

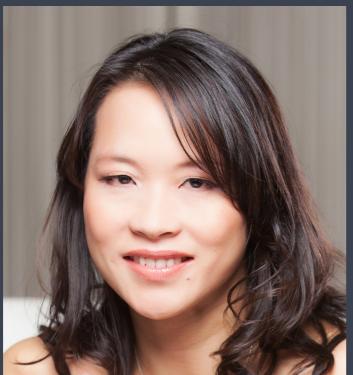
Introduction to bulk RNA-seq (Part I)

Harvard Chan Bioinformatics Core

in collaboration with

HMS Research Computing

<https://tinyurl.com/hbc-rnaseq>



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



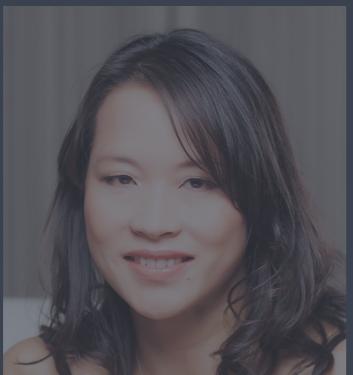
James Billingsley



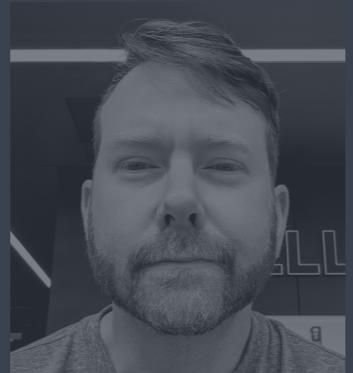
Sergey Naumenko



Peter Kraft
Faculty Advisor



Shannan Ho Sui
Director



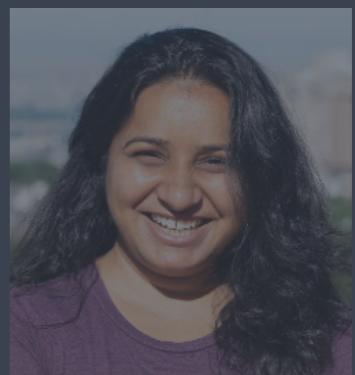
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Consulting

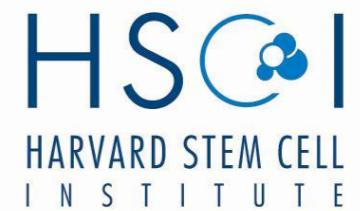
- RNA-seq analysis: bulk, single cell, small RNA
- ChIP-seq and ATAC-seq analysis
- Genome-wide methylation
- WGS, resequencing, exome-seq and CNV studies
- QC & analysis of gene expression arrays
- Functional enrichment analysis
- Grant support

