

# Introduction to ChIP-seq (Part I)

Harvard Chan Bioinformatics Core  
in collaboration with  
HMS Research Computing

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



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

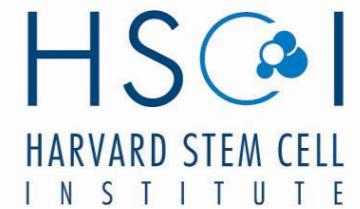
- RNA-seq analysis: bulk, single cell, small RNA
- ChIP-seq and ATAC-seq analysis
- Genome-wide methylation
- WGS, resequencing, exome-seq and CNV studies
- QC & analysis of gene expression arrays
- Functional enrichment analysis
- Grant support

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



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

NIEHS



# Training

We have divided our short workshops into 2 categories:

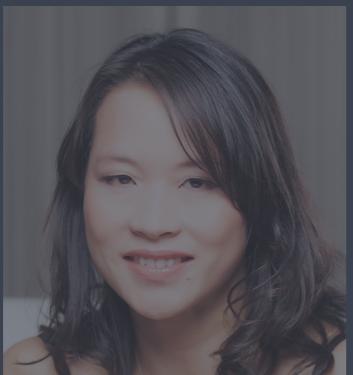
1. Basic Data Skills - No prior programming knowledge needed (no prerequisites)
2. Advanced Topics: Analysis of high-throughput sequencing (NGS) data - Certain “Basic” workshops required as prerequisites.

