DEPARTMENT OF BIOINFORMATICS
SCHOOL OF BIOENGINEERING
SRM UNIVERSITY

BI0303- MOLECULAR PHYLOGENY AND EVOLUTION

LECTURE PLAN

SEMESTER: V **Course: Molecular Phylogeny And Evolution**
CODE: BI0303 **Staff Handling: Mr. P.P . Karthikeyan**
Section: III **Total Hours: 45**

LECTURE	TOPIC	LEARNING OUTCOME
1	**UNIT I-PHYLOGENETIC TREES** Types- rooted , unrooted, dendograms, cladogram, phylogram	○ **Introduction to phylogeny** ○ **Types of methods to study phylogeny** ○ **Different distance based methods**
2	Gene Trees versus Species trees	
3	Topological differences- d H between trees	
4	Tree building methods	
5	Distance methods: UPGMA	
6	LS methods	
7	Minimum evolution methods	
8	NJ methods	
9	Phylogenetic reconstruction	
10	**UNIT II- METHODS** Maximum parsimony method	○ **Character based methods** ○ **Branch length estimation** ○ **Weighted parsimony**
11	Informative sites	
12	Strategies of searching for MP trees- Subtree pruning, neighbor swapping	
13	Consensus trees	
14	Branch length estimation	
15	Weighted parsimony	
16	MP methods for protein data	
17	Maximum likelihood method	
18	Maximum likelihood concluded	
19	**UNIT III- STATISTICAL APPROACH** Optimization principle & Topological errors	○ **Validation of phylogenetic trees** ○ **Molecular clocks and linearized trees**
20	Interior branch tests- Z test	
21	Bootstrap tests	
22	Tests of topological differences-Minimum evolution method,	
23	Tests of topological differences- Parsimony approach	

24	Tests of topological differences -Likelihood approach	
25	advantages and disadvantages of tree building methods	
26	Molecular clocks - Two cluster test	
27	Linearized trees	
28	**UNIT IV-ANCESTRAL SEQUENCES** Inferences of ancestral sequences- parsimony approaches	○ **Reconstruction of ancestral sequences** ○ **Analyzing whether a evolutionary change is parallel or convergent**
29	Bayesian approaches- two types Distance based approach	
30	Parsimony based approach	
31	Introduction to Synonymous and non-synonymous	
32	Estimating bs & bn from ansetral nucleotides, counting methods	
33	Convergent and parallel evolution- Introduction	
34	Convergent and parallel amino acid changes with example	
35	Significance of convergent evolution	
36	Tests for convergent and parallel evolution	
37	**UNIT V-EVOLUTION** Molecular basis of evolution	○ **Concepts in evolution** ○ **Genetic variation and genetic distance**
38	Codon usage bias and the theory behind it	
39	Synonymous and non-synonymous substitutions method- Evolutionary pathway methods	
40	Kimura two parameter model	
41	Allele frequency and hardy Weinberg equations & Deviations from hardy Weinberg- fixation index	
42	Genetic variation in subdivided population	
43	Genetic variation in many loci	
44	Population trees from genetic markers	
45	Genetic distance calculation methods	

TEXT BOOKS

1. Masatoshi Nei, *Molecular Evolution and Phylogenetics*, Oxford University Press, 2000.
2. *Roderick D.M. Page, Dr Edward C. Holmes*, Molecular Evolution: A Phylogenetic Approach, *Blackwell Publishing, 1998*.

REFERENCE BOOKS

1. David W Mount, *Bioinformatics- Sequence and genome analysis* , Cold Spring Harbor Laboratory Press, second edition, 2004.
2. Jin Xiong, *Essential Bioinformatics*, Cambridge University Press, 2006.

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