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



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NIEHS



Training



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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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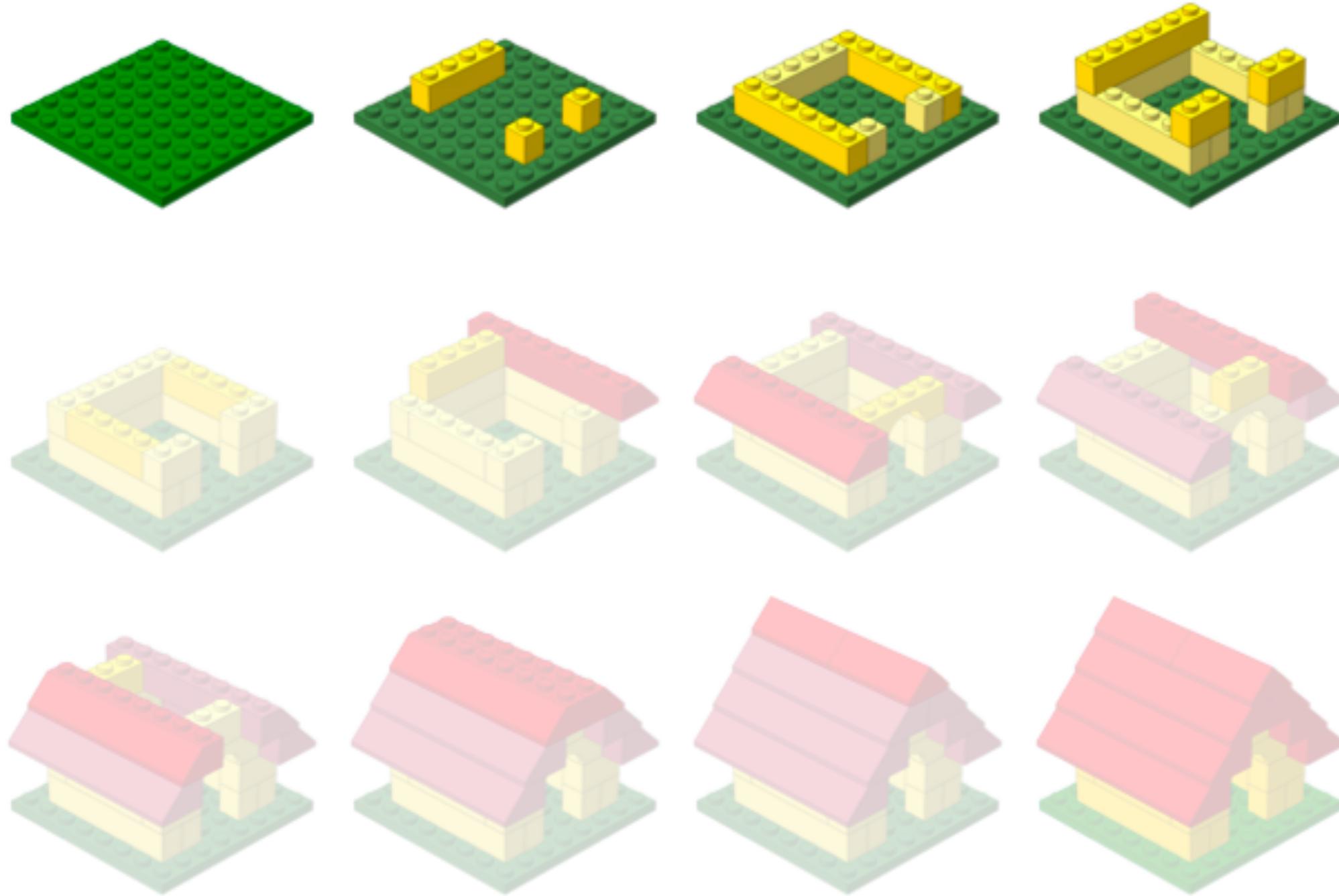