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

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

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





Shannan Ho Sui  
*Director*



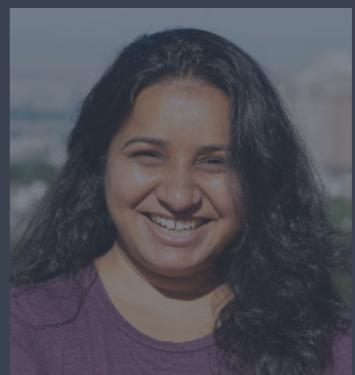
John Hutchinson  
*Associate Director*



Victor Barrera



Zhu Zhuo



Preetida Bhetariya



Radhika Khetani  
*Training Director*



Meeta Mistry



Mary Piper  
*Assoc. Training Director*



Jihe Liu



Will Gammerdinger



Maria Simoneau



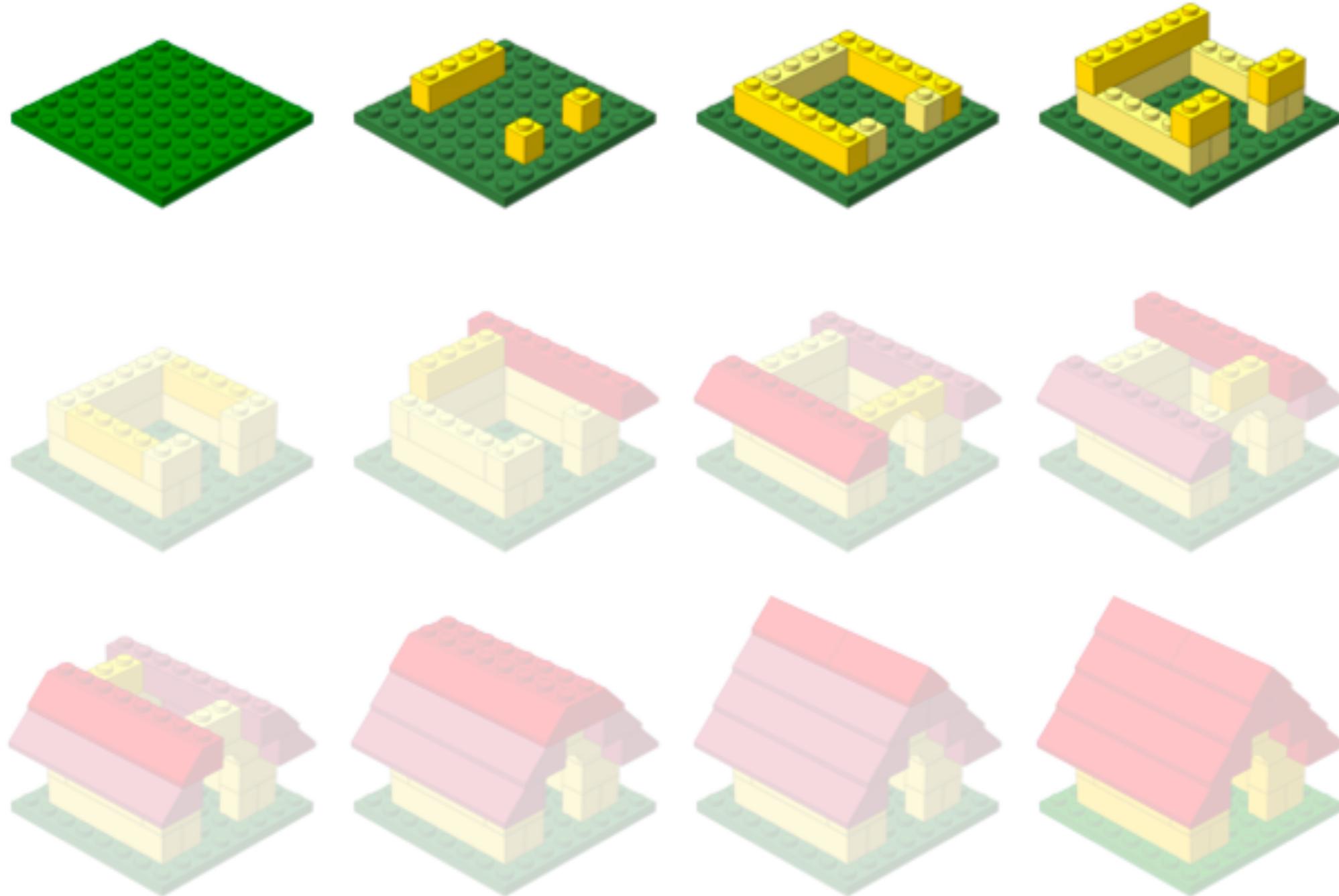
James Billingsley



Sergey Naumenko



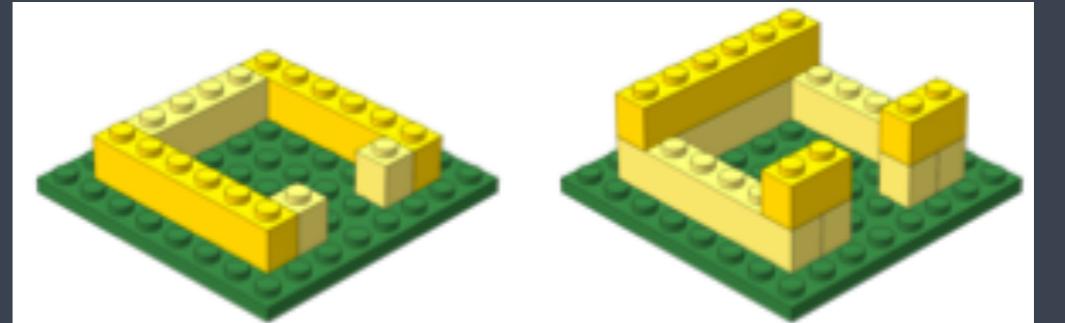
Peter Kraft  
*Faculty Advisor*



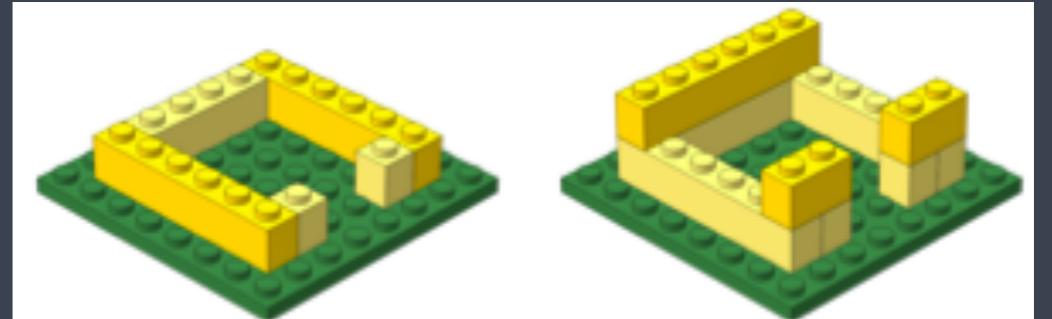
<http://anoved.net/tag/lego/page/3/>

Setting up to perform Bioinformatics analysis

# Setting up...

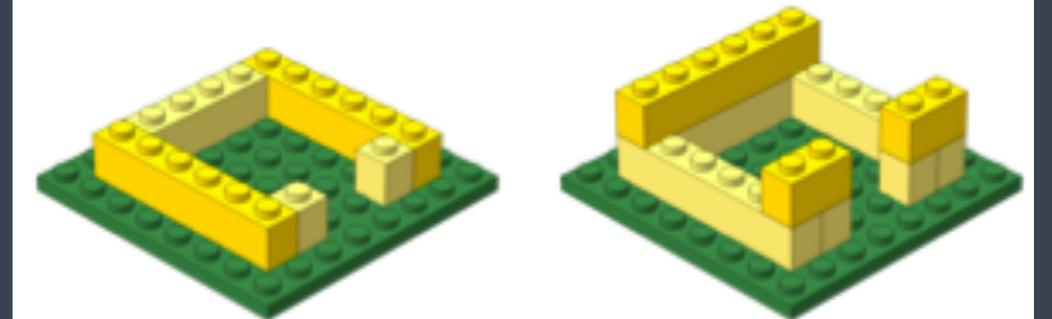


# Setting up...



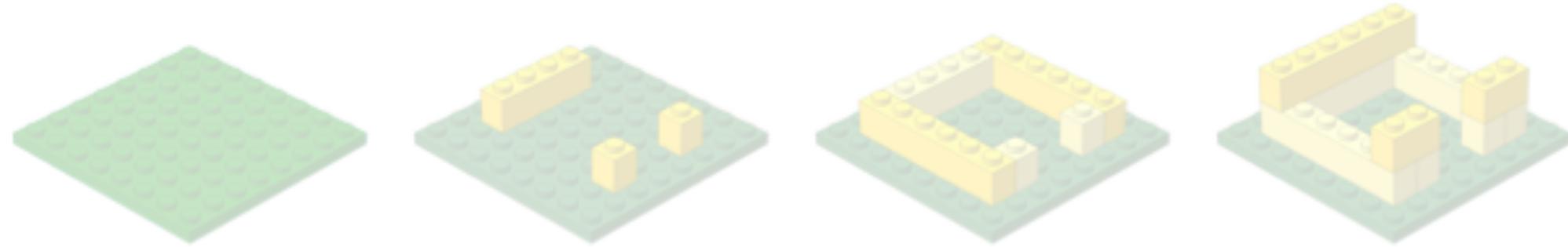
- ✓ Introduction to the command-line interface (shell, Unix, Linux)
  - Dealing with large data files
  - Performing bioinformatics analysis
    - Using tools
    - Accessing and using compute clusters

