

# Introduction to the command-line interface (shell)

Harvard Chan Bioinformatics Core  
in collaboration with  
HMS Research Computing

<https://tinyurl.com/hbc-shell-online>



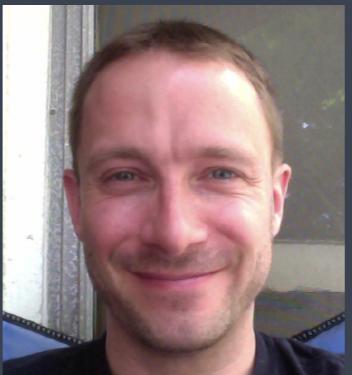
Shannan Ho Sui  
*Director*



John Hutchinson  
*Associate Director*



Victor Barrera



Rory Kirchner



Zhu Zhuo



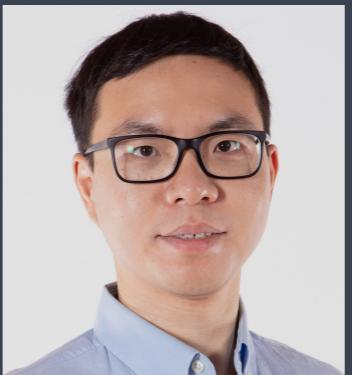
Preetida Bhetariya



Meeta Mistry



Mary Piper  
*Assoc. Training Director*



Jihe Liu



Radhika Khetani  
*Training Director*



Ilya Sytchev



James Billingsley



Sergey Naumenko



Joon Yoon



Peter Kraft  
*Faculty Advisor*

# Consulting

- RNA-seq analysis: bulk, single cell, small RNA
- ChIP-seq and ATAC-seq analysis
- Genome-wide methylation
- WGS, resequencing, exome-seq and CNV studies
- QC & analysis of gene expression arrays
- Functional enrichment analysis
- Grant support

<http://bioinformatics.sph.harvard.edu/>



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NIEHS



# Training

We have divided our short workshops into 2 categories:

1. Basic Data Skills - No prior programming knowledge needed (no prerequisites)
2. Advanced Topics: Analysis of high-throughput sequencing (NGS) data - Certain “Basic” workshops required as prerequisites.

*Any participants wanting to take an advanced workshop will have to have taken the appropriate basic workshop(s) within the past 6 months.*

<http://bioinformatics.sph.harvard.edu/training/>

<https://hbctraining.github.io/main/>



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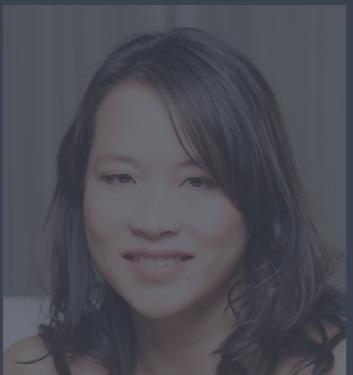
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# Introductions!