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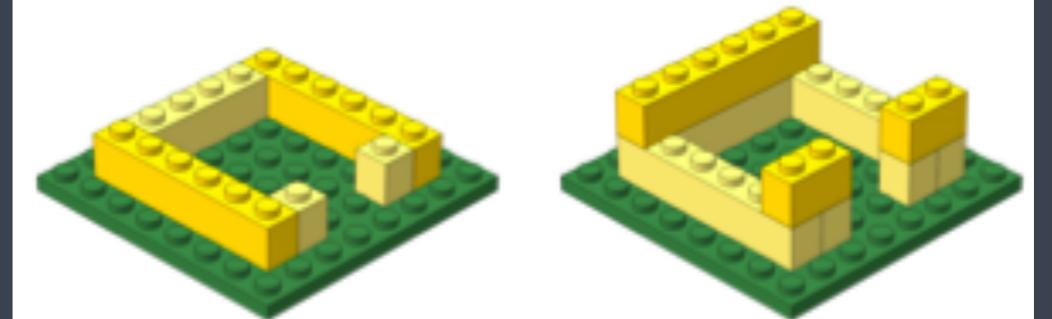
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<http://anoved.net/tag/lego/page/3/>

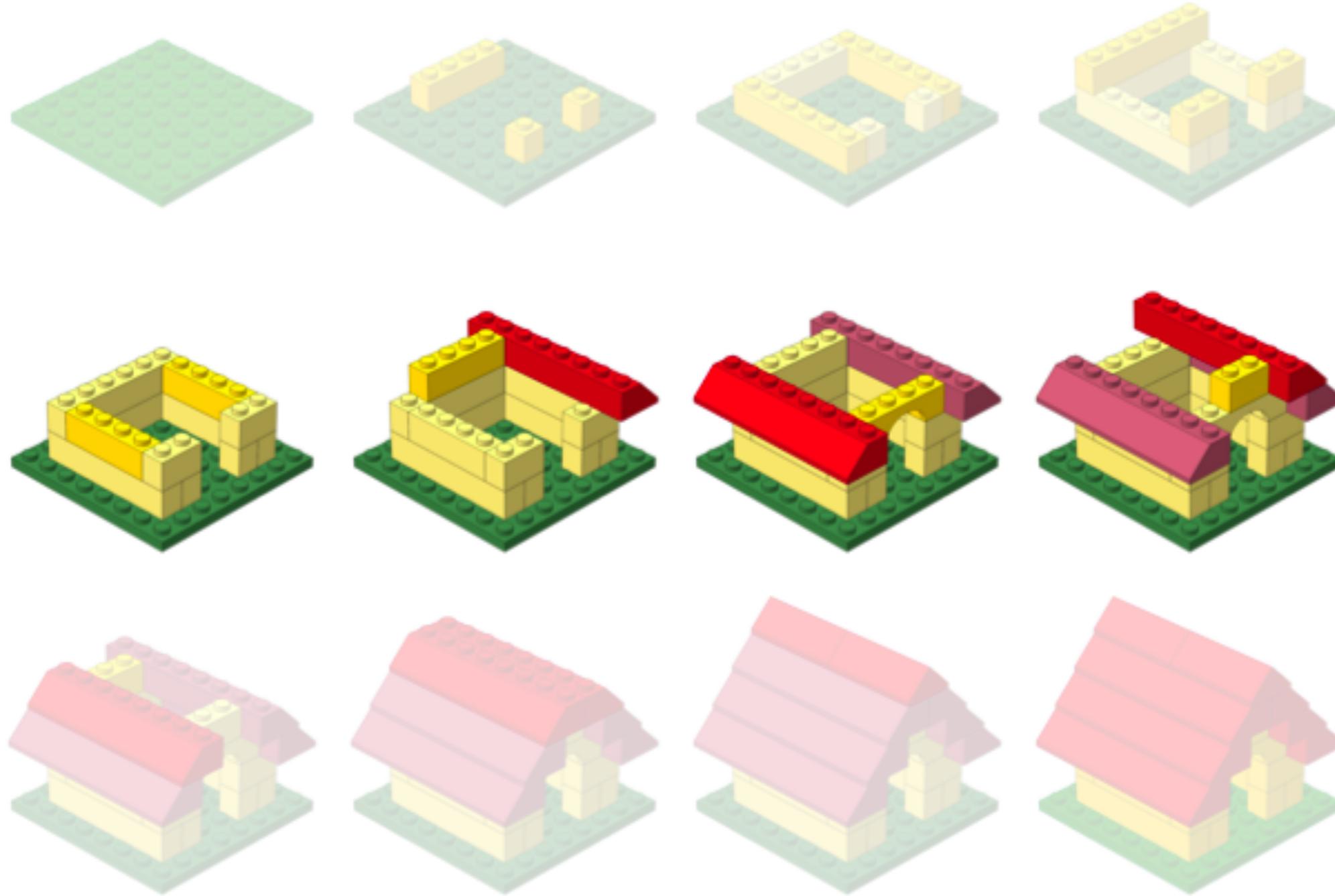
Setting up to perform Bioinformatics analysis

