

The syllabus (mostly the schedule) will be updated throughout the semester. I have also embedded it below.

## Phylogenetic Methods (PhyloMeth). Spring 2018

UT students may sign up at EEB 603, CRN 30253 (grad students) or EEB 504, CRN 31819 (advanced undergrads)

Syllabus version: 12:22 PM, 10 January, 2018

Instructor: **Brian O'Meara** (bomeara@utk.edu)

Course website: <http://phylometh.org>

Office Hours (446 Hesler) by appointment.

##### Anonymous feedback <http://www.brianomeara.info/feedback>

### What you will learn

This is a modern class in phylogenetic methods. You will learn how to get data, build a tree, use comparative methods, and how to make new methods. More importantly, you will learn *why* to do all this.

### Requirements

- A laptop on which you can install software (have root / admin access)
  - It'll be easiest if this is a Mac; less easy is Linux; Windows will be hard
- A question and some data to answer it
- GitHub account
- Slack
- R
- And other software we'll learn about during the course

I am writing a textbook as part of the course \* HTML version \* PDF

It will be updated as we go, so check back frequently.

### Evaluation

Grading will be based on effort and performance. Some of the things will be harder for some students than others just given differences in what they've been exposed to so far, and I don't want to penalize students who are less skilled at R, for example. But I do require that you put in work on this class: work through the exercises, think about the papers, etc. Much of the homework is chewy, so it will take some thought to get through, and you might not be able to do all of this. That's ok.

- EEB603 final project will be done solo (though consulting is ok)
- EEB504 final project will be done in pairs

### Teaching

The class is generally flipped: rather than me droning at the front of the room, I'll be releasing videos online for you to watch. They will be linked to from this syllabus. In class, talk about what was not clear from the videos about methods, and we'll dig into that. We can also work on problematic parts of the exercises (you should do most of them before class) and talk about papers.

### Online option

There is a no-credit online option, as well.

## Schedule

- Week 1, Jan 11
  - Topic: Getting ready
  - Items: R, github, gitter, unit testing
  - Instructions: <http://rpubs.com/bomeara/phylomethsoftwareinstall>
  - Exercise: Getting Started
  - One way to do the exercise is to fork the github repo, clone it to your computer, start editing documents (such as those in `exercises/gettingstarted`), then `git commit -m"done homework"` -a, then do a pull request.
  - Recorded class
- Week 2, Jan 16
  - Topic: Gathering data
  - Reading: Chapter 3 of the textbook.
  - Videos: See videos in this playlist
  - Items: Sequences, trees, name resolution, alignment
  - Exercise: Getting trees: <https://github.com/bomeara/phylometh/blob/master/exercises/gettingtreesanddata/exercise.R>
  - In class: Discussion of what kinds of data you need for your questions, what kind of trees you need.
  - Recorded class
- Week 3, Jan 23 & Jan 25
  - Topic: Building trees
  - Videos: Terminology, Tree space, Likelihood vs Bayes
  - Reading
    - \* Felsenstein 1978
    - \* Felsenstein 1985
    - \* Lewis 2001
    - \* Drummond & Rambaut 2007
  - Items: Likelihood; Bayes; Parsimony
  - Potential exercises (choose your own)
    - \* RAxML tutorial: Fast maximum likelihood tree inference program.
    - \* RevBayes tutorials: Bayesian program with many different models.
    - \* BEAST tutorials: Bayesian tree inference program, especially used for getting chronograms.
    - \* Cyverse discovery environment: Free service (thanks, NSF!) for running phylogenetic (and other) software
  - Recorded class
- Week 4, Jan 30 & Feb 1
  - Topic: Building trees
  - Items: Gene tree species tree; Network
  - Reading
    - \* Maddison 1997: Gene trees in species trees
    - \* Heled & Drummond 2009: A method for inferring species trees given gene trees inside them
    - \* Degnan & Rosenberg 2000: Cases where the most frequent gene tree does not match the species tree
    - \* Solís-Lemus & Cécile Ané, 2016: Phylogenetic networks. A bit mathy for many students in this class, but worth introducing quartets, reticulation, and an existing method.
  - Class exercise: R Markdown
- Week 5, Feb 6 & Feb 8
  - Topic: Dating trees
  - Items: Beast, r8s
  - Reading
    - \* Sanderson, 2002: Penalized likelihood.
    - \* Drummond et al. 2006: Bayesian dating. And good paper title.
    - \* Drummond and Rambaut, 2007: BEAST description.

- \* Beaulieu et al., 2015: One possible caveat to Bayesian dating.
  - \* Heath et al. 2015: Using fossils as tips.
  - \* Course book
- Exercise
  - \* RevBayes tutorials on dating.
- Recorded class
- Week 6, Feb 13 & Feb 15
  - Topic: Discrete character models
  - Items: Pagel 1994, corHMM, geiger
  - Video: PhyloMeth discrete characters
  - Reading
    - \* Pagel, 1999: Ancestral state reconstruction
    - \* Lewis, 2001: MKV model
    - \* O’Meara, 2012: Review of models
  - Exercise
- Week 7, Feb 20 & Feb 22
  - Topic: Continuous character models
  - Items: Surface, OUwie, geiger
  - Videos: OU, BM, etc
  - Reading:
    - \* Hansen and Martins, 2006: Linking micro and macroevolutionary models. TL;DR: Table 1 shows that many microevolutionary models reduce to Brownian motion.
    - \* Felsenstein 1988: Biology behind the model.
    - \* O’Meara, 2012: Not nearly as important as the ones above, but an intro to models that shows how I think.
    - \* Course Book
  - Exercise
- Week 8, Feb 27 & Mar 1
  - Topic: Correlating characters
  - Items: independent contrasts, Pagel 1994, Hansen OU
  - Reading
    - \* Felsenstein, 1985: Independent contrasts
    - \* Pagel, 1994: Pagel 94 correlation
    - \* Maddison & FitzJohn, 2015: A big problem with correlation (and other issues)
  - Exercise
- Week 9, Mar 6 & Mar 8
  - Topic: Biogeography and optimization (guest week by Katie Massana)
  - Reading
    - \* Ronquist and Sanmartin, 2011
    - \* Ree and Smith, 2008
    - \* Matzke, 2014
- Week 10, Mar 20 & Mar 22
  - Topic: Diversification and SSE models
  - Items: diversitree, hisse
    - \* Magallon and Sanderson, 2001: As an empirical paper of ages, later work has improved on this, but it has extremely clear explanations of the math behind these methods.
    - \* Maddison, FitzJohn, and Otto, 2007: The BiSSE paper. Download it as a PDF: the equations do not render in the HTML.
    - \* Maddison & FitzJohn, 2015: Already read it, but reread for this week.
    - \* Beaulieu & O’Meara, 2016: A hidden state version of the BiSSE model.
  - Exercise
- Week 11, Mar 27 & Mar 29
  - Topic: Simulating data
  - Items: TreeSim, geiger

- Week 12, Apr 3 & Apr 5
  - Topic: Building a new comparative method
- Week 13, Apr 10 & Apr 12
  - Topic: Testing a new comparative method
- Week 14, Apr 17 & Apr 19
  - Topic: Student choice
- Week 11, Aprl 24 & Aprl 26
  - Topic: Student choice

**Course made possible by:** NSF CAREER grant to O'Meara & ongoing support from the Department of Ecology & Evolutionary Biology, U. of Tennessee, Knoxville.