Phylogenetic Biology
BI 450/550, winter 2006

Time: Tuesday/Thursday 2-3:50, Room 139A SB2 for lectures and labs
Instructor: Dr. Susan Masta; email smasta@pdx.edu; office room 515 SB1; phone 725-8505
Office hours: T/Th 3:50-4:30, Room 139A SB2 (computer lab); Wed. 1-2 in office, room 515 SB1

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 class participation (5%), 3 quizzes (30%), computer analysis assignments (25%), and a final phylogenetic analysis project with a written paper (30%) and class presentation (10%).

Reading Material: There is no assigned textbook for this class. Instead, reading material will be handed out in class or posted on WebCT each week. 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
10 January: Introduction – uses of trees.

12 January: History and philosophy of phylogenetics, concept of homology, choice of characters.
Guidelines for phylogenetic analysis project. Reading: pp 38-47 of MacClade Manual by Maddison and Maddison.

17 January: Sequences as phylogenetic characters.
Computer lab: Tree of Life, NCBI, Downloading sequences from GenBank.
Exercise 1

19 January: 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.

24 January: Introduction to parsimony, rooting trees.
Computer lab: Introduction to PAUP* and parsimony analysis
Exercise 3: Beasties; creating a data matrix in MacClade (not graded)

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

31 January: Tracing character change I.
Quiz 1
Reading: Felsenstein 1985 “Phylogenies and the comparative method” American Naturalist Vol. 125, pp. 1-15.
Computer lab: work on independent project; get instructor approval for project

2 February: 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.

7 February: Tracing character change III; Assessing support for a hypothesis.
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

9 February: Assessing support; Introduction to maximum likelihood.
Computer lab: bootstrap analyses with PAUP*; creating log files.
Reading: pp 193-201 in Molecular Evolution: a Phylogenetic Approach by Page and Holmes

14 February: 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

16 February: Maximum likelihood and models of sequence evolution.
Computer lab: Maximum likelihood searches with PAUP*

21 February: Molecular clocks.
Computer lab: Using ModelTest to find a model of sequence evolution
Quiz 2

23 February: Distance-based phylogenetic methods; Comparison of tree reconstruction methods.
Computer lab: estimating divergence times

28 February: Species concepts; Gene trees versus species trees
Computer lab: open

2 March: Phylogeography
Computer lab: open

7 March: Applications: Biogeography.
Computer lab: open

9 March: Applications: Conservation.
Computer lab: open

14 March: Applications: Lateral Gene Transfer.
Computer lab: open
Quiz 3

16 March: Applications: Gene trees.
***written project due**

20 March: Final exam period Monday 10:15-12:05: Presentation of term projects.