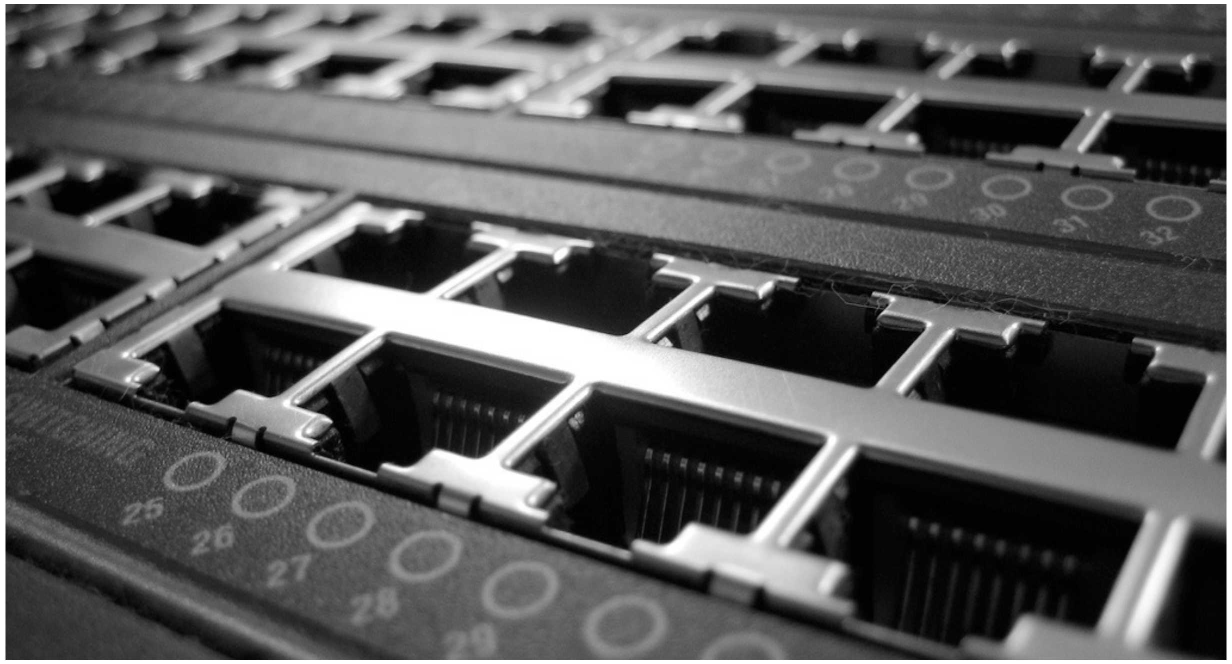


Introduction to the command-line interface (shell)

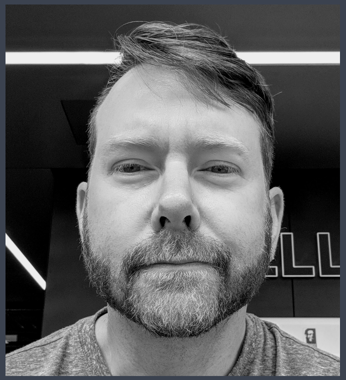
Harvard Chan Bioinformatics Core

in collaboration with

FAS Research Computing

https://tinyurl.com/hbc-shell-fasrc-online

Shannan Ho Sui
Director


John Hutchinson
Associate Director

Victor Barrera

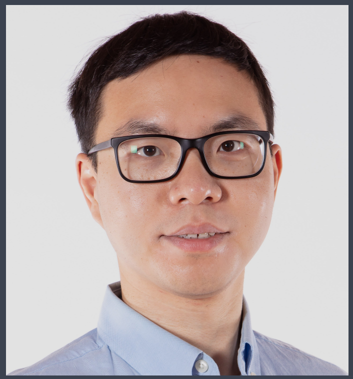
Zhu Zhuo

Preetida Bhetariya

Radhika Khetani
Training Director

Meeta Mistry

Mary Piper
Assoc. Training Director


Jihe Liu

Will Gammerdinger

Maria Simoneau

James Billingsley

Sergey Naumenko

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/

CFAR
HARVARD UNIVERSITY
CENTER FOR AIDS RESEARCH

HARVARD
T.H. CHAN
SCHOOL OF PUBLIC HEALTH

NIEHS

HSCI
HARVARD STEM CELL
INSTITUTE

HARVARD
CATALYST
THE HARVARD CLINICAL
AND TRANSLATIONAL
SCIENCE CENTER

HARVARD
MEDICAL SCHOOL

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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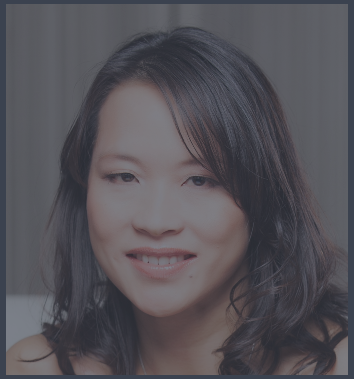
Introductions!



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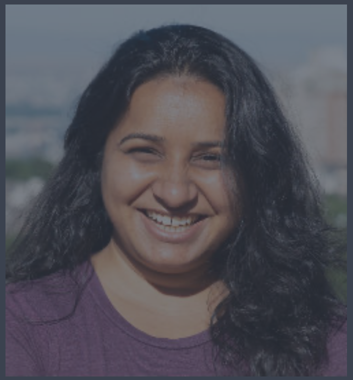

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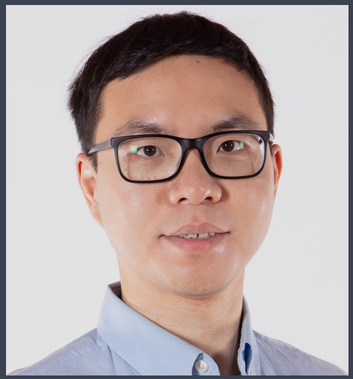

