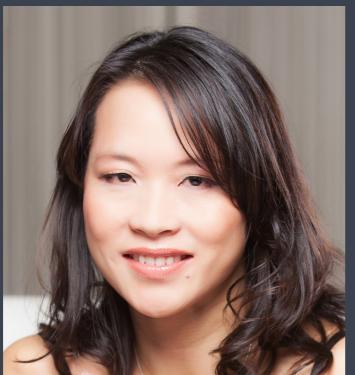


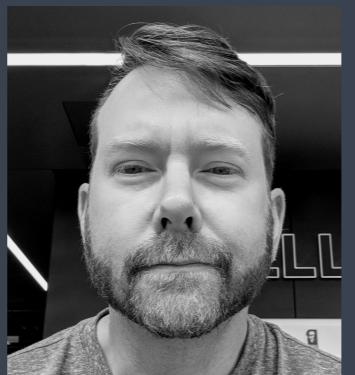
Introduction to the command-line interface (shell)

Harvard Chan Bioinformatics Core
in collaboration with
HMS Research Computing

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



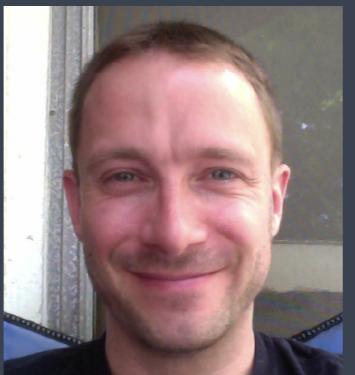
Shannan Ho Sui
Director



John Hutchinson
Associate Director



Victor Barrera



Rory Kirchner



Zhu Zhuo



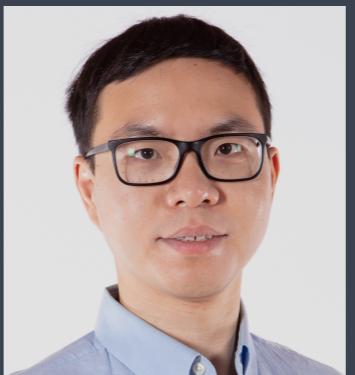
Preetida Bhetariya



Meeta Mistry



Mary Piper
Assoc. Training Director



Jihe Liu



Radhika Khetani
Training Director



Maria Simoneau
Project coordinator



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/>



**HARVARD
T.H. CHAN
SCHOOL OF PUBLIC HEALTH**

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.

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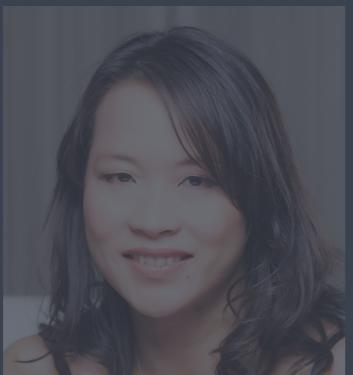
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Introductions!



