

Welcome to BCB/EEOB546X!

Computational Skills for Biological Data

Instructors:

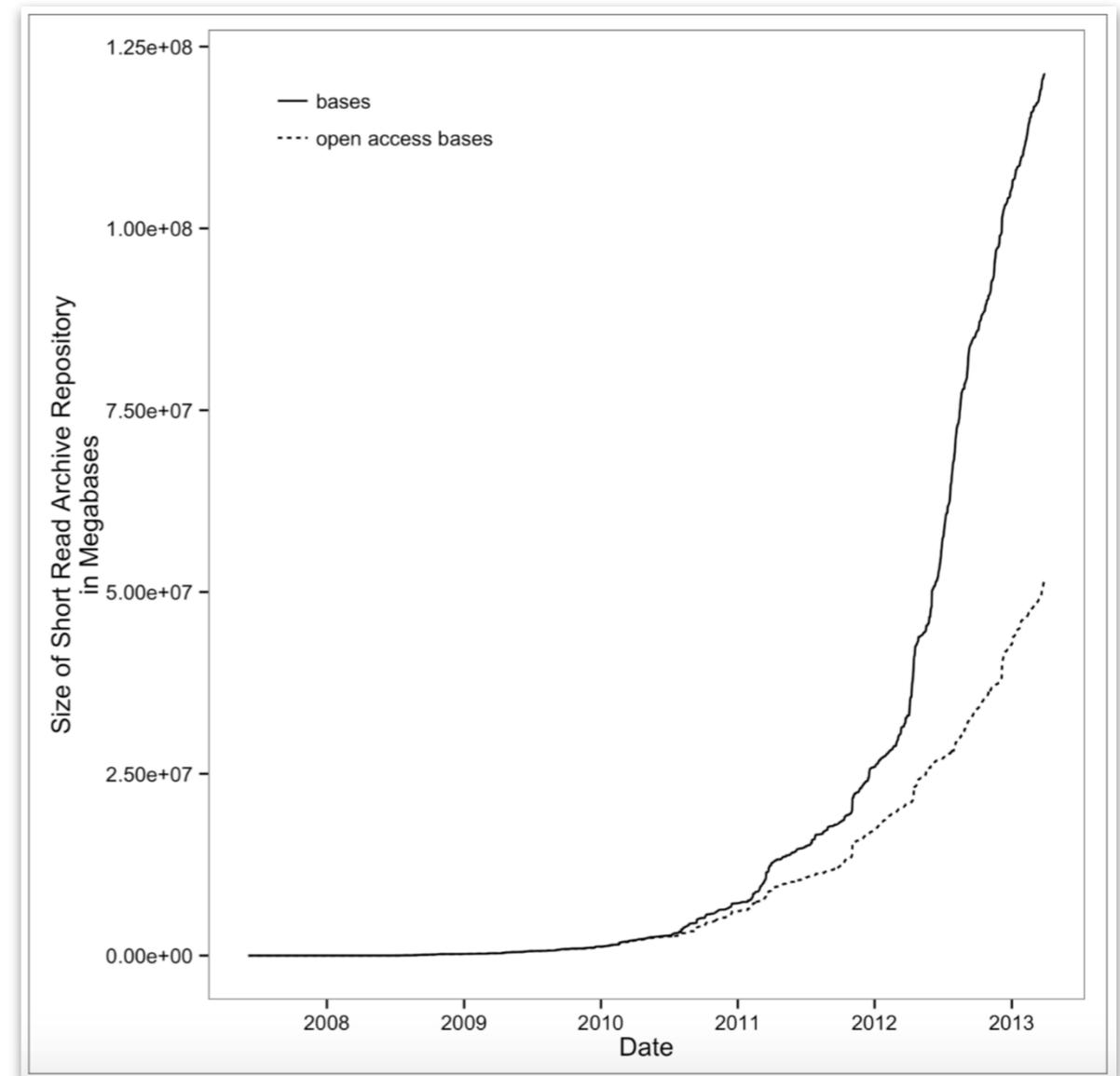
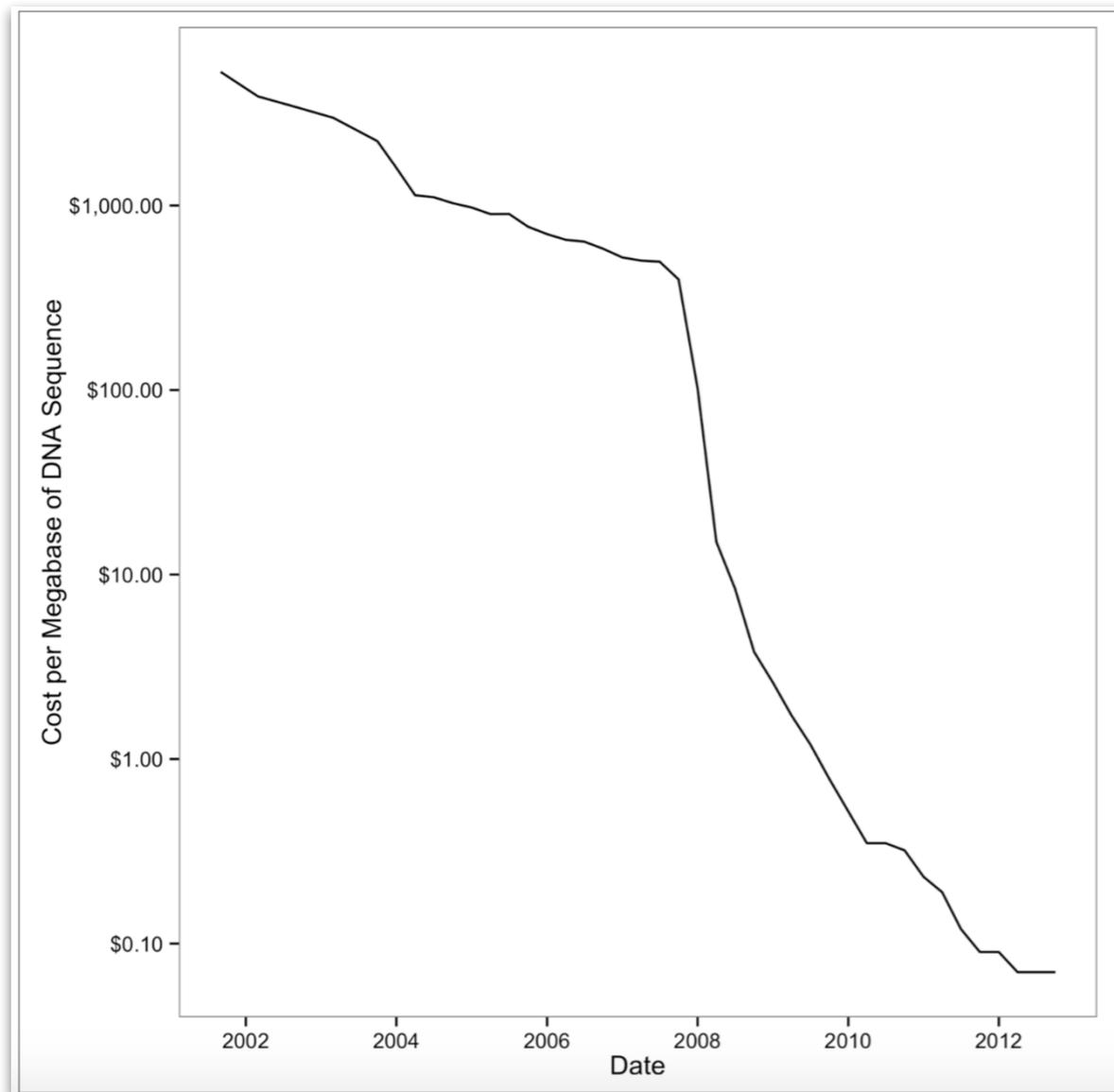
Matt Hufford