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Workshop scope

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http://www.UNIX-systems.org
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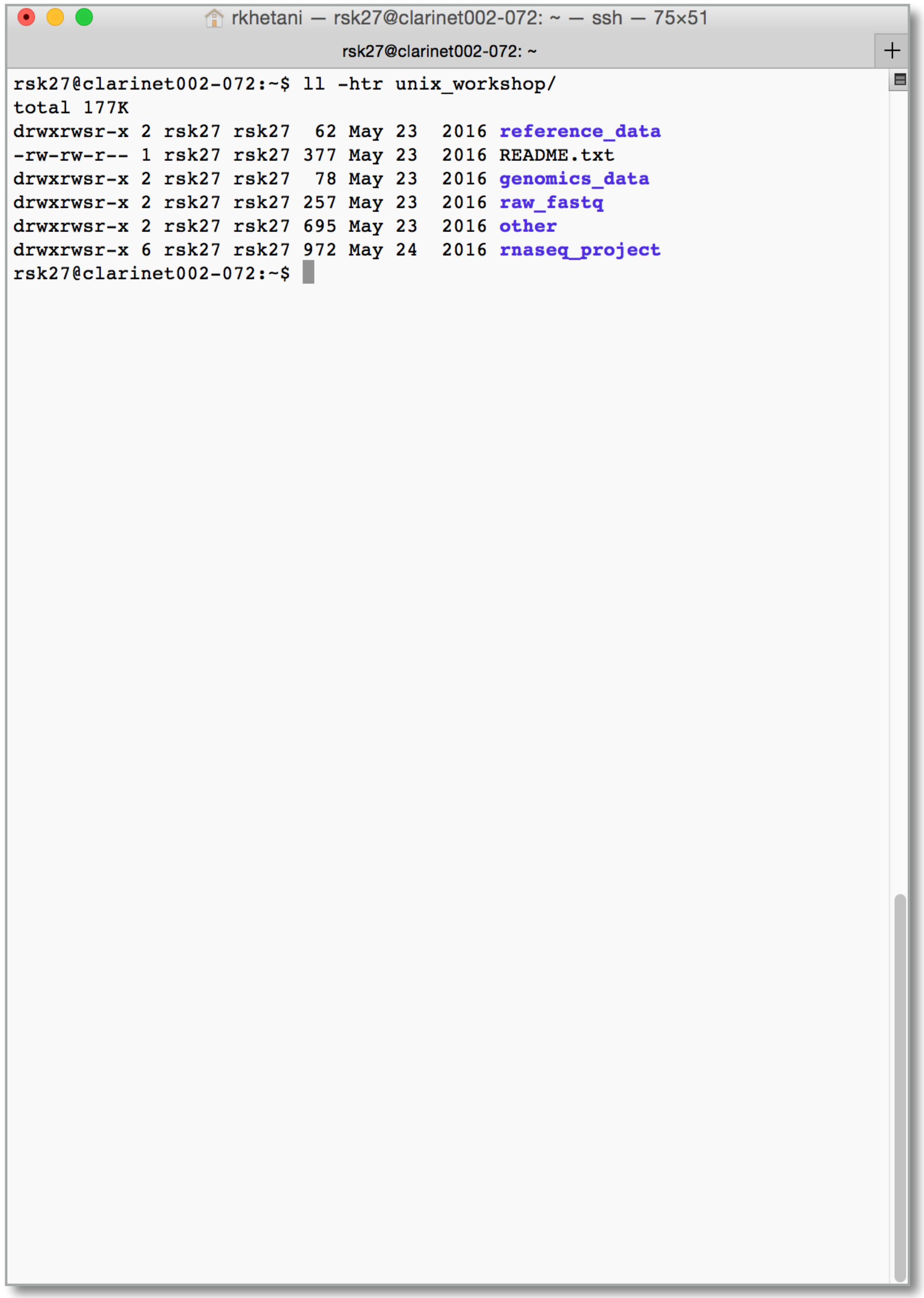
UNIX is a Registered Trademark of The Open Group



