

# BOT6935/ZOO6927 – Phylogenomics

Spring 2016, 3 credits

## I. Class Meetings

<b>Lecture:</b> Tuesday, Thursday	Period 3	9:35 AM–10:25 AM	Carr 222
<b>Lab:</b> Friday	Periods 6–7	12:50 PM–2:45 PM	Carr 222

## II. Instructors

**Emily Sessa**, Ph.D.  
Department of Biology  
Office: Bartram 521A  
Office Hours: by appointment  
Phone: 392-1098  
Email: [emilysessa@ufl.edu](mailto:emilysessa@ufl.edu)

**TA: Blaine Marchant**  
Department of Biology & FLMNH  
Office: Dickinson Hall  
Office Hours: by appointment  
Email: [dbmarchant@ufl.edu](mailto:dbmarchant@ufl.edu)

## III. Course Communications

Course Website: <http://lss.at.ufl.edu> (select Canvas)

We will also use Dropbox to share larger files; please set up a Dropbox account prior to the start of the course if you do not already have one.

## IV. Course Goals and Objectives

The goal of this course is to acquaint graduate students with the theory and methods used in modern phylogenetic analyses, particularly those that involve “big” data sets, either in terms of numbers of taxa or markers. Topics covered will include:

- Review of ML and BI methods, including scripts for running RAxML and MrBayes
- Alignment and multiple alignment, and profile HMM analyses
- Assessing support, conflict, and hypothesis testing with phylogenies
- Supertree and supermatrix approaches
- Handling “big data” in phylogenetics, including MPI parallelization approaches
- Ancestral state reconstruction, concordance analyses, biogeographic and molecular dating analyses, phylogenetic comparative methods (e.g., independent contrasts)
- Extensive use of Hipergator and introduction to using the command line

By the end of the course, students will be able to do the following:

- Execute a complete phylogenetic pipeline, from alignment of sequence data to various applications of trees to test hypotheses and reconstruct ancestral and historical scenarios.
- Understand and explain the challenges posed by “big data” for programs like RAxML and MrBayes, and how new software or methods can cope with these problems.
- Design a phylogenetic experiment and assess various forms of support and error.
- Evaluate transcriptome and genome assemblies reported in the literature.
- Assemble transcriptomes and identify orthologs and paralogs between/within taxa.
- Operate many standard and specialized software packages for phylogenetic analyses, both on the command line and locally on a laptop.

## V. HPC Use

Students enrolled in this course will need an HPC account that is tied to the class. Please follow the instructions under the Assignments tab in Canvas to register for an account. **Please do this even if you already have an account.** We don't want you to use up your advisor's HPC space (which he/she pays for) to work on assignments for class. Please only use the course HPC account for running jobs directly related to the class.

## VI. Assessments and Grading

Your grade will be based on 1) participation, 2) weekly lab assignments, 3) an individual (not a group) project, and 4) two exams. Point breakdown and grade determination are as follows:

	Points		Points		Points
Participation	60	<b>A</b>	450–500	<b>C</b>	350–366
Lab work	140	<b>A-</b>	433–449	<b>C-</b>	333–349
Project	100	<b>B+</b>	416–432	<b>D+</b>	316–332
Exams	200	<b>B</b>	400–415	<b>D</b>	300–315
<b>Total</b>	<b>500</b>	<b>B-</b>	383–399	<b>E</b>	below 300
		<b>C+</b>	367–382		

- 1) **Participation grade** will be based on you asking questions during lecture and lab, contributing to discussions of literature, etc.
- 2) **Weekly assignments** will be handed out in lab and are due before you leave that day.
- 3) **Projects** will involve choosing from a set of pre-selected papers, and copying the methods of that paper using a different data set of your choosing or construction. You will write up your methods and results, and hand these in along with the code you used to do the analyses. More information will be provided later in the course.
- 4) **Exams** will be take-home, sent out electronically, and you will have approximately one week to complete each of them. They will be open-notebook, but I expect you to work independently.

## VII. UF Counseling Services

Resources are available on-campus for students having personal problems:

- UF Counseling & Wellness Center, 3190 Radio Rd, 392-1575, provides psychological and psychiatric services, and can assist with stress & anxiety issues (<http://www.counsel.ufl.edu/>)

A recent series of articles has documented the prevalence of depression, anxiety, and other mental illnesses among graduate students and academics. If you are struggling with any of these issues, please let your instructor or another faculty member know, and we will help you. We are all members of our shared academic community and UF family; no one should feel alone.

### VIII. Attendance and Conduct in Class

Students are expected to be on time for class, and attendance in all class periods is mandatory. Please contact the instructor at least a week in advance if you must be absent. The policies for allowable absences and make-up work follow the university attendance policies: <https://catalog.ufl.edu/ugrad/current/regulations/info/attendance.aspx>.

Only approved electronic devices may be used in class. Approved electronic devices are laptop computers (when used to take notes or otherwise participate in classroom activities) and voice recording devices. Unapproved electronic devices include cell phones, MP3 players, etc.

