

BIOL 659 Advanced Studies in Genetics: Molecular Evolution & Phylogenetics (MEP)

Instructor: Michael A. Thomas, Ph.D.

Office: 256 Gale Life Science
Office Hours: 11 AM–Noon, Tuesday, Wednesday & Thursday
Phone: 282-2396
Email: mthomas@isu.edu

Class meets:

Tuesdays & Thursdays, 9:30-10:45 AM in Nursing 334 or LS 205/208 (for computer labs).

Overview

Molecular Evolution & Phylogenetics (MEP) is a graduate-level course emphasizing both the theory and practice of reconstructing evolutionary history using molecular data. MEP is designed to meet the “statistics & research design” tool requirement for Biology graduate students with molecular research emphases. Accordingly, MEP will concentrate on the algorithmic basis of probabilistic approaches such as maximum likelihood (ML) & Bayesian inference. Students learn how to use these approaches and critically evaluate the phylogenetic literature, with discussion of principles in statistics accompanied by laboratory exercises that ensure students have skills to test hypotheses. We will explore:

- 1) The major approaches to evolutionary reconstruction and hypothesis testing.
- 2) The historical phylogenetic controversies and philosophical arguments.
- 3) Various models of evolution for inferring rates of substitutions.
- 4) Estimating and using molecular clocks to test hypotheses about divergence times, rates, etc, and recent controversies surrounding molecular clocks.
- 5) Using relative substitution rates to test hypotheses about the activity of Darwinian and purifying selection.
- 6) Various approaches to determining the accuracy and robustness of evolutionary reconstructions (bootstrapping, statistical tests, etc).
- 7) Genetic polymorphism and population trees.
- 8) Computational approaches: Using computer tools (desktop and cluster-based) in evolutionary reconstructions.

MEP will feature an interactive lecture format, hands-on demonstrations and computer lab-based exercises, and an emphasis on applying new knowledge to novel explorations of your data.

Course information and computational resources can be accessed at <http://egg.isu.edu>.

Topics covered

Please see attached schedule. Coverage and dates are subject to change.

Prerequisites

A background in molecular genetics and experience with biological computing will be helpful but not essential.

Textbook & References

Required

- Masatoshi Nei & Sudhir Kumar, *Molecular Evolution & Phylogenetics*, Oxford University Press, 2000, ISBN: 0-19-513585-7 (about \$65). This book is available from OUP online (<http://www.oup.com/us/>), Amazon, and elsewhere.

Optional

- Roderic D. Page & Edward C. Holmes, *Molecular Evolution: A phylogenetic approach*, Blackwell Science, 1998, ISBN: 0-86542-889-1. This book is available from Blackwell online (<http://www.blackwellpublishing.com>), Amazon, and elsewhere.
- Joseph Felsenstein, *Inferring Phylogenies*, Sinauer, 2004, ISBN: 0-87893-177-5– this book provides informatics on certain phylogenetic methods not covered by Nei, such as Bayesian approaches. I'll be providing electronic copies of useful chapters as needed, but it's still worth having on your bookshelf.

Grading

Your grade will consist of the following components, weighted as shown:

Final Exam	30%
Assignments (6)	60%
Participation, intangibles	10%

Final letter grades depend upon the overall performance and may be adjusted upward.

Final Exam

The Final Exam will be take-home, open-book format. Students will have 1 week to complete the exam. The exams will feature problems to be solved using informatics, tools, and approaches covered in the class. Students will work alone (i.e., not in collaboration with other students).

Assignments

Six (6) homework assignments will be assigned. These will consist of problems to be solved using tools, and approaches covered in the class, providing practice on some of the major concepts in the class. Students will work alone (i.e., not in collaboration with other students).

Late policy

Assigned work in this course must be turned in by the specified due date. Late work will **not** be accepted.