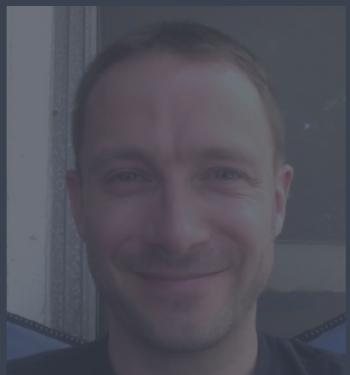
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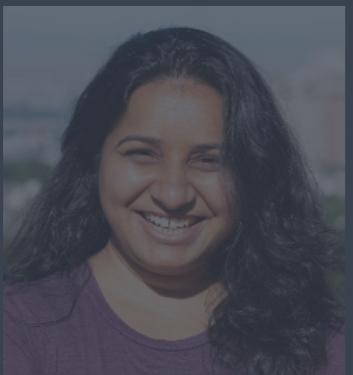
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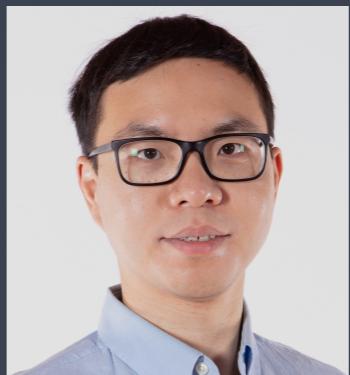
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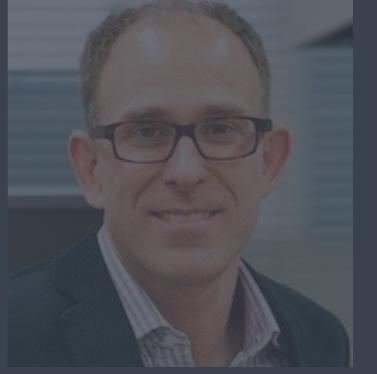
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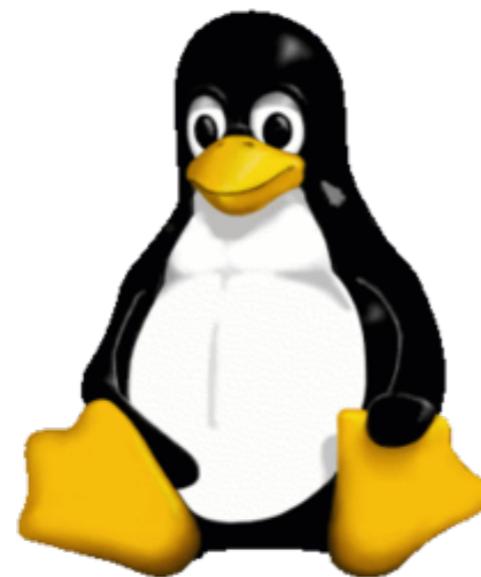


Joon Yoon



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

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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
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ubuntu



