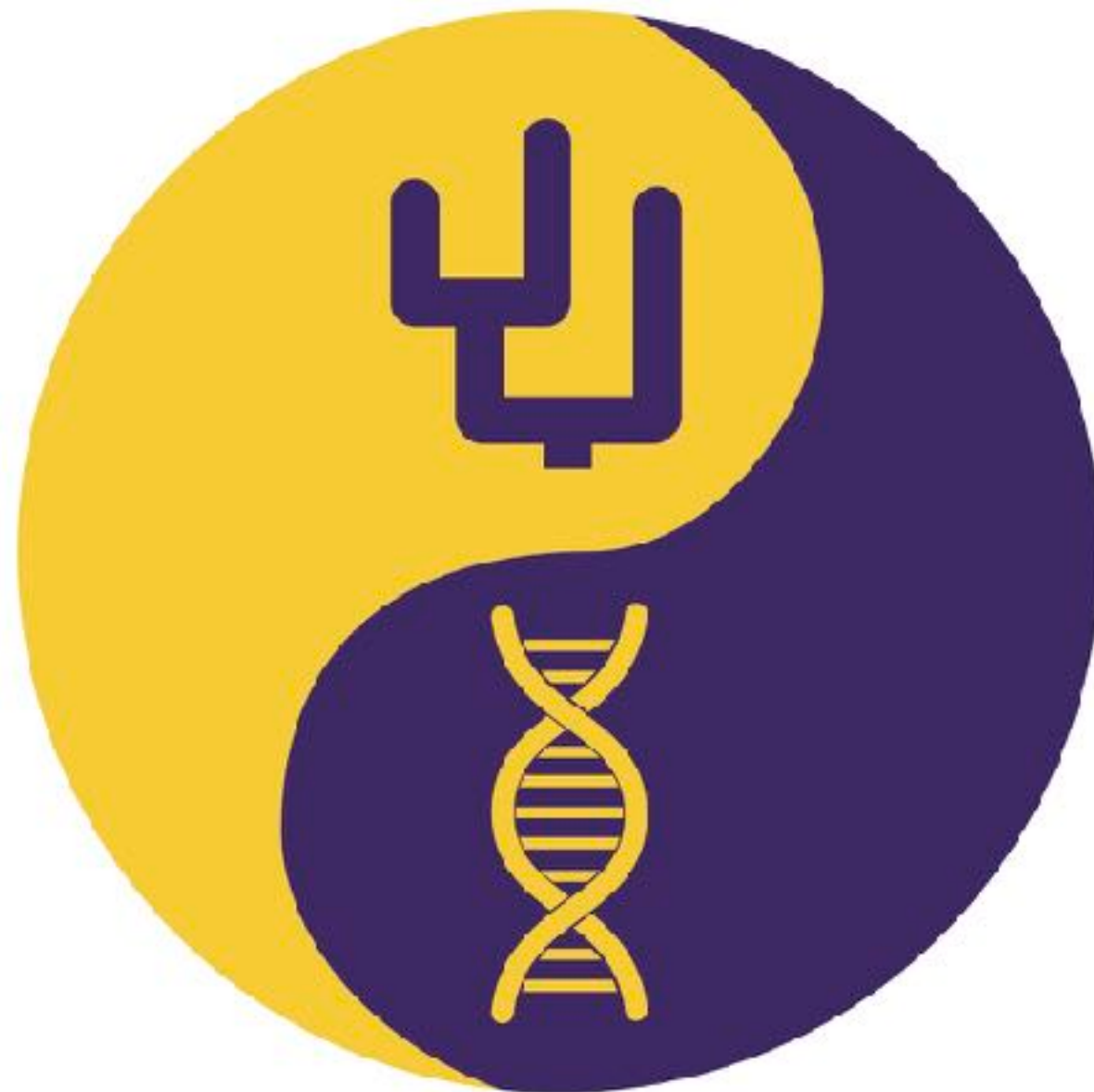


Computational Phylogenetics (BIOL 7800)



