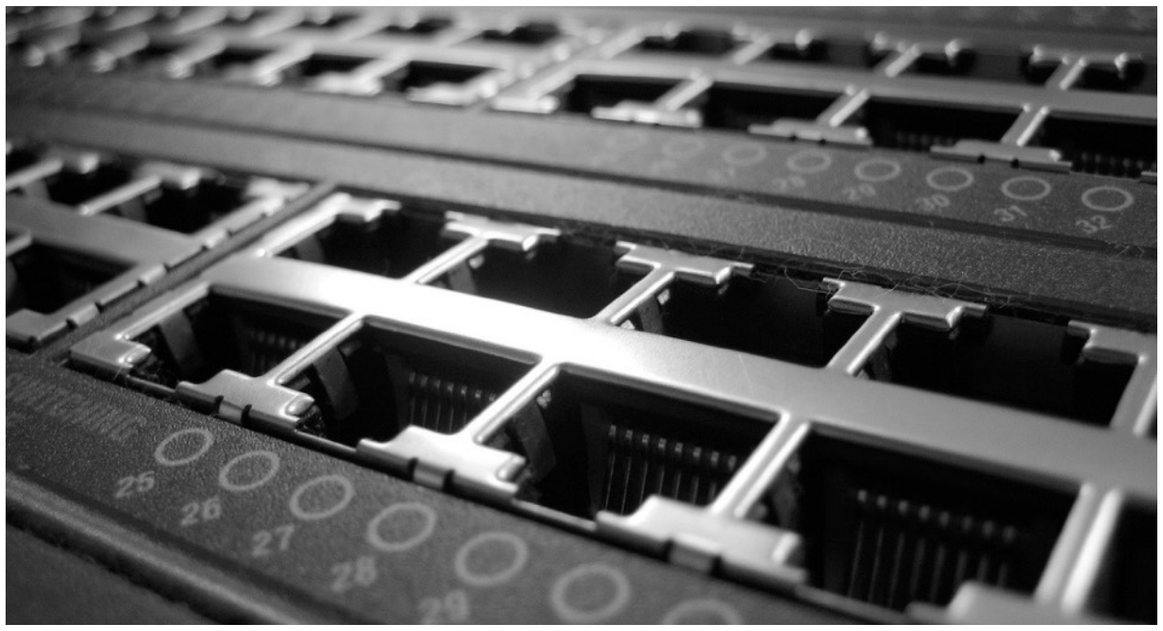


Introduction to the command-line interface

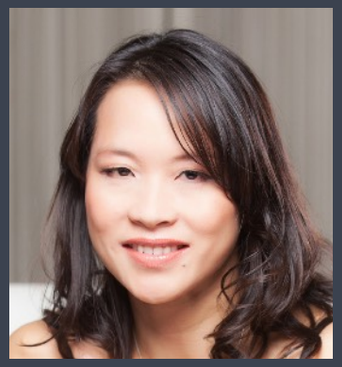
(shell)

Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

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



Shannan Ho Sui
Director

Victor Barrera

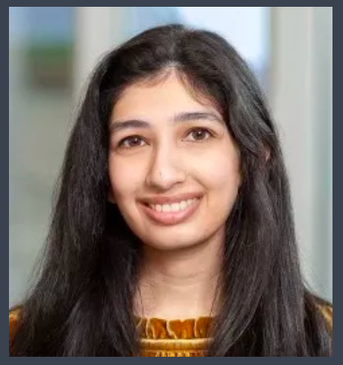
James Billingsley

Zhu Zhuo

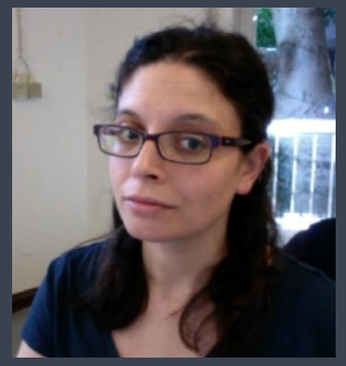
Meeta Mistry
Interim Director of Education

Heather Wick

Will Gammerdinger



Noor Sohail

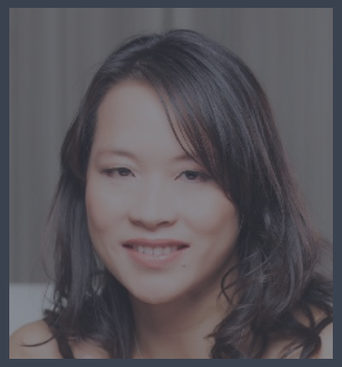


Emma Berdan

Sergey Naumenko

Maria Simoneau

Introductions!



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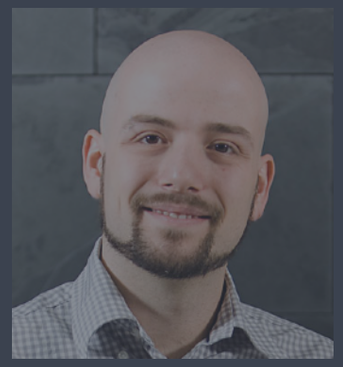

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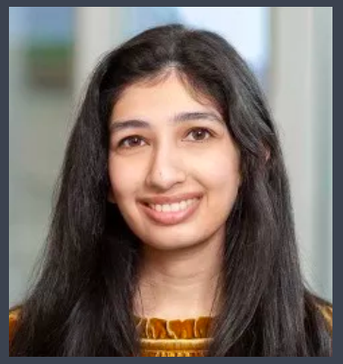

