Phylogenetic comparative methods  
CEB 35300, Winter 2018

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# Course overview

**Time:** Winter quarter 2016, beginning January 9, Tuesdays, 9:30 a.m. to 12:20 (10 classes altogether)

**Location:** The field museum, Botany classroom every day except for 1/23 (Volunteer Center Conference Room, formerly BioSynC; 10:00 to 12:20) and 2/27 (Bill Stanley (Zoology) Classroom).

**Goals and summary:** This is a graduate seminar course about the uses of phylogenetic trees in evolution and ecology, emphasizing historical inference and hypothesis tests of lineage diversification, phenotypic traits, geographic ranges, and community ecology. This is not a course on how to infer phylogenies, or their uses in studies of molecular evolution and population genetics. Readings and discussion focus on analysis of continuous traits, primarily regression-based methods.

We will work our way from model assumptions and statistical underpinnings to practical implementation of methods. The 3-hour weekly meeting will be split between discussion of primary literature, hands-on tutorials on data analysis in R, and student presentations of methods, providing hands-on tutorials in how to conduct analyses covered.

**Prerequisites:** (1) A course in phylogenetics or systematics, or general familiarity with methods for estimating phylogenies; (2) ability to work in R, and access to a laptop computer that can be brought to the course.

**Labs:** The lab component of the course will be a hands-on practice in using R to perform phylogenetic comparative analysis. Students should bring a laptop with R installed. Students who do not already have R programming background should, at a minimum, [install R](https://www.r-project.org/) and are encouraged to work through the first three chapters of [An Introduction to R](https://cran.r-project.org/doc/manuals/r-release/R-intro.html) prior to the course. The following packages should be installed prior to the first class: ape, phytools, geiger, nlme, magrittr, ggplot2, ggtree.

Students will need a phylogenetic dataset to work on in the lab component. The dataset should comprise an ultrametric tree of ca. 20-500 tips (not much smaller or larger, though this is not a firm boundary); at least two continuous traits; and at least one categorical trait. Students who don’t have such a dataset at hand may use one provided by the instructor. This dataset will be revisited during the labs, providing an opportunity for students to work on their data from multiple angles.

Tutorials will be posted at <https://github.com/andrew-hipp/PCM-2018>.

**Student presentations:** Student presentations should do one of two things: (1) introduce a method that complements the methods we are already covering in class and provide sufficient background that other students in the class can follow the method, regardless of how far we are in class; or (2) work through a recent empirical paper that presents a particularly strong suite of phylogenetic comparative analyses. Students searching for possible topics are referred to the document “Ideas for student presentations.” In any case, the presenter should divide the presentation between an overview of the papers / methods presented and a hands-on tutorial, with code, allowing everyone in class to execute the analyses presented. The presentation will thus provide all participants in the class with a model for executing the analyses presented and code that they may be able to repurpose in their own research.

**Grades:** Grades in the course will be based 70% on attendance and participation in discussion, 30% on the presentation. Students who need to miss a class session will be expected to provide a one-page essay that raises questions about the readings and identifies points of connection between the readings and past discussions, other articles read in the class, or issues relative to the student’s research. This essay is to be turned in within one week of the missed class period. Each class period counts for 1/10 of the participation grade. Presentation grades will be weighted 1/2 to clarity of presentation, and 1/2 to clarity of the code / lab portion. Final letter grades will be assigned based on [University Grading Policies](https://registrar.uchicago.edu/page/university-grading-policies).

# Course schedule

**Week 1 (9 January):** Trees, traits, and covariance: importing and visualizing comparative data   
*Lab: reading, editing, and visualizing phylogenetic data*

**Week 2 (16 January):**Independent contrasts and its extensions: addressing phylogenetic autocorrelation. *Lab:* PIC

**Week 3 (23 January; Volunteer center classroom):**Generalized linear models (GLS). *Lab: GLS*

**Week 4 (30 January):**Fitting and evaluating alternative models (including multimodel inference)  
*Lab: AIC, parametric bootstrapping, model-averaging*

**Week 5 (6 February):** Stretching the tree: evolutionary rates and models of continuous trait evolution  
*Lab: stretching the tree and modifying the covariance matrix*

**Week 6 (13 February):** Ornstein-Uhlenbeck models. *Lab: fitting O-U models*

**Week 7 (20 February):**Multivariate vs univariate; and accounting for intraspecific variation and error. *Lab: incorporating phylogenetic error and measurement error in analysis*

**Week 8 (27 February; Zoology classroom):**Phylogenetic diversity and phylogenetic methods in community ecology part I. *Lab: metrics and permutation tests*

**Week 9 (6 March):** Phylogenetic diversity and phylogenetic methods in community ecology part II.  
*Lab: PGLMM*

**Week 10 (13 March):** Effects of traits on lineage diversification.   
*Lab: lineage diversification methods*