Syllabus

OEB275r – Fall 2022

Scott V. Edwards, Landen Gozashti, OEB/MCZ

Comparative Genomics: Phylogenetic Approaches to Linking Genomes and Phenotypes

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Weekly meeting time: Thursdays 12-2:45 pm EST. GEOL 103A

Course overview:

Three major themes: 1) fundamentals of population genetics and phylogenetics; 2) models for simple and multivariate trait evolution on trees 3) new models for mapping genes for phenotypic traits using trees

Course structure: The course will begin with introductory lectures and demonstrations so that everyone is on the same page. We will introduce basic models of phylogenetics of single- and multigene data sets including methods using the multi-species coalescent model. In mid-course, we will get treated to state-of-the-art presentations by some of the world leaders in methods of comparative biology and genotype-phenotype mapping on trees. The course will be punctuated with recaps during which we conduct in-class analysis of data sets and short presentations. A short (10 double-spaced pages) final project, consisting of analysis of a comparative data set (genomic and phenotypic data) and write-up set be due at the end of the course, during reading period.

Week 1 (Sept. 1) – **Course introduction**

Course themes, historical perspective from phylogenetics and population genetics to comparative methods.

Week 2 (Sept. 8) – Neutral theory of molecular evolution: implications for population genetics and phylogenetics (lecture/discussion)

Estimating pop gen parameters: Software: PopGenome (R package); migrate-n

Week 3 (Sept. 15) – Phylogenetics: single gene and multigene coalescent approaches (lecture/discussion)

Software: IQ-tree; MP-EST; ASTRAL

Week 4 (Sept. 22) – **Joe Felsenstein – University of Washington**

 Introduction to character evolution on trees (lecture/discussion)

Software: Phylip (contrast module)

Week 5 (Sept. 29) – **Dean Adams - Iowa State University –** comparative methods for multivariate traits

Software: RRPP, Geomorph, PACA (R packages)

Week 6 (Oct. 6) – **Matt Pennell, University of Southern California.**

Rates of trait evolution;   o

Week 7 (Oct. 13) – **Jeremy Beaulieu – University of Arkansas**

Comparative methods with Hidden Markov Models; Software: corHMM (R package)

Week 8 (Oct. 20) – –   Recap: review of recent class discussions and prospects for the next step:S linking genomes and phenotypes (Lecture discussion). Begin thinking about final projects.

Week 9 (Oct. 27) – **Zhirui Hu - University of California San Francisco; Gregg Thomas - Harvard**

PhyloAcc and PhyloAcc-GT: Associating rates of genome change to specific phenotypes using Bayesian inference

Week 10 (Nov. 3) – **Patrick Gemmel - Harvard**

Linking genomic variation and continuous traits; Software: PhyloACC-continuous (R package)

Week 11 (Nov. 10) **Michael Hiller, Loewe Center for Translational Biodiversity Genomics** (lecture/software demo)

Linking genomes and traits through comparative genomics. Software: TOGA (Tool to infer Orthologs from Genome Alignments)

Week 12 (Nov. 17) – **Russell Dinnage, Florida International University**

Deep learning for morphometrics and phylogenetics

Week 13 (Dec. 1) – Wrap up: the future of mapping genes via phylogenies

Final project due: December 7.