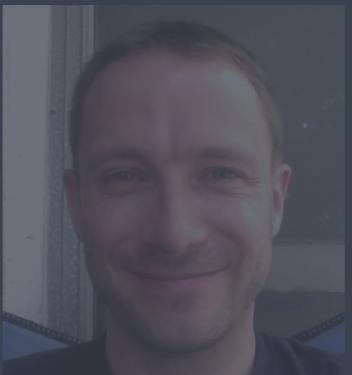
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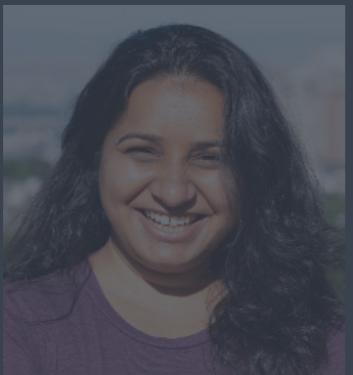
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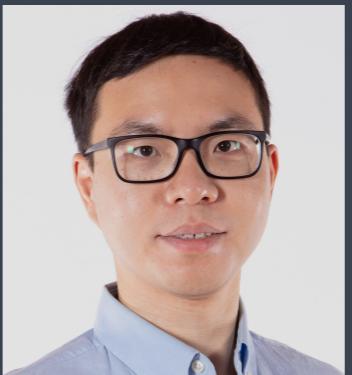
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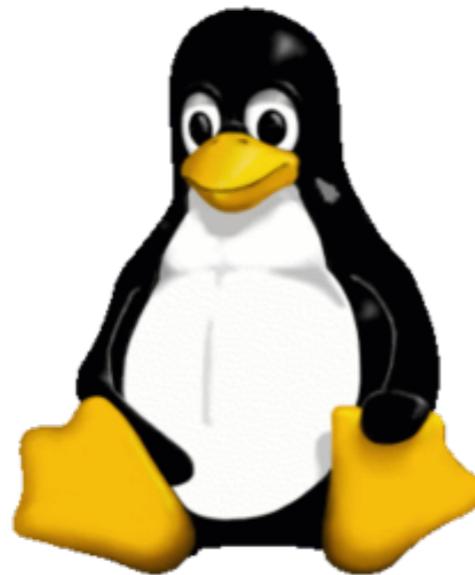


Joon Yoon



Peter Kraft  
*Faculty Advisor*

# Workshop scope



```
rkhetani — rsk27@clarinet002-072: ~ — ssh — 75x51
rsk27@clarinet002-072:~$ ll -htr unix_workshop/
total 177K
drwxrwsr-x 2 rsk27 rsk27 62 May 23 2016 reference_data
-rw-rw-r-- 1 rsk27 rsk27 377 May 23 2016 README.txt
drwxrwsr-x 2 rsk27 rsk27 78 May 23 2016 genomics_data
drwxrwsr-x 2 rsk27 rsk27 257 May 23 2016 raw_fastq
drwxrwsr-x 2 rsk27 rsk27 695 May 23 2016 other
drwxrwsr-x 6 rsk27 rsk27 972 May 24 2016 rnaseq_project
rsk27@clarinet002-072:~$
```

*“Unix is user-friendly.*

*It's just very selective about who its friends are.”*

# The Unix command-line interface

- ◆ Unix is a stable, efficient and powerful operating system
- ◆ It can easily coordinate the use and sharing of a computer's (or a system's) resources, i.e. built to allow multi-user functionality
- ◆ Can easily handle complex and repetitive tasks easily on large and small datasets
- ◆ Usually, written commands are used to work with this OS, instead of the pointing and clicking used with operating systems like Windows and OSX

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## *Bioinformatics:*

- ◆ A lot of NGS-analysis tools are created for the Unix OS
- ◆ High-performance compute clusters which are necessary to analyze large datasets require a working knowledge of Unix