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rsk27@clarinet002-072:~$ 
```

"Unix is user-friendly.

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

http://en.wikipedia.org/wiki/Unix, http://en.wikipedia.org/wiki/Tux

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

CentOS

ubuntu

debian

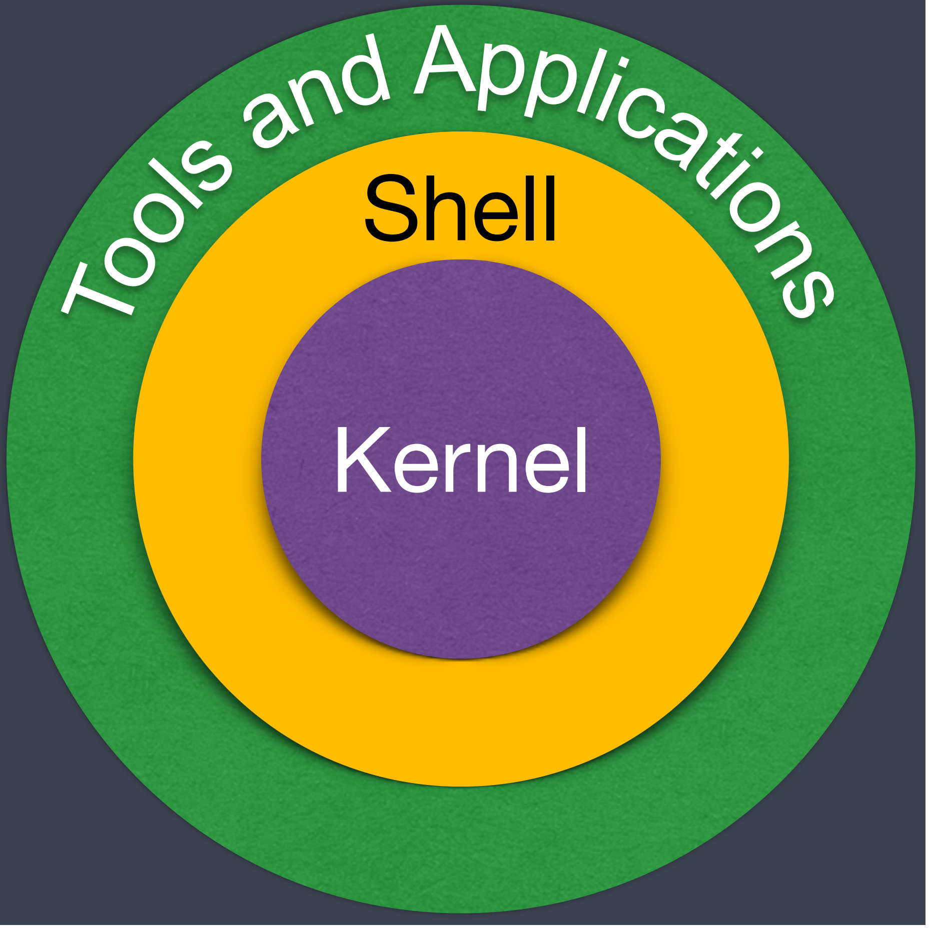
fedora

redhat

Components

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

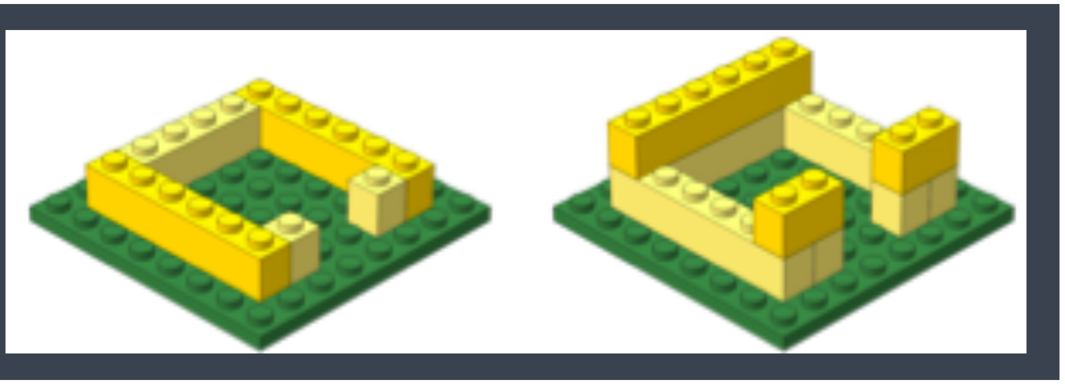
- ✦ The kernel, which schedules tasks and manages storage: ***the brain of the system***
- ✦ The shell, ***an interpreter*** that helps interprets our input for the kernel
- ✦ Utilities, tools and applications, which use the shell to communicate with the kernel