Tracy Heath

Dennis Lavrov

Introduction and Basic Unix

What motivated us to teach this class?



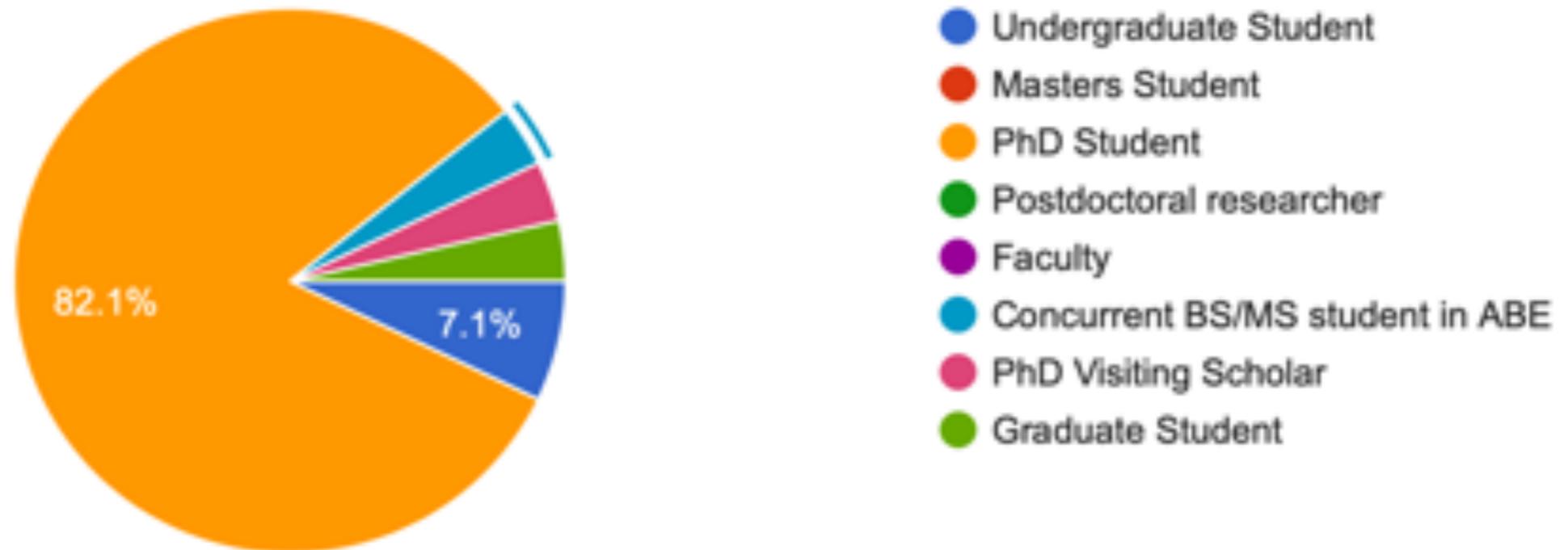
Introduction and Basic Unix

What motivated you to take this class?

Course Make Up

What is your current academic level?