### IX. Accommodations for Students with Disabilities

Students who require accommodations for a disability must contact the Dean of Students Office of Disability Resources, in Peabody 202 (phone: 352-392-1261). Please see the DRC website (<http://www.dso.ufl.edu/drc/>) for more information. The student should provide documentation of accommodation requirement **by the second week of classes**. No accommodations are available to students who lack this documentation. It is the policy of the University of Florida that the student, not the instructor, is responsible for arranging accommodations when needed. Once notification is complete, the Dean of Students Office of Disability Resources will work with the instructor to accommodate the student.

**X. Lecture & Lab Schedule (subject to change)**

Week	Lect #	Date	Topic
1	1	5-Jan	<ul style="list-style-type: none"> <li>• Course introduction, logistics</li> <li>• What is phylogenetics/phylogenomics, basic phylogenetic pipeline</li> </ul>
	2	7-Jan	<ul style="list-style-type: none"> <li>• Sources of sequence data: Sanger, NGS overview</li> </ul>
	Lab 1	8-Jan	Lab: HPC introduction, command line basics
2	3	12-Jan	<ul style="list-style-type: none"> <li>• Homology, identity, similarity</li> <li>• Alignment and multiple sequence alignment</li> </ul>
	4	14-Jan	<ul style="list-style-type: none"> <li>• BLAST</li> </ul>
	Lab 2	15-Jan	Lab: Alignment and BLAST
3	5	19-Jan	<ul style="list-style-type: none"> <li>• Profile analysis, profile HMMs</li> </ul>
	6	21-Jan	<ul style="list-style-type: none"> <li>• Gene family circumscription</li> </ul>
	Lab 3	22-Jan	Lab: OrthoMCL
4	7	26-Jan	<ul style="list-style-type: none"> <li>• Assembly (Guest lecturer: Blaine Marchant)</li> <li>• deBruijn graphs</li> </ul>
	8	28-Jan	<ul style="list-style-type: none"> <li>• Assembly statistics, assessing quality (Guest lecturer: Blaine Marchant)</li> <li>• Genome vs. transcriptome assembly</li> </ul>
	Lab 4	29-Jan	Lab: Assembly
5	9	2-Feb	<ul style="list-style-type: none"> <li>• Treespace - what is it?</li> <li>• Various ways of exploring treespace</li> <li>• Brief discussion of parsimony methods</li> </ul>
	10	4-Feb	<ul style="list-style-type: none"> <li>• Maximum likelihood approaches</li> </ul>
	Lab 5	5-Feb	Lab: RAxML, ExaML
6	11	9-Feb	<ul style="list-style-type: none"> <li>• Bayesian inference in phylogenetics</li> </ul>
	12	11-Feb	<ul style="list-style-type: none"> <li>• Models in ML and BI</li> <li>• Ways of choosing between models</li> </ul>
	Lab 6	12-Feb	Lab: PartitionFinder, MrBayes, PhyloBayes
7	13	16-Feb	<ul style="list-style-type: none"> <li>• Assessing conflict</li> <li>• Topology tests</li> </ul>
	14	18-Feb	<ul style="list-style-type: none"> <li>• Support in phylogenetics</li> <li>• Bootstrapping, jackknifing</li> </ul>
	Lab 7	19-Feb	Lab: Topology tests, support, etc.

8	<b>15</b>	23-Feb	• Supertrees
	<b>16</b>	25-Feb	• Supermatrices • <b>Exam 1 sent out (by email)</b>
	Lab 8	26-Feb	Lab: Supertrees, Superfine-MRP
Spring break			
9	<b>17</b>	8-Mar	• Ancestral state reconstruction • <b>Exam 1 due (by email)</b>
	<b>18</b>	10-Mar	• Hypothesis testing • Tests for selection
	Lab 9	11-Mar	Lab: PAML
10	<b>19</b>	15-Mar	• Gene trees and species trees • Reasons for discordance
	<b>20</b>	17-Mar	• Bayesian concordance analysis
	Lab 10	18-Mar	Lab: Bucky, MP-EST
11	<b>21</b>	22-Mar	• Comparative methods I (Guest lecturer: Brian Stucky)
	<b>22</b>	24-Mar	• Comparative methods II (Guest lecturer: Brian Stucky)
	Lab 11	25-Mar	Lab: Comparative methods (Guest lab-leader: Brian Stucky)
12	<b>23</b>	29-Mar	• Biogeography
	<b>24</b>	31-Mar	• Molecular dating
	Lab 12	1-Apr	Lab: BioGeoBEARS, BEAST
13	<b>25</b>	5-Apr	• Diversification rates • Detecting rate shifts
	<b>26</b>	7-Apr	• Diversification and character evolution
	Lab 13	8-Apr	Lab: BAMM, Diversitree
14	<b>27</b>	12-Apr	• Gene expression profiling I (Guest lecturer: Clayton Visger)
	<b>28</b>	14-Apr	• Gene expression profiling II (Guest lecturer: Clayton Visger) • <b>Project/paper due (by email)</b>
	Lab 14	15-Apr	Lab: Gene expression profiling (Guest lab-leader: Clayton Visger)
15	<b>29</b>	19-Apr	• RAD sequencing & GBS (Guest lecturer: Sally Chambers) • <b>Exam 2 sent out (by email)</b>
		26-Apr	• <b>Exam 2 due (by email)</b>