

Educational Objectives:

1. The field of molecular phylogenetics has grown, both in size and in importance, since its inception in the early 1990s, attributable mostly to advances in molecular biology and more rigorous methods for phylogenetic tree building. The importance of phylogenetics has also been greatly enhanced by the successful application of tree reconstruction, as well as other phylogenetic techniques, to more diverse and perplexing issues in biology. Today, a survey of the scientific literature will show that molecular biology, genetics, evolution, development, behaviour, epidemiology, ecology, systematic, conservation biology, and forensics are but a few examples of the many disparate fields conceptually united by the methods and theories of molecular phylogenetics. Phylogenies are used essentially the same way in all of these fields, either by drawing inferences from the structure of the evolutionary tree or from the way the character states map onto the tree. Virologists can then use these clues to build hypotheses and models of important events in history. Broadly speaking, the relationships established by phylogenetic trees often describe a species evolutionary history and, hence, its phylogeny—the historical relationships among lineages or organisms or their parts, such as their genes. Phylogenies may be thought of as a natural and meaningful way to order data, with an enormous amount of evolutionary information contained within their branches. Scientists working in these different areas can then use these phylogenies to study and elucidate the biological processes occurring at many levels of life's hierarchy. The evolutionary information about any organism including viruses helps us to trace its origin, diversity and biogeography. In case of viruses it becomes more important because viruses can only propagate in their hosts and if they are going to be evolving in a speedy way their pathogenasty may increase. This also concludes that virus has a good reservoir in host population that supports virus evolution. Studying of molecular phylogenetics becomes more important when the cases of human viruses (HIV, HCV, etc.) are in consideration. By using evolutionary information one can derive strategies for viral disease management at population scale. Molecular evolution is a young and exciting field and combines advancements in molecular biology and computer technology. This course will cover major areas of molecular evolution and phylogenetics. The student is expected to learn

about different types of molecular data and their collection; major transitions of evolution; genomic evolution and genome projects; comparison of DNA and amino acid (protein) sequences to calculate genetic distances; phylogeny reconstruction by parsimony, distance, and likelihood methods; test of the molecular clock and dating speciation events; Darwinian selection at the molecular level and methods for detecting it; within-species variation and evolution of modern humans; the mechanisms of molecular evolution and the neutral theory. A computer-based bioinformatics practical offer the students opportunities to get familiar with software used in molecular phylogenetics. The course is designed to attract a diverse range of students, from Biology, Virology, Ecology, Genetics, Human Genetics, Zoology, Anthropology, Earth Sciences, and Human Sciences.

Course Outcomes:

2. This is an advance level course that describes the different aspects of the field of the molecular phylogenetics, its application in the various fields of science. This course is designed to train the researcher in the field of modern phylogenetics. The trained students will be able to generate evolutionary information about living organisms especially viruses that can be utilized for research and developments in above mentioned fields.

3. **Course Contents:**

- a. A short history of molecular phylogenetics
 - (1) Introduction to molecular phylogenetics
 - (2) Foundations of phylogenetics
 - (3) Terminologies/definitions
 - (4) ICTV database and other databases
 - (5) Bases of classifications of various organisms
- b. Sources of data for evolutionary information
 - (1) Types of data used in evolutionary analysis

- (2) Preparations of data matrixes
 - (3) Criteria for the selection of molecular phylogenetic characters
 - (4) Data retrieval in phylogenetics
 - (5) Designing of laboratory work in phylogenetics
- c. Evolutionary trees
- (1) Introduction to evolutionary trees
 - (2) Tree topologies
 - (3) Distance based trees
 - (4) Tree sorting strategies
 - (5) Tree interpretation and Labeling
- d. Statistics of molecular phylogenetics
- (1) Failure of Distance based methods in molecular phylogenetics
 - (2) Method and Model selection in molecular phylogenetics
 - (3) Bayesian inference in phylogenetics and concept of posterior probabilities
 - (4) Maximum like hood phylogenetics
 - (5) Application of maximum parsimony algorithm in phylogenetics
- e. Recent research trends in molecular phylogenetics
- (1) Dated phylogenetics
 - (2) Biogeography and molecular phylogenetics
 - (3) Tracing origin of organisms
 - (4) Applications of molecular phylogenetics in various fields of science
 - (5) Character mapping and molecular phylogenetics
- f. The lab work includes:
- (1) Retrieving of molecular phylogenetic data from different sources like wet lab and gene banks
 - (2) Preparation of different data matrixes for phylogenetic analysis

- (3) Process of alignment of amino acid and nucleotide sequences
- (4) Learning of different software/bioinformatics tools for Phylogenetics
- (5) Understanding of evolutionary methods and models
- (6) Labeling and interpretation of phylogenetic trees

Recommended Books:

1. Page, R. and E. Holmes. 1998. *Molecular evolution: a phylogenetic approach*. Blackwell, London.
2. Yang Z. 2006. *Computational Molecular Evolution*. Oxford University Press, Oxford, England.
3. Geneious (Bioinformatics Software) manual. Latest Edition (<http://www.geneious.com>)