28 responses



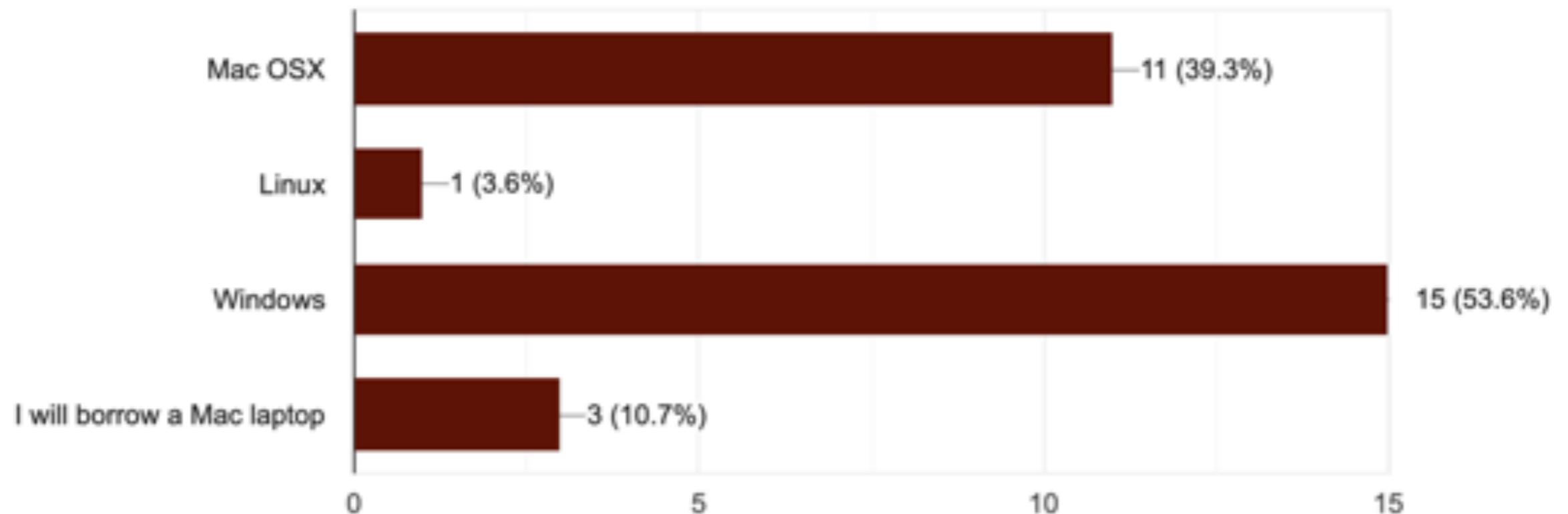
Introduction and Basic Unix

What motivated you to take this class?

Platform Use

If you own a laptop, what operating system do you have? (Please select all that apply.)

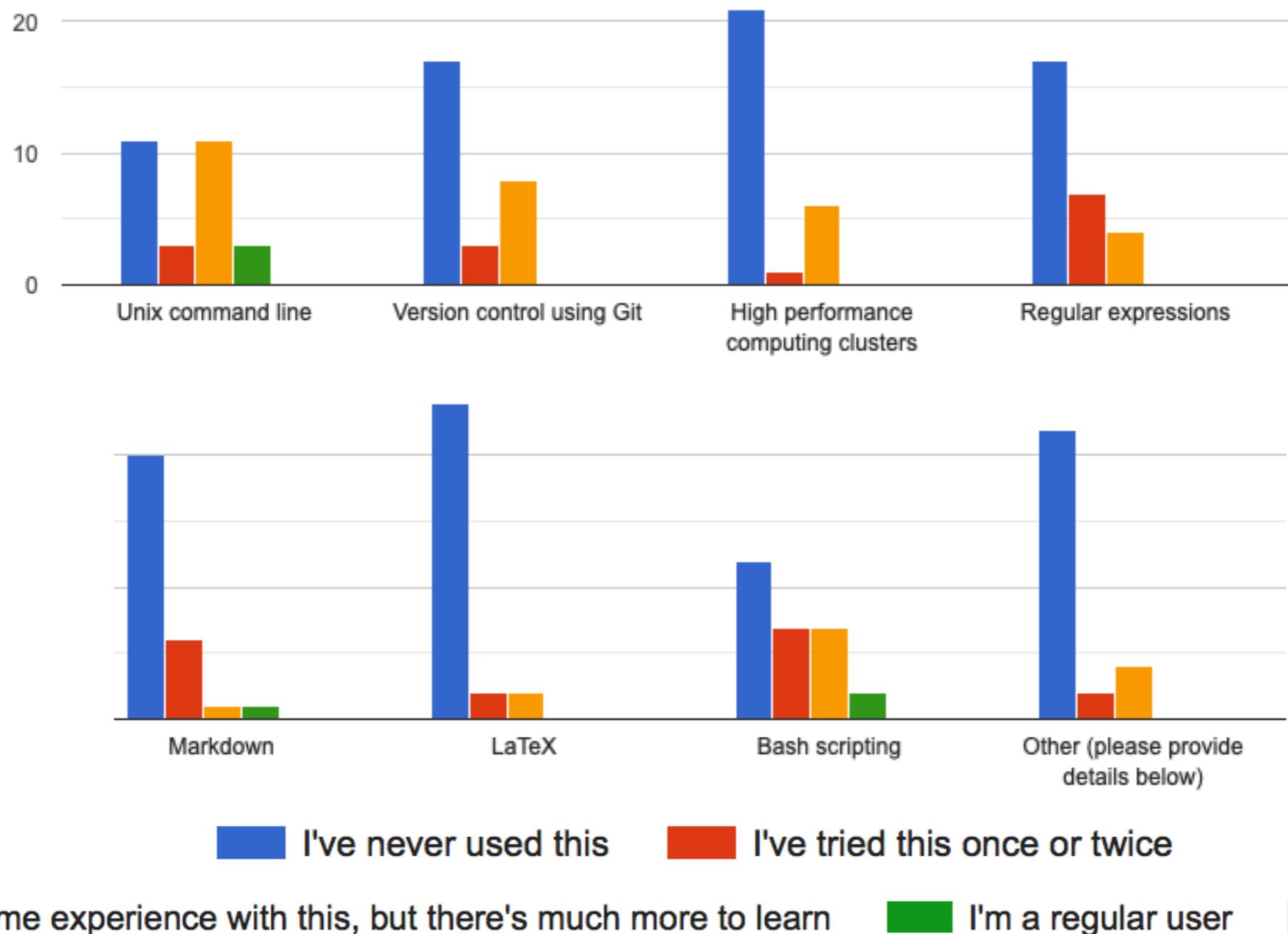
28 responses



Introduction and Basic Unix

What motivated you to take this class?