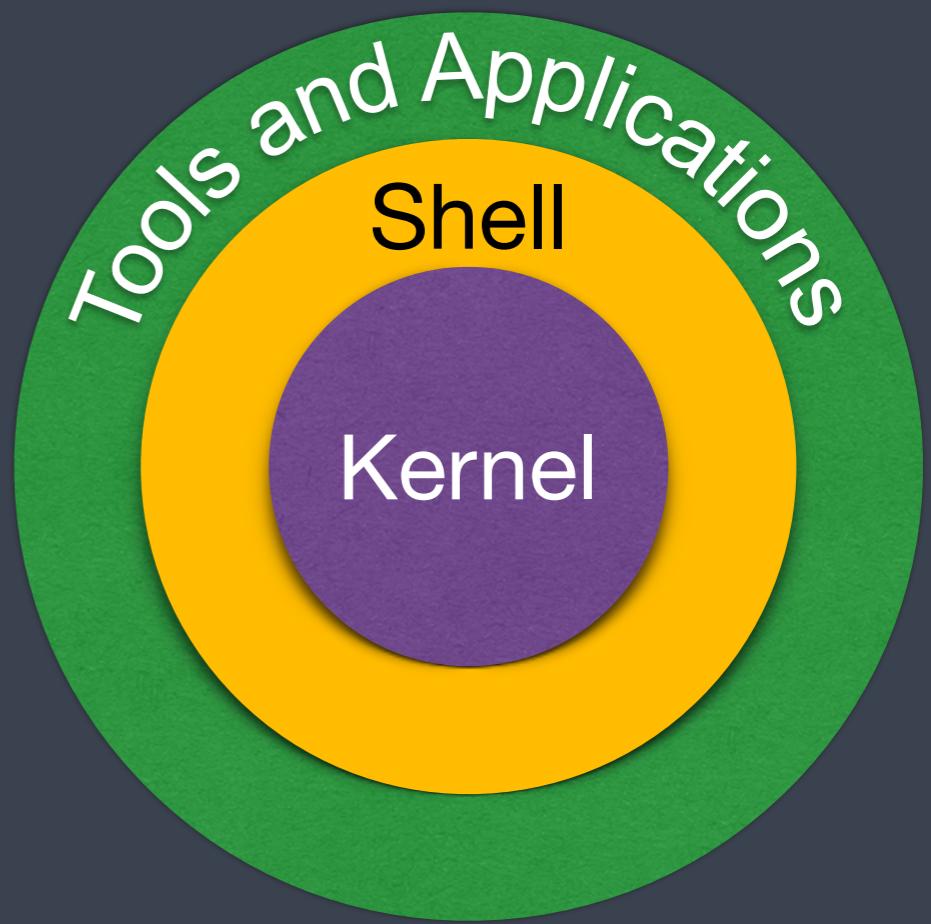
fedora



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



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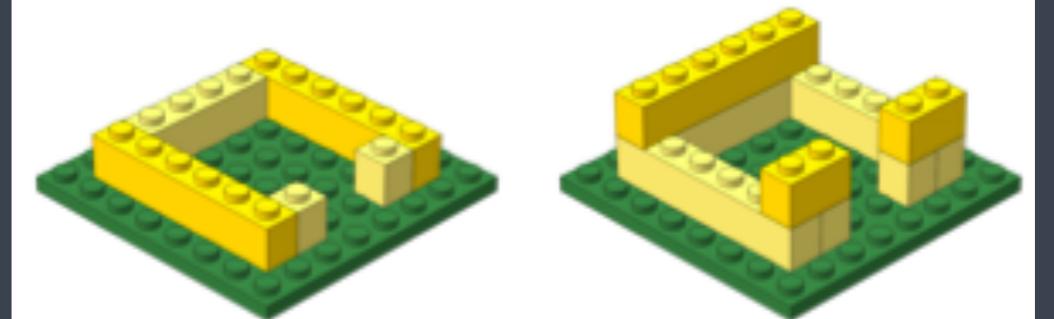
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- ◆ Dozens of shells have been developed throughout UNIX history, and a lot of them are still in use
- ◆ The most commonly used shell is **bash**

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

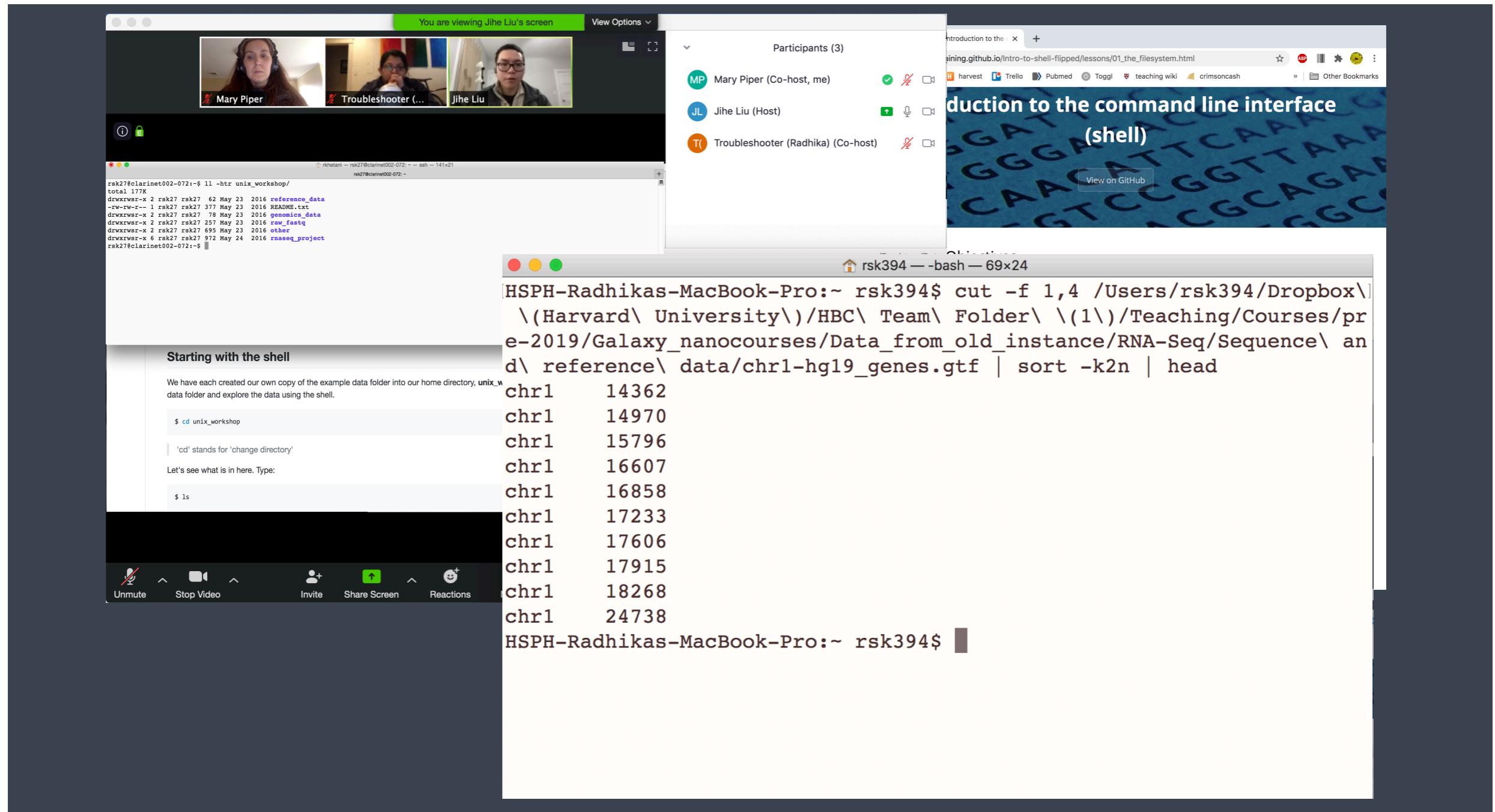
- How do you access the shell?
- How do you use it?
 - Getting around the Unix file system
 - looking at files
 - manipulating files
 - automating tasks
- What is it good for?