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



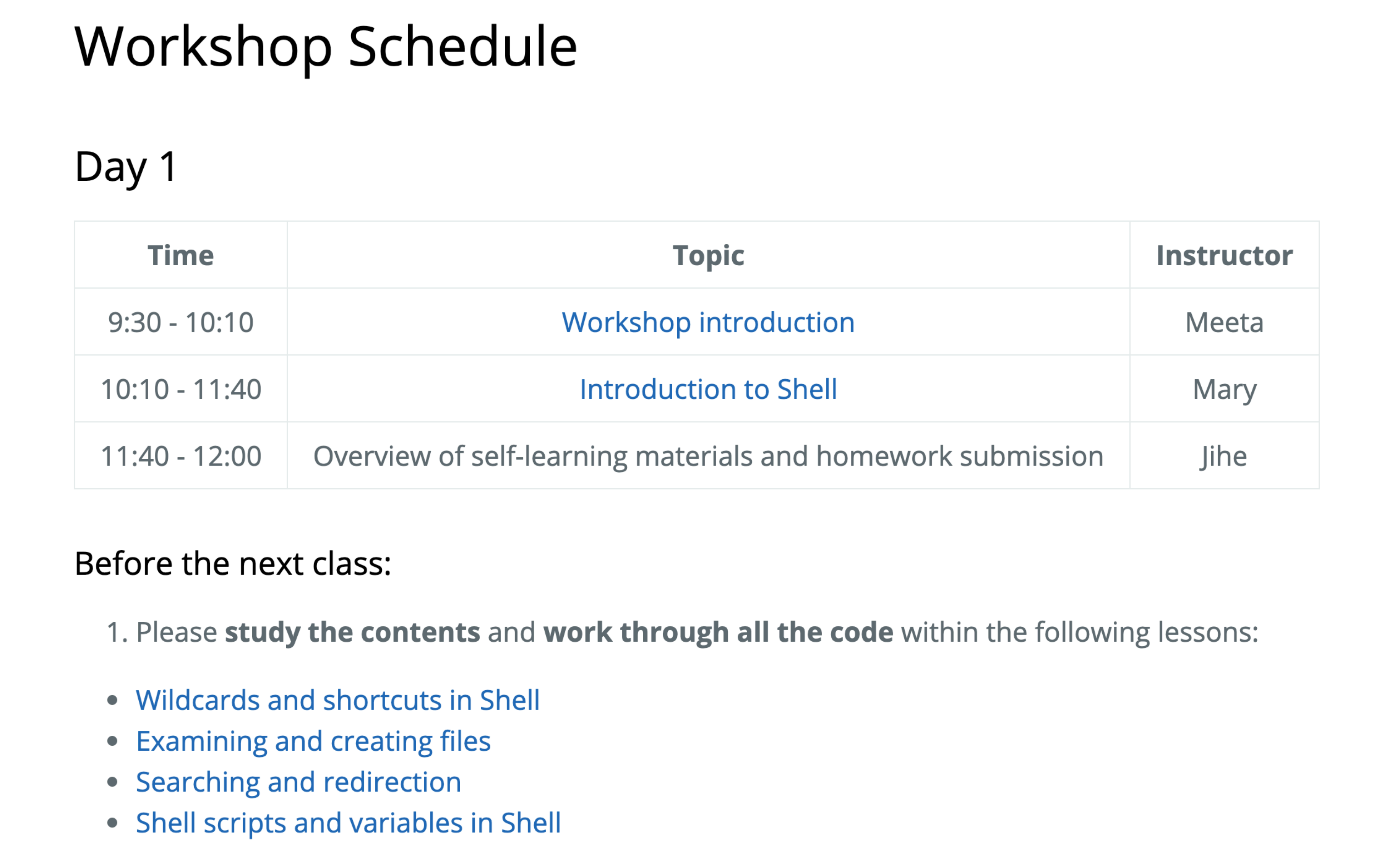
- ✓ Learn what a “shell” is and become comfortable with the command-line interface
  - Find your way around a filesystem using written commands
  - Work with small and large data files
  - Become more efficient when performing repetitive tasks
- ✓ Understand what a computational cluster is and why we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

Logistics

Course webpage

https://tinyurl.com/hbc-shell-fasrc-online

Course schedule online



Workshop Schedule

Day 1

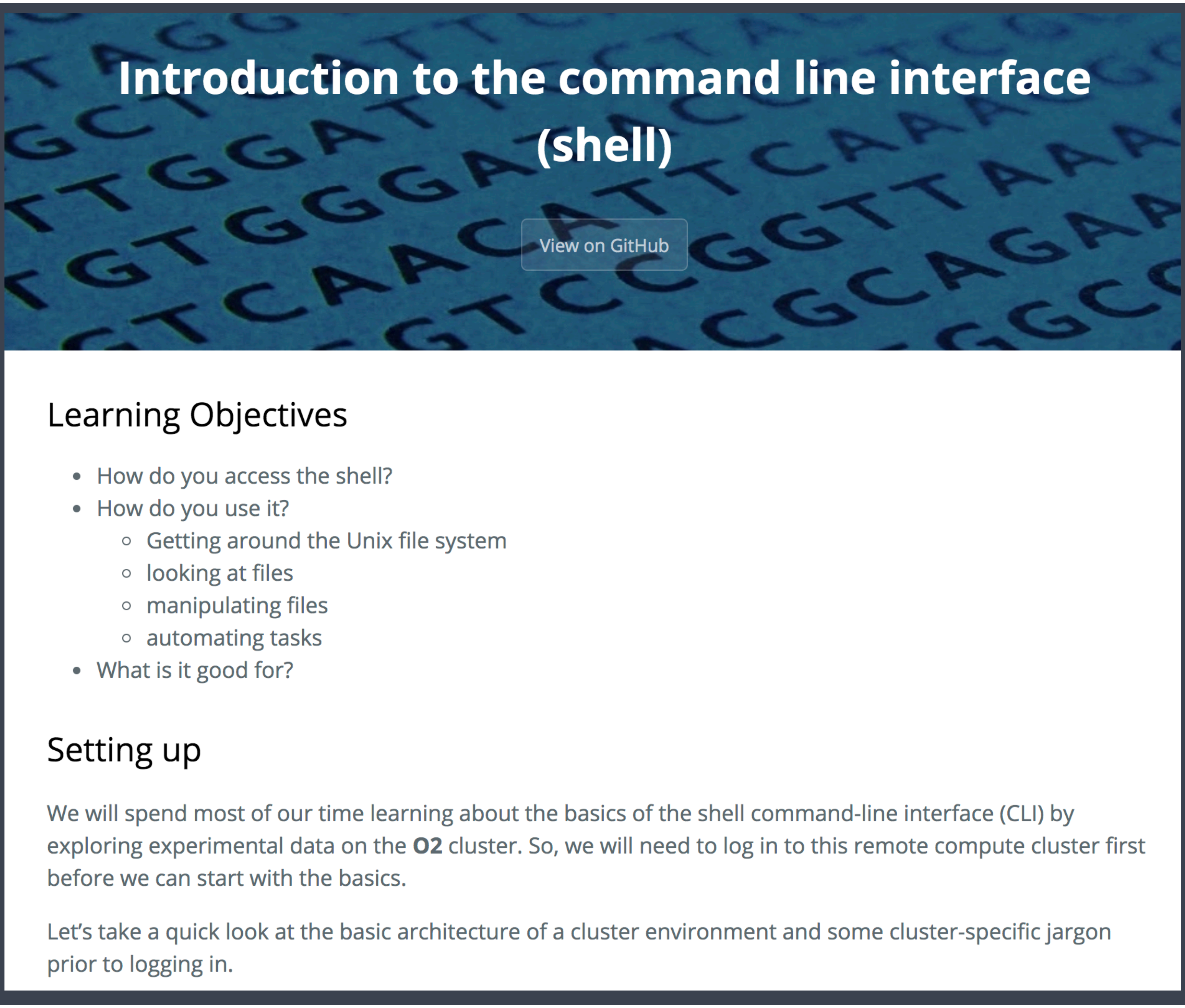
Time	Topic	Instructor
9:30 - 10:10	Workshop introduction	Meeta
10:10 - 11:40	Introduction to Shell	Mary