# Linux

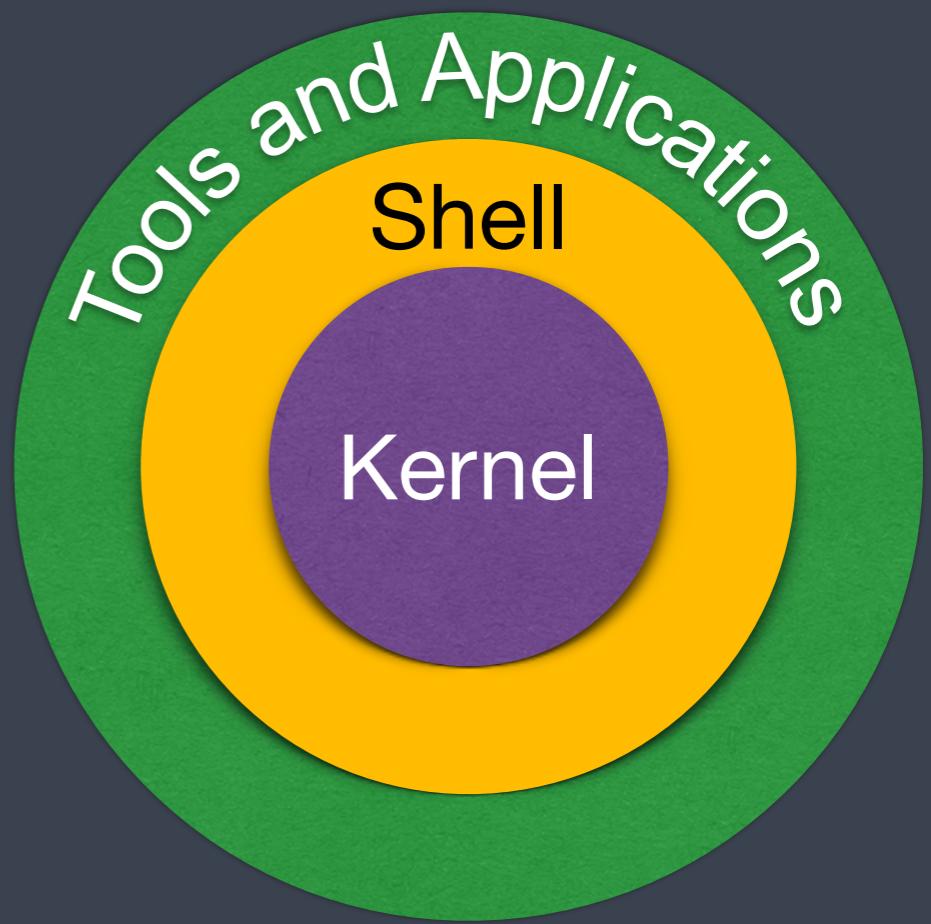
- ❖ Linux is a free, open-source operating system based on Unix
- ❖ It has the same components as the original, but the open source community is involved in active development of various distinct distributions of Linux



# Components

The Unix/Linux system is functionally organized at 3 levels:

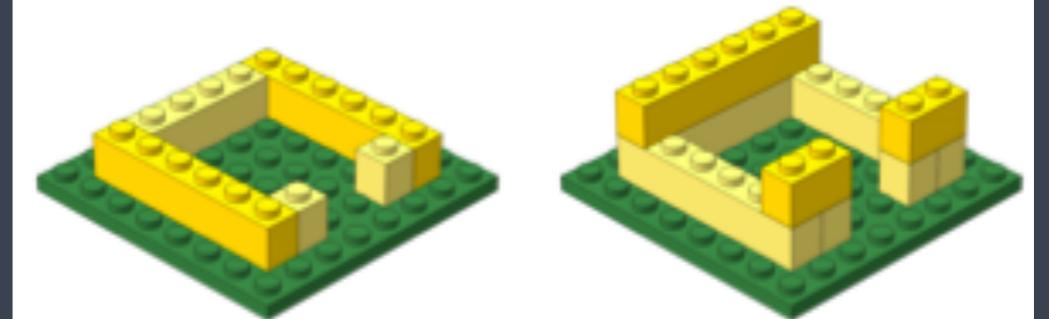
- ◆ **The kernel**, which schedules tasks and manages storage: *the brain of the system*
- ◆ **The shell**, *an interpreter* that helps interprets our input for the kernel
- ◆ **Utilities, tools and applications**, which use the shell to communicate with the kernel



# The “shell”

- ◆ The shell is **an interpreter**
- ◆ It is independent of the operating system
- ◆ Dozens of shells have been developed throughout UNIX history, and a lot of them are still in use
- ◆ The most commonly used shell is **bash**

# Learning Objectives



- ✓ Learn what a “shell” is and become comfortable with the command-line interface
  - Find your way around a filesystem using written commands
  - Work with small and large data files
  - Become more efficient when performing repetitive tasks
- ✓ Understand what a computational cluster is and why we need it

# Logistics

# Course webpage

<https://tinyurl.com/hbc-shell-online>

# Course schedule online

## Workshop Schedule

### Day 1

Time	Topic	Instructor
10:00 - 10:30	Workshop introduction	Radhika
10:30 - 11:45	Introduction to Shell	Radhika
11:45 - 12:00	Overview of self-learning materials and homework submission	Jihe

### Self Learning #1

- Wildcards and shortcuts in bash
- Searching and redirection
- Examining and creating files
- Shell scripts and variables in bash

### Assignment #1

- All exercise questions from the self-learning lessons have been put together in a [text file](#) (download for local access).
  - The text file can be opened with any text editor application (i.e. Notepad++, TextWrangler) on your local computer
- Add your solutions to the exercises in the downloaded .txt file and **upload the saved text file** to [Dropbox](#) **day before the next class**.