Setting up

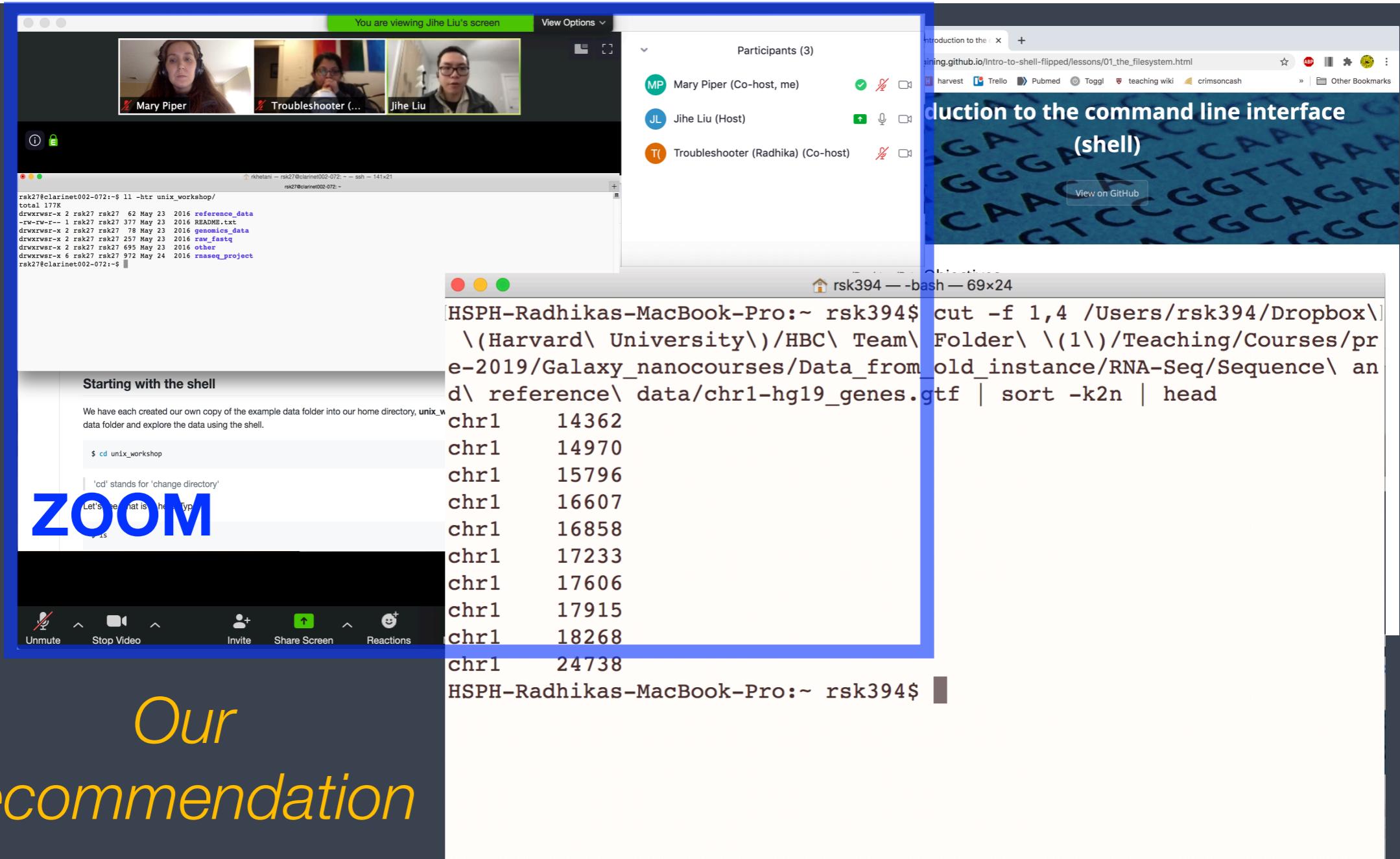
We will spend most of our time learning about the basics of the shell command-line interface (CLI) by exploring experimental data on the **O2** cluster. So, we will need to log in to this remote compute cluster first before we can start with the basics.