11:40 - 12:00	Overview of self-learning materials and homework submission	Jihe

Before the next class:

1. Please **study the contents** and **work through all the code** within the following lessons:

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

Course materials online



Introduction to the command line interface (shell)

Learning Objectives

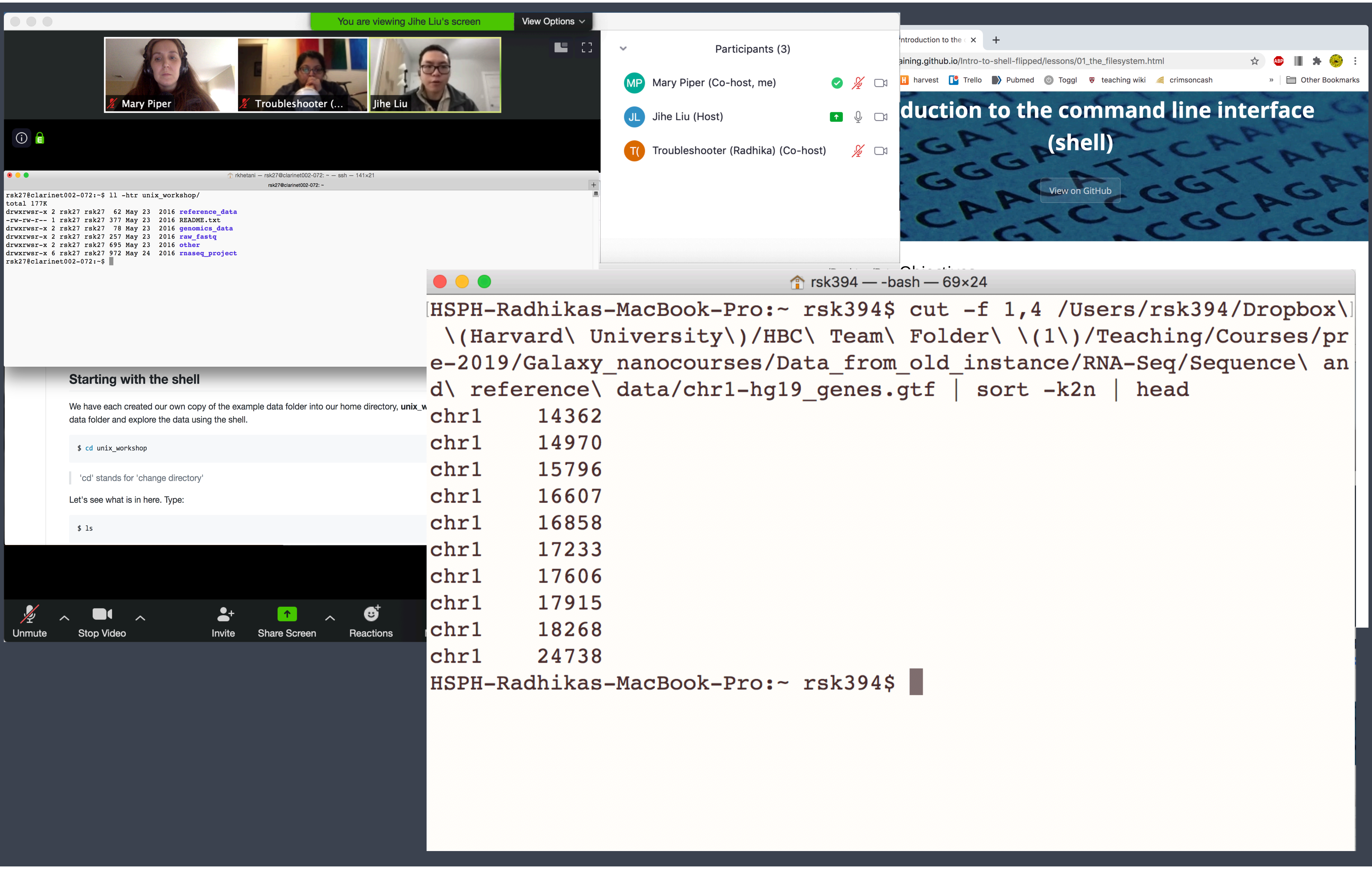
- How do you access the shell?
- How do you use it?
  - Getting around the Unix file system
  - looking at files
  - manipulating files
  - automating tasks
- What is it good for?

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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rsk27@clarinet002-072:~$ 
```

