Phylogenetic Biology

BI 450/550, CRN 15167, 15168 winter 2009

Time: Tuesday/Thursday 10-11:50, Room 247 SB2 for lectures, 139A SB2 for labs
Instructor: Dr. Susan Masta; email smasta@pdx.edu; office room 606 SB1; phone 725-8505
Office hours: Wed. 12-1 in room 606 SB1
Computer lab: room 139A SB2: you must have a student ID to enter this room, and an Odin account to log onto the computers. The ID will gain you access at any time to this room. You can purchase a student ID in Neuberger Hall if you do not have one.

Course Description: Phylogenetic biology explores how organisms, genes, and traits have evolved, and seeks to represent the history of life's divergence through the use of phylogenetic trees. Phylogenetic biology has contributed to a wide variety of disciplines and pursuits. Developing flu vaccines, conducting forensic tests, tracking the origin and spread of HIV, understanding the human genome, constructing the Tree of Life, and determining how many times eyes have evolved, all require constructing and understanding evolutionary trees. This course will focus on the use, interpretation, and methods of reconstructing evolutionary trees, and on methods to trace the evolution of traits on these trees. The course will combine lectures with hands–on computer analyses of data. Each student will develop and work on an independent project during the course of the term, culminating in a written paper and a class presentation.

Course Objectives: You will become familiar with:

- The uses of phylogenetics, and how to apply phylogenetics to evolutionary questions
- The history of phylogenetics and systematics
- How to extract and align DNA sequences from public databases
- How to construct phylogenetic trees, using a variety of methods
- How to trace characters on phylogenetic trees
- How to evaluate the robustness of phylogenetic hypotheses

Grading: Grades for the course will be based on two class presentations (10 and 20%), computer analysis assignments (30%), a phylogenetic analysis project with a written paper (30%), and class participation (10%). Graduate students will also lead an in-class discussion of recent papers in molecular phylogenetics and systematics.

Reading Material: There is no assigned textbook for this class. Instead, reading material will be handed out in class or posted on Blackboard. You may also wish to consult several books as background references: *Molecular Evolution: A Phylogenetic Approach* 1998 by R. Page ad E. Holmes; *Inferring Phylogenies* 2004 by J. Felsenstein (recommended for graduate students); Chapter 11 from *Molecular Systematics*, 2nd edition 1996 edited by D. Hillis. C. Moritz, and B. Mable; and *Phylogenetic Trees Made Easy* by B. Hall.

Syllabus

29 September: Introduction – uses of trees.

1 October: History and philosophy of phylogenetics, concept of homology, choice of characters.
Guidelines for term project. Reading: pp 38-47 of MacClade Manual by Maddison and Maddison.
Computer lab: Tree of Life excercise

6 October: Morphological characters
Creating a data matrix; Term projects approved

Bioinformatics

8 October: Sequences as phylogenetic characters.
Computer lab and Exercise 1: NCBI, Downloading sequences from GenBank.

13 October: Presentations of term project topics
Computer lab: Download project sequences from GenBank.

15 October: Sequence alignment, data matrices.
Computer lab and Exercise 2: sequence alignment with ClustalX.
Reading: Chapter 2 of Fundamental Concepts of Bioinformatics, Data Searches and Pairwise Alignments by Krane and Raymer.

20 October: Parsimony theory, rooting trees.
Computer lab: Introduction to PAUP* and parsimony analysis
Exercise 3: creating a data matrix in MacClade.

22 October: Parsimony methods, weighting characters.
Computer lab and Exercise 4: Parsimony analysis with PAUP*; create a phylogenetic tree with sequences.

Trait Evolution

27 October: Tracing character change I.
Computer lab: work on independent project
Reading: Felsenstein 1985 "Phylogenies and the comparative method" American Naturalist Vol. 125, pp. 1-15.

29 October: Tracing character change II.
Computer lab and Exercise 5: Introduction to MacClade and character evolution.
Reading: de Queiroz 1996 "Including the characters of interest during tree reconstruction and the problems of circularity and bias in the studies of character evolution" American Naturalist Vol. 148, pp. 700-708.

3 November: Tracing character change III.
Computer lab and Exercise 6: MacClade and tracing character evolution.
Reading: Chapter 6, pp 216-227 in Molecular Evolution: a Phylogenetic Approach by Page and Holmes

Advanced Phylogenetics: Theory, Techniques, and Applications

5 November: Assessing support for a hypothesis.
Computer lab: bootstrap analyses with PAUP*; creating log files.

10 November: Systematics (Graduate student led discussion).
Computer lab: morphological data matrices and parsimony analysis.

12 November: Introduction to maximum likelihood.
Computer lab: translating nucleotides to amino acids.
Reading: pp 193-201 in Molecular Evolution: a Phylogenetic Approach by Page and Holmes

17 November: Maximum likelihood and models of sequence evolution.
Computer lab: Introduction to likelihood analyses with PAUP*.
Reading: pp 145-161 in Molecular Evolution: a Phylogenetic Approach by Page and Holmes

19 November: Distance-based phylogenetic methods. Comparison of tree reconstruction methods.
Computer lab: Maximum likelihood searches with PAUP*; Using ModelTest to find a model of sequence evolution.

24 November: Molecular clocks.
Computer lab: estimating divergence times.

26 November: PSU CLOSED for Thanksgiving

1 December: Student project presentations.

3 December: Student project presentations.

8 December: Final exam period Tuesday 10:15-12:05: Written term project reports due.