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

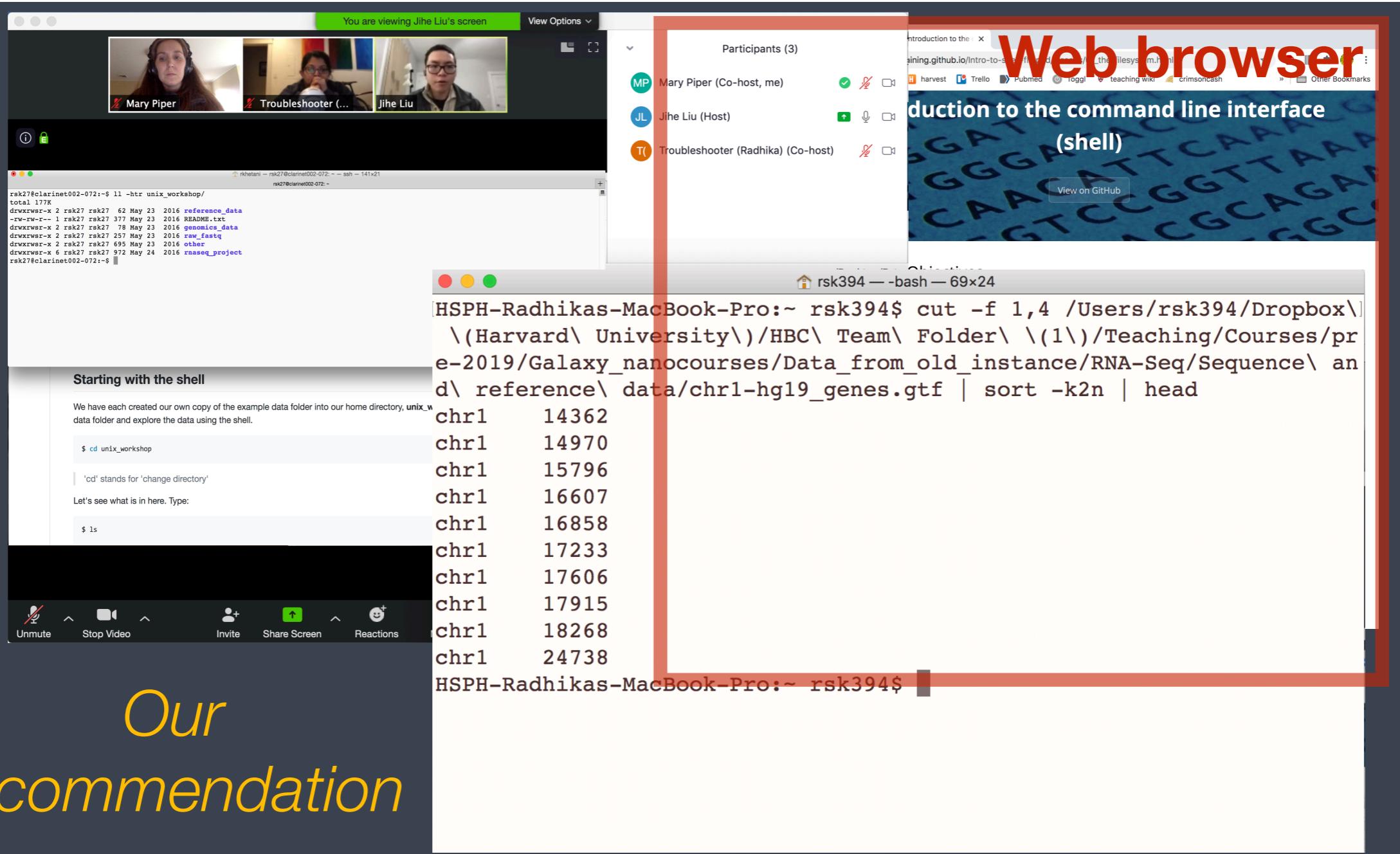
Single screen & 3 windows?