duction to the command line interface (shell)

Starting with the shell

We have each created our own copy of the example data folder into our home directory, **unix_w**
data folder and explore the data using the shell.

```
$ cd unix_workshop
```

> 'cd' stands for 'change directory'

Let's see what is in here. Type:

```
$ ls
```

```
HSPH-Radhikas-MacBook-Pro:~ rsk394$ cut -f 1,4 /Users/rsk394/Dropbox\
 \(Harvard\ University\)/HBC\ Team\ Folder\ \(1\)/Teaching/Courses/pr
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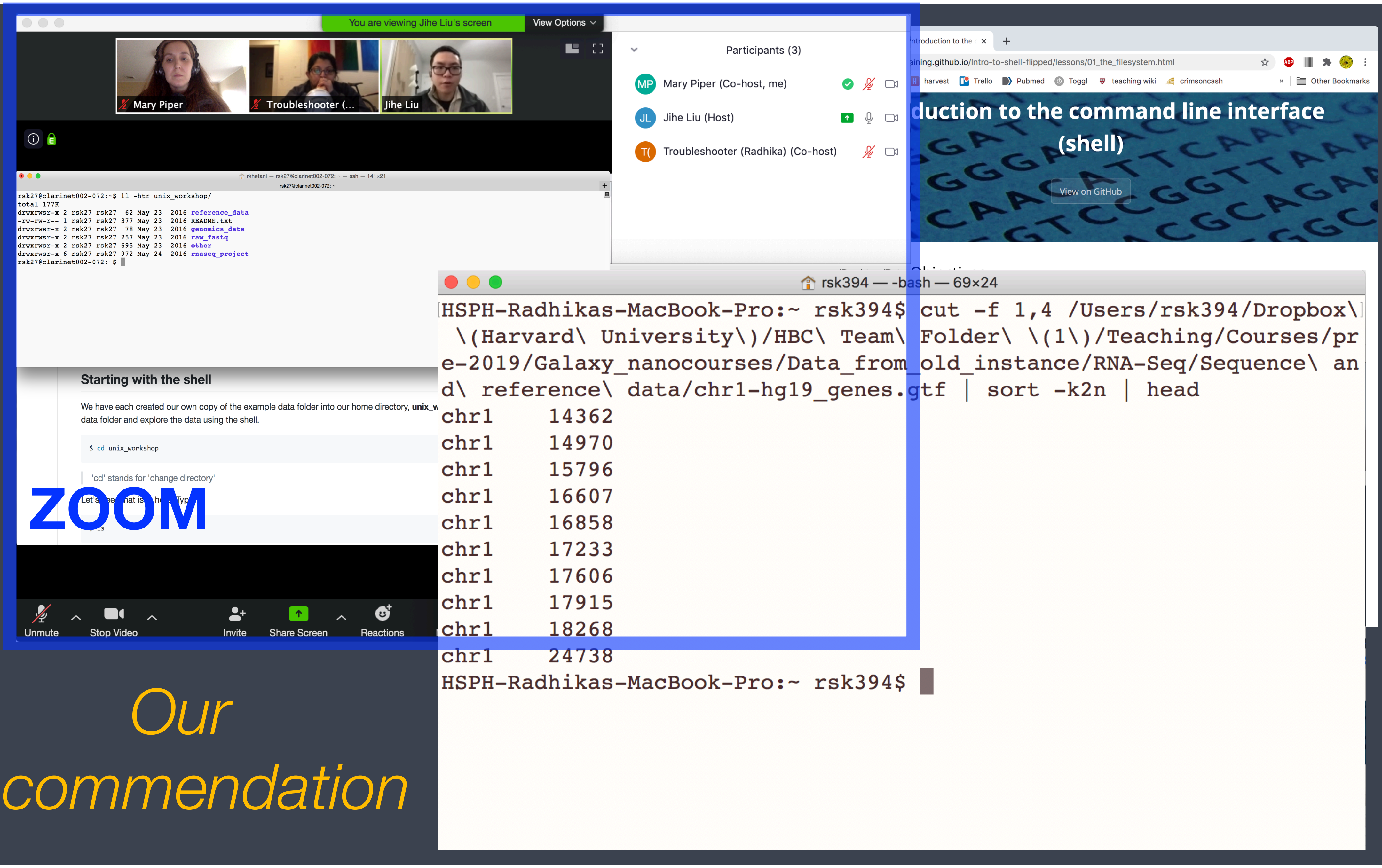