# Course materials online



## Introduction to the command line interface (shell)

[View on GitHub](#)

### Learning Objectives

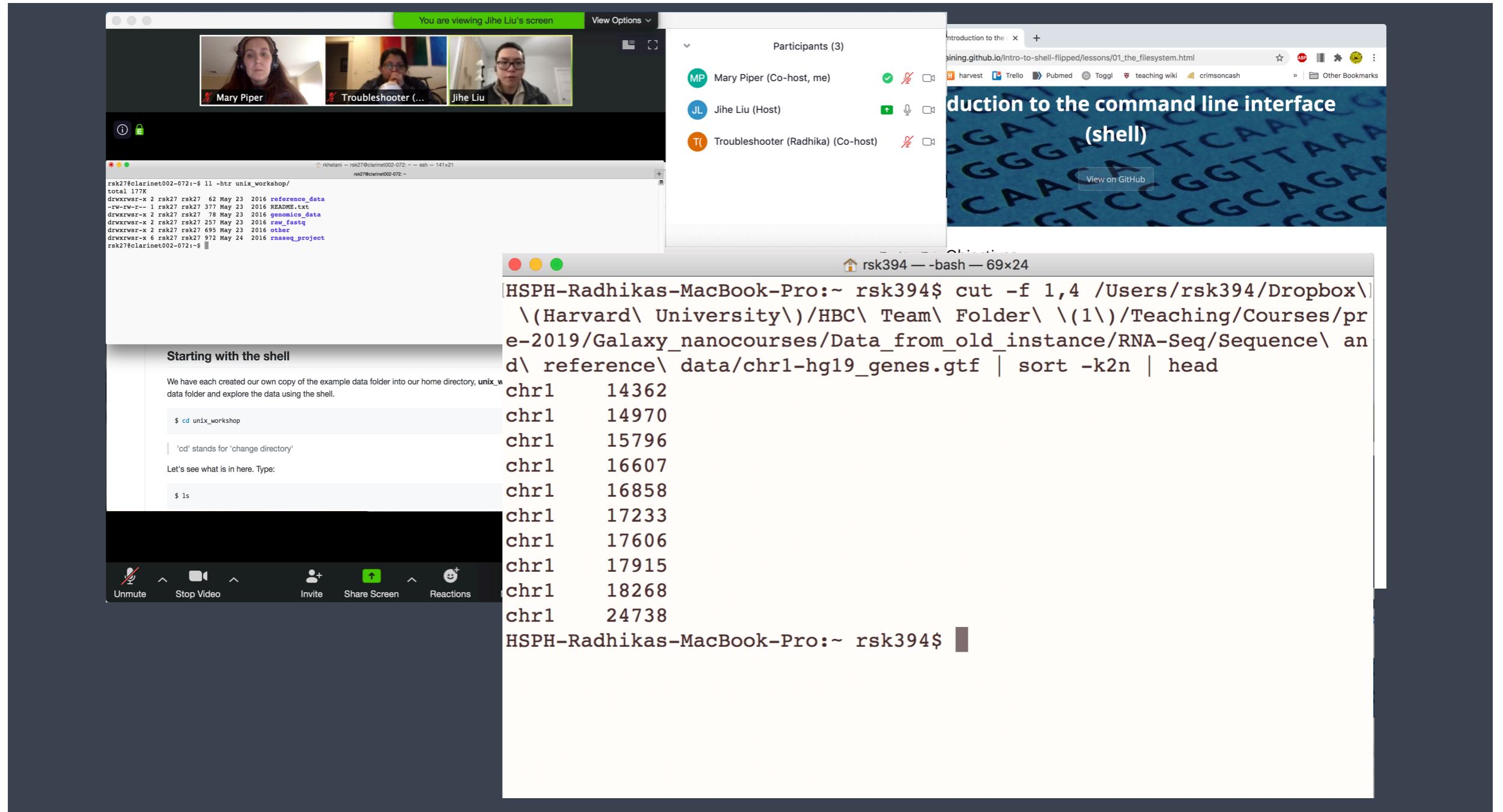
- How do you access the shell?
- How do you use it?
  - Getting around the Unix file system
  - looking at files
  - manipulating files
  - automating tasks
- What is it good for?