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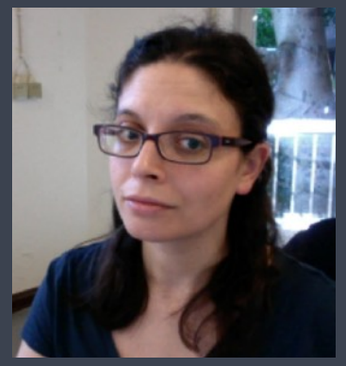

Emma Berdan

Sergey Naumenko

Maria Simoneau

Consulting

- Transcriptomics: bulk, single cell, small RNA
- Epigenomics: ChIP-seq, CUT&RUN, ATAC-seq, DNA methylation
- Variant discovery: WGS, resequencing, exome-seq and CNV
- Multiomics integration
- Spatial biology
- Experimental design and grant support

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

CFAR
HARVARD UNIVERSITY
CENTER FOR AIDS RESEARCH

HARVARD
T.H. CHAN
SCHOOL OF PUBLIC HEALTH

NIEHS

HARVARD
CATALYST
THE HARVARD CLINICAL
AND TRANSLATIONAL
SCIENCE CENTER

HARVARD
MEDICAL SCHOOL

Training

A key component of the HBC's mission is its training initiative. Our dedicated training team holds workshop to help researchers at Harvard better understand analytical methods for NGS data.

HBC's training team is made up of four PhD-level scientists who devote substantial time to material development, training and community building/outreach. All members of the training team also participate in consultations on research projects to ensure they remain up-to-date on current best practices in NGS analysis.

Our hands-on workshops focus on **basic data skills** and **analysis of high-throughput sequencing data**, with an emphasis on **experimental design**, current **best practices** and **reproducibility**. Our workshops are designed for **wet-lab biologists** aiming to independently design sequencing-based experiments and analysing the resulting data.

We offer three types of workshops:

1. Short, 3-hour monthly workshops (*Current topics in bioinformatics*)
2. Basic Data Skills**
3. Advanced Topics: Analysis of high-throughput sequencing (NGS) data**

***The basic data skills workshops serve as the foundation for the advanced workshops.*

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

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

Training

A key component of the H
researchers at Harvard b

HBC's training team is m
training and community b
research projects to ensu

Our hands-on workshops
an emphasis on **experim
for **wet-lab biologists** ai
data.

We offer three types of w

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3. Advanced Topics: Ana

**The basic data skills

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HARVARD
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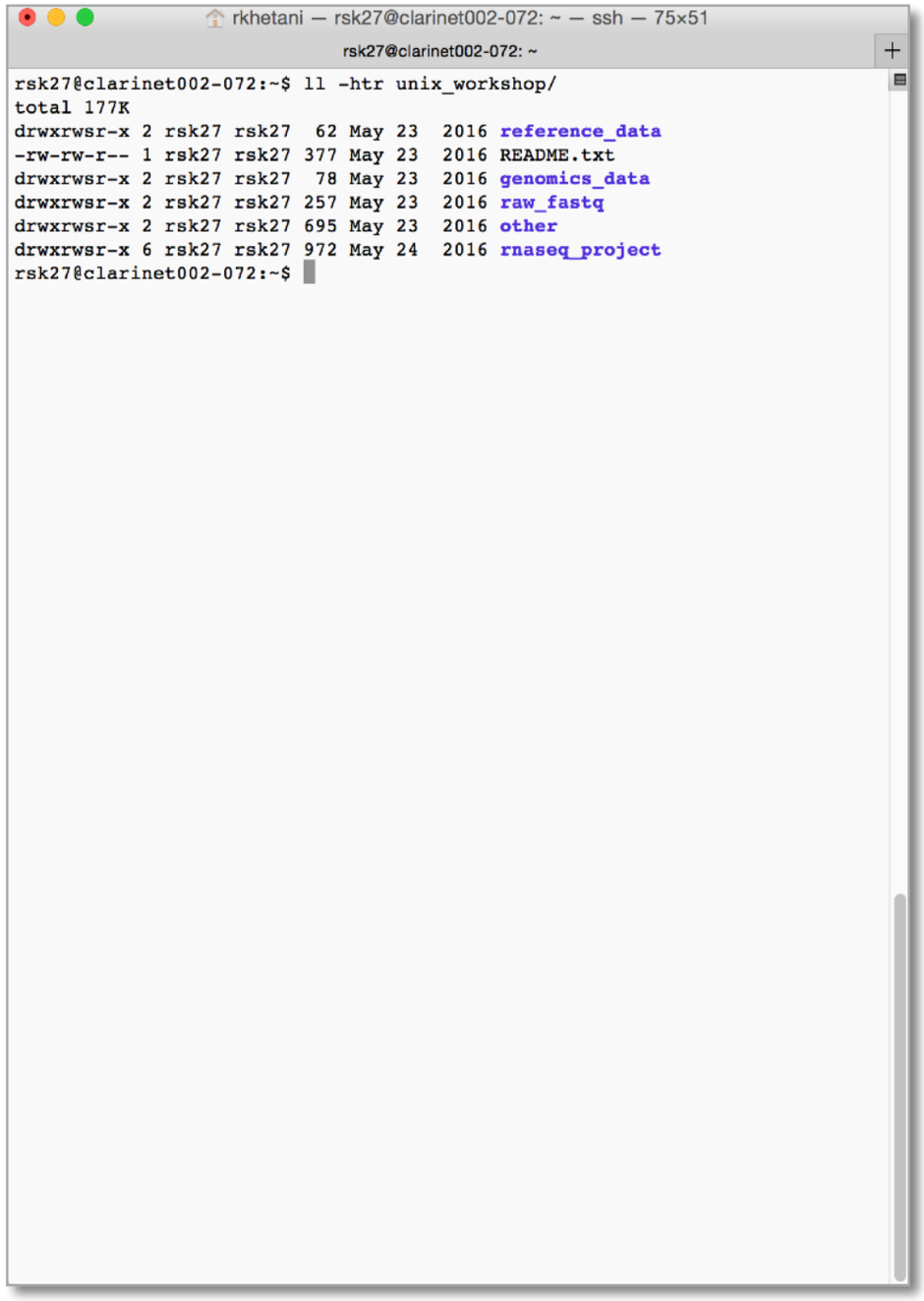
Workshop scope