Single screen & 3 windows?



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Single screen & 3 windows?

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

- Top Left Window:** A video feed showing three participants: Mary Piper, Troubleshooter (Radhika), and Jihe Liu.
- Top Right Window:** A participant list titled "Participants (3)" showing Mary Piper (Co-host, me), Jihe Liu (Host), and Troubleshooter (Radhika) (Co-host).
- Bottom Window:** A terminal window titled "rsk394 — bash — 69x24" displaying command-line output. The output shows the user navigating to a directory and running a command to extract specific lines from a GTF file, followed by a list of chromosome IDs and their corresponding values.

Terminal Output:

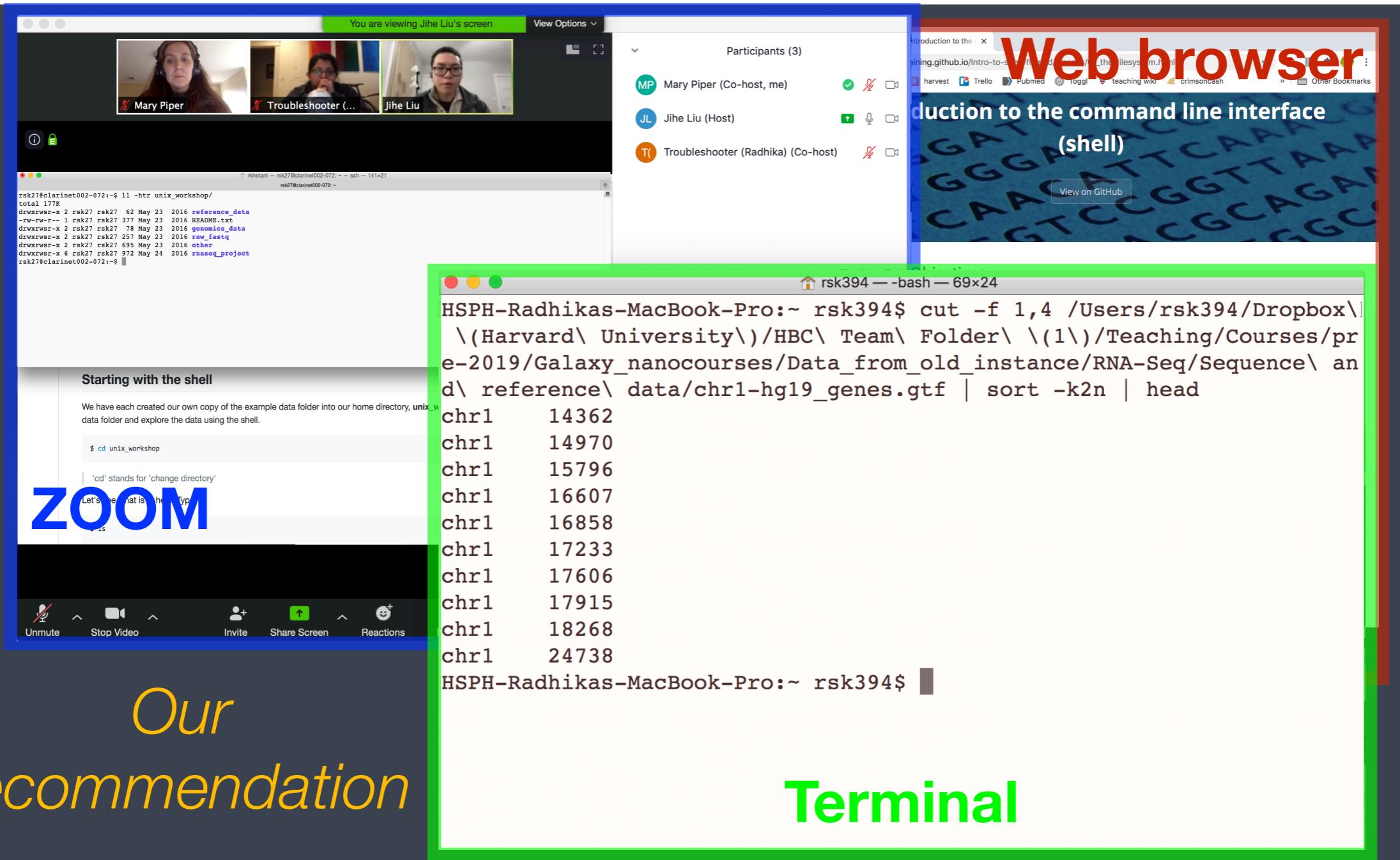
```
HSPH-Radhikas-MacBook-Pro:~ rsk394$ cut -f 1,4 /Users/rsk394/Dropbox\\(Harvard\\ University\\)/HBC\\ Team\\ Folder\\ \\(1\\)/Teaching/Courses/pre-2019/Galaxy_nanocourses/Data_from_old_instance/RNA-Seq/Sequence\\ and\\ reference\\ data/chrl-hg19_genes.gtf | sort -k2n | head
chr1    14362
chr1    14970
chr1    15796
chr1    16607
chr1    16858
chr1    17233
chr1    17606
chr1    17915
chr1    18268
chr1    24738
```