Class Details

Meeting Time: 10:30-11:50 T/Th

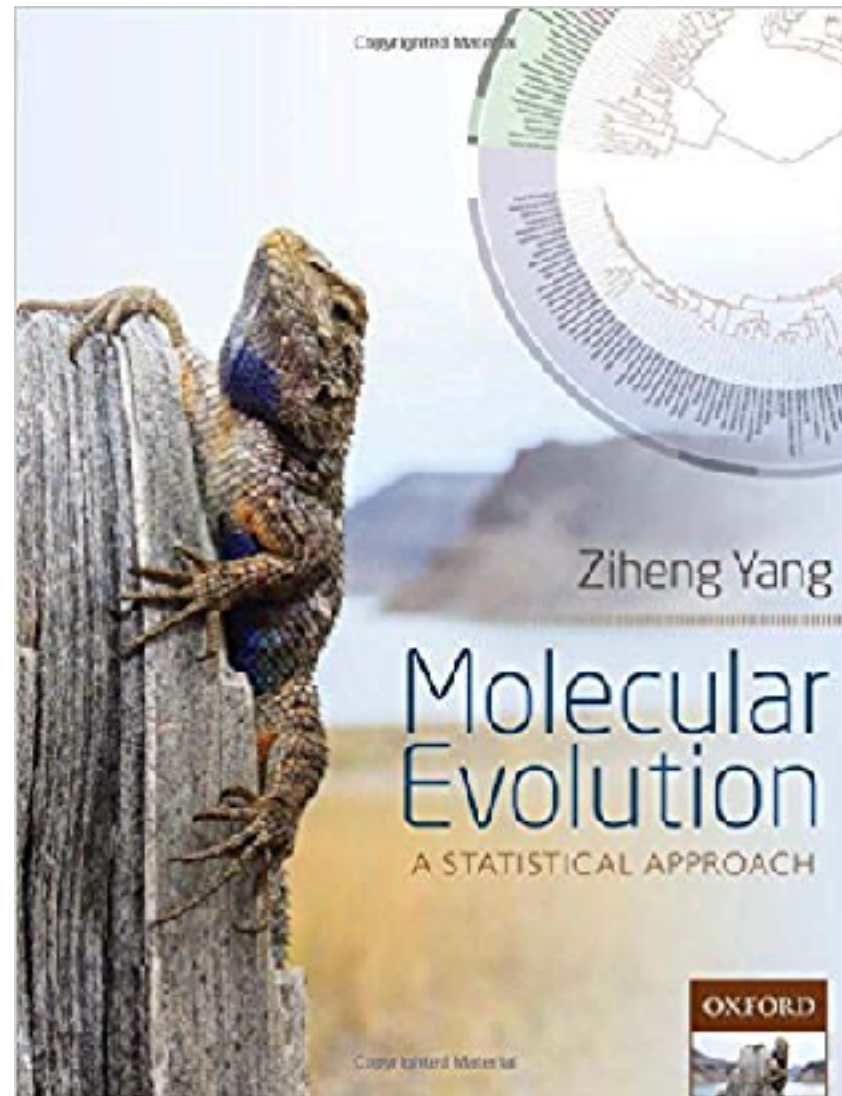
Location: PFT 1244 (For now, but if this doesn't work we can move to my lab, LSB 248)

Open Office Hours

Students in previous classes have suggested that having dedicated time to work together where I'm around is helpful, because they can ask questions as they arise.

I'm happy to do this, but figured we could find a time that works for everyone.

Required Textbook



Molecular Evolution: A Statistical Approach

Supplemental readings will be posted to Moodle

Grading Structure

Grades will be based on completion of regular assignments (75%), which will culminate in an end-of-semester project (25%). Assignments should be posted to a GitHub repository.

A Bit About You

- What do you work on?
- Have you run phylogenetic analyses before?
- Have you done any programming?



GitHub

<https://github.com>

Will be used to post code from class and submit assignments. The most commonly used platform for collaborative scientific coding.

We will discuss the use of GitHub next week.

Your first assignment will be to sign up for a GitHub account.



<https://github.com/CompPhyloLSU>

Computer Setup

Most assignments will use RevBayes code. Some of it will be executed through Jupyter notebooks. The easiest way to install and run Jupyter is using Anaconda.

Ideally, all students will have access to a Mac or Linux laptop. We may occasionally use Terminal commands, which are not available on Windows. Let me know if you have a Windows-only computer.



<https://www.anaconda.com/download/>



ANACONDA NAVIGATOR

Desktop Portal to Data Science

ANACONDA PROJECT

Portable Data Science Encapsulation

DATA SCIENCE LIBRARIES

Data Science IDEs



Analytics & Scientific Computing



Visualization



Machine Learning



...and many more!