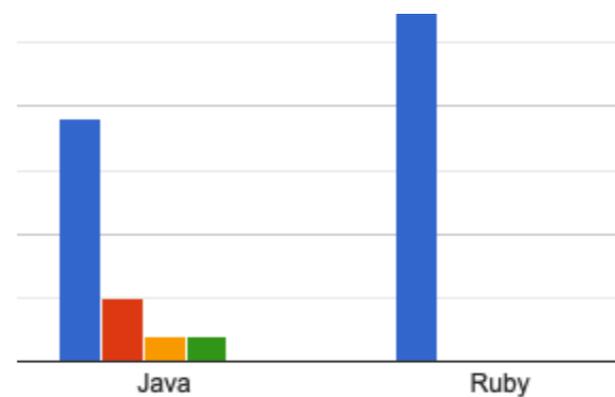
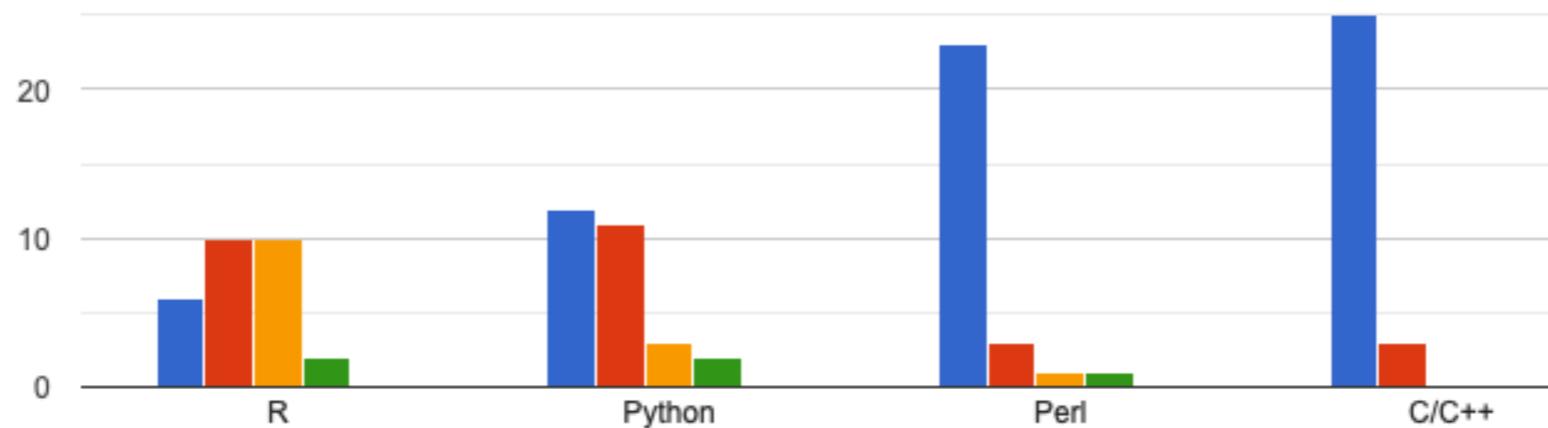
Familiarity with Topics



Introduction and Basic Unix

What motivated you to take this class?

Familiarity with Coding Languages



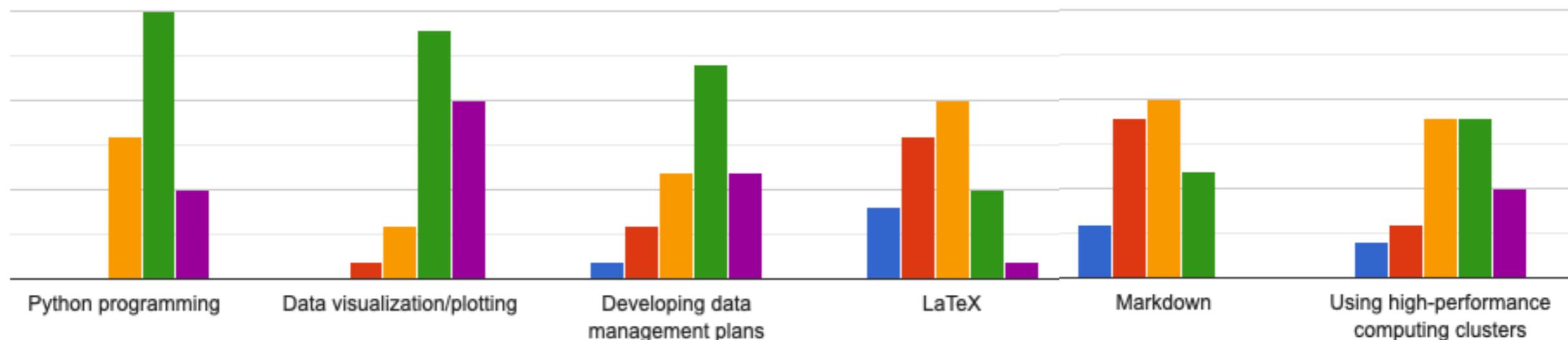
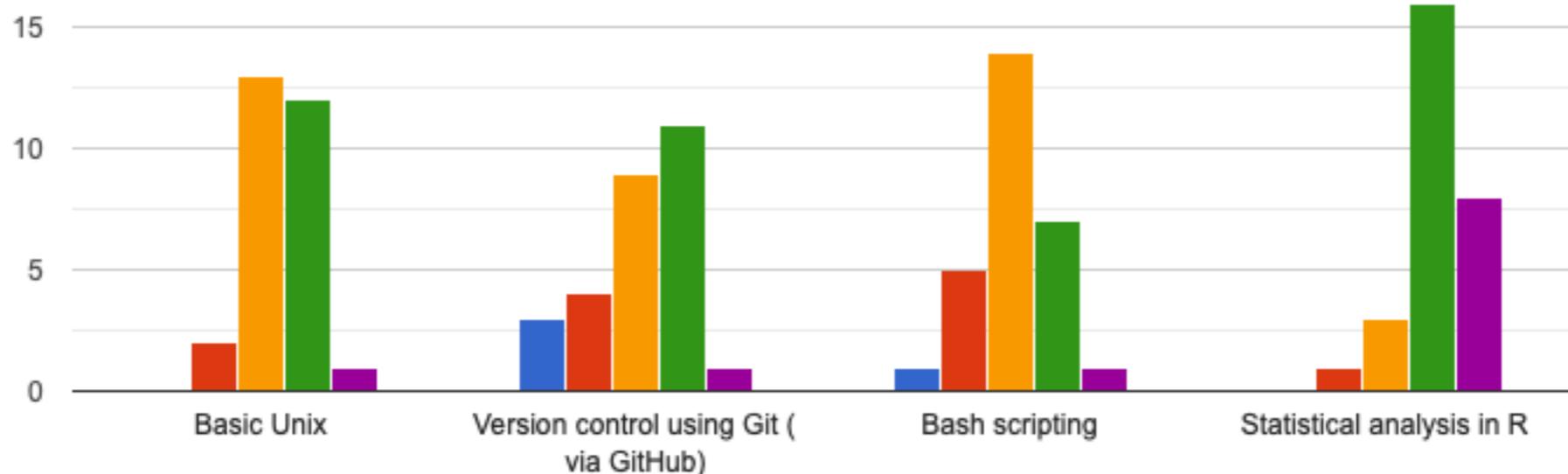
■ Unfamiliar ■ Novice programmer or limited previous experience ■ Occasional user

■ Regularly program in this language ■ Expert programmer

Introduction and Basic Unix

What motivated you to take this class?