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Our recommendation

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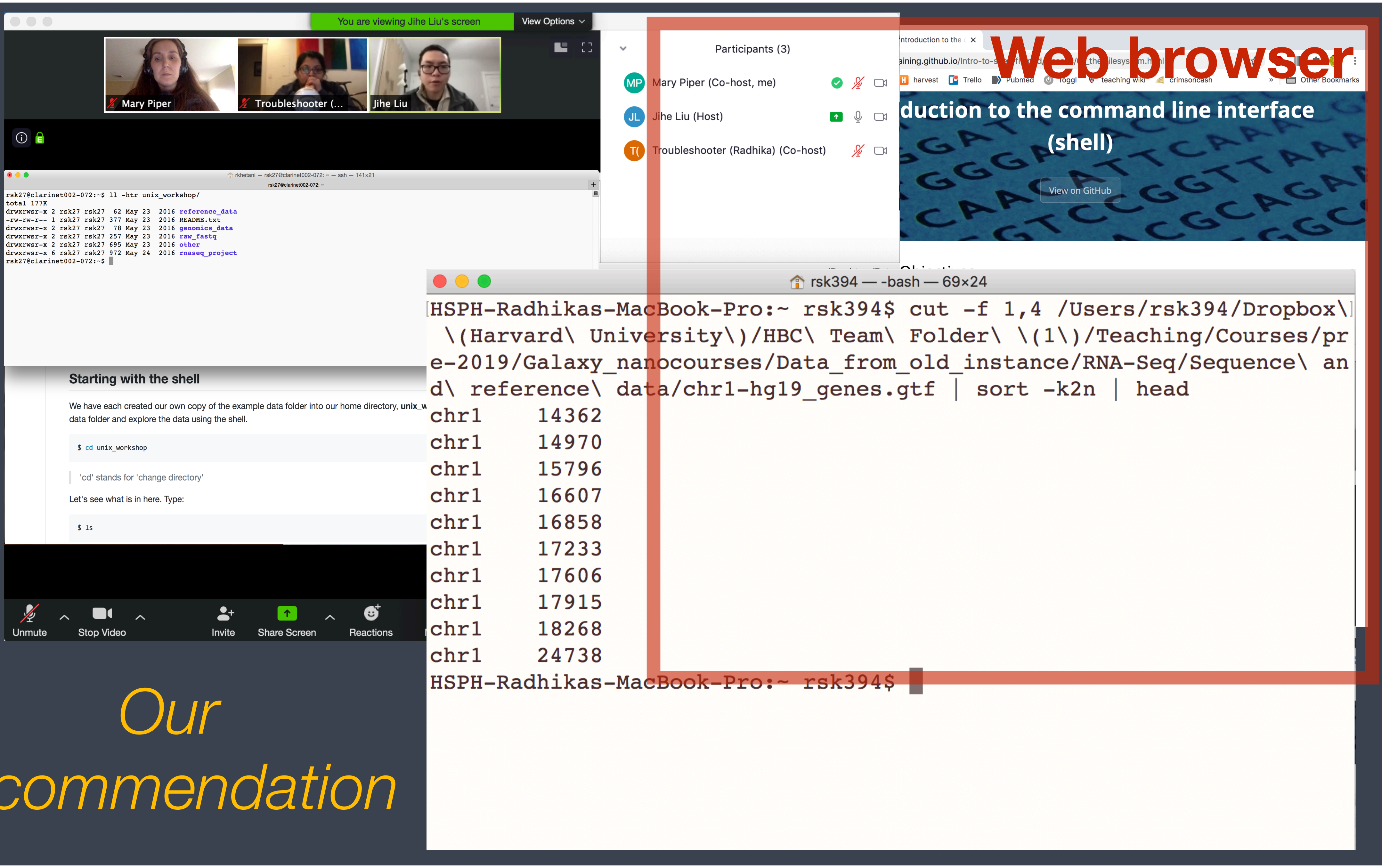

rkhetani — rsk27@clarinet002-072: ~ — ssh — 141×21

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rsk394 — -bash — 69×24

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Our recommendation

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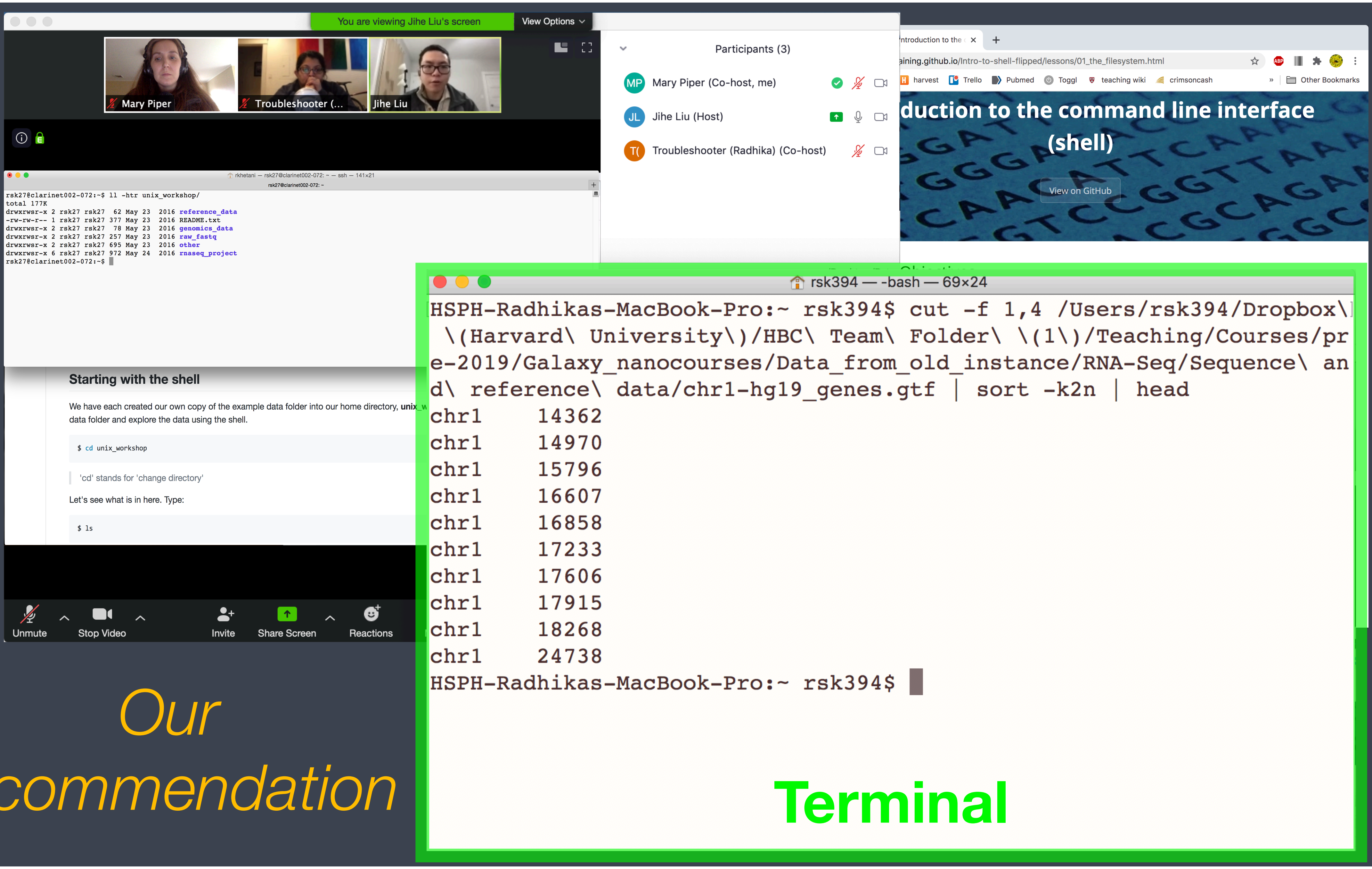

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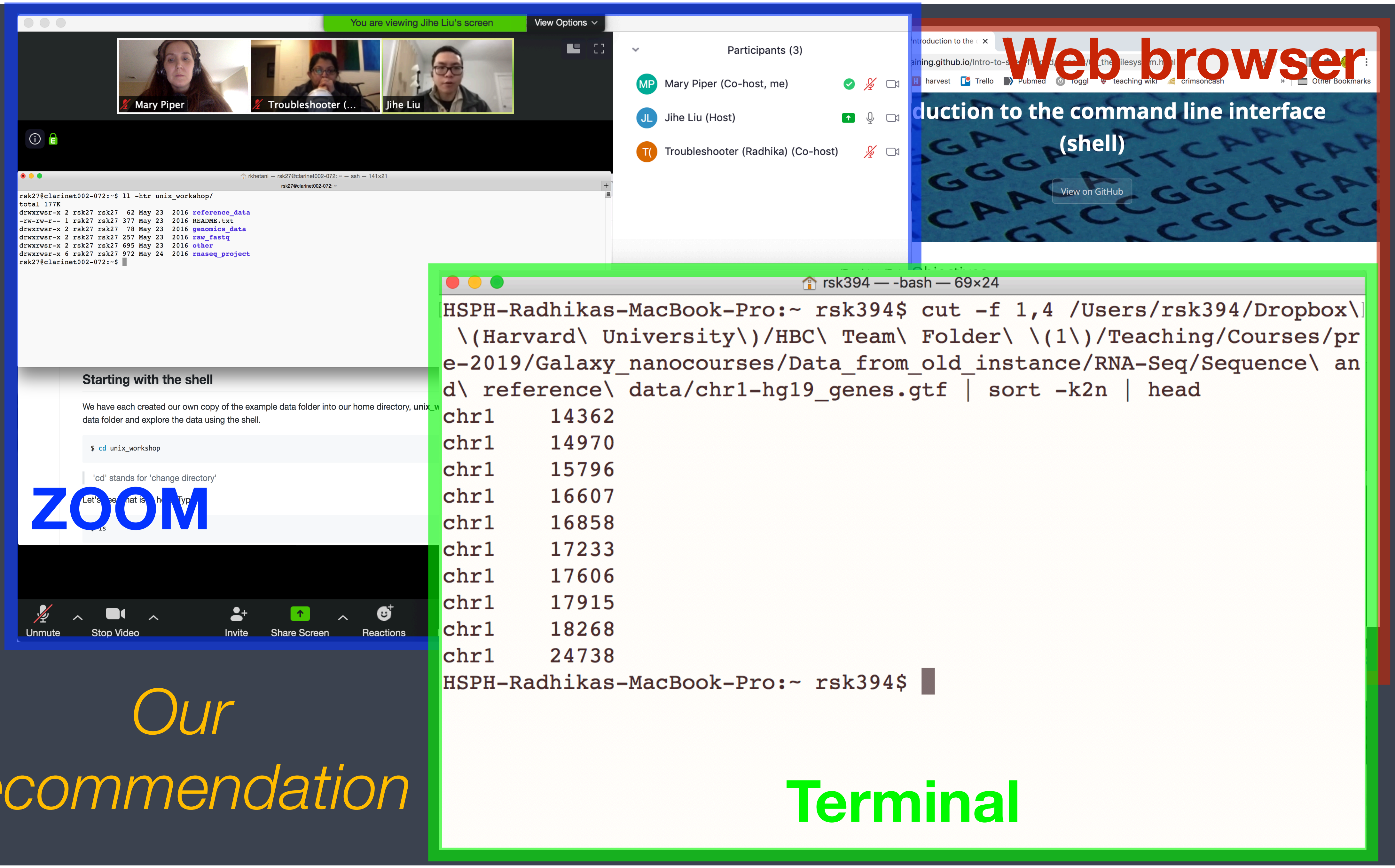
```