# Setting up...



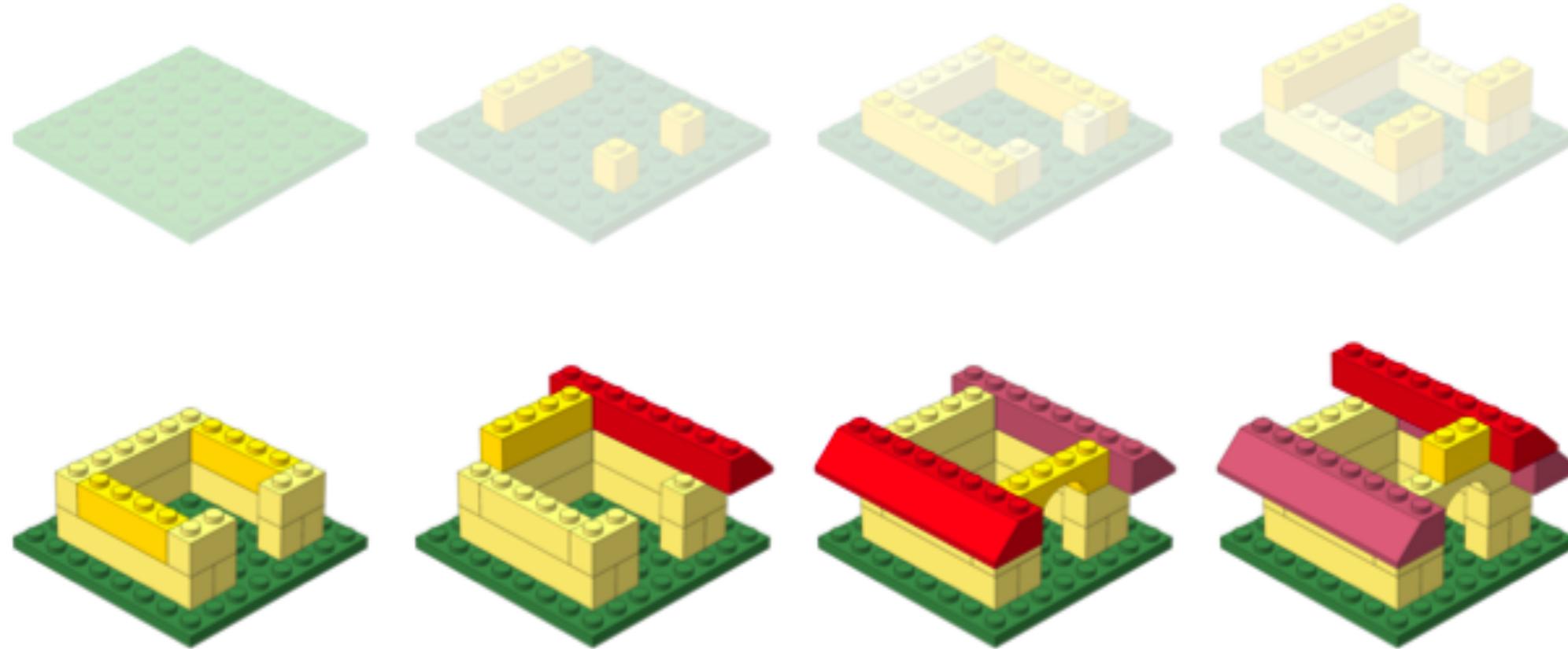
- ✓ Introduction to the command-line interface (shell, Unix, Linux)
  - Dealing with large data files
  - Performing bioinformatics analysis
    - Using tools
    - Accessing and using compute clusters
- ✓ R
  - Parsing and working with smaller BED files
  - Statistical analysis, e.g. differential binding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