### Setting up

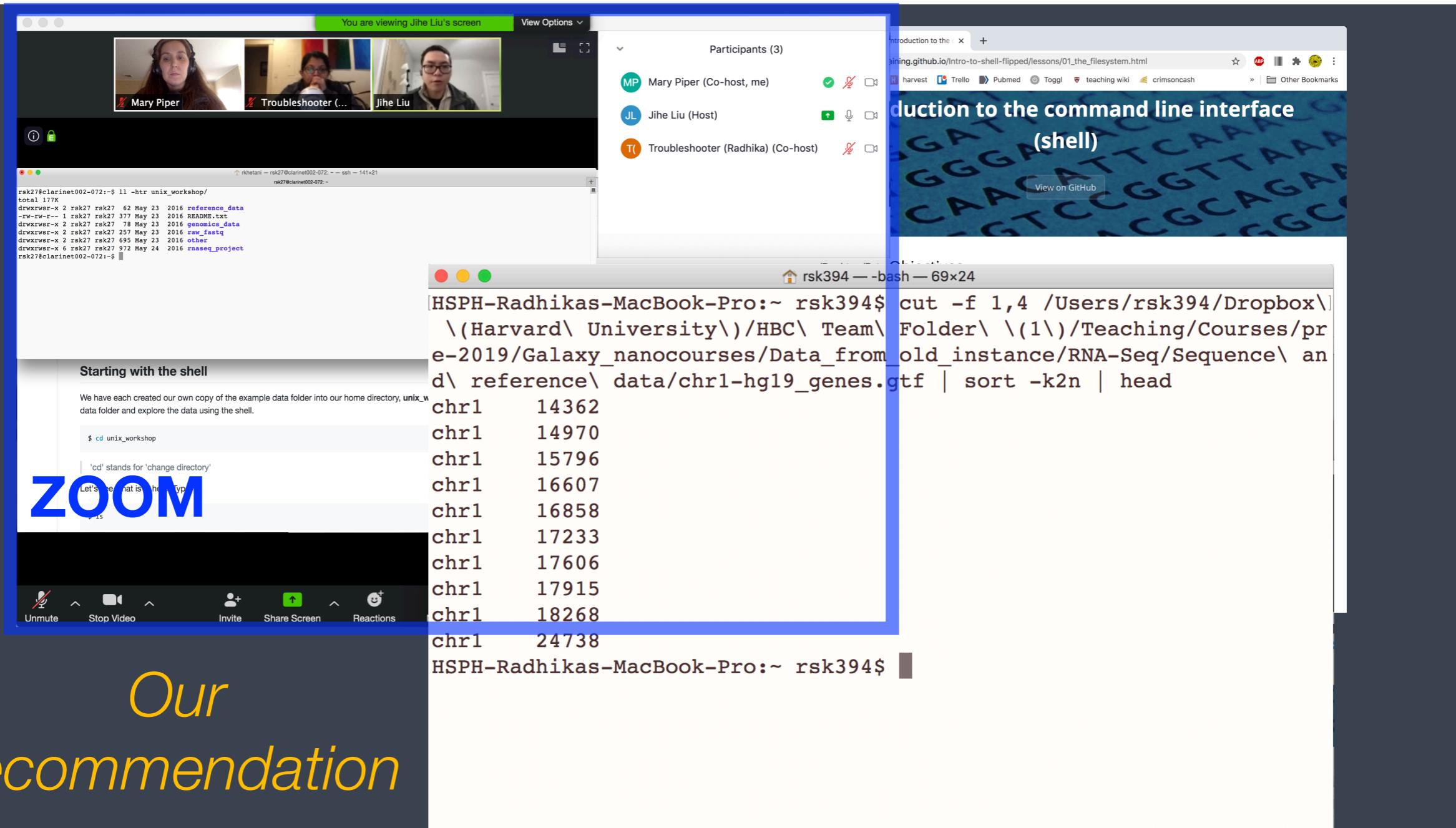
We will spend most of our time learning about the basics of the shell command-line interface (CLI) by exploring experimental data on the **O2** cluster. So, we will need to log in to this remote compute cluster first before we can start with the basics.

