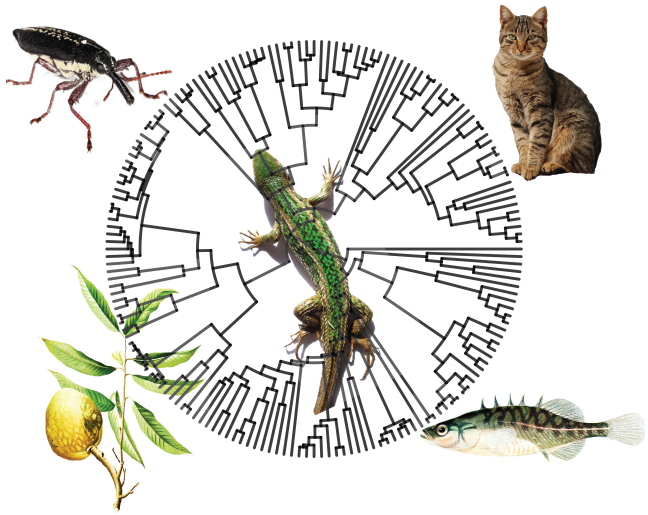
BYU-Department of Biology

Biology 559R: Introduction to Phylogenetic Comparative Methods

Instructor Juan C. Santos, Postdoctoral Fellow
Office: LSB 4136
Phone: 801-422-4398
e-mail: infraguttatus@gmail.com
Office Hours: by appointment



Term Winter (2015)

Times T-Th, 2:00 – 2:50 p.m.

Room 2142 LSB (2nd floor LSB)

Credits 2 credits

Prerequisites A graduate-level course in 'Phylogenetic Systematics' and basic knowledge of R scripting (recommended)

Course Description

This course is a 'hands on' practice and application of phylogenetic comparative methods. For this purpose, I will introduce different statistical and quantitative methods for analyzing character evolution and ecological and evolutionary processes along phylogenetic trees. We will use different R packages and other freely available software that allow us to analyze and retrieve data from online repositories, but students are also encouraged to use their own research data for this purpose. The statistical and theoretical foundations of techniques will be discussed, but the emphasis of this course is on the analysis, visualization and implementation of the current comparative methodologies. The main topics include: (1) brief introduction to R scripting and environment, (2) data retrieval from online databases for the construction of phylogenetic trees, (3) sequence alignment and phylogenetic inference, (4) tree manipulation and visualization, (5) ancestral state reconstruction, (6) diversification analyses and trait evolution inferences, (7) tree and data simulations, and (8) multivariate comparative methods. The list of R packages and software that we will review and implement are provided below. Students will conduct a course project based on their own datasets and prepare a final report and presentation.

Course Format

The course will consist of lab sessions during each class with an introduction of the methodologies and a brief discussion of relevant key literature. During the

first nine classes, students will develop and present a work plan for their course projects using their own data. Subsequent meetings will cover additional topics with the opportunity for the students to request practice of specific methodologies in support of their projects. For suggestions about methods, you are encouraged to visit the CRAN Task View: Phylogenetics, Especially Comparative Methods (http://cran.r-project.org/web/views/Phylogenetics.html). The final evaluation will be student-led presentations of their projects and a written report in manuscript format.

*2142 LSB (computer room) is equipped with PC computers, but most of software runs at its best in MAC OS systems. Students are encouraged to bring their own computer to the lab.

Prerequisites

Students should have had at least one upper-level course in Evolutionary Biology or 'Phylogenetic Systematics'. It is also recommended some basic univariate statistics methods and knowledge of statistical inference, but these latter components are not a requirement. The instructor's consent is required after discussing possible course projects, as students need to have a suitable dataset for their final projects.

Textbooks

There are no required textbooks and all course material will be provided as pdf files. Students are encouraged to read the manuals of each software or R package. However, the following reference may be useful for the course:

Emmanuel Paradis (2012) Analysis of Phylogenetics and Evolution with R. Second Edition. Springer. ISBN 978-1-4614-1742-2*

*This book is available to download at the Harold B. Lee Library

Grading

	Total Grade (%)	Due Date
Participation (showing up in class, asking questions, participating in the discussions)	20	
Project Proposal (5-10 minute presentation)	10	Feb-5
Final Presentation (10-15 minute presentation)	20	Apr 9 and Apr 14
Final Project Report	50	Day of presentation

Course Topics and Schedule

Date	Topic	Software and R packages
Jan 6	Introduction to R and comparative methods	--
Jan 8	Introduction to R basic functions	--
Jan 13	Getting sequences from GenBank into R	'ape', 'seqinr'
Jan 15	Alignment: Simultaneous alignment and tree estimation Alignment visualization and manipulation	'Sate-II', 'Mesquite'
Jan 20	Statistical estimation of models of sequence evolution	'jmodeltest'
Jan 22	Implementation of models of sequence evolution and phylogenetic inference	'Garli-2.0', 'RAxML'
Jan 27	Chronogram estimation	'BEAST'
Jan 29	Tree visualization, plotting	'FigTree', 'ape'
Feb 3	Tree retrieval, manipulation and simulations	'ape', 'geiger'
Feb 5	**Project Proposal Presentation**	**--**
Feb 17	Ancestral state reconstruction (discrete)	'ape', 'phytools'
Feb 19	Ancestral state reconstruction (continuous)	'ape', 'phytools'
Feb 24	Diversification Analysis	'ape', 'geiger'
Feb 26	Diversification Analysis: BiSSE based models	'diversitytree'
Mar 3	Diversification Analysis: GoeSSE based models	'diversitytree'
Mar 5	Trait evolution: Data manipulation and exploration	--
Mar 10	Trait evolution: Correlation analyses (continuous traits)	'geiger', 'caper'
Mar 12	Trait evolution: Correlation analyses (discrete traits)	'geiger', 'caper'
Mar 17	Trait evolution: Rates of trait evolution	'geiger', 'phytools'
Mar 19	Trait evolution: Trait simulations	'geiger', 'caper'
Mar 24	Trait evolution: Multivariate methods (e.g., PPCA)	'phytools', "caper'
Mar 26	Request to practice specific methodologies	--
Mar 31	Request to practice specific methodologies	--
Apr 2	Request to practice specific methodologies	--
Apr 7	Request to practice specific methodologies	--
Apr 9	**Student presentations of final project**	**--**
Apr 14	**Student presentations of final project**	**--**