# Workshop scope



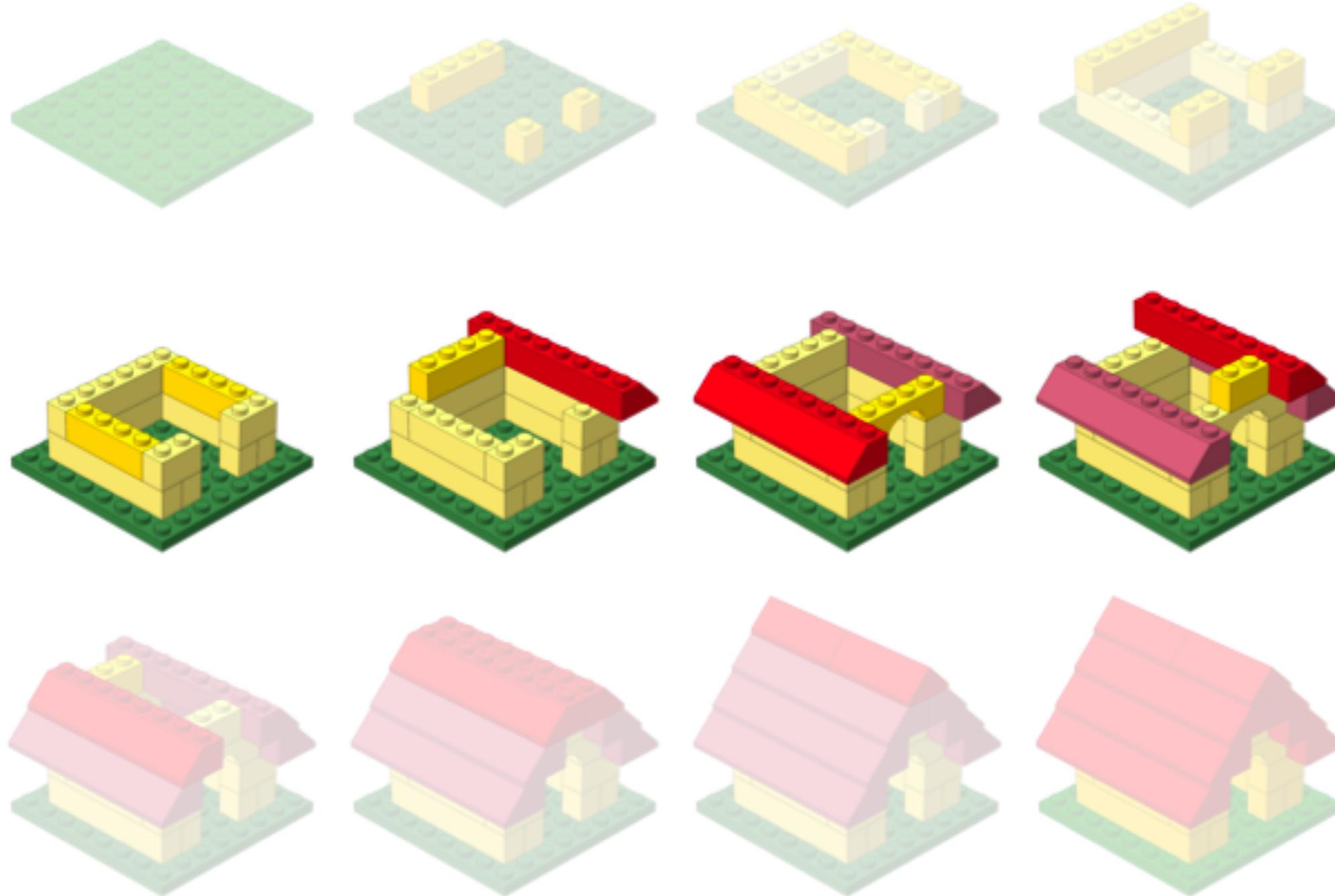
<http://anoved.net/tag/lego/page/3/>

Bioinformatics data analysis



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

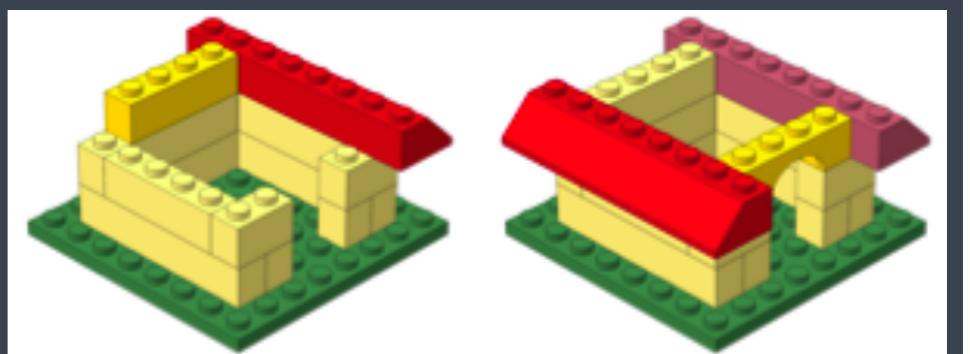
Bioinformatics data analysis



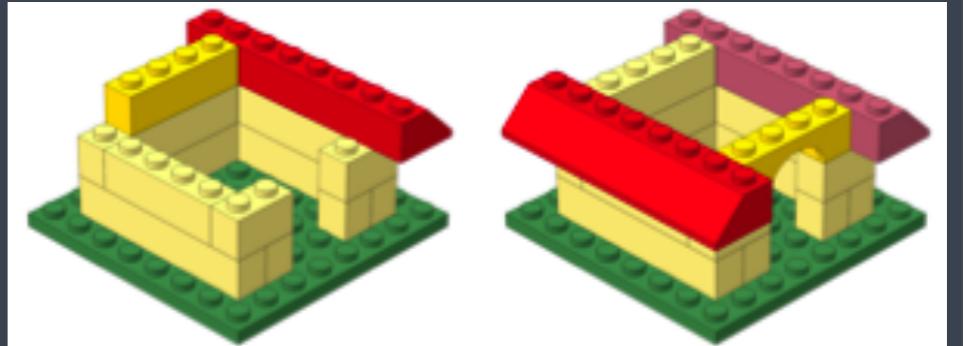
<http://anoved.net/tag/lego/page/3/>

Bioinformatics data analysis

# Learning Objectives

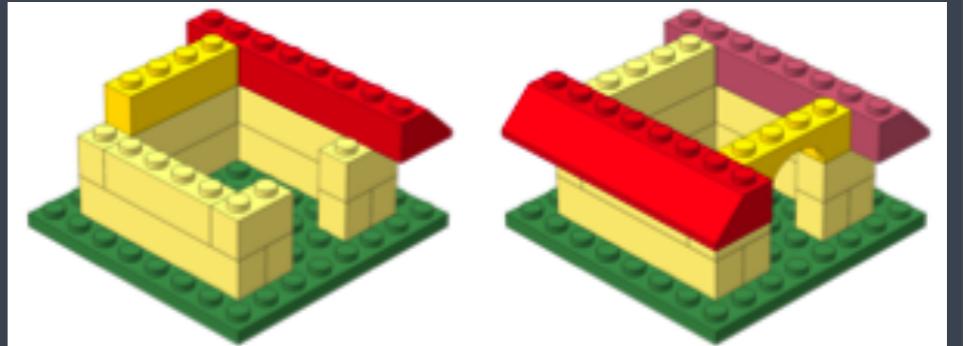


# Learning Objectives



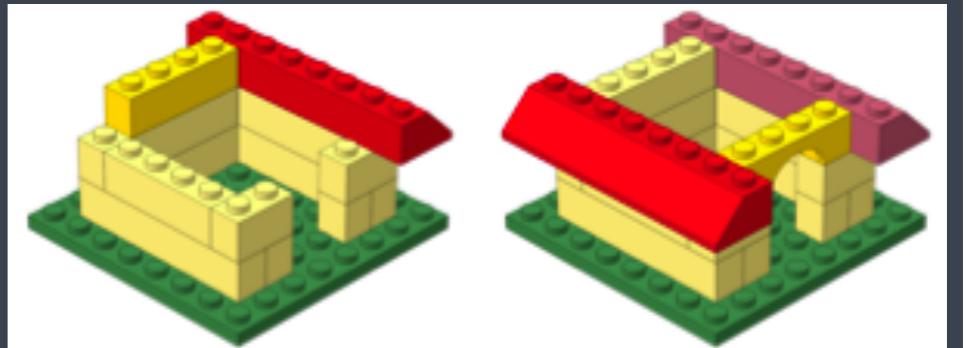
- ✓ Describe best practices for designing a good ChIP-seq experiment

