



Course Title: Concepts of Molecular Phylogenetics
Course Code: BIOF303

Units: 03

L	T	P/S	Lab	TOTAL CREDIT UNITS
2			2	03

Course Objectives:

Theory: This course applies a combination of molecular and statistical techniques to infer evolutionary relationships among organisms, genes or proteins.
Practical: This course will help the students to gain hands on experience for the phylogenetics software platform. They will be able to draw a phylogenetic tree and analyze the result.

Pre-requisites: Basic knowledge about the biological databases and data structure.

Student Learning Outcomes:

- The student will be able to describe evolutionary process at molecular level.
- The student will apply molecular methods to study genetic variation within and between species.
- The student will explain and evaluate different phylogenetic optimality criterion and use software for biological problems.

Course Contents/Syllabus- Theory:

	Weightage (%)
Module I	30
Descriptors/Topics: Introduction to Molecular Phylogeny and Evolution Tree of Life, Basic Terminology associated with a phylogenetic tree, Trees and Homology, orthology and paralogy. Molecular basis of evolution- synonymous and non- synonymous mutations- genetic polymorphism and evolution- Population trees from genetic markers.	
Module II	40
Descriptors/Topics: Evolutionary Models & Statistical Approach Jukes-Cantor Model, Kimura Model, Statistical Models of evolution, Optimization principle and topological errors interior branch tests- bootstrap tests- Tests of topological differences- advantages and disadvantages- molecular clocks and linearized trees.	

Module III	30
Descriptors/Topics: Phylogenetic Evaluation and analysis General protocol of phylogenetic tree construction, UPGMA, evaluation methods- NJ methods- phylogenetic reconstruction, Maximum parsimony methods- Strategies of searching for MP trees- consensus trees- branch length estimation-weighted parsimony- MP methods for protein data- Maximum likelihood methods	

Pedagogy for Course Delivery:

Theory

Lectures	: 25
Presentation	: 4
Class Test	: 1
Total	: 30

Practical

Practical	: 28
Lab internal	: 2
Total	: 30

List of Experiments:

1. Sequence retrieval.
2. Biological Databases: Study of different Biological databases (esp. the ones given below), Format, their distinguishing features, Uses and Applications.
3. Databases search for homologous sequence using (BLAST) and (FASTA)
4. MSA: (Clustal W, Clustal X, PILE UP)
5. Algorithms-MSA, Progressive alignment etc
6. Problems with MSA method, Statistics behind MSA
7. Phylogenetic prediction using SDSC biology workbench.
8. Phylogenetic prediction using MEGA4.
9. Phylogenetic prediction using Phylip.

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