COURSE TITLE	**PHYLOINFORMATICS**
COURSE CODE	**01CB0602**
COURSE CREDITS	**3**

Objective:

1 Develop a Comprehensive Understanding of Phylogenetic concepts to impact the scientific base among students for globally desirable important areas of evolutionary biology.

Course Outcomes: After completion of this course, student will be able to:

1 Apply phylogenetic concepts and methods to construct evolutionary trees.

2 Implement distance-based methods to generate and interpret phylogenetic trees.

3 Analyze sequence data using character-based phylogenetic methods.

4 Compare models of molecular evolution to interpret genetic changes.

5 Evaluate phylogenetic inferences using statistical validation techniques.

Pre-requisite of course: Basic knowledge of Bioinformatics

Teaching and Examination Scheme

Theory Hours	Tutorial Hours	Practical Hours	ESE	IA	CSE	Viva	Term Work
2	1	0	50	30	20	25	25

Contents : Unit	Topics	Contact Hours
1	**Introduction to phylogenetic Analysis** Terminology of phylogenetic tree root, internal nodes, internal branches, external branches, terminal nodes, rooted and unrooted trees, cladograms vs. phylograms, phylogeny, species trees, gene tree, characters, cladistics, evolutionary tree, properties of phylogenetic trees: Ultrametric trees and Additive trees	7
2	**Distance matrix methods** clustering, algorithms, measuring genetic change; models of sequence evolution, introduction to maximum likelihood, UPGMA, neighbor joining methods, Fitch-Margolish method	5
3	**Character based method of phylogenetics** Parsimony, maximum parsimony method, maximum likelihood method, Markov model, dynamic programming, analysis of true tree, Tree construction using partial distance matrices, consensus trees, Tree confidence, minimum distance trees.	5
4	**Model of molecular evolution** Introduction to molecular, mode of evolutionary process, genome and biological network evolution, evolutionary change in nucleotide sequences, mathematical modeling of nucleotide substitution in a DNA sequence, Probabilistic models of evolution, HMM	6

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Contents : Unit	Topics	Contact Hours
5	**Evaluation and softwares** Perfect phylogeny, compatibility, bootstrap, Jacknife, PHYLIP, PAUP, WGCNA	5
Total Hours		**28**

Suggested List of Experiments:

Contents : Unit	Topics	Contact Hours
1	**Module1: Introduction to Phylogenetic Analysis** To perform the installation of phylogenetic software tools	1
2	**Module1: Introduction to Phylogenetic Analysis** To analyze and compare different types of trees	1
3	**Module2: Distance matrix methods** To apply the UPGMA method to conduct phylogeny	1
4	**Module2: Distance matrix methods** To apply the neighbor-joining method to conduct phylogeny	1
5	**Module3: Character-based method of phylogenetics** To apply maximum parsimony algorithm to conduct phylogeny	1
6	**Module3: Character-based method of phylogenetics** To apply the maximum likelihood algorithm to conduct phylogeny	1
7	**Module3: Character-based method of phylogenetics** To apply Hidden Markov Models (HMMs) in phylogeny	1
8	**Module3: Character-based method of phylogenetics** To compare the file formats of different types of phylogenetic trees	1
9	**Module4: Model of molecular evolution** To identify molecular evolution roots using phylogeny	1
10	**Module4: Model of molecular evolution** To analyze phylogenetic trees using partial distance matrices	1
11	**Module4: Model of molecular evolution** To classify consensus trees from multiple phylogenetic analyses	1
12	**Module4: Model of molecular evolution** To analyze phylogenetic trees by bootstrapping	1
13	**Module5: Evaluation and Software** To compare phylogenetic trees tools such as Phylip, Mega, Clustal	1
14	**Module5: Evaluation and Software** To evaluate Jackknife analysis to assess the sensitivity of phylogenetic trees	1
Total Hours		**14**

Textbook :

1 Bioinformatics: Sequence and genomic analysis (2nd eds.), Mount, D.W., CBS Publishers and Distributors, New Delhi., 2005

Textbook :

2 Molecular evolution, A phylogenetic approach, Roderic, D. M., Edward, C.M., Blackwell science., 1998

References:

1 Bioinformatics: concept, skill and applications (2nd eds.), Bioinformatics: concept, skill and applications (2nd eds.), Rastogi, S.C., Mendiratta, N. and Rastogi, CBS Publishers and distributors, New Delhi, 2007

2 Instant notes in bioinformatics, Instant notes in bioinformatics, Westhead, Parish and Twyman, Taylor & Francis Group, 2009

Suggested Theory Distribution:

The suggested theory distribution as per Bloom's taxonomy is as follows. This distribution serves as guidelines for teachers and students to achieve effective teaching-learning process

Distribution of Theory for course delivery					
Remember / Knowledge	**Understand**	**Apply**	**Analyze**	**Evaluate**	**Higher order Thinking / Creative**
20.00	30.00	20.00	10.00	10.00	10.00

Instructional Method:

1 The course delivery method will depend upon the requirement of content and need of students. The teacher in addition to conventional teaching method by black board, may also use any of tools such as demonstration, role play, Quiz, brainstorming, MOOCs etc.

2 The internal evaluation will be done on the basis of continuous evaluation of students in the laboratory and class-room.

3 Practical examination will be conducted at the end of semester for evaluation of performance of students in laboratory.

Supplementary Resources:

1 https://cci.charlotte.edu/departments/bioinformatics/seminars/

2 Students will use supplementary resources such as online videos, NPTEL videos, e-courses, Virtual Laboratory.

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