Setting up...



- ✓ Introduction to the command-line interface (shell, Unix, Linux)
 - Dealing with large data files
 - Performing bioinformatics analysis
 - Using tools
 - Accessing and using compute clusters
- ✓ R
 - Parsing and working with smaller results text files
 - Statistical analysis, e.g. differential expression analysis
 - Generating figures from complex data

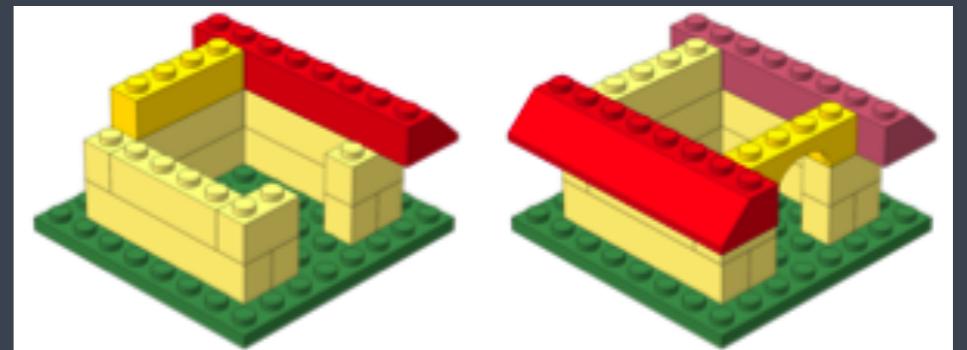
Workshop scope



<http://anoved.net/tag/lego/page/3/>

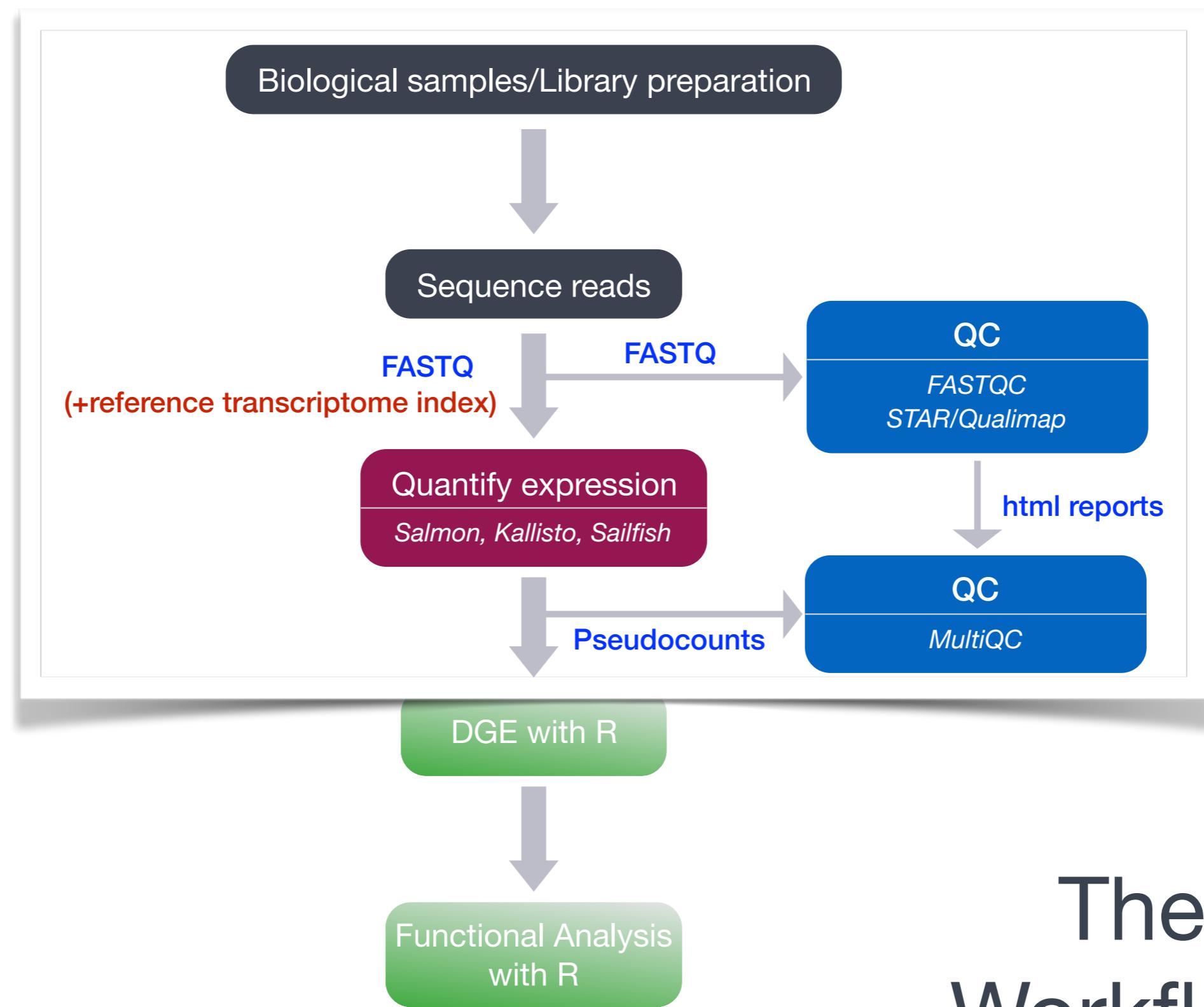
Bioinformatics data analysis

Learning Objectives



- ✓ Describe best practices for designing a bulk RNA-seq experiment
- ✓ Describe steps in an RNA-seq analysis workflow (from sequence data to expression quantification).
- ✓ Implement shell scripts on a high-performance compute cluster to perform the above steps.

We won't be covering how to perform differential gene expression (DGE) analysis on count data in this workshop.



The Workflow

Logistics

Course webpage

<https://tinyurl.com/hbc-rnaseq>

Course schedule online

Workshop Schedule

NOTE: The *Basic Data Skills Introduction to the command-line interface* workshop is a prerequisite.

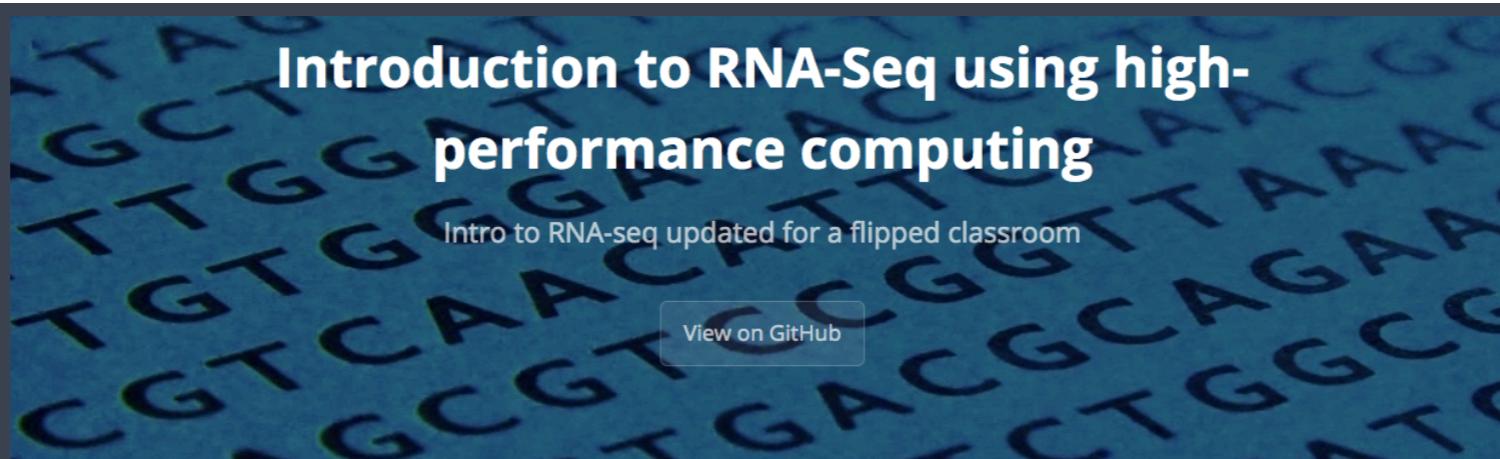
Pre-reading

- [Shell basics review](#)
- [Introduction to RNA-seq](#)