CONDA

Data Science Package & Environment Manager



ANAACONDA NAVIGATOR

Sign in to Anaconda Cloud

Home

Environments

Projects (beta)

Learning

Community

Documentation

Developer Blog

Feedback

Applications on root Channels Refresh

jupyterlab0.27.0

An extensible environment for interactive and reproducible computing, based on the Jupyter Notebook and Architecture.

Launch

jupyter notebook5.0.0

Web-based, interactive computing notebook environment. Edit and run human-readable docs while describing the data analysis.

Launch

IPyQtqtconsole4.3.1

PyQt GUI that supports inline figures, proper multiline editing with syntax highlighting, graphical celltips, and more.

Launch

spyder3.2.3

Scientific Python Development Environment. Powerful Python IDE with advanced editing, interactive testing, debugging and introspection features.

Launch

glueviz0.10.4

Multidimensional data visualization across files. Explore relationships within and among related datasets.

Install

orange33.4.1

Component based data mining framework. Data visualization and data analysis for novice and expert. Interactive workflows with a large toolbox.

Install

rstudio1.0.153

A set of integrated tools designed to help you be more productive with R. Includes R essentials and notebooks.

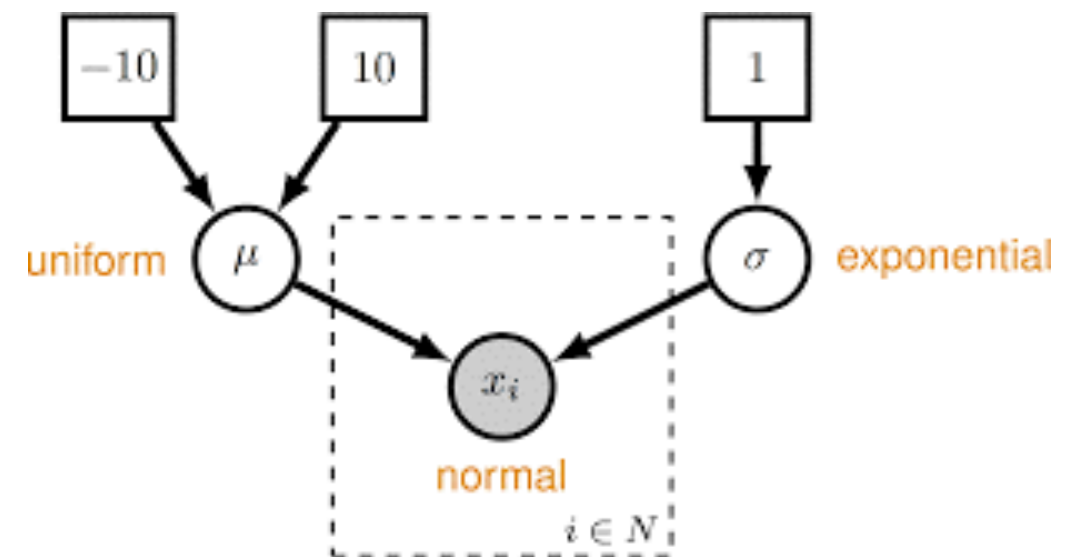


RevBayes

New software for Bayesian inference, primarily in phylogenetics.

Uses graphical models.

Has its own R-like language to specify models and run analyses.





RevBayes

<https://revbayes.github.io>

Download the codebase by
following the instructions here:

<https://revbayes.github.io/software>

Sorry, this is probably the least fun
thing we'll do all semester.

Terminal



On Mac:

Applications -> Utilities -> Terminal

On Ubuntu Linux:

Applications -> Terminal

Introduction to Paths

- The Unix root (/)
 - The very base of the filesystem
- Absolute paths
 - All absolute paths begin at the root - start with /
- Relative paths
 - don't start with /
 - Working directories
 - Shortcuts for current and parent directories
- Hidden files and folders
 - Names begin with .
 - Usually used for configuration files