“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

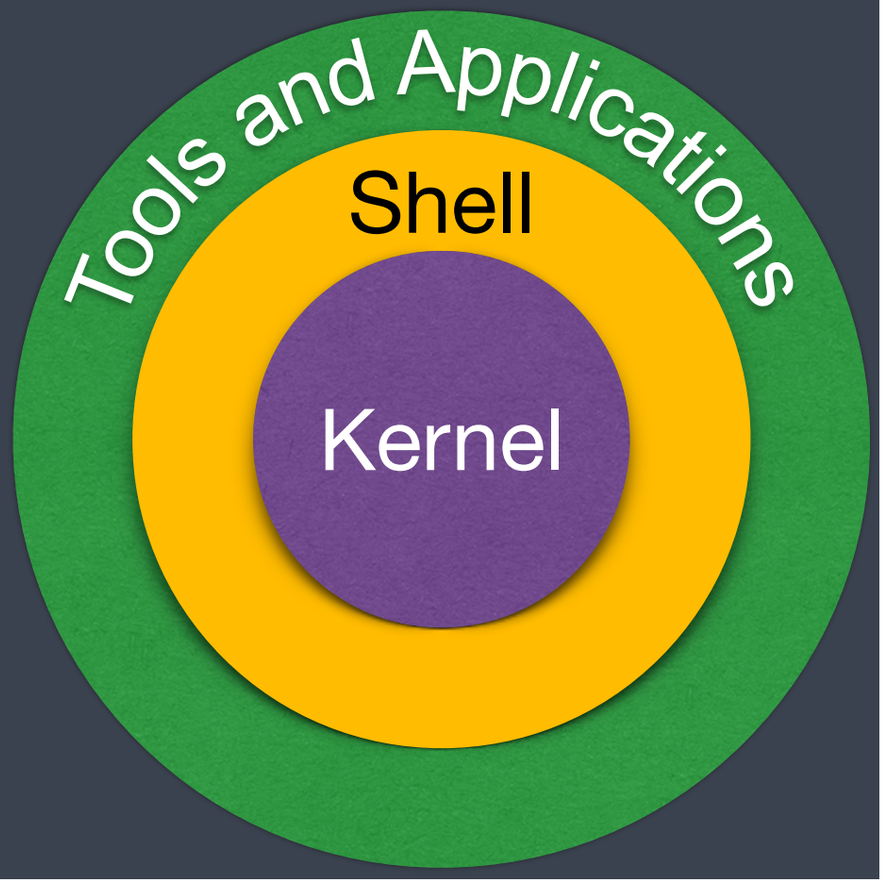
Linux

- 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

Components

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

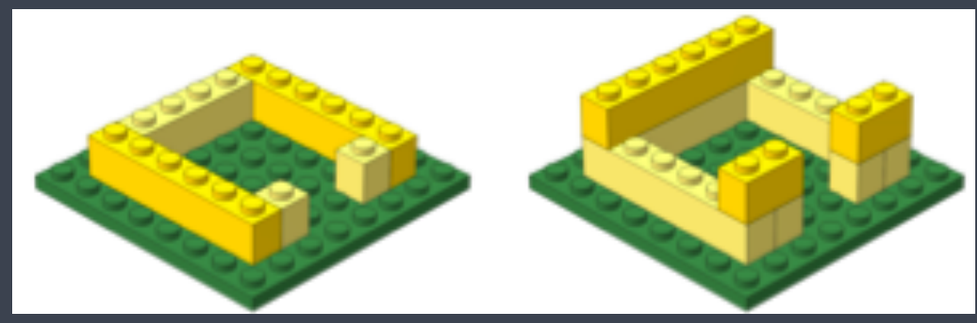
- The kernel, which schedules tasks and manages storage: ***the brain of the system***
- The shell, ***an interpreter*** that helps interprets our input for the kernel
- Utilities, tools and applications, which use the shell to communicate with the kernel



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
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

> **NOTE:** To run through the code above, you will need to be **logged into O2** and **working on a compute node** (i.e. your command prompt should have the word `compute` in it).
>
> 1. Log in using `ssh rc_trainingXX@o2.hms.harvard.edu` and enter your password (replace the "XX" in the username with the number you were assigned in class).
> 2. Once you are on the login node, use `srun --pty -p interactive -t 0-2:30 --mem 1G`

