Phylogenetic Biology and Analysis, BIO 549 (tentative number)
Syllabus, Fall Semester 2010 (will be taught as BIO 598)

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Preferred prerequisites: undergraduate course in Evolution, Bioinformatics
Course credit hours: 4

Course description. Phylogenies, or trees, are basic branching diagrams that provide a powerful tool for the study of relationships between organisms, their genes/genomes, or an understanding of the evolutionary history of life itself. This course will cover the basic theory and general concepts of phylogenetic inference as well as provide practical, hands-on experience with many of the commonly used methods for inferring phylogenetic trees (e.g., maximum parsimony, distance, and maximum likelihood) emphasizing currently used software programs and tools for reconstructing trees using molecular sequences or morphological data as characters for analysis. Other topics that will be explored include re-sampling techniques (e.g., bootstrapping), testing models of character evolution, tree comparison methods, estimation of divergence times, and the advantages and disadvantages of the various approaches for inferring and interpreting trees. In addition, examples of exemplary phylogenetic studies taken from the primary literature will be examined in detail to gain insights into the application, efficacy, and limitations of approaches and methods to specific questions or problems.

      The course is structured as presentation and practice, and will meet for 2 hours each on Monday and Wednesday. Following short presentation(s) on a particular topic(s), students will be instructed in the use (direct hands-on experience) of several of the software packages/programs that are widely used for sequence analysis, phylogeny reconstruction, and evolutionary analysis on desktop computers (e.g., *PAUP**, MEGA, Mesquite, MrBayes, ClustalX, Muscle) and/or available on the WWW, using real data sets (such as their own). Students are expected to have access to a personal computer (laptop or desktop running Macintosh OSX or Windows) for use during the class and outside of class time.

      This course is intended for, and appropriate to, graduate and advanced undergraduate students in the Anthropology, Biology, Computational Biosciences, Evolutionary Biology, Microbiology, Molecular and Cellular Biology, and Plant Biology graduate programs, as well as the Molecular Biosciences & Biotechnology undergraduate programs.

Course goals. This course is intended for students with little or no experience in phylogenetic methods, or their application, using standard computer programs. The goal is to familiarize students with the theory, conceptual framework, and practice of phylogenetic approaches and methodologies that are typically used in studies of organismal systematics, comparative and evolutionary biology, and molecular evolution. This will be accomplished through the use of representative data sets of molecular sequences for direct computational analyses, hypothesis testing, and tree comparisons, employing standard phylogenetic methods (i.e., distance, maximum parsimony, maximum likelihood, Bayesian inference). In addition, selected published papers will be discussed in detail to illustrate the various methodological approaches and analyses used in contemporary phylogenetic studies ("case studies") and their results. Students are expected to demonstrate knowledge of phylogenetic methodology by completing a project utilizing the approaches and methods of analysis they have learned as applied to sequence data derived from their own research project(s) or obtained from existing public databases such as Genbank [www.ncbi.nlm.nih.gov/Genbank/], TreeBase [www.treebase.org/] or Phylota [ceiba.biosci.arizona.edu/cgi-bin/pb.cgi], and present the results of their analyses to the class.

Required & recommended texts. *The Phylogenetic Handbook*, 2nd edition (2009) by P. Lemey, M. Salemi and A.-M. Vandamme (Cambridge University Press, ISBN 978-0-521-73071-6) is the primary text for this course and is required. Supplemental readings will be assigned from selected chapters of *Inferring Phylogenies*, by J. Felsenstein (2003, Sinauer Associates), as well as from recently published articles from selected journals (provided as pdf files).

Course grading. The final grade for the course is based upon a student's performance in three areas:
(i) Attendance, demonstrated knowledge of assigned readings, and thoughtful contributions to discussions in class (20% of grade)
(ii) Completion of four short homework assignments (30% of grade). Assignments will be evaluated on accuracy, clarity and documentation of results obtained from analyses.
(iii) Completion of a detailed phylogenetic analysis of a molecular data set. The results of this project will form the basis for a 12 – 15 minute oral and media-based presentation (e.g., powerpoint) to the class during the final week of the semester (50% of grade). While the format for the presentations will be discussed in more detail later in the semester, presentations will be graded on scientific content (discussion of methods used, results from analyses), clarity of presentation, and ability to answer questions from the audience. Students are expected to provide a short list of literature articles relevant to the topic of their project one week prior to their scheduled presentation.
          Course grades will be calculated on a 100-point scale, with 90-100% an A, 80-89% a B, 70-79% a C, 60-69% a D, <60% an E.

Blackboard. The course will use *Blackboard* for posting course information (e.g., the syllabus), sample data sets, supplementary readings and assignments. Log in to *Blackboard* on MyASU regularly to view announcements for the course. Instructor presentations & notes will be posted under Course Documents as soon as possible, following each session.

Academic Integrity and Ethics
Under the **ASU Student Academic Integrity Policy** (http://provost.asu.edu/academicintegrity), "[e]ach student must act with honesty and integrity, and must respect the rights of others in carrying out all academic assignments." This policy also defines academic dishonesty and sets a process for faculty members and colleges to sanction dishonesty. Violations of this policy fall into five broad areas that include but are not limited to: Cheating on an evaluation or assignment; Plagarism; Academic deceit, such as fabrication of data or information; Aiding academic Integrity Policy violations and inappropriate collaboration; Falsifying academic records.

ASU Policy on Academic Dishonesty: "In the 'Student Academic Integrity Policy' manual, ASU defines ***plagiarism*** [as], 'using another's words, ideas, materials or work without properly acknowledging and documenting the source. Students are responsible for knowing the rules governing the use of another person(s) work or materials and for acknowledging and documenting the source appropriately. You can find this definition at: **http://www.asu.edu/studentaffairs/studentlife/judicial/academic_integrity.htm#definitions**. Academic dishonesty, including inappropriate collaboration, will not be tolerated.