Text Overlay:

Our recommendation

Terminal

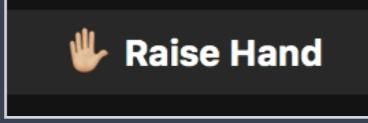
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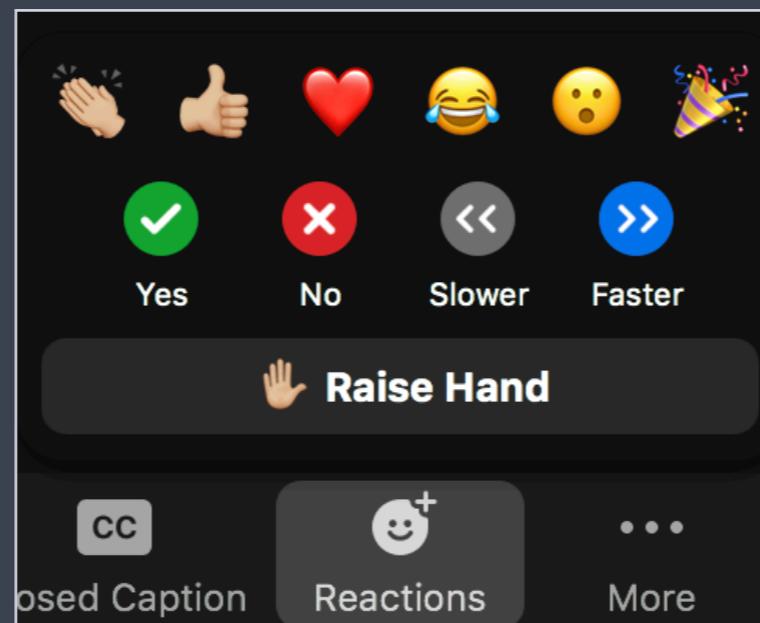


Odds and Ends

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- ❖ 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!

HBC training team: hbctraining@hsph.harvard.edu

O2 (HMS-RC): rchelp@hms.harvard.edu

HBC consulting: bioinformatics@hsph.harvard.edu

Twitter

HBC: @bioinfocore

HMS-RC: @hms_rc