Topics of Interest



Introduction and Basic Unix

What motivated you to take this class?

A few more take-homes...

- ◆ Many of you likely also have interest in more specific applications (e.g., transcriptomics, formal sequence analysis, GWAS, etc...)
- ◆ This course will focus on basic skills that will be necessary for working with large data sets and will be useful in these applications...it's a first step
- ◆ You all are drinking from the data firehose!

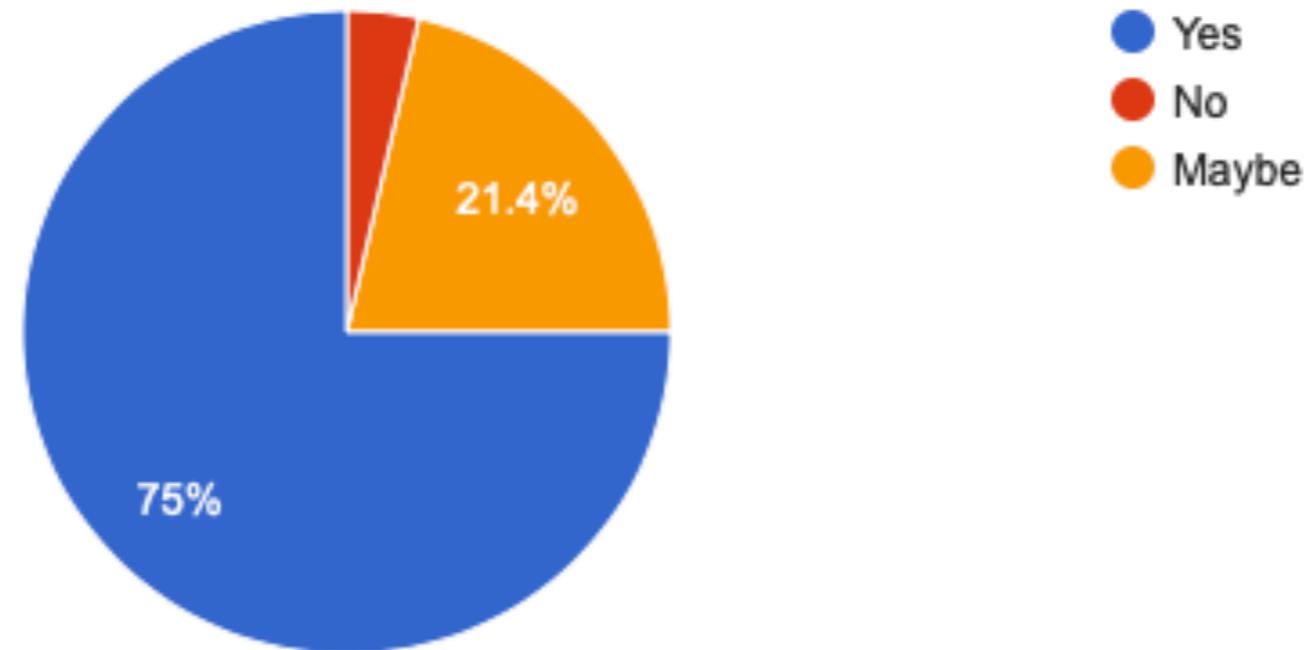
Introduction and Basic Unix

What motivated you to take this class?

A few more take-homes...

Are you currently involved in research that requires computational skills?

28 responses



Introduction and Basic Unix

Our Objectives

By the end of this course, you should:

- Navigate through your computer, create and modify files and directories, and process data using basic Unix commands
- Become familiar with basic R syntax and data structures and implement these in data analysis and plotting.
- Utilize the Python scripting language for more sophisticated data processing.