Day 1

Time	Topic	Instructor
09:30 - 09:45	Workshop introduction	Radhika
09:45 - 10:25	Working in an HPC environment	Radhika
10:25 - 11:05	Project Organization and Best Practices in Data Management	Meeta
11:05 - 11:45	Quality Control of Sequence Data: Running FASTQC	Jihe
11:45 - 12:00	Overview of self-learning materials and homework submission	Jihe/Meeta

Course materials online

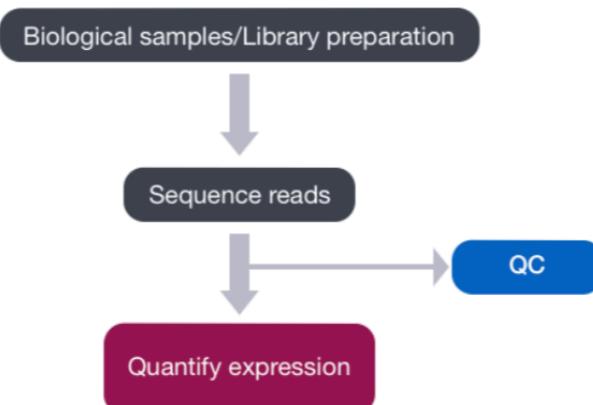


Learning Objectives:

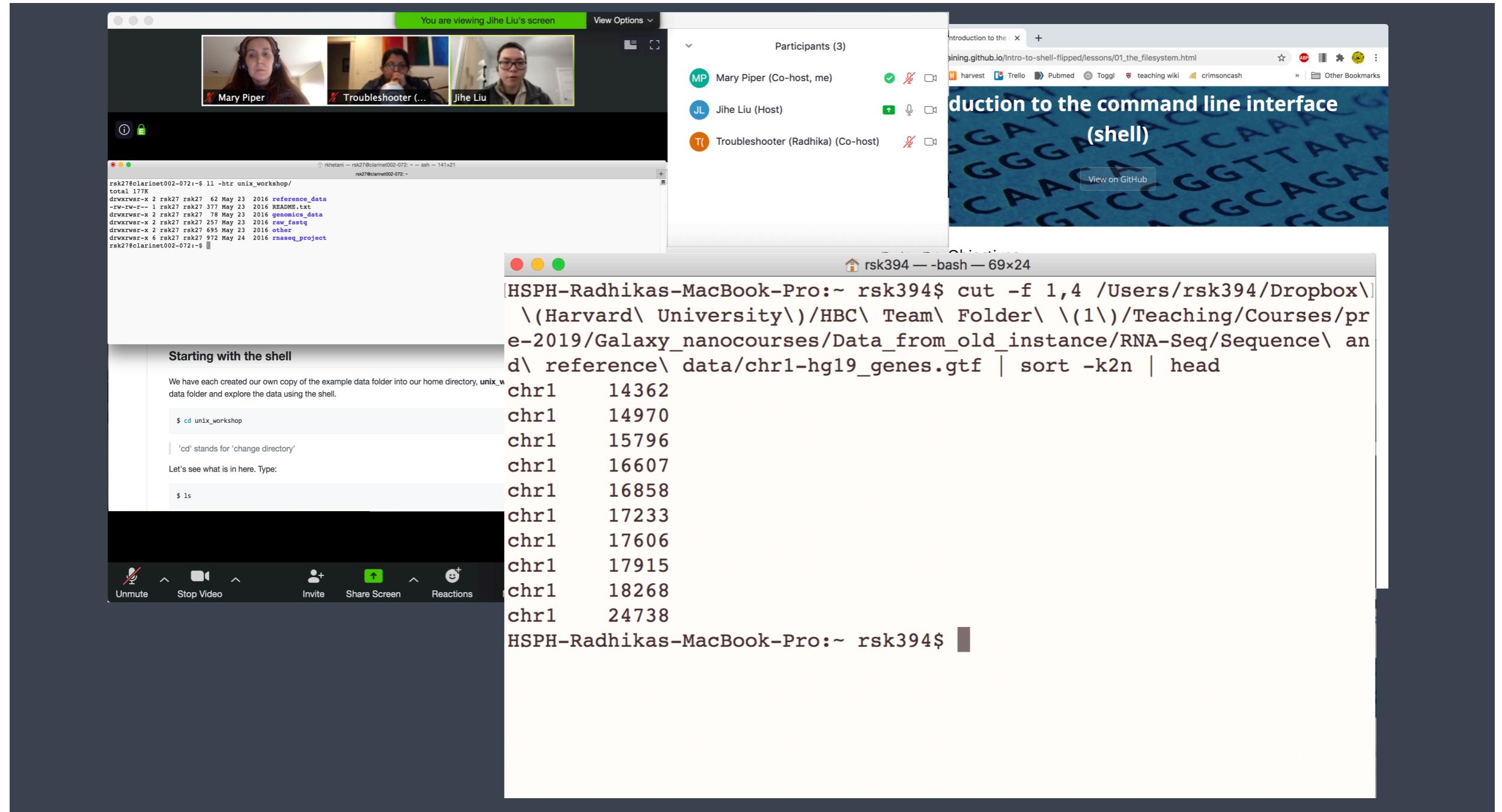
- Understand the quality values in a FASTQ file
- Create a quality report using FASTQC

