

# BIOLOGY 848: PHYLOGENETIC METHODS

Syllabus for Fall, 2017

Last Modified: August 21, 2017

**Lecture location and time:**

HAW 2025. MWF 2:00-2:50

**Computer lab:**

HAW 2025. F 3:00-4:50.

Mark Holder – 6031 Haworth Hall. [mtholder@ku.edu](mailto:mtholder@ku.edu)

Office hours: Monday 11am. Friday 10am. and by appointment.

**Source of course info:**

Links to the course reading materials will be available from:

<http://phylo.bio.ku.edu/courses/phylomethods>

**Recommended Text:**

Joseph Felsenstein. 2004. *Inferring Phylogenies*. Sinauer Associates, Inc. Sunderland, MA.

**Course goals:** This course covers state-of-the-art methods for reconstructing phylogenies. We will cover the theoretical basis for different phylogenetic analyses and learn how to use some of the software packages available for conducting these analyses. Inferences that rely heavily on phylogenetic trees (eg. analyses of character evolution, divergence time estimation, and studies of diversification rates) will also be covered.

**Grading:**

Your grade will be determined by homework assignments and a project that will be due the last week of class. The term paper will make up 40% of your grade. The project can consist of a new phylogenetic analysis (of your own data or published data) or a paper reviewing a research topic in phylogenetic analysis. Please talk to me about your planned project before spending too much time so that we can agree that the scope is appropriate.

**Plagiarism:**

No form of plagiarism will be tolerated in this course. This includes copying material from another student, but also includes failing to cite sources. See the writing guides posted at:

<http://writing.ku.edu/writing-guides>

for a discussion of types of plagiarism.

The homework assignments should be worked on your own.

**Students with Disabilities:**

The staff of Services for Students with Disabilities coordinates accommodations and services for KU courses. Their contact information is:

<http://access.ku.edu/> If you have a disability for which you may request accommodation in KU classes and have not contacted them, please do as soon as possible. Please also see me privately in regard to this course.

<b>Lecture topics</b>	<b>Software</b>
Intro, Statistical inference, tree terminology	
Hennigian Inference	
Compatibility/Parsimony	UNIX, text editors
Parsimony	PAUP*
Distance-based tree estimation	FastME, FastTree
Distance methods/Searching	
Models and Model selection	PAUP*
Maximum likelihood	PAUP*, GARLI, RAxML, IQTree
Rate heterogeneity	
Consistency	seq-gen
Topology testing	PAUP / CONSEL
Branch Support	
Bayesian Phylogenetics	MrBayes & PhyloBayes & RevBayes
Ancestral character state reconstruction	Mesquite; Simmap
Comparative methods	Mesquite
Divergence time estimation	BEAST
Multiple Sequence Alignment	
Coalescent	Migrate

It is *very* likely that we will run out of time, and not be able to cover all of these topics; so please, speak up and give me some feedback about what topics are most important to you!