Introduction and Basic Unix

Our Objectives

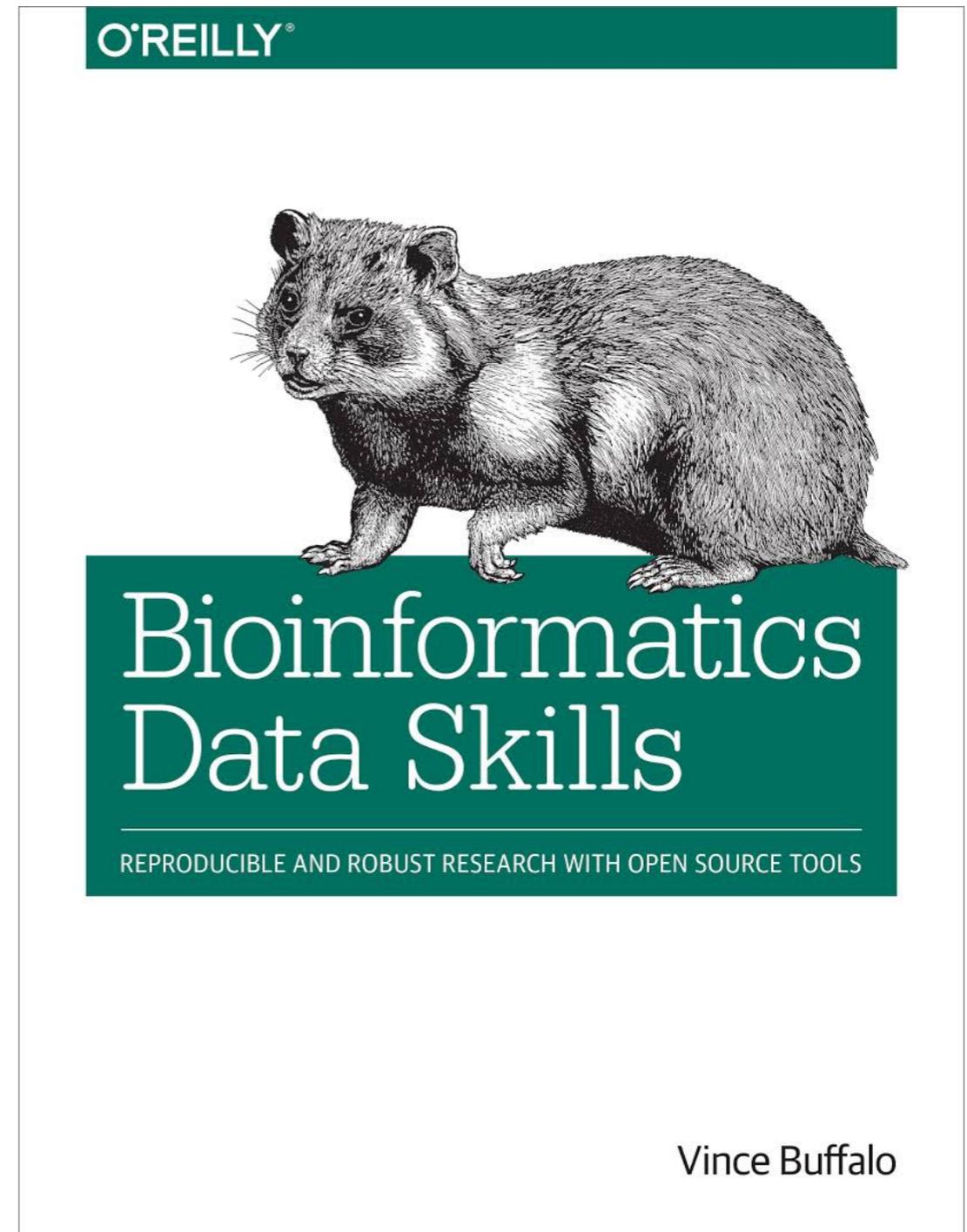
By the end of this course, you should:

- Become familiar with various genomic data types (range, sequence, and alignment data) and learn how to write scripts and analysis pipelines for working with these data.
- Become familiar with high performance computing resources at Iowa State as well as how and when to employ these resources.
- Explore additional resources/topics in computational biology including manuscript preparation in LaTeX and Overleaf and creation of NSF-style Data Management Plans.

Introduction and Basic Unix

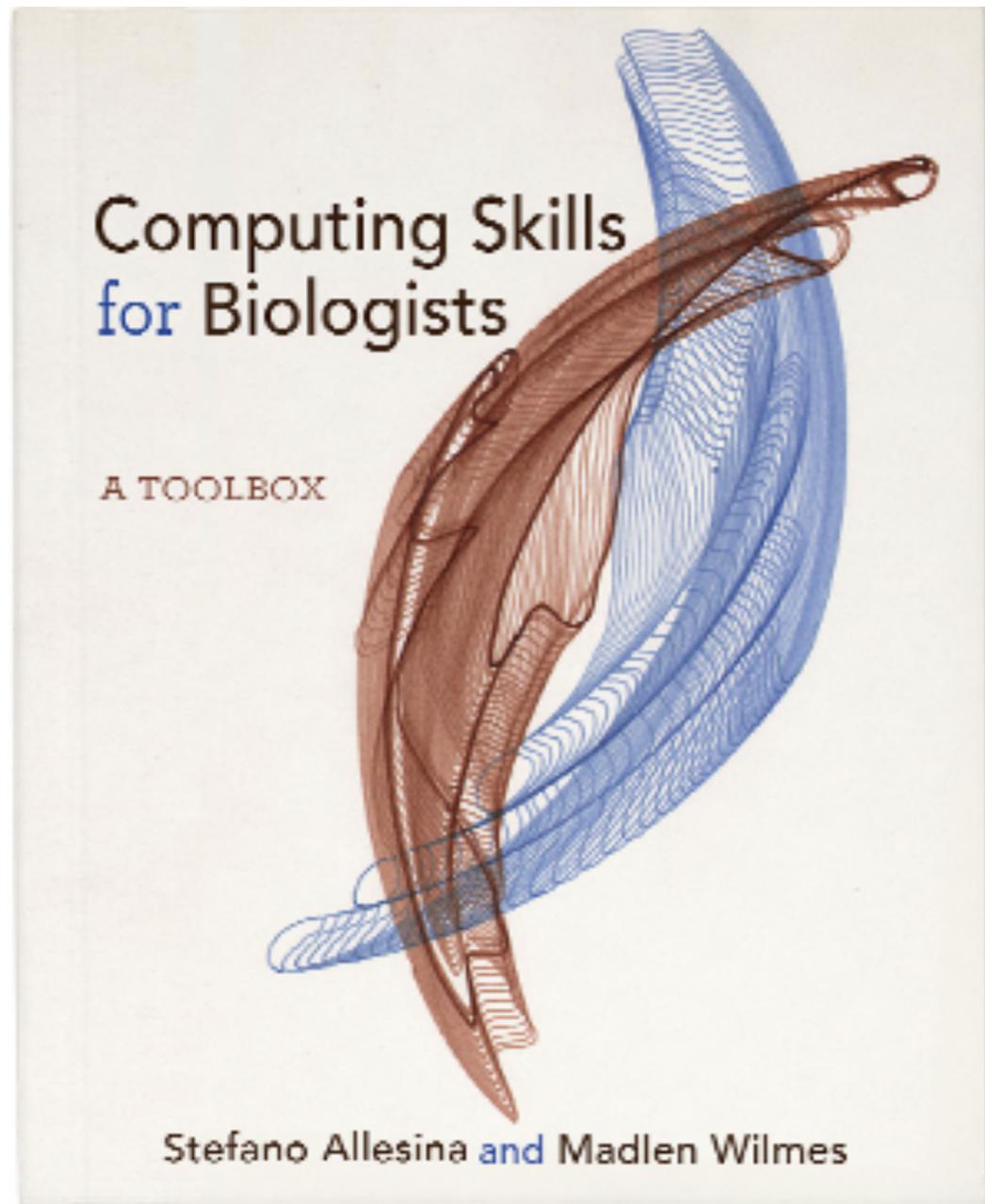
Our Textbooks

- ◆ Written to help address sudden need in biology to be able to handle Big Data
- ◆ Available through Amazon (hard copy), O'Reilly (hard copy and eBook), and ISU Library (eBook, FREE!!)