Quality Control of FASTQ files

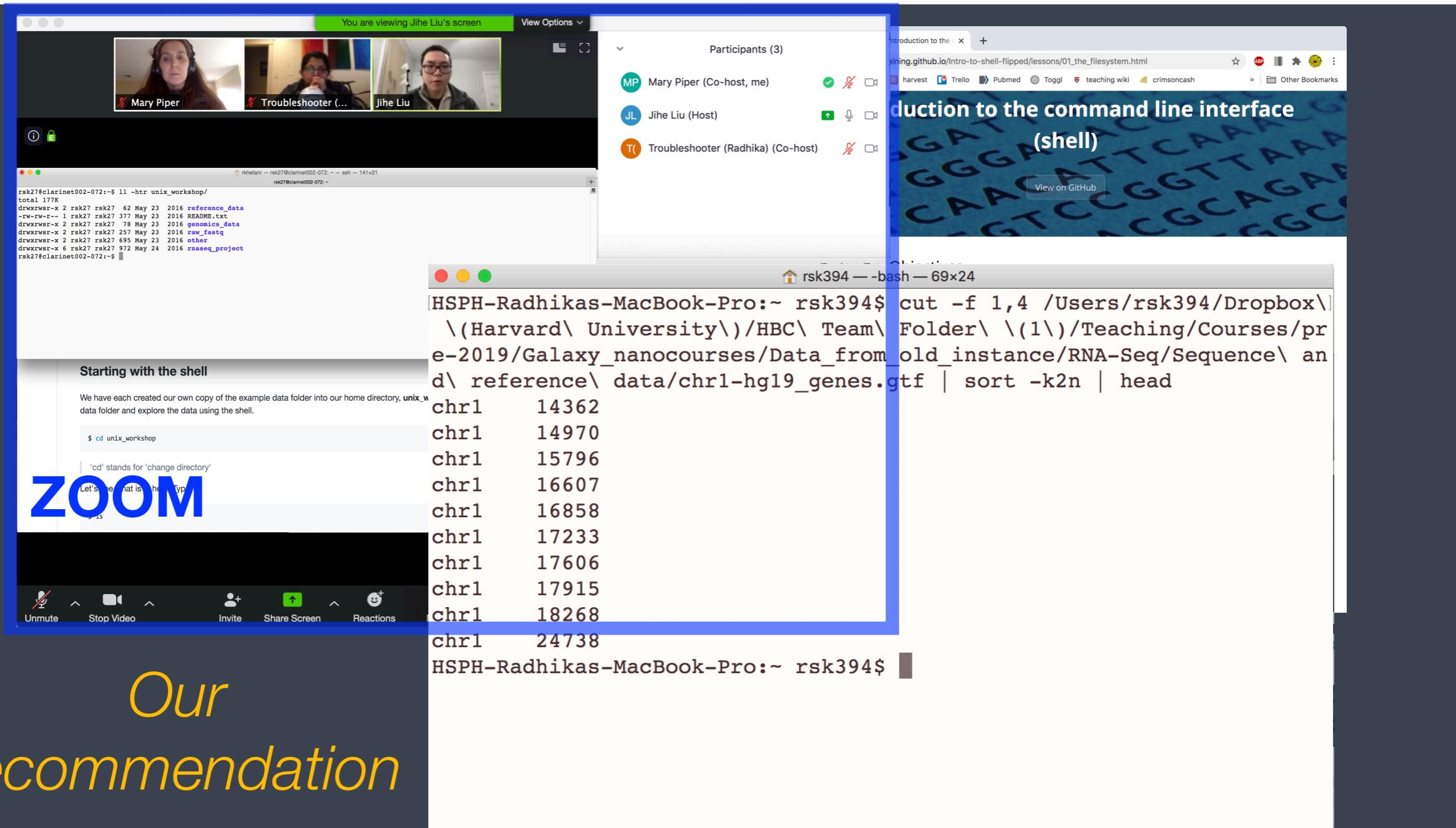
The first step in the RNA-Seq workflow is to take the FASTQ files received from the sequencing facility and assess the quality of the sequence reads.



