

University of Montana

ScholarWorks at University of Montana

Syllabi

Course Syllabi

Spring 2-1-2017

BIOB 483.01: Phylogenetics and Evolution

Scott R. Miller

University of Montana - Missoula

Follow this and additional works at: <https://scholarworks.umt.edu/syllabi>

Let us know how access to this document benefits you.

Recommended Citation

Miller, Scott R., "BIOB 483.01: Phylogenetics and Evolution" (2017). *Syllabi*. 4718.

<https://scholarworks.umt.edu/syllabi/4718>

This Syllabus is brought to you for free and open access by the Course Syllabi at ScholarWorks at University of Montana. It has been accepted for inclusion in Syllabi by an authorized administrator of ScholarWorks at University of Montana. For more information, please contact scholarworks@mso.umt.edu.

BIOB 483 Phylogenetics and Evolution

Contact information:

Instructor: Scott Miller

Office hours: By appointment

Office location: ISB 318

Phone: 243-5149

E-mail: scott.miller@umontana.edu

Goals: Phylogenetics and related molecular evolutionary methods provide powerful approaches for testing evolutionary hypotheses and have recently become pervasive throughout biology and beyond. In this course, we will: (1) become familiar with the theoretical foundations of popular methods of reconstructing phylogenies from molecular sequence data and other select molecular evolutionary analyses; (2) gain hands-on experience with phylogenetic datasets and computational software; and (3) learn how to critically evaluate other people's phylogenies.

Learning outcomes: Following the course, it is expected that a student can: understand and apply (1) terms used in phylogenetics and evolution; (2) strengths and weaknesses of different methods of inferring evolutionary relationships among organisms/molecular sequences; (3) existing computational approaches to infer evolutionary relationships among organisms/molecular sequences; (4) algorithms for aligning molecular sequences; (5) different models of DNA substitution and statistical methods for selecting the model of DNA substitution appropriate for a data set; (6) resampling techniques for testing robustness of phylogenies; (7) methods for incorporating rate heterogeneity into models of DNA evolution; (8) statistical tests of molecular adaptation using codon models of evolution; and (9) the above approaches in an independent phylogeny project. A student should also learn how: to critically evaluate phylogenies; to correct for phylogenetic correlation with phylogenetic comparative methods when testing hypotheses of phenotypic evolution with comparative data; and to use publicly-available computational resources to obtain molecular sequence data and related information.

Text: There is no text for this course. Readings from the primary literature will be provided as appropriate. Some good general introductions to the subject matter that you may wish to check out:

Baum, D. and S. Smith. 2013. *Tree Thinking: An Introduction to Phylogenetic Biology*. Roberts & Company.

Swofford, D. et al. 1996. Phylogenetic inference. In: *Molecular Systematics*, 2nd ed. (D. M. Hillis, C. Moritz and B. K. Mable, eds.). Sinauer.

Felsenstein, J. 2004. *Inferring Phylogenies*. Sinauer.

Avise, J. 2004. *Molecular Markers, Natural History, and Evolution*, 2nd ed. Sinauer.

General policies: University policies on drops, adds, grade changes, changes of status and disability services for students will be observed in this course.

Assessment: Performance will be evaluated according to the following +/- grading system: A (>93-100); A- (>90-93); B+ (>87-90); B (>83-87); B- (>80-83); C+ (>77-80); C (>73-77); C- (>70-73); D+ (>67-70); D (>63-67); D- (>60-63); F (<60). Assessment will be based on the following criteria:

(1) Attendance and participation: 20% of grade. Discussion, sharing of ideas and asking of questions are encouraged. Missing class without a valid, documented reason will result in a 5 point deduction from your final grade.

(2) Assignments (computer lab exercises etc.): 40% of grade. To guarantee full consideration, assignments must be turned in by the specified deadline. If you elect to submit by email, please do so at least 20 minutes before the beginning of class. If you prefer to submit a hard copy, typed responses are preferred but not required; however, written responses must be legible to receive full consideration.

(3) An independent research project to be explained in detail at a later date and to be developed in consultation with the instructor: 40% of grade. Briefly, this will consist of development of a phylogenetic hypothesis; molecular sequence data set acquisition (either as part of your own research or from a public database); data analysis; and interpretation. You will submit a short (~ 8-10 pages) paper of your findings and deliver a short (ca. 15 minute) presentation to the group near the end of the semester (details on respective formats to follow).

Graduate Increment: To obtain graduate credit, a student will be expected to satisfactorily address an additional synthesis question for each computer exercise that relates applied data analysis with theoretical issues discussed in the classroom. All questions including the synthesis question will be graded with equal weight. For the final project, additional and more sophisticated analyses developed in consultation with the instructor will be required, as will greater integration with existing literature via a more extensive literature review requirement.

Writing course: Writing assignments completed as a part of this course satisfy **1/3 of the Upper Division Writing Requirement** for DBS majors (Biology, Microbiology, and Medical Technology). Detailed written feedback on a draft of the project paper will be provided by the instructor two weeks in advance of the paper deadline to accommodate opportunity for revision. A draft of the paper will be turned in on 4/25, instructor comments will be returned by 5/2, and the final paper will be due on 5/12.

UM Online Course Supplement: Course documents including lectures will be posted on the course's Moodle site. If you have not used such a course supplement before or have difficulty accessing the site, please contact technical support at UM Online (<http://www.umt.edu/xls/techsupport/default.aspx>). Lectures will be posted following the day's session.

Schedule:

Week	Topics
Jan 23	Introduction to phylogenetics
Jan 30	The parsimony criterion; Statistical properties of parsimony
Feb 6	<i>Computer lab</i> : Sequence alignment and parsimony
Feb 13	DNA substitution models and distance methods <i>Computer lab</i> : Distance methods
Feb 20	Introduction to maximum likelihood; How “good” is my tree? <i>Computer lab</i> : Selecting DNA substitution models and likelihood
Feb 27	Hypothesis testing in a likelihood framework <i>Computer lab</i> : Testing competing phylogenetic hypotheses
Mar 6	Bayesian methods and phylogeny reconstruction <i>Computer lab</i> : Bayesian methods
Mar 13	Critically evaluating trees; Open lab
Mar 20	Spring Break
Mar 27	Phylogenetic comparative methods: Testing hypotheses of phenotypic evolution <i>Computer lab</i> : Are two traits correlated?
Apr 3	Ancestor reconstruction: Inferring ancient phenotypes
Apr 10	Investigating molecular adaptation <i>Computer lab</i> : Testing for positive selection
Apr 17	Open lab; Gene trees vs. species trees
Apr 24	Phylogenomics: Tree-building on a genome-wide scale <i>Computer lab</i> : Species trees
May 1	Project presentations
May 12	Final paper due; There is no final exam for the course

* Timing of topics subject to change