# Learning Objectives



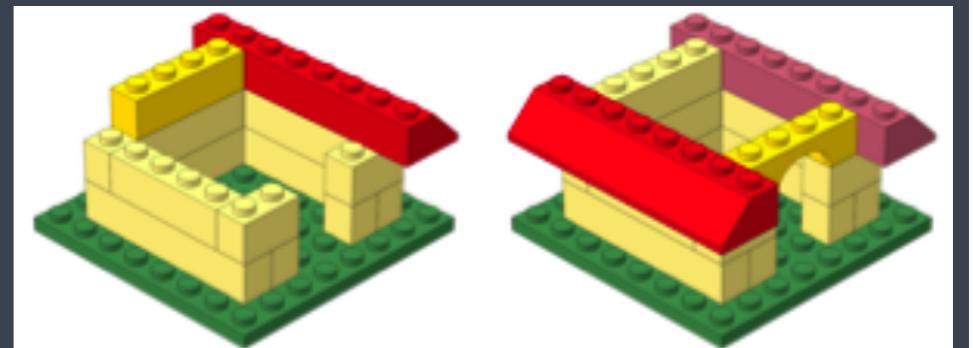
- ✓ Describe best practices for designing a good ChIP-seq experiment
- ✓ Describe steps in an ChIP-seq analysis workflow (from sequence data to peak calls)

# Learning Objectives



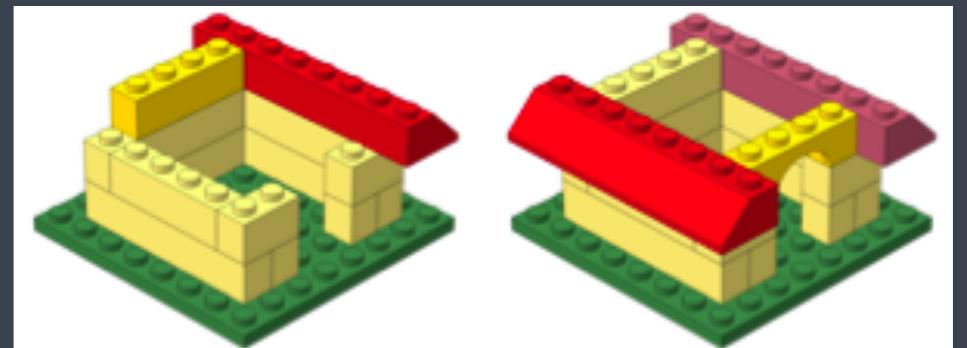
- ✓ Describe best practices for designing a good ChIP-seq experiment
- ✓ Describe steps in an ChIP-seq analysis workflow (from sequence data to peak calls)
- ✓ Learn how to handle various file formats encountered with ChIP-seq analysis

