

Skill Enhancement Course
Virtual Certificate Course on
Course title: Molecular Phylogenetics
Course Credit: 30

Course Description:

Molecular Phylogenetics is an advanced course that explores the methods and principles used to infer evolutionary relationships among organisms using molecular data. This course provides a comprehensive understanding of the theory and practice of reconstructing phylogenies, analyzing genetic sequences, and interpreting evolutionary histories.

Course Objectives:

- To understand the fundamental concepts of molecular evolution and phylogenetics.
- To learn the various methods for sequence alignment and phylogenetic tree construction.
- To analyze and interpret phylogenetic trees and evolutionary relationships.
- To gain practical experience with software tools and databases used in molecular phylogenetics.
- To apply molecular phylogenetic methods to real-world biological problems.

Minimum Qualification: B.Sc Biological Sciences and having basic knowledge of computation.

Duration: One Month

Mode of Teaching: Online

Mode of Examination: Online (Departmental)

Course fee: Rs 8000.00

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CHAIRMAN

Board of Studies in Zoology

University of Jammu

2023-24

Course title: Molecular Phylogenetics

Course Code: ZOO- SKC-301 (Theory)

Course Credit: 10

1. Introduction to Molecular Phylogenetics

- Overview of phylogenetics and its significance
- Historical development of molecular phylogenetics

2. Molecular Evolution

- DNA, RNA, and protein evolution
- Mutation rates and molecular clocks
- Concept of the molecular clock and methods for estimating divergence times

3. Molecular Data and Databases

- GenBank and other sequence databases
- Methods for retrieving molecular sequences from online databases (NCBI, EMBL).

4. Sequence Alignment

- Pairwise and multiple sequence alignment
- Algorithms and software tools for sequence alignment

5. Phylogenetic Tree Construction Methods

- Introduction to distance-based methods (UPGMA, Neighbor-Joining)
- Introduction to character-based methods (Maximum Parsimony, Maximum Likelihood)
- Principles of maximum parsimony and its application in phylogenetics
- Maximum likelihood methods and their advantages
- Introduction to Bayesian methods and Markov Chain Monte Carlo (MCMC) techniques

6. Evaluating Phylogenetic Trees

- Bootstrapping and statistical support
- Model selection and model testing
- Tree reliability and robustness
- Tools and techniques for visualizing and annotating phylogenetic trees

7. Advanced Topics

- Phylogenomics and whole-genome phylogenetics
- Molecular dating and biogeography
- Recent advances and applications of molecular phylogenetics in various fields.

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Suggested Reading:

1. Felsenstein, J. 2003. Inferring Phylogenies. Sinauer Associates.
2. Kitching, I., Forey, P. L., Humphries, C. J. & Williams, D. M. 1998. Cladistics: The Theory and Practice of Parsimony Analysis, 2nd ed. The Systematics Association Publication No. 11. Oxford University Press.
3. Nei, M. & Kumar, S. 2000. Molecular Evolution and Phylogenetics. Oxford University Press.
4. Page, R.D.M. & Holmes, E.C. 1998. Molecular Evolution: A Phylogenetic Approach. Blackwell Science.
5. Swofford, D. L., Olsen, G.J., Waddell, P. J. & Hillis, D.M. 1996. Phylogenetic inference. Pages 407-514 in Molecular Systematics, 2nd Ed. (D. M. Hillis, C. Moritz, & B. K. Mable, Eds.). Sinauer, Sunderland, Massachusetts.

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Course title: Molecular Phylogenetics

Course Code: ZOO- SKC-302 (Practical)

Course Credit: 20

1. **Introduction to Molecular Phylogenetics Tools and Resources**
 - Introduction to bioinformatics databases: NCBI, GenBank
 - Installation and setup of phylogenetic analysis tools MEGA, itaxotool, BEAST, RAxML
2. **DNA Sequence Retrieval and Data Preparation**
 - Retrieving DNA sequences from GenBank
 - Cleaning and preparing sequence data for analysis
3. **Sequence Alignment**
 - Hands-on practice with multiple sequence alignment
 - Evaluating alignment quality
 - Preparing aligned sequences for phylogenetic analysis
4. **Models of Nucleotide Substitution**
 - Model selection using tools like jModelTest or MEGA
 - Applying the chosen model to sequence data
5. **Phylogenetic Tree Construction - Distance Methods**
 - Constructing trees using distance methods (Neighbor-Joining, UPGMA)
 - Interpreting distance-based phylogenetic trees
6. **Phylogenetic Tree Construction - Maximum Parsimony**
 - Constructing and evaluating parsimony trees using MEGA
 - Comparing parsimony results with distance methods
7. **Phylogenetic Tree Construction - Maximum Likelihood**
 - Using software like RAxML for maximum likelihood analysis
 - Interpreting maximum likelihood trees and assessing tree reliability
8. **Phylogenetic Tree Construction - Bayesian Inference**
 - Running Bayesian analyses using BEAST or MrBayes
 - Evaluating and interpreting Bayesian phylogenetic trees
9. **Bootstrapping and Confidence Intervals**
 - Performing bootstrap analyses using MEGA or RAxML
 - Interpreting bootstrap support values and confidence intervals
10. **Molecular Clock Hypothesis and Dating Divergence Times**

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