Course materials online

Learning Objectives

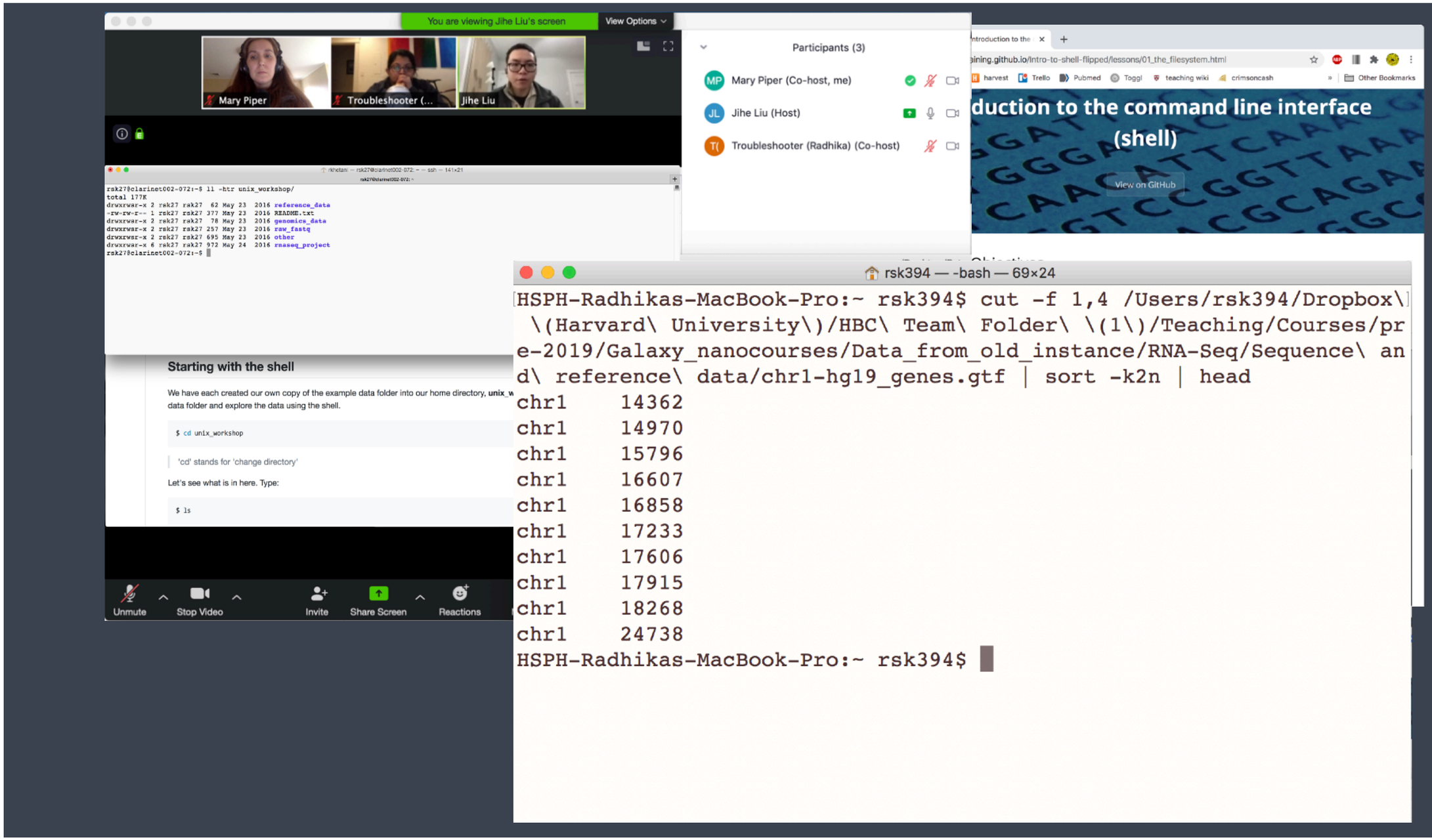
- How do you access the shell?
- How do you use it?
  - Getting around the Unix file system
  - looking at files
  - manipulating files
  - automating tasks
- What is it good for?