# Learning Objectives

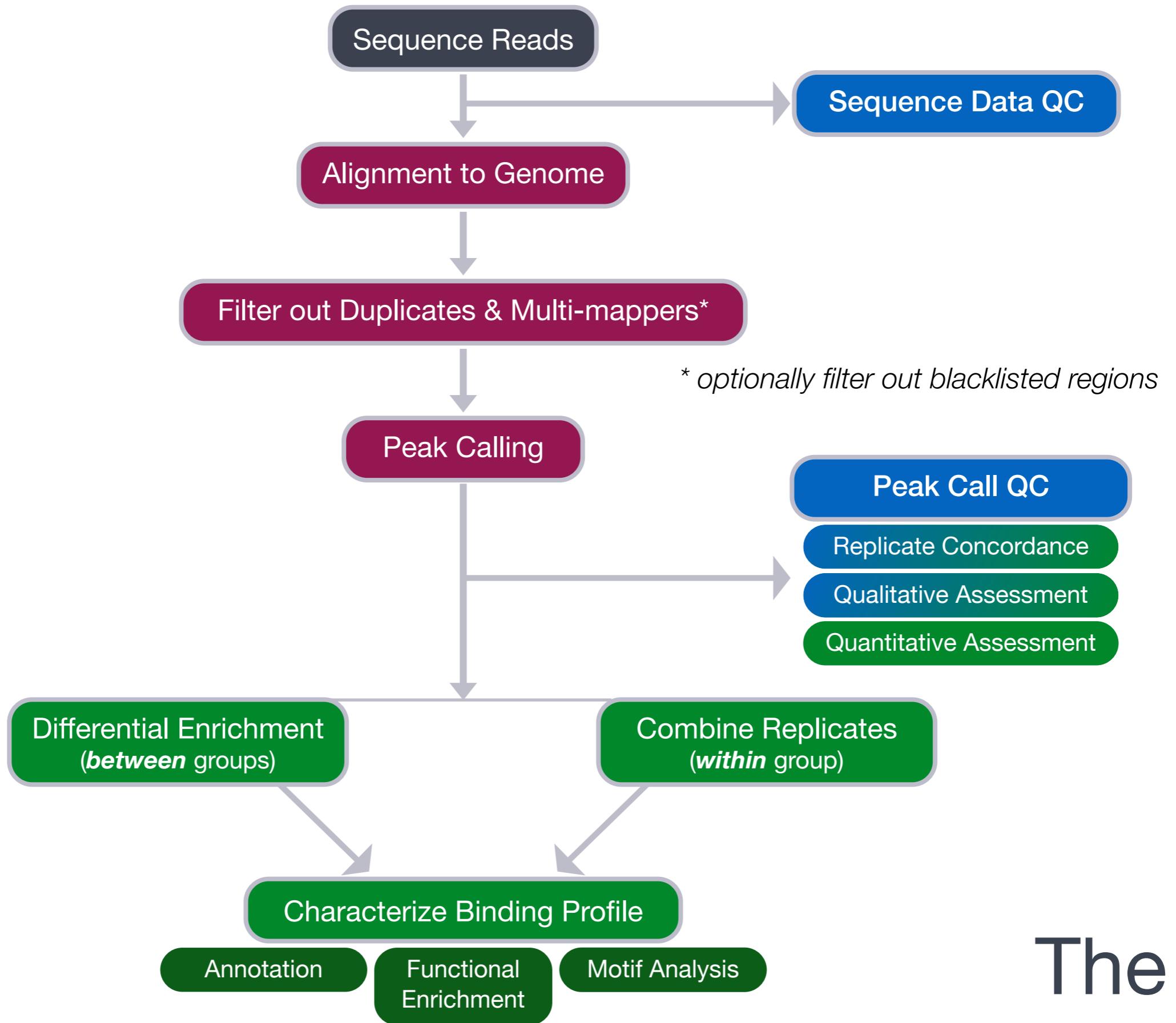


- ✓ Describe best practices for designing a good ChIP-seq experiment
- ✓ Describe steps in an ChIP-seq analysis workflow (from sequence data to peak calls)
- ✓ Learn how to handle various file formats encountered with ChIP-seq analysis
- ✓ Implement shell scripts on a high-performance compute cluster to perform the above steps