Let's take a quick look at the basic architecture of a cluster environment and some cluster-specific jargon prior to logging in.

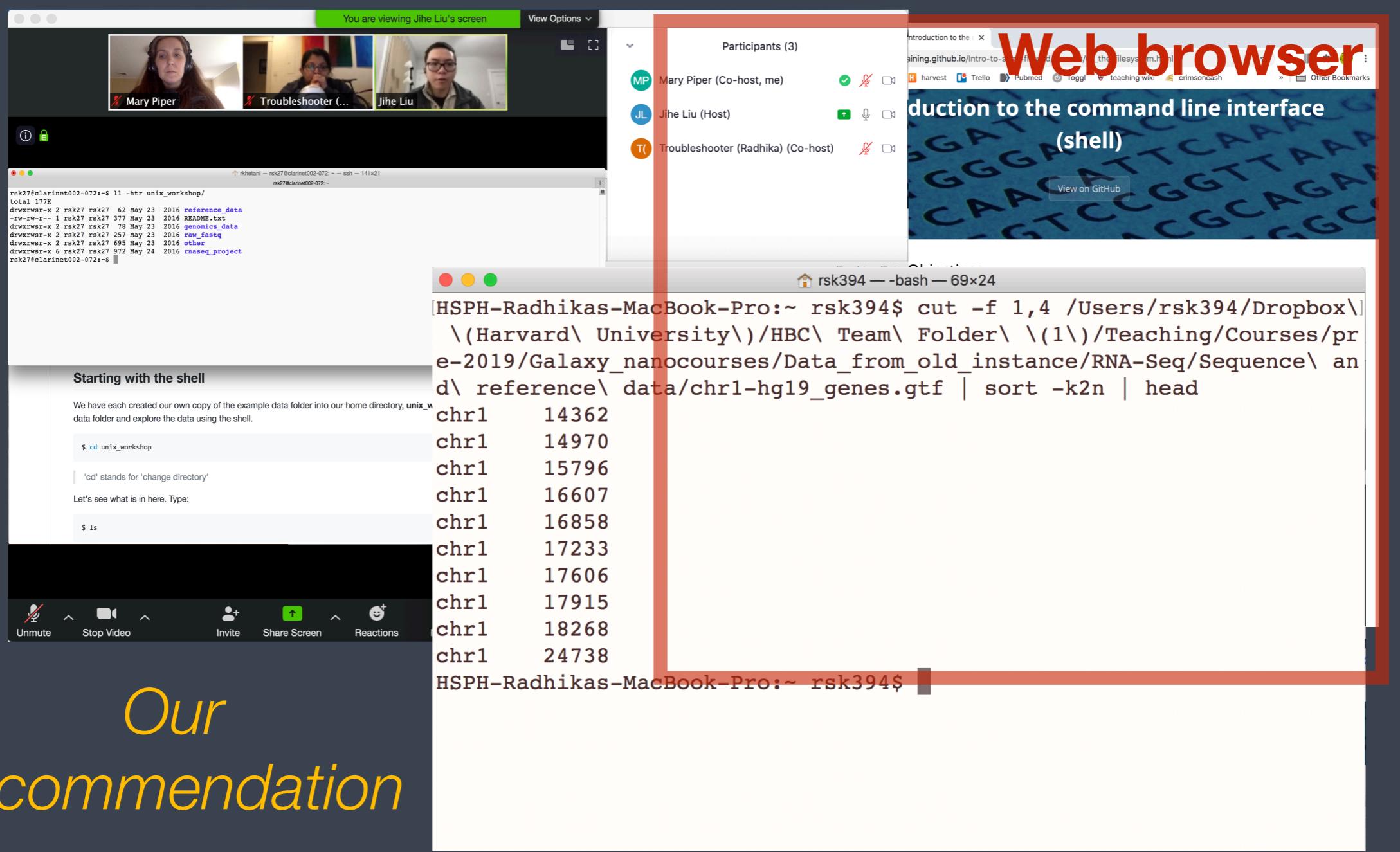
# Single screen & 3 windows?