Running RevBayes

<PATH_TO_REVBAYES>/revbayes/projects/cmake/rb

<PATH_TO_REVBAYES>/revbayes/projects/cmake/rb-jupyter

Running RevBayes in Jupyter

To run RevBayes through Jupyter, we will need to install a kernel. This is a recently developed feature and requires a little extra work. Instructions are here:

https://github.com/revbayes/revbayes_kernel

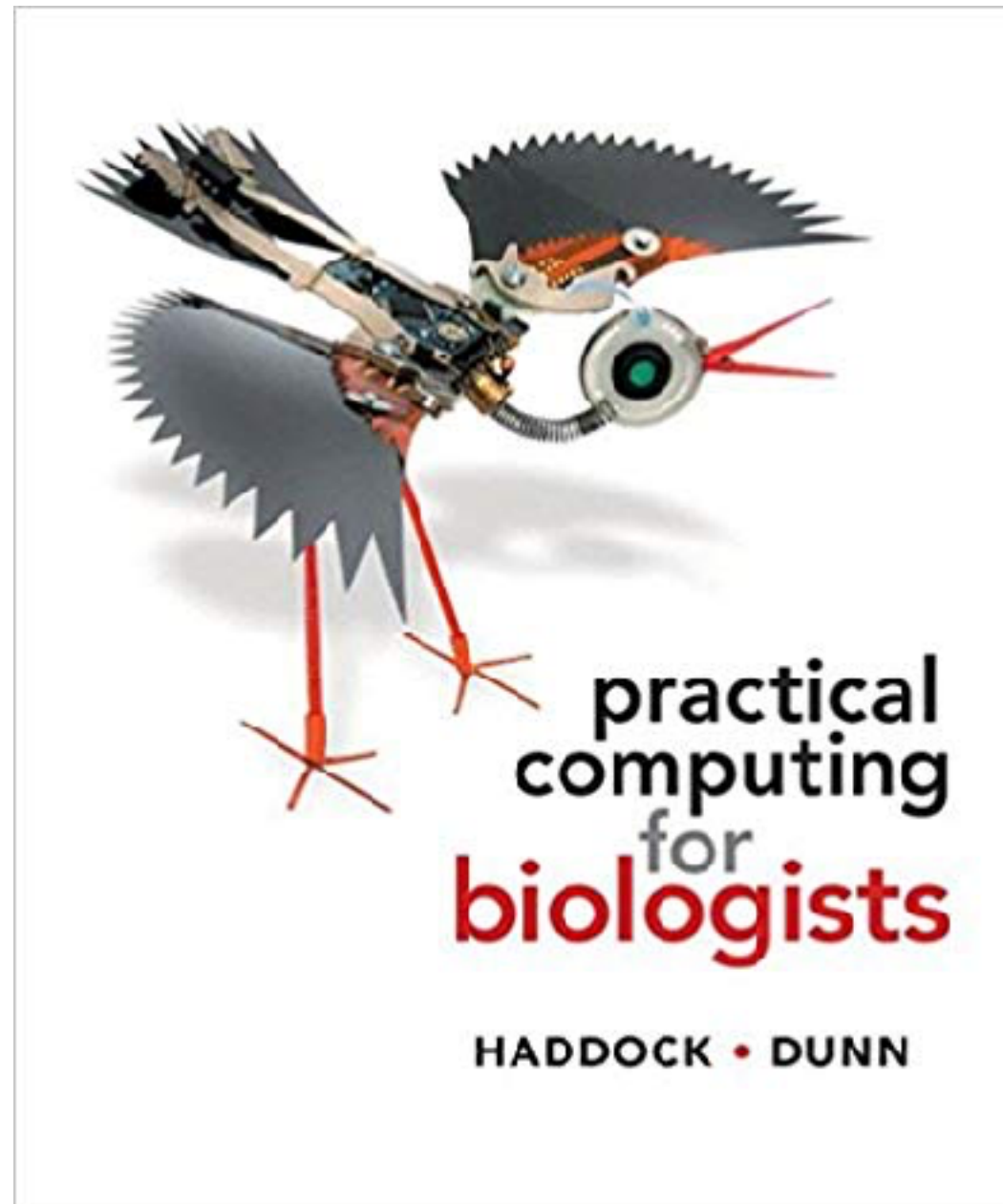
Before you run these commands, you'll need to change directories (cd) into the revbayes_kernel folder.