Setting up

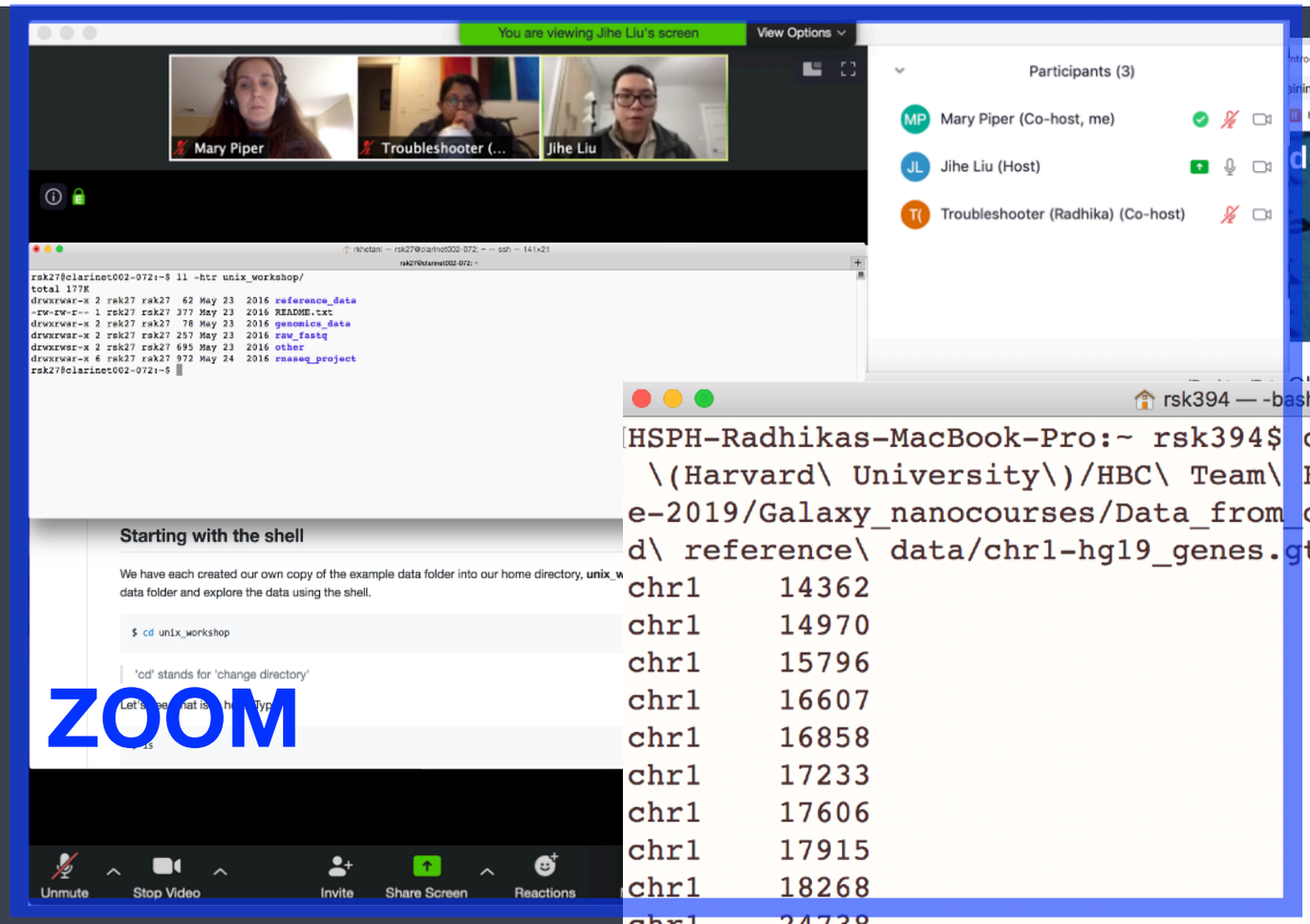
We will spend most of our time learning about the basics of the shell command-line interface (CLI) by exploring experimental data on the **O2** cluster. So, we will need to log in to this remote compute cluster first before we can start with the basics.

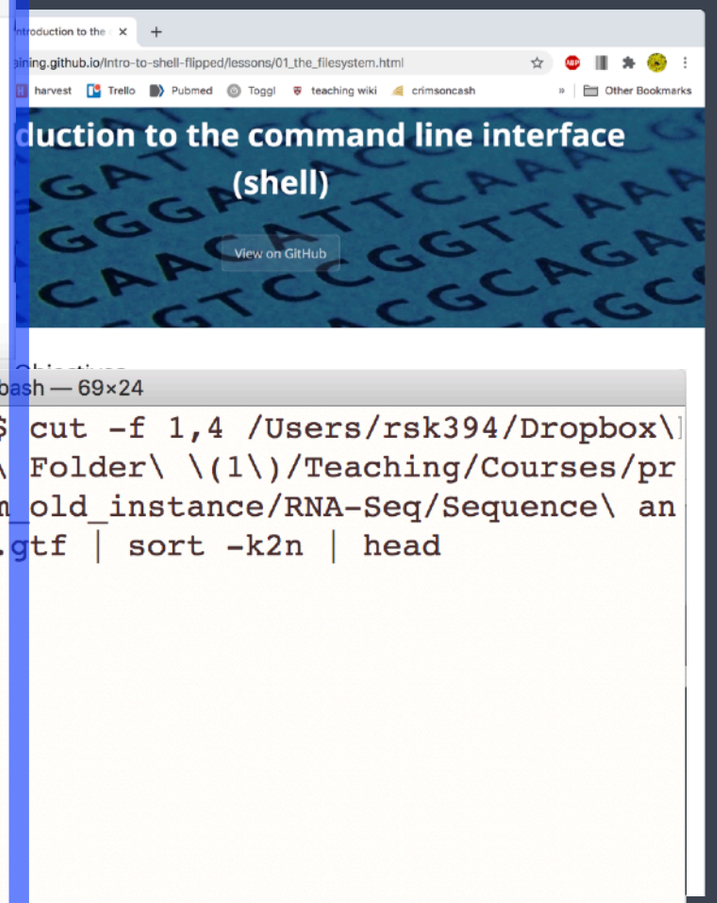
Let's take a quick look at the basic architecture of a cluster environment and some cluster-specific jargon prior to logging in.

Single screen & 3 windows?



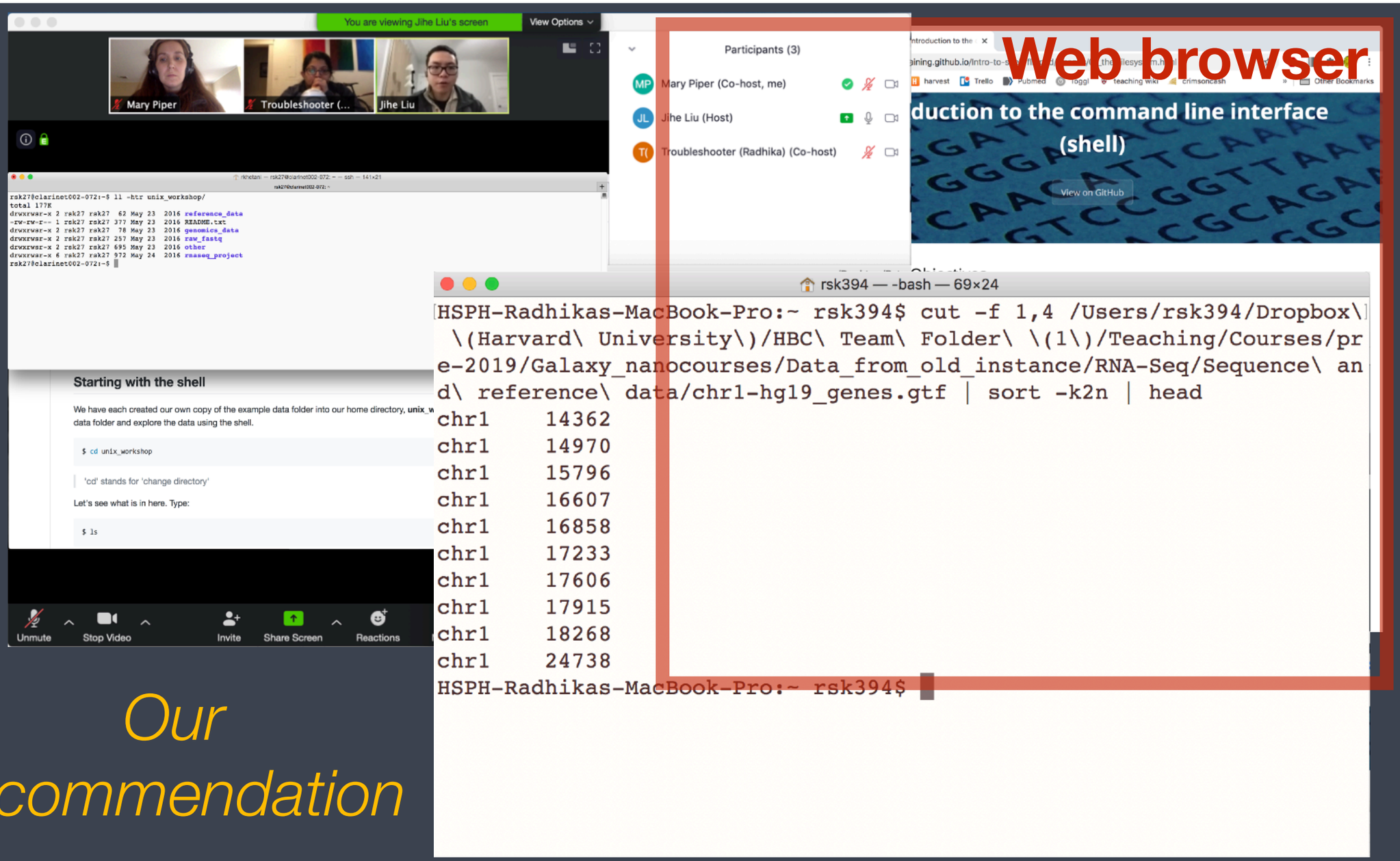
Single screen & 3 windows?





Our recommendation

Single screen & 3 windows?



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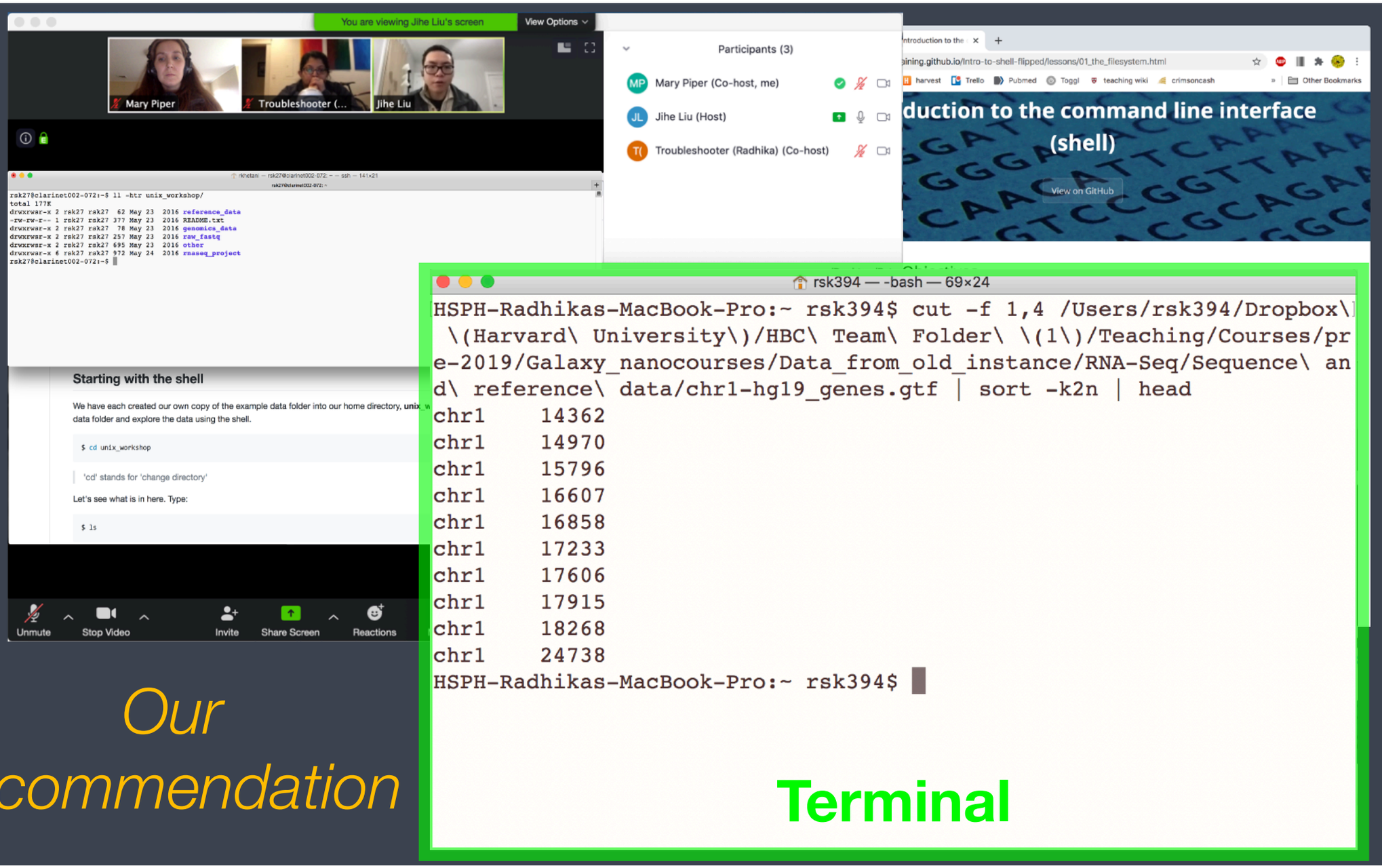
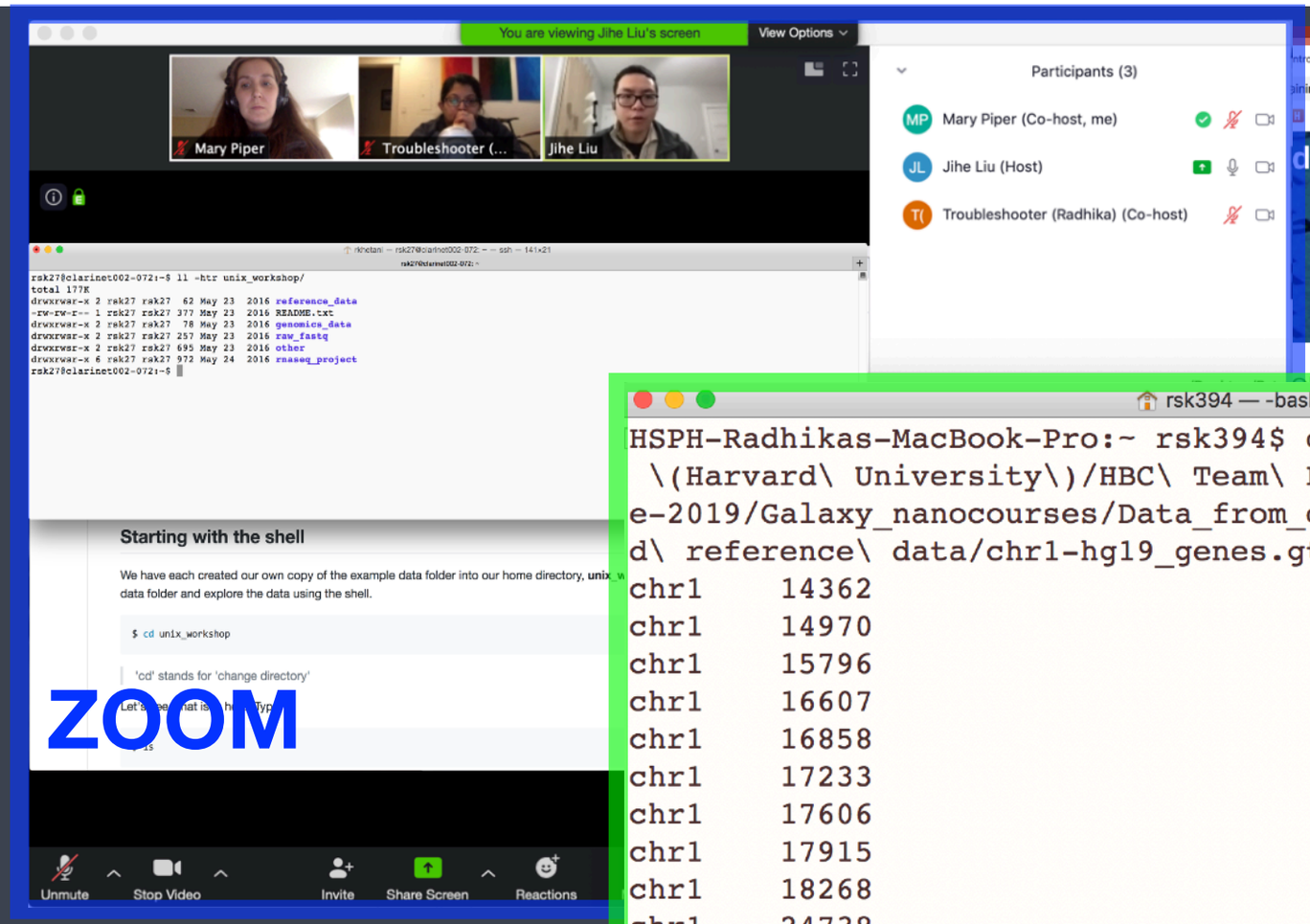
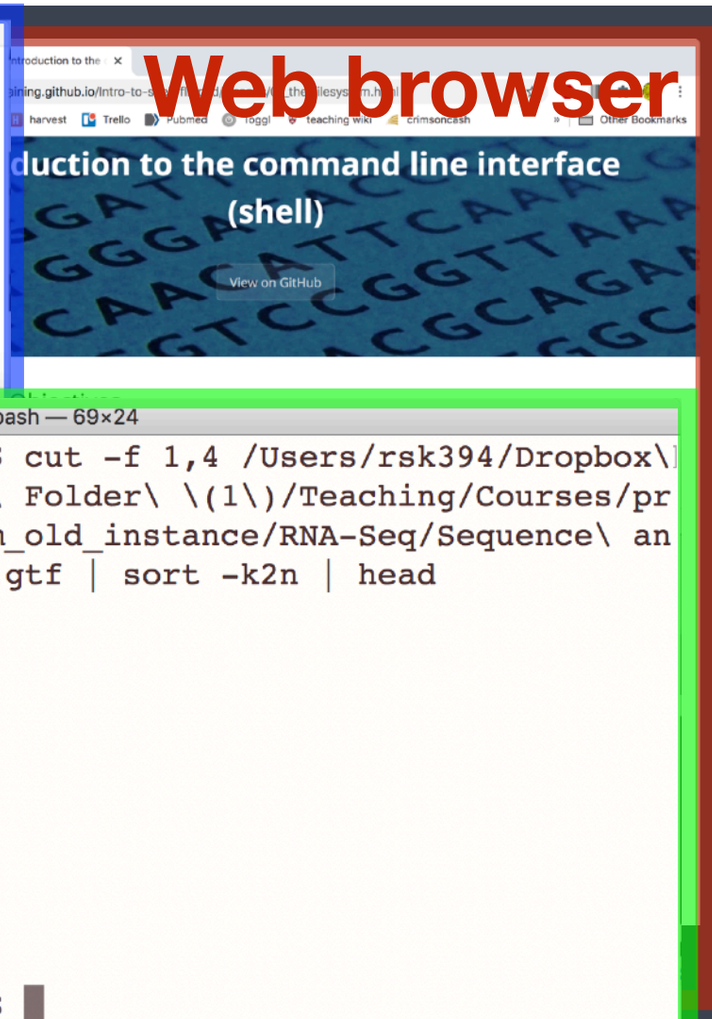


Our recommendation

Terminal

Single screen & 3 windows?





Our recommendation

Course participation

- Please keep your videos on, we would love to see your faces!
- Mandatory review of self-learning lessons and assignments
- Attendance required for all classes
- Your questions and active participation drive learning
- We look forward to all of your questions!

Homework and Expectations

- At-home lessons and exercises after each session
- Cover material not previously discussed
- Provides us feedback to help pace the course appropriately
- 3-5 hours to complete
- Homework load is heavier in the beginning of this workshop series and tapers off

Odds and Ends (1/2)

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

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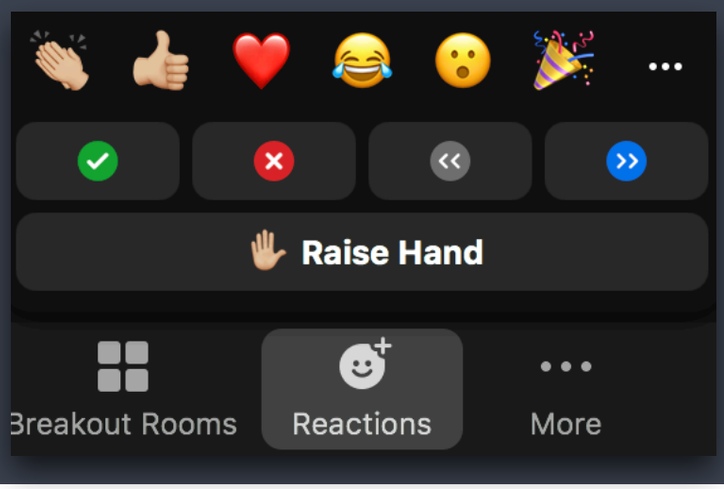
- Captioning is available upon request

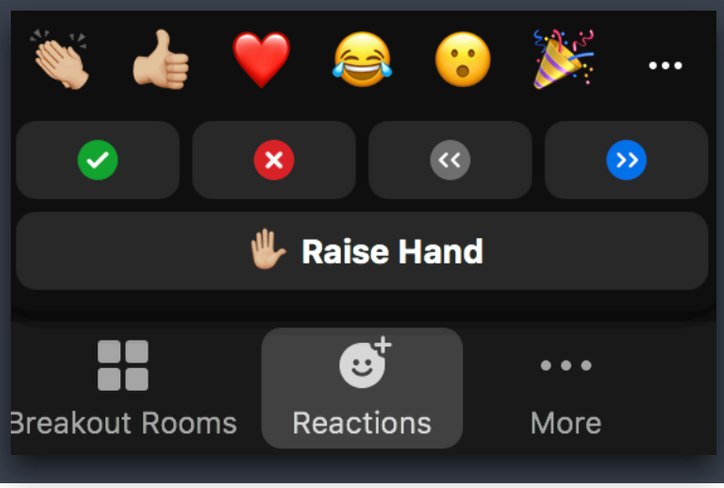
Odds and Ends (1/2)

- Quit/minimize all applications that are not required for class
- Captioning is available upon request
- 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
  - ✋ **Raise Hand** when the presenter asks for questions
  - Let the **Moderator** know
- Technical difficulties with software?
  - Start a private chat with the **Troubleshooter** with a description of the problem.



Thanks!

- **Kathleen Chappell** and **Andy Bergman** from HMS-RC
- Data Carpentry

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