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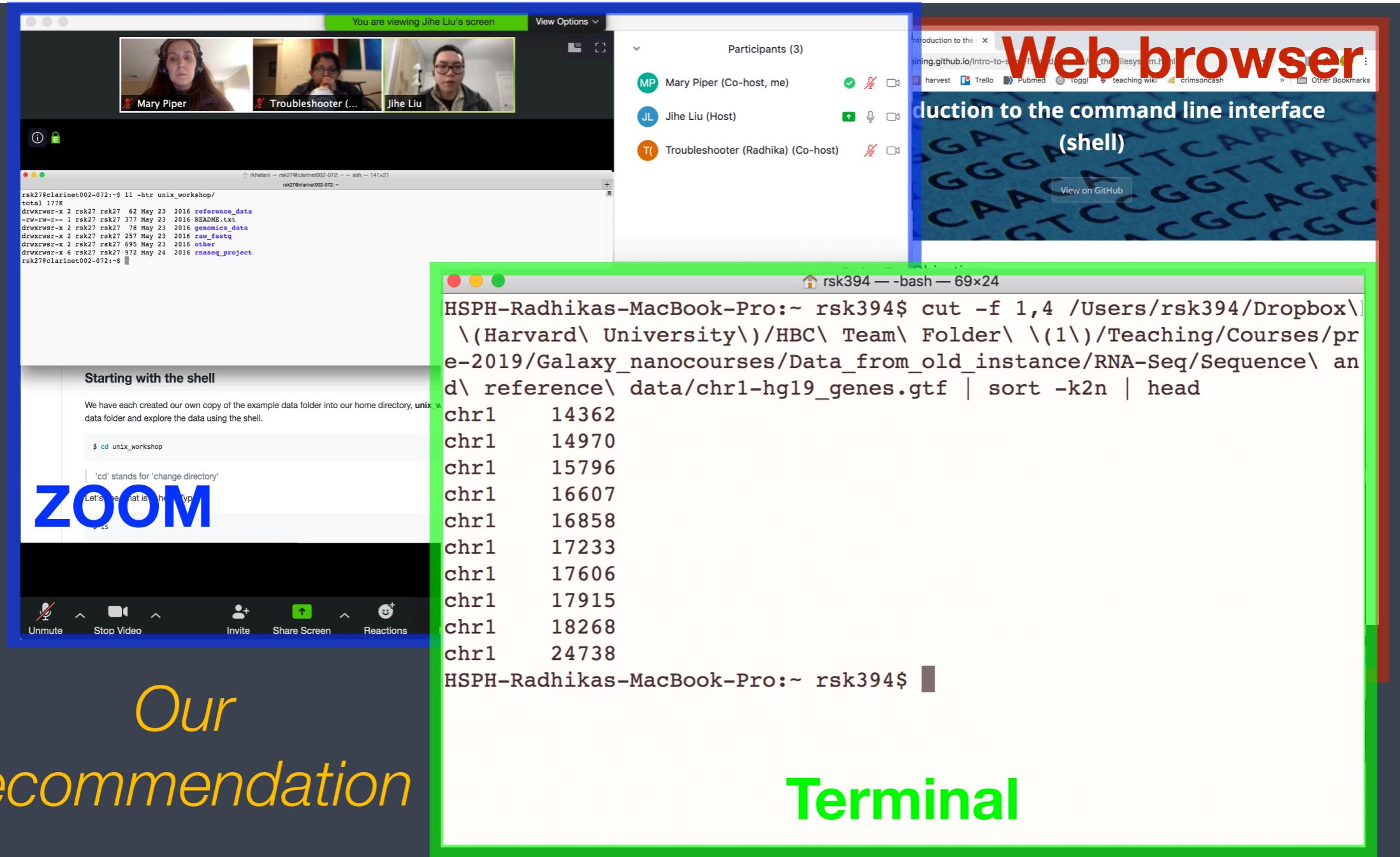
The image shows a video conference interface with three main windows:

