# “Agenda”: Class One: Introductions

# Introductions

To get to know each other, to help build community, and to get a feel for the diversity of backgrounds present

Who are you, what are you interested in, why are you here, and what is your background in phylogenetics?

## Instructors

Carl, Will, John

## Students

# Course goals

## To provide a venue to explore topics in phylogenetics

Basically, the instructors wanted an excuse to learn new things and be brought up-to-date with the literature

Community and involvement are very important (everyone, instructors included, needs to conscientiously make space for everyone else). If anyone feels that the instructors are overly dominating the conversation, call them out. If anyone feels that another student is overly dominating the conversation, please notify one of the instructors

# Course structure

## Introductory meetings

The first few (four?) lectures will be general introductions, given by the instructors.

## Core meetings

Then we’ll transition to a student-led format, with each student responsible for leading a session on a topic of their choice. Each week the student leader will produce an annotated bibliography of the relevant papers (both classic and recent), select two(ish) papers for the class to read, and deliver a short (15 min) introductory lecture, before we move to a discussion format for the rest of the session.

### Possible topics

modeling migration/hybridization/introgression; state-dependent diversification models; modeling gene duplication and loss; POMO models; covarion/hidden state models; model testing, model adequacy; posterior predictive tests; demographic inference (e.g., inferring population size changes through time); the multispecies coalescent, genetrees/species tree; the BAMM controversy; divergence time dating; inferring selection from sequence alignments; alignment inference (alignment-phylogeny co-inference?); community phylogenetics; spatial phylogenetics; phylogenetic networks; inferring phylogenies from morphological data; heterogeneous models, e.g., non-stationary base frequencies; ancestral state reconstruction; phylogenomics (strengths, pitfalls?); inferring correlated evolution of traits; assessing support; hypothesis testing of relationships; reconstructing morphological evolution on a phylogeny; ABC approaches; hidden Markov models; mixture models; species delimitation; microbial community analysis; etc; etc; etc; etc

Please consulate an instructor before settling on a topic

## Course website

The course will be largely run through our course website: https://github.com/wf8/IB290 (under the hood version); https://wf8.github.io/IB290/ (pretty version)

### Website tutorial

Will

# Introduction to phylogenies and “tree thinking”

Short lecture – Carl.