Introduction and Basic Unix

Our Textbooks



0	Introduction	1
1	Unix	12
2	Version Control	55
3	Basic Programming	81
4	Writing Good Code	120
5	Regular Expressions	165
6	Scientific Computing	185
7	Scientific Typesetting	220
8	Statistical Computing	249
9	Data Wrangling and Visualization	300
10	Relational Databases	337
11	Wrapping Up	366

Introduction and Basic Unix

How will we communicate?

Slack

The screenshot shows a Slack interface for a channel named "BioDataSkills". The left sidebar lists various channels and direct messages. The main area displays a message from Tracy Heath in the "#general" channel, dated December 15th, 2017. The message is a welcome email for students, asking them to fill out a feedback survey. Below this, a message from Ben Cortes indicates he joined the channel along with Brittany Cavazos on Monday, August 20th. Another message from Matthew Hufford, dated "Yesterday", welcomes the 2018 folks and mentions previous messages. A final message from Débora Brito Goulart shows she joined along with 16 others. The interface includes a search bar, a list of channels, and a message input field at the bottom.

BioDataSkills | Matthew Hufford

Jump to...

All Threads

Channels

- # buffalo-book-bugs
- # final-project
- # general
- # reading-discussion
- # resources
- # scripting_help

Direct Messages

- slackbot
- Matthew Hufford (...)
- Basanta Bista
- Ben Cortes
- Brittany Cavazos
- Débora Brito Goulart
- Dennis Lavrov, Tracy H...
- Gaosh01 Hylia, Lucas ...
- Henrique Uliana Trenti...
- Lucas Koester, Dennis ...
- Maxwell McReynolds, ...

Apps

+ Add Apps

#general | 25 | 0 | Company-wide announcements and work-based m. | December 15th, 2017

December 15th, 2017

Tracy Heath 11:58 AM
Hi @channel! I just sent the following email to the class. Please fill out our feedback survey.

Dear BCB/EEOB 546X Students,

Thank you all for a great semester! Matt, Dennis, and I were all very impressed with all of your hard work in our course. We are currently working on grading your data management plan assignments and your final projects. We should have your final grades submitted early next week.

In the meantime, **we would really appreciate your feedback!** Please be sure to fill out your course instructor evaluations (there should be three of them) that are sent to you by the university. In addition to the official ISU evaluations, we would like you to provide some feedback on the course so that we can continue to make it better next year. The feedback from our spring 2017 students certainly helped us improve how we structured and taught the course this semester.

Please take time time to fill out our course feedback survey:

<https://goo.gl/forms/8JCh6plfO18fMtl72> (edited)

👉 Feel free to fill out the survey even if you were not officially enrolled in the course.

Monday, August 20th

Ben Cortes 12:44 PM
joined #general along with Brittany Cavazos.

Yesterday

Matthew Hufford 5:58 PM
Welcome 2018 Folks! You'll see several messages in this space from previous offerings...they may help you get a feel for the course and see how things have gone in previous years. We've left them here just in case it's helpful for you to look through, but also feel free to ignore these for now and just pay attention to new messages.

Débora Brito Goulart 6:02 PM
joined #general along with 16 others.

+ Message #general

Introduction and Basic Unix

What is our schedule?

Google Sheet

https://docs.google.com/spreadsheets/d/1DifkzshtsZhbD8eTw1SGMFCQ9MhqZSe02_b_GhFmFqo/edit?usp=sharing

Introduction and Basic Unix

How will grades be assigned?

Grading:

Assignment 1: Unix	15%
Assignment 2: R	15%
Assignment 3: Python	15%
Assignment 4: Data Management Plan	15%
Group Project and Presentation	40%

Chapter 1

- ◆ Our two main goals in bioinformatics are to have research that is *reproducible* and *robust*
- ◆ How can we make our analysis reproducible?
- ◆ How can we make our analysis robust?

Chapter 1

- ◆ Writing code for humans makes it reproducible, but it must still be readable by your computer

```

#!/ user/bin/perl
# PatHaps.pl by Matthew Hufford
use strict;
use warnings;

open AF, "<AllFreq.txt" or die "fail!\n\n";
my %data;
while (<AF>) {
    chomp;
    my $AllFreq = $_;
    my ($locus, $allele, $freq) = split("\t", $AllFreq);
    $data{$locus}->{$allele}=$freq;
}
close AF;

#define a hash of allele frequencies from the bulked seed

#always name "IN" file uniquely to avoid corrupting files
# removing endlines

#creating a hash of hashes--locus and allele are keys to the $freq value

open PG, "<PatGenosIN(-9).txt" or die "fail!\n\n";
my ($patallele_id, @genos) = <PG>;
close PG;
print `cp Pools2Format.txt outfile.txt`;
my @patallele_id = split("\t", $patallele_id);
open OUT, ">>outfile.txt";
print (OUT "\n");

#read in the set of dad haplotypes from file "PatGenosIN.txt"
#first line turned into string, rest of file turned into an array

#creating array of loci names from string of first line

foreach my $dad (@genos) {
    chomp $dad;
    my ($dadID, @linedata) = split ("\t", $dad);
    print (OUT "$dadID\t0\t0\t");

    #splitting paternal ID from array of genotypes
    #printing dad ID with a tab

    for my $a (0..$#linedata) {
        my $allele=$linedata[$a];

        #creating a list from 0 to the number of scalars in each line of the array; the $# notation indicates the total number in array
        #putting list into the array and creating a string of allele calls that are at those positions.

        if ($allele =~ m/&/) {
            my ($allele1, $allele2) = split ("&", $allele); #matching all alleles that contain an ampersand
            my $freq1=$data{$patallele_id[$a]}->{$allele1}; #creating an array of the two possible alleles
            my $freq2=$data{$patallele_id[$a]}->{$allele2}; #creating frequency scalar for each allele 1
            my $freq2=$data{$patallele_id[$a]}->{$allele2}; #creating frequency scalar for each allele 2

            if (rand()<($freq1/($freq1+$freq2))) {
                print (OUT "$allele1\t-9\t");
            }
            else {
                print (OUT "$allele2\t-9\t");
            }
        }
    }
}

#assessing whether random number between 0 and 1 is less than freq 1