All contents of our course materials, including lectures, exercises, exams, etc. are under copyright protection. *You may NOT distribute, post, sell, or buy any notes, exercises, or exams without our written permission*.

The course syllabus is a "contract" between student and instructor. I will do my best to uphold my part of the deal and help you understand the standards of academic scholarship, and I expect you to behave in a mature, responsible, and ethical fashion as outlined in this document. **If you do not accept the rules for conduct in this class, please drop the class now.**

Course Schedule

Date	Topic; Relevant Readings; Assignments Due
August 19	Introduction to course; basic concepts and applications of phylogenetics Readings*: Baldauf (2003)
August 24 August 26	Characters, homology, homoplasy, types of data used for phylogenetics Introduction to trees, topologies, tree interpretation and evolution Readings*: Lemey et al. (2009), chapter 1; Felsenstein (2003), chapter 10
August 31 September 2	Sequence databases, internet resources, software programs Multiple sequence alignment, data file formats Readings*: Lemey et al. (2009), chapters 2, 3
September 7 September 9	Phylogenetic inference: overview of methods Phylogenetic inference: use of models, rooting trees Readings*: Holder and Lewis (2003) Homework assignment #1 due
September 14 September 16	Models of molecular evolution (nucleotide substitution) Phylogenetic inference: distance methods Readings*: Lemey et al. (2009), chapters 4, 5, 10
September 21 September 23	Phylogenetic inference: maximum parsimony methods Phylogenetic inference: maximum parsimony, searching for optimal trees Readings*: Lemey et al. (2009), chapter 8 Homework assignment #2 due
September 28 September 30	Phylogenetic inference: maximum likelihood methods 1 Phylogenetic inference: maximum likelihood methods 2 Readings*: Lemey et al. (2009), chapter 6
October 5 October 7	Bayesian inference and phylogenetics 1 Bayesian inference and phylogenetics 2 Readings*: Lemey et al. (2009), chapter 7 Homework assignment #3 due
October 12 October 14	Testing models of evolution, tree topologies, molecular clock analysis Case Study #1 (Zanis et al. 2002) Readings*: Lemey et al. (2009), chapters 11, 12; Felsenstein (2003), chapters 18, 19
October 19 October 21	Reliability of inferred trees: non-parametric and parametric bootstrap Reliability of inferred trees: accuracy and error Readings*: Lemey et al. (2009), chapters 12; Felsenstein, chapter 20
October 26 October 28	Inferring 'big' trees: supermatrix and supertree approaches Case Study #2 (Sanderson et. al. 2003) Readings*: Bininda-Emonds (2004); Delsuc et al. (2005) Homework assignment #4 due

November 2	Estimating divergence times on phylogenies 1
November 4	Estimating divergence times on phylogenies 2
	Readings*: Rutschmann (2006)
November 9	Case Study # 3 (Hughes and Eastwood, 2006; Poux et al. 2006)
November 11	Veterans Day Holiday (no class)
November 16	Reconstructing character evolution 1
November 18	Reconstructing character evolution 2
	Readings*: Maddison and Maddison (2003), chapter 4
November 23	Open lab for working on course projects
November 25	Thanksgiving Holiday (no class)
November 30	Open lab for working on course projects
December 2	Student presentations
December 7	Student presentations (Last day of classes)
December 9/14	Student presentations (Final exam period)

*Readings: chapters from following book and/or relevant primary literature articles:
Lemey, P., M. Salemi and A.-M. Vandamme. 2009. *The Phylogenetic Handbook*, 2nd edition. Cambridge University Press, Cambridge, UK. [primary text]

Baldauf, S. L. 2003. Phylogeny for the faint of heart: a tutorial. *Trends in Genetics* 19: 345-351.
Bininda-Emonds, O. R. P. 2004. The evolution of supertrees. *Trends in Ecology and Evolution* 19: 315-322.
Delsuc, P. H., H. Brinkmann, and N. Lartillot. 2005. Phylogenomics. *Annual Review of Ecology, Evolution and Systematics* 36: 541-562.
Felsenstein, J. 2003. *Inferring Phylogenies*. Sinauer Associates, Sunderland, MA, USA.
Holder, M., and P. O. Lewis. 2003. Phylogeny estimation: traditional and Bayesian approaches. *Nature Reviews Genetics* 4: 275-284.
Maddison, D. R., and W. P. Maddison. 2003. *MacClade 4.0 Manual*. Sinauer Associates, Sunderland, MA, USA.
Rutschmann, F. 2006. Molecular dating of phylogenetic trees: a brief review of current methods that estimate divergence times. *Diversity and Distributions* 12: 35-48.

References for Case Studies:
Hughes, C., and R. Eastwood. 2006. Island radiation on a continental scale: Exceptional rates of plant diversification after uplift of the Andes. *Proceedings of the National Academy of Sciences USA* 103: 10334-10339.
Poux, C., P. Chevret, D. Huchon, W. W. de Jong, and E. J. Douzery. 2006. Arrival and diversification of caviomorph rodents and platyrrhine primates in South America. *Systematic Biology* 55: 228-244.
Sanderson, M. J., A. C. Driskell, R. H. Ree, O. Eulenstein, and S. Langley. 2003. Obtaining maximal concatenated phylogenetic data sets from large sequence databases. *Molecular Biology and Evolution* 20: 1036-1042.
Zanis, M. J., D. E. Soltis, P. S. Soltis, S. Mathews, and M. J. Donoghue. The root of angiosperms revisited. 2002. *Proceedings of the National Academy of Sciences USA* 99: 6848-6853.