After installation, you'll also need to add this line to your .bash_profile file in your home directory.

```
export REVBAYES_JUPYTER_EXECUTABLE=<revbayes_path>/revbayes/projects/cmake/rb-jupyter
```

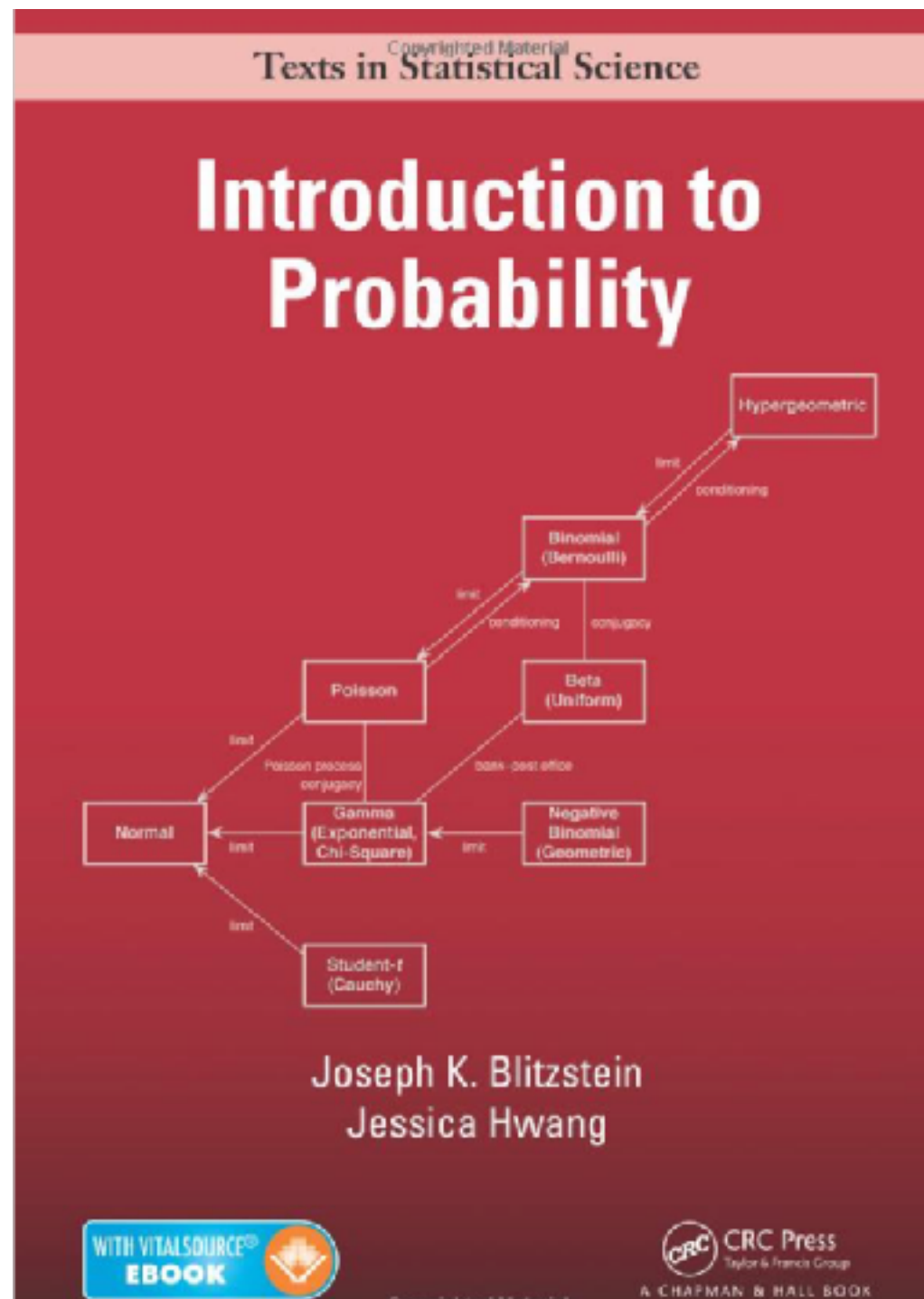
Additional Resources

Practical Computing for Biologists by Haddock and Dunn



Additional Resources

Introduction to Probability by Blitzstein and Hwang



Additional Resources

Udacity Course on the Command Line

<https://www.udacity.com/course/linux-command-line-basics--ud595>

Software Carpentry - Introduction to the Shell

<http://swcarpentry.github.io/shell-novice/>