- Video Feed:** Shows three participants: Mary Piper, Troubleshooter (Radhika), and Jihe Liu.
- Participants List:** Shows three participants: Mary Piper (Co-host, me), Jihe Liu (Host), and Troubleshooter (Radhika) (Co-host).
- Terminal Session:** A green-highlighted window showing a command-line interface (CLI) session. The command `cut -f 1,4 /Users/rsk394/Dropbox\[Harvard\ University\)/HBC\ Team\ Folder\ \((1\)/Teaching/Courses/pre-2019/Galaxy\_nanocourses/Data\_from\_old\_instance/RNA-Seq/Sequence\ and\ reference\ data/chrl-hg19\_genes.gtf | sort -k2n | head` is run, displaying a list of chromosomes and their lengths:

```
chr1    14362
chr1    14970
chr1    15796
chr1    16607
chr1    16858
chr1    17233
chr1    17606
chr1    17915
chr1    18268
chr1    24738
```

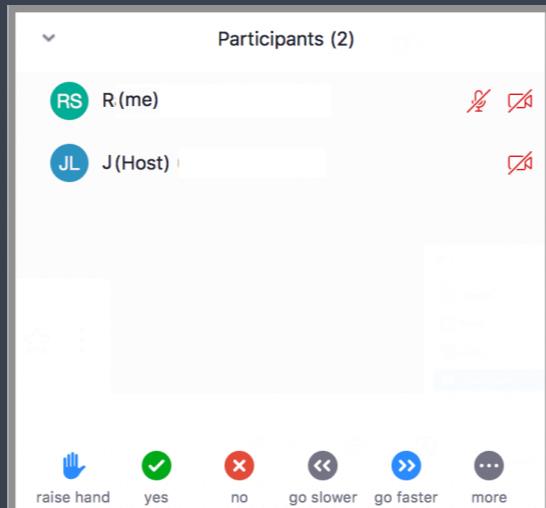
*Our recommendation* **Terminal**

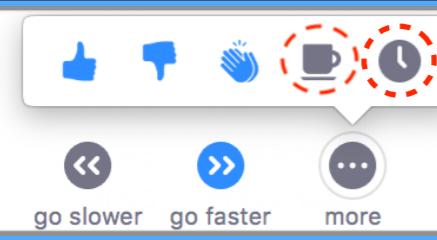
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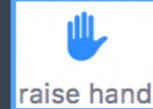
# Odds and Ends (1/2)

- ❖ Quit/minimize all applications that are not required for class
- ❖ Click on “Participants” to open that panel in Zoom



- ▶  = "agree", "I'm all set" (equivalent to a **green post-it**)
- ▶  = "disagree", "I need help" (equivalent to a **red post-it**)
- ▶  If you are away from the computer use the coffee cup or clock icon

# Odds and Ends (2/2)

- ❖ Questions for the presenter?
  - Post the question in the Chat window OR
  - Raise your hand  when the presenter asks for questions
- ❖ Technical difficulties with logging in or running commands?
  - Start a private chat with the *Troubleshooter* with a description of the problem.

# Thanks!

- Kathleen Keating and Andy Bergman from HMS-RC
- Data Carpentry

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# Contact us!

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*HBC consulting:* [bioinformatics@hsph.harvard.edu](mailto:bioinformatics@hsph.harvard.edu)

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