Computational Phylogenetics (BIOL 7800) Syllabus – Spring 2015

Meeting Time:	10:30-11:50 T/Th
Location:	LSA A245
Instructor:	Dr. Jeremy Brown
Email:	jembrown@lsu.edu
Office/Lab:	LSA A243/LSB 248
Office Phone:	578-1745
Office Hours:	By appointment.
Course Website:	www.phyleauxgenetics.org (teaching tab), Moodle, GitHub
Required Texts:	*Molecular Evolution: A Statistical Approach* by Yang *(Advanced) Python for Biologists* by Jones
Course Objectives:	Phylogenetic analyses are a fundamental tool for evolutionary biologists and programming skills have become a *de facto* requirement for dealing with most modern datasets. This course will cover the foundational concepts of phylogenetics, while teaching you to program in Python.
Grading Structure:	Grades will be based on completion of regular programming assignments (75%) and participation in class discussions (25%). Assignments should be posted to a GitHub repository. Grading of programming will be equally weighted on the functionality of the code and associated structure, clarity, and comments.
Grading Scale:	A: 90-100, B: 80-89, C: 70-79, D: 60-69, F: < 60

Rough Outline of Topics

<u>Python and Computing</u>

Working at the command line
Variable types
Flow and functions
Complex variable types
Defining new functions
Defining new classes
Recursion
Specialized phylogenetic topics
Version control

<u>Phylogenetics</u>

Intro. to probability
Intro. to Markov chains
Models of nucleotide evolution
Simulating nucleotide evolution
Maximum likelihood inference
Bayesian inference
Markov chain Monte Carlo
Calculating likelihoods on trees
Amino acid models of sequence evolution
Codon models of sequence evolution
Covarion models of sequence evolution
Graphical models in phylogenetics