

BI549: Molecular Phylogenetics and Evolution

Fall 2007 (*preliminary syllabus*)

Course Description: Phylogenetic analyses are increasingly important in many different fields of biological research, particularly as advances in molecular genetic techniques have made large DNA sequence data sets readily available. This course covers the basic methods of phylogenetic analysis and their application in fields such as systematics, comparative biology, and molecular evolution. Lectures will emphasize the logical basis and computational details of various tree-building algorithms and associated methods of hypothesis testing, as well as novel applications of phylogenetic analysis in various fields of biology. Computer-based labs will give students the opportunity to implement these methods using a variety of phylogenetic software.

Lecture: T Th 9:30-10:50, BRB 122

Lab/Discussion: W 10:00-11:50, BRB 122

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Suggested Texts:

Felsenstein, J. 2003. *Inferring Phylogenies*. Sinauer Associates.

Kitching, I., Forey, P. L., Humphries, C. J. & Williams, D. M. 1998. *Cladistics: The Theory and Practice of Parsimony Analysis*, 2nd ed. The Systematics Association Publication No. 11. Oxford University Press.

Nei, M. & Kumar, S. 2000. *Molecular Evolution and Phylogenetics*. Oxford University Press.

Page, R.D.M. & Holmes, E.C. 1998. *Molecular Evolution: A Phylogenetic Approach*. Blackwell Science.

Salemi, M. & A.-M. Vandamme, Eds. 2003. *The Phylogenetic Handbook: A Practical Approach to DNA and Protein Phylogeny*. Cambridge University Press.

Swofford, D. L., Olsen, G.J., Waddell, P. J. & Hillis, D.M. 1996. Phylogenetic inference. Pages 407-514 in *Molecular Systematics*, 2nd Ed. (D. M. Hillis, C. Moritz, & B. K. Mable, Eds.). Sinauer, Sunderland, Massachusetts.

Primary Computer Programs (provided):

Maddison, W. P. & D. R. Maddison. 2000-2005. MacClade: Analysis of phylogeny and character evolution. Version 4.08. Sinauer Associates, Sunderland, MA.

or Maddison, W. P. & D. R. Maddison. *Mesquite* (<http://mesquiteproject.org/>). Version 1.12.

Swofford, D. L. 2002. PAUP*: Phylogenetic Analysis Using Parsimony (and Other Methods). Version 4.0b10. Sinauer Associates, Sunderland, MA.

Ronquist, F. & J. P. Huelsenbeck. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19: 1572-1574.

Drummond A.J. & Rambaut A. 2006. BEAST v1.4.5, available from <http://beast.bio.ed.ac.uk/>

Course Requirements:

1. One mid-term exam and one final exam
2. Attend all lectures and labs
3. Participate in weekly lab and discussion sections
4. Complete computer-based laboratory assignments
5. Write one 15-20 page research paper that 1) considers a basic issue in phylogenetic analysis and 2a) includes a compilation and re-analysis of published data, **or** 2b) analyzes new character data collected in your own research, **and/or** 2c) analyzes simulated data.
6. Present research paper to class (25 minute oral presentation)

Grading:

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| Computer Analysis Assignments | 10% |
| Class Participation | 10% |
| Research Paper | 25% |
| Oral Presentation | 15% |
| Mid-term Exam | 20% |
| Final Exam | 20% |

Lecture/Lab Schedule – **subject to revision**

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| September 4-6 | Introduction to Phylogenetic Analysis: trees, characters, cladistics, parsimony (Ch. 1 in Kitching et al., 1998) |
| September 11-13 | Parsimony: character state reconstruction, tree length and other indices, tree-searching algorithms, homoplasy and weighted parsimony, Bremer support (or decay) index, consensus trees (Swofford & Sullivan, Ch. 7 in Salemi & Vandamme, Eds.) (Sennblad B, Bremer B 2000 <i>Syst. Biol.</i> 49: 101-113.) (Broughton RE, Stanley SE, Durrett RT 2000 <i>Syst. Biol.</i> 49: 617-627.) |
| September 18-20 | Distance Methods: models of nucleotide and protein evolution, UPGMA, neighbor-joining |
| September 25-26 | Sequence Alignment: gaps, gap-coding, Clustal, MALIGN, POY |
| September 27-Oct. 3 | Maximum Likelihood theory and methods: systematic versus random error, the long branch attraction problem and performance of phylogenetic methods, model selection and adequacy |
| October 4-11 | Bayesian Inference: MrBayes, BEAST |

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| October 16-17 | Hypothesis Testing: tree comparisons and statistical tests, parametric bootstrapping |
| October 17 | Take-home Mid-term handed out (due 19 Oct.) |
| October 18-25 | Data heterogeneity: base and amino acid compositional biases, tests of homogeneity, total evidence versus taxonomic congruence, mixed models |
| October 30 - Nov. 1 | Gene trees, species trees and the coalescent |
| November 6-8 | Lineage sorting and multilocus methods |
| November 13-15 | Rates and Dates: relative rates tests, calibrating the molecular clock, time-dependency of evolutionary rates?! |
| November 20-29 | Comparative Analyses: concentrated changes test, independent contrasts, ancestral state reconstruction of continuous characters |
| December 4-6 | Phylogenomics; Co-evolution, co-phylogeny: TreeMap |
| ~December 6 | Student Presentations |
| Final Exam: TBA | |