that are essential for application in Biotechnology.

**Pre-requisites:** Basic knowledge about molecular biology & computers.

**Student Learning Outcomes:**

- The student will choose biological data, submission and retrieval it from databases and design databases to store the information.
- The student will employ skills to make inferences and analysis of a problem using a uniform schema.

**Course Contents/Syllabus- Theory:**

	Weightage (%)
<b>Module I</b>	<b>15</b>
<b>Descriptors/Topics: Introduction to Bioinformatics</b>  Overview of Bioinformatics and computational biology. Importance of databases - EMBL – NCBI nucleic acid sequence databases - protein sequence databases (SwissProt) - structure databases (PDB) - bibliographic databases.	
<b>Module II</b>	<b>25</b>
<b>Descriptors/Topics: Sequence Alignment Methods</b>  Sequence analysis of biological data - methods of alignment - methods for optimal alignments; using gap penalties and scoring matrices- multiple sequence alignment – introduction - tools for MSA (MUSCLE, T-coffee) - application of multiple sequence alignment. Similarity Searching Tools: BLAST and FASTA, Theory and Algorithms, variants of	

BLAST and FASTA, PSI-BLAST and PHI BLAST, Statistical Significance.	
<b>Module III</b>	<b>20</b>
<p><b>Descriptors/Topics: Molecular Phylogenetics and Methods</b></p> <p>The concept of evolutionary tree, terminology of phylogenetics, introduction to evolutionary models, Types of phylogenetic trees (rooted vs. unrooted trees). Phylogenetic analysis algorithms: UPGMA, Neighbors-Relation, Neighbor-Joining, maximum Parsimony, maximum likelihood. Tree evaluation methods: Bootstrapping, Randomized and jack-knifing methods, Phylogenetic analysis software: PHYLIP, MEGA, and PhyML.</p>	
<b>Module IV</b>	<b>20</b>
<p><b>Descriptors/Topics: Predictive methods using DNA and protein sequences</b></p> <p>Concepts of motif, pattern and profile, Gene Identification methods, Gene predictions strategies – Prokaryotic and Eukaryotic, Identification and characterization of proteins, Protein structure prediction methods: Secondary and tertiary approaches. Protein Identification and characterization: ProtParam, Peptide cutter.</p>	
<b>Module V</b>	<b>20</b>
<p><b>Descriptors/Topics: Introduction to Chemoinformatics, Molecular modelling &amp; Drug designing</b></p> <p>Chemical similarity search methods, Designing focused chemical libraries, Comparative protein modelling, Molecular docking and virtual high-throughput screening, Search algorithms, Scoring methods, Challenges in Molecular docking, Introduction of receptor flexibility through multiple receptor conformations (MRC docking), Hit-to-lead optimization, Introductory concept of Activity Cliffs.</p>	

### **Pedagogy for Course Delivery:**

The class will be taught using theory and practical. In addition to assigning the practical studies, the course instructor will spend considerable time in understanding the concept of bioinformatics and its integration to different biological sciences. The instructor will cover the strategies used to analyze the biological data.

Lectures: 42

Tutorial:

Presentation/ Seminar: 2

Class Test: 1

Total: 45

## Practical

Practical : 30

Lab internal : 1

Total : 31

## List of Experiments

- Biological databases: NCBI, EMBL, DDBJ, iHOP, PDB, UniProt, KEGG, Ensembl, STRING; Sequence file formats: GenBank, FASTA, EMBL, PDB format
- DotPlot Analysis: DOTPLOT, DOTTER, DOTMATCHER., Pairwise Sequence Alignment programs: LALIGN, EMBOSS NEEDLE, EMBOSS Water, Clustalw, Muscle, T-Coffee, Similarity Searching: BLAST, Variants of Blast.
- Phylogenetic analysis software: MEGA, PHYLIP.
- Primer Designing: PRIMER3, Gene Identification Programs: GENSCAN, ORF finder. Fgenesh, Glimmer, Protein Identification and characterization: Protparam, Peptide cutter, Motif and Patterns program: Prosite, InterProScan, Pfam.
- Modelling software: Swiss Model workspace, ArgusLab, Model Evaluation: PROcheck. Docking-Hex

## Assessment/ Examination Scheme:

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

## Theory Assessment (L&T):

Continuous Assessment/Internal Assessment					End Term Examination
Components (Drop down)	Class Test 1	Viva	Home Assignment	Attendance	
Weightage (%)	10	5	10	5	70

## Lab/ Practical/ Studio Assessment:

	Continuous Assessment/Internal Assessment	End Term Examination
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<b>Components (Drop down)</b>	<b>Performance</b>	<b>Lab record</b>	<b>viva</b>	<b>Attendance</b>	<b>Lab record</b>	<b>Performance</b>	<b>Viva</b>	<b>Total</b>
<b>Weightage (%)</b>	15	5	5	5	10	50	10	70

### **TEXT BOOKS**

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

### **REFERENCES**

- Introduction to Bioinformatics, Teresa Attwood, David Parry-Smith, 1st edition, May 2001, Pearson Education
- 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
- Introduction to Bioinformatics, Arthur M. Lesk, 2002, Oxford University Press

### **Any other Study Material:**

- Online tutorials