```

Chapter 1

- ◆ Adding in tests for your code helps avoid the dreaded silent errors and makes your research more robust

```
def add(x, y):  
    """Add two things together.""" return x + y
```

```
def test_add():  
    """Test that the add() function works for a variety of numeric types.""" assert(add(2, 3) == 5)  
assert(add(-2, 3) == 1)  
assert(add(-1, -1) == -2)  
assert(abs(add(2.4, 0.1) - 2.5) < EPS)
```

Chapter 1

- ◆ If a library already exists for what you want to do, why not use it?
- ◆ Do not modify your raw data directly (treat as “Read Only”)
- ◆ If you’re going to use a script multiple times, turn it into a tool:
 - ◆ document it
 - ◆ create versions
 - ◆ make your command-line arguments clear
 - ◆ sharing in a version-controlled repository

Chapter I

- ◆ Publish both your scripts and data
- ◆ Also publish your documentation and document everything!
- ◆ *What's the difference between documenting a script and a project? How might we do both?*
- ◆ Make an analysis and the figures showing the results of an analysis the product of a script

Intro. to Computational Methods

UNIX

- ◆ UNIX is an operating system originally developed by AT&T's Bell Labs in the 1960's (then Novell, then The Open Group)
- ◆ “Operating System” = Suite of programs that make your computer work
- ◆ Mac OSX is one flavor of UNIX; others are Linux, Solaris, BSD

Intro. to Computational Methods

UNIX

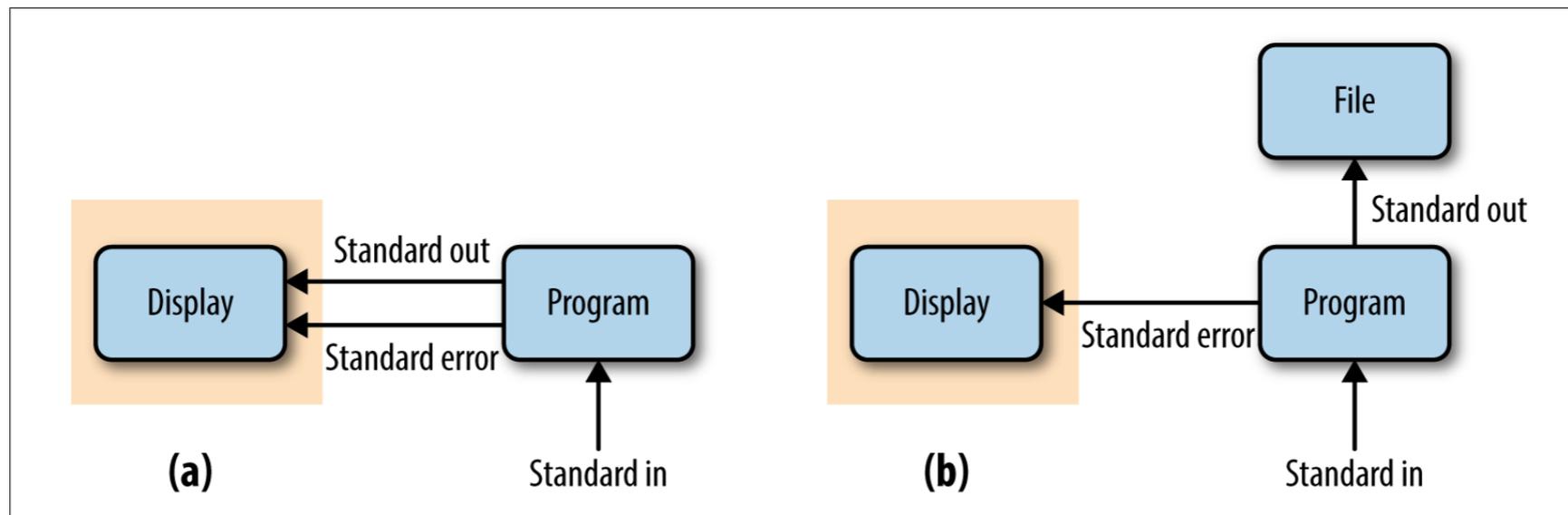
The UNIX OS has three components:

- (1) The Kernel: OS Hub; allocates memory and time
- (2) The Shell: Interface between user and the kernel; the shell searches for command files called by user and passes requests to the kernel
- (3) Programs: Commands called by the user

Intro. to Computational Methods

UNIX

- ◆ UNIX is modular: **What does this mean?**
- ◆ UNIX handles data as a stream
- ◆ A given program generates standard output and standard error streams: **What is the difference?**
- ◆ How can we redirect streams?



Introduction and Basic Unix

Our Computational Goals for Today

1. Make sure everyone has a Shell solution
2. Installation of GitBash and/or Git
3. Clone the Git repository for the textbook and the course
4. Work through a Basic Unix example

Introduction and Basic Unix

Where to from here?

1. If the basic Unix commands in our example were all new (and even if they weren't!), you should consider working through the Unix portions of these tutorials :

<https://sites.google.com/site/eeob563/computer-labs/lab-1>

http://korflab.ucdavis.edu/Unix_and_Perl/

2. If you haven't already, read Chapters 1-3 of Buffalo
 - For Chapter 1, create a text snippet in Slack with a few favorite points and any questions on points that were not clear, and we'll discuss these on Friday
 - We'll also discuss and work through examples from Chapter 3 on Friday