Our recommendation

Terminal

Single screen & 3 windows?



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harvest Trello Pubmed Toggl teaching wiki crimsoncash » Other Bookmarks

duction to the command line interface (shell)

View on GitHub

rsk394 — -bash — 69×24

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```

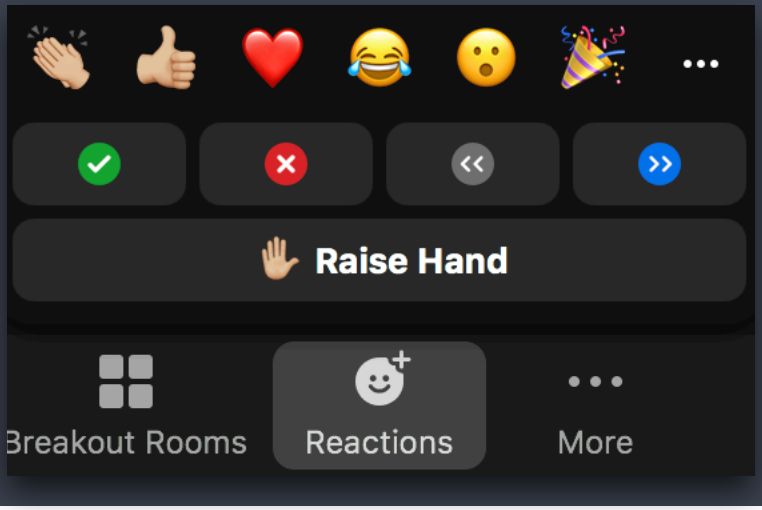
Our recommendation

Odds and Ends

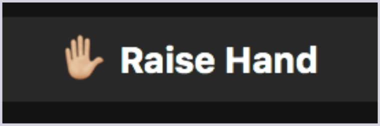
- Quit/minimize all applications that are not required for class

Odds and Ends (1/2)

- Quit/minimize all applications that are not required for class
- Are you all set?
  - ✅ = "agree", "I'm all set" (equivalent to a green post-it)
  - ❌ = "disagree", "I need help" (equivalent to a red post-it)

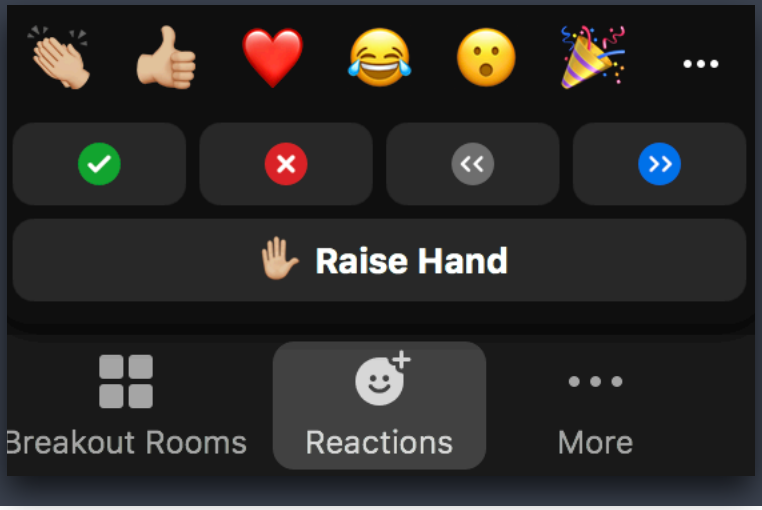


Odds and Ends (2/2)

- Questions for the presenter?
  - Post the question in the Chat window OR
  - 

when the presenter asks for questions
  - Let the **Moderator** know

- Technical difficulties with software?
  - Start a <u>private</u> chat with the **Troubleshooter** with a description of the problem.



Thanks!

- **Daniel Caunt** and **Maggie McFee** from FAS-RC
- Data Carpentry

Contact us!

HBC training team: hbctraining@hsph.harvard.edu

HBC consulting: bioinformatics@hsph.harvard.edu

FAS-RC: create a ticket

Twitter

HBC: @bioinfocore

FAS-RC: @fasrc