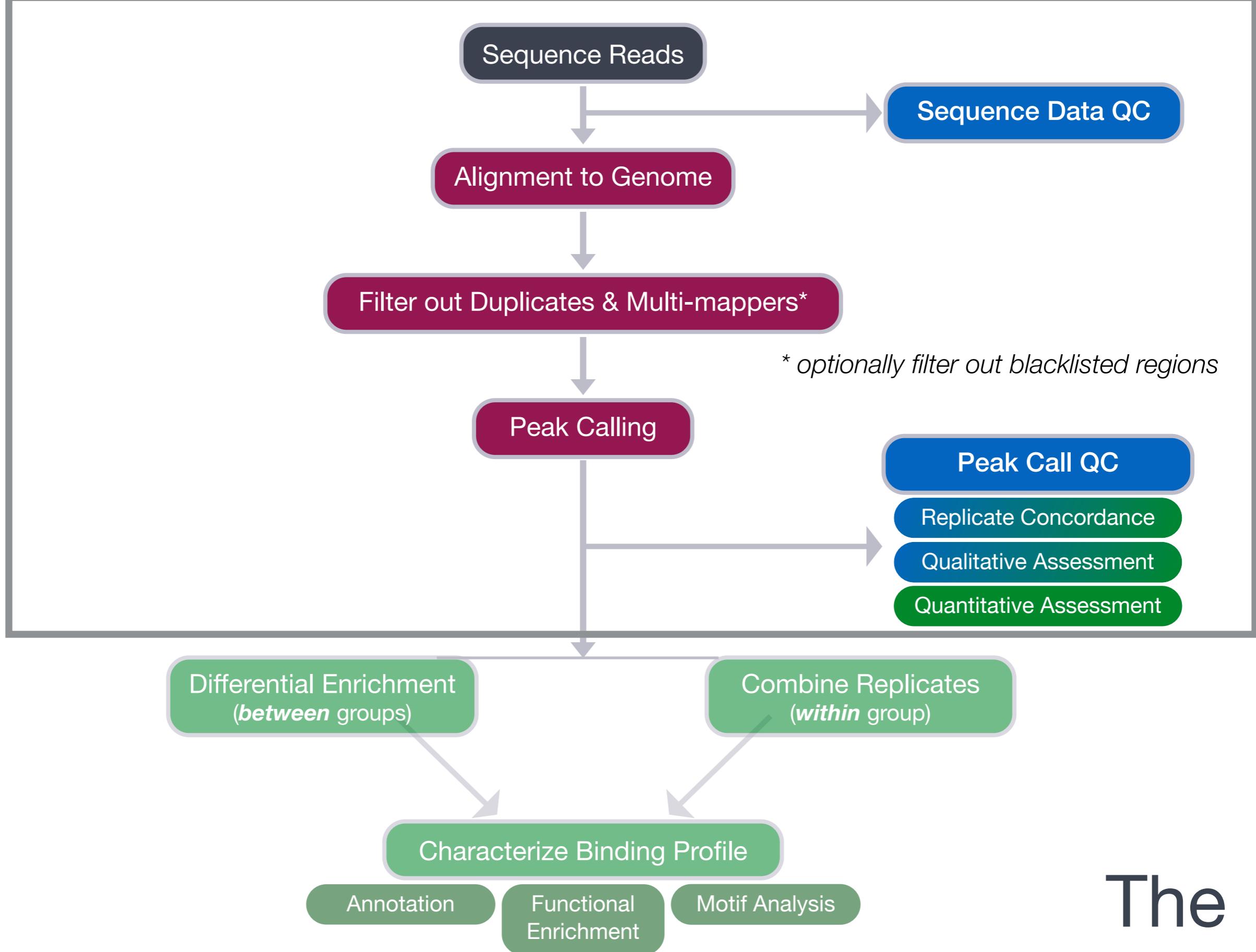
# Learning Objectives



- ✓ Describe best practices for designing a good ChIP-seq experiment
- ✓ Describe steps in an ChIP-seq analysis workflow (from sequence data to peak calls)
- ✓ Learn how to handle various file formats encountered with ChIP-seq analysis
- ✓ Implement shell scripts on a high-performance compute cluster to perform the above steps



# The Workflow



# The Workflow

Boxes in green represent parts of the workflow that will be covered in ChIP-seq Part II

# Logistics

# Course webpage

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

# Course schedule online

## Workshop Schedule

**NOTE:** The *Basic Data Skills* [Introduction to the command-line interface](#) workshop is a prerequisite.

### Pre-reading:

- Please **study the contents** and **work through all the exercises** within the following lessons:
  - [Shell basics review](#)
  - [Best Practices in Research Data Management \(RDM\)](#)

### Day 1

Time	Topic	Instructor
09:30 - 09:45	Workshop Introduction	Meeta
09:45 - 11:00	Introduction to ChIP-seq	Dr. Shannan Ho Sui
11:00- 11:05	Break	
11:05 - 11:50	Working in an HPC environment	Radhika

# Course materials online



## FastQC for quality assessment

[View on GitHub](#)

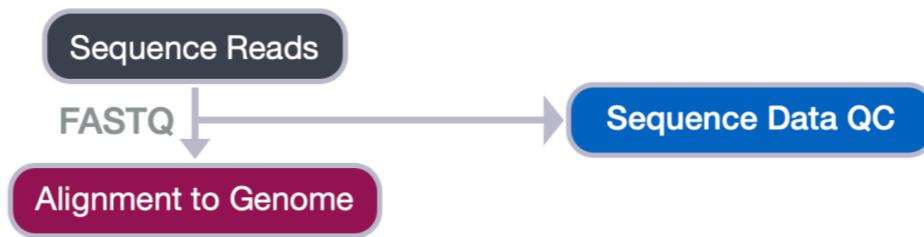
Contributors: Mary Piper, Radhika Khetani, Jihe Liu, Will Gammerdinger

Approximate time:

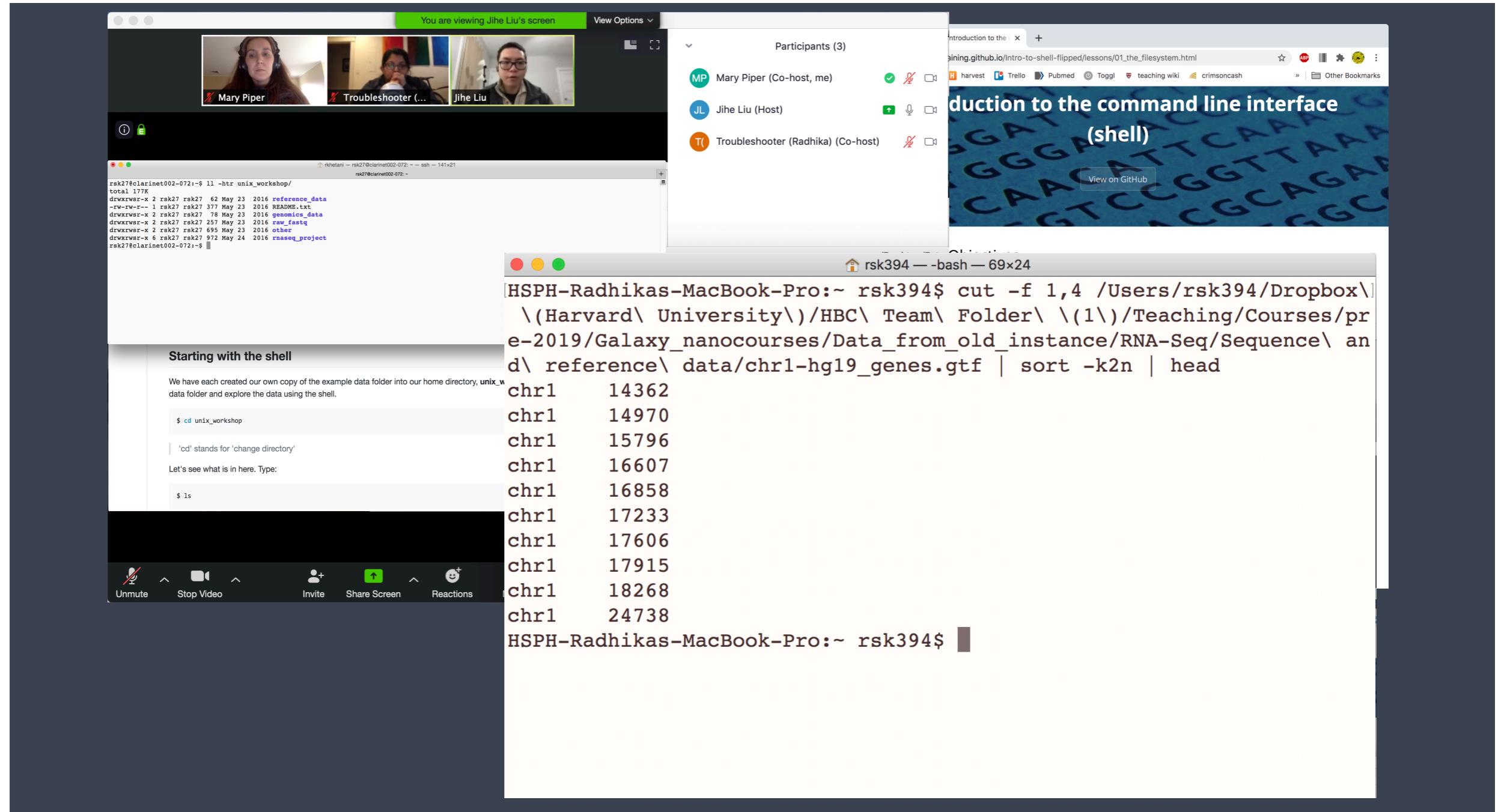
### Learning Objectives

- Explain the components of a FASTQ file
- Evaluate the quality of the sequencing data using FastQC

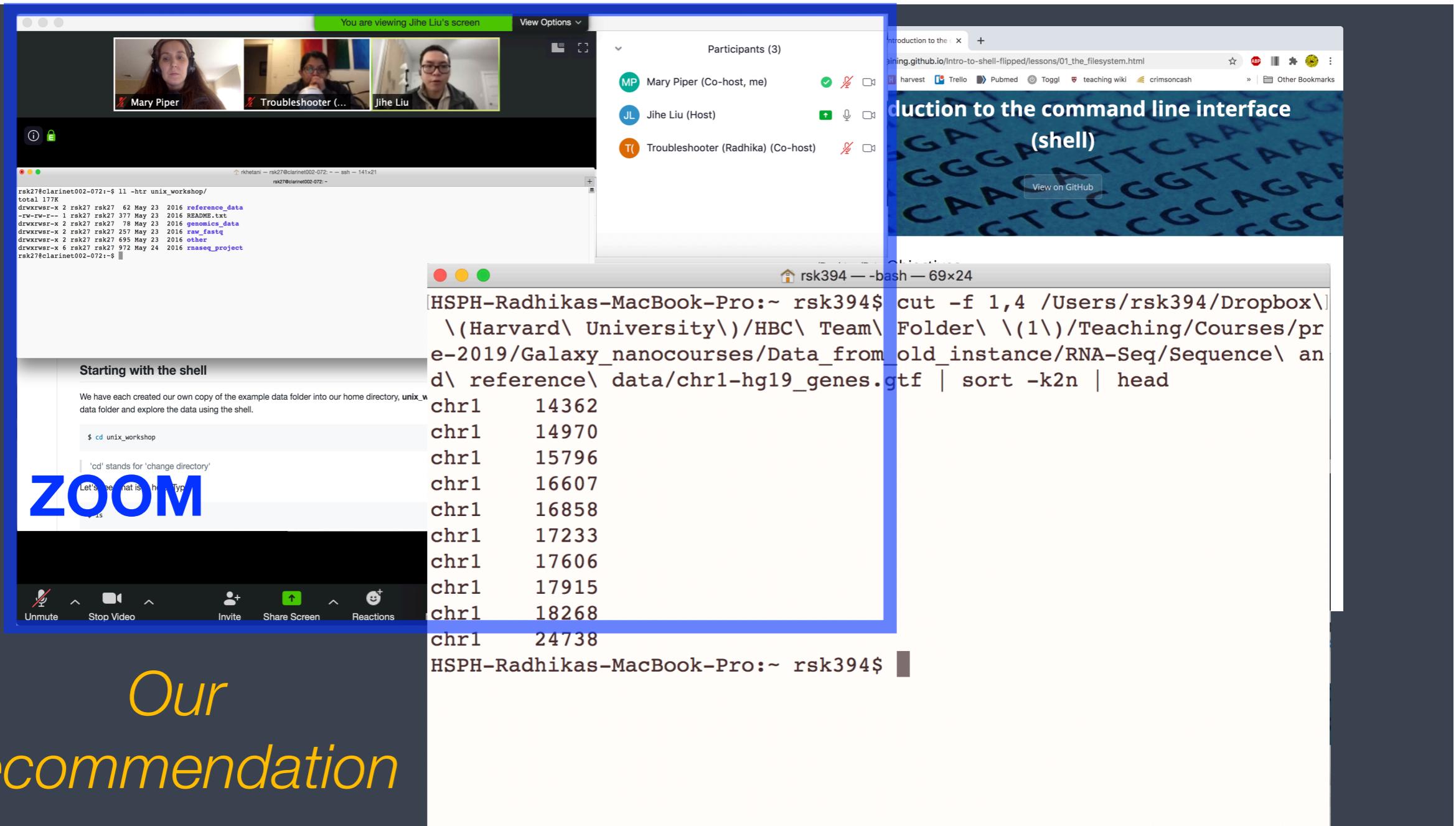
### Quality control of sequence reads