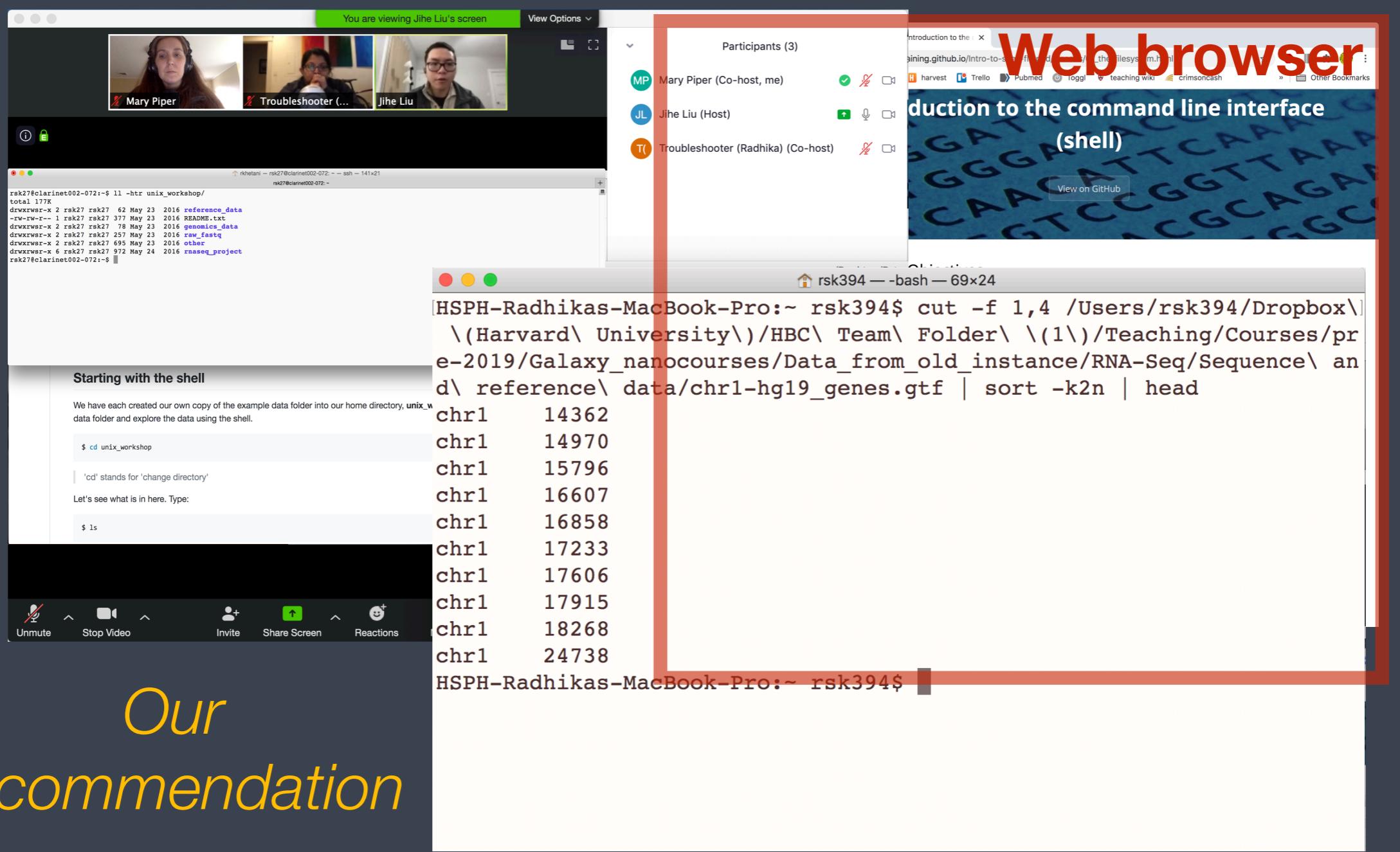
Single screen & 3 windows?



Single screen & 3 windows?



Single screen & 3 windows?



Single screen & 3 windows?

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-bordered window titled "rsk394 — bash — 69x24" displays a command-line interface. The command run is:

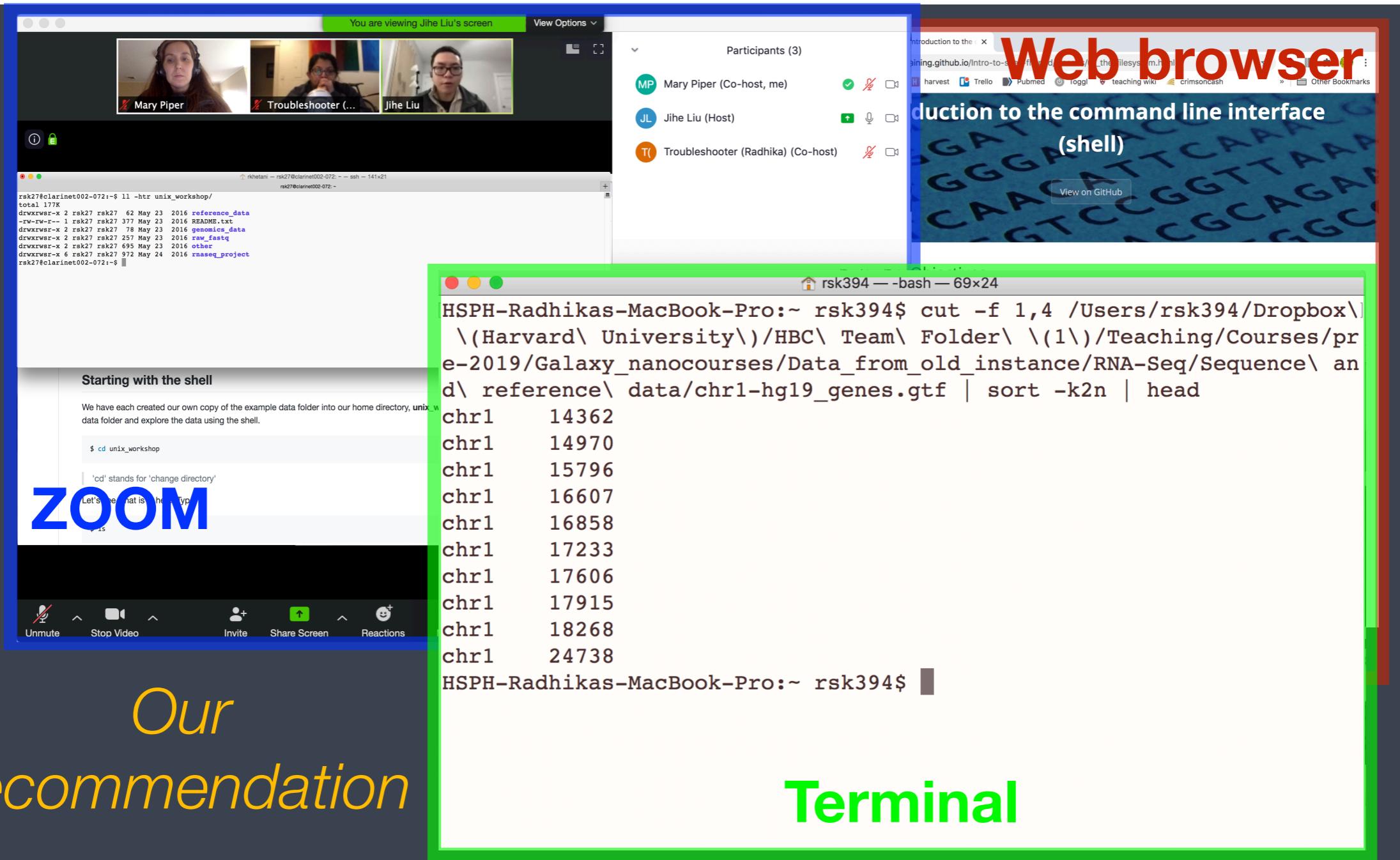
```
HSPH-Radhikas-MacBook-Pro:~ rsk394$ cut -f 1,4 /Users/rsk394/Dropbox\\(Harvard\\ University\\)/HBC\\ Team\\ Folder\\ \\(1\\)/Teaching/Courses/pre-2019/Galaxy_nanocourses/Data_from_old_instance/RNA-Seq/Sequence\\ and\\ reference\\ data/chrl-hg19_genes.gtf | sort -k2n | head
```

Output:

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

Our recommendation **Terminal**

Single screen & 3 windows?

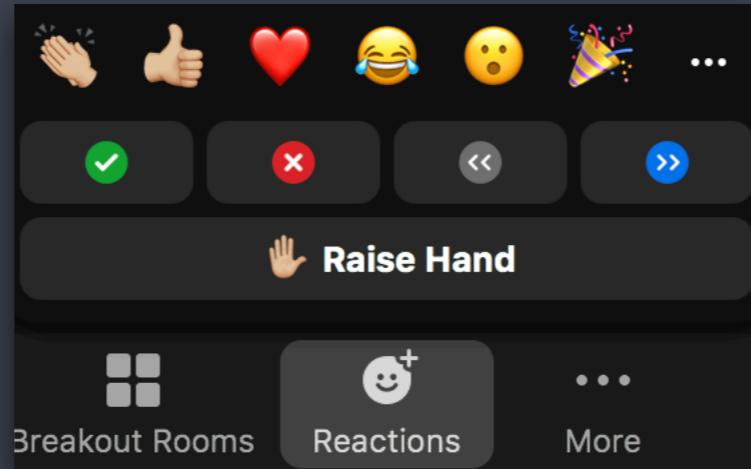


Odds and Ends

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

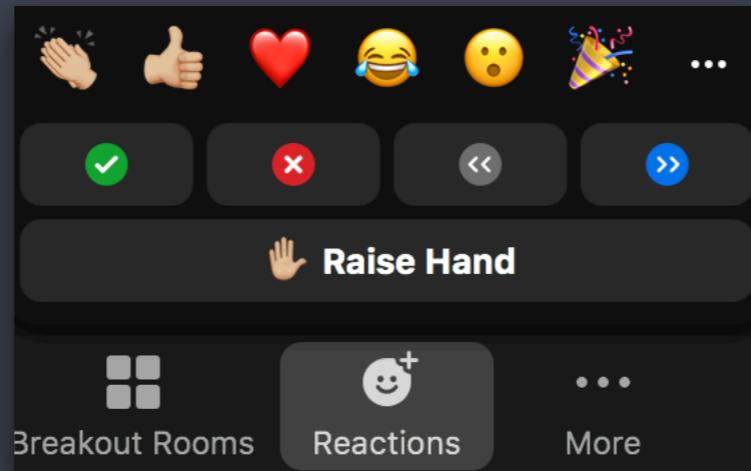
Odds and Ends

- ❖ 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 (contd.)

- ❖ Questions for the presenter?
 - Post the question in the Chat window OR
 -  when the presenter asks for questions
- ❖ Technical difficulties with software?
 - Start a *private* chat with the *Troubleshooter* with a description of the problem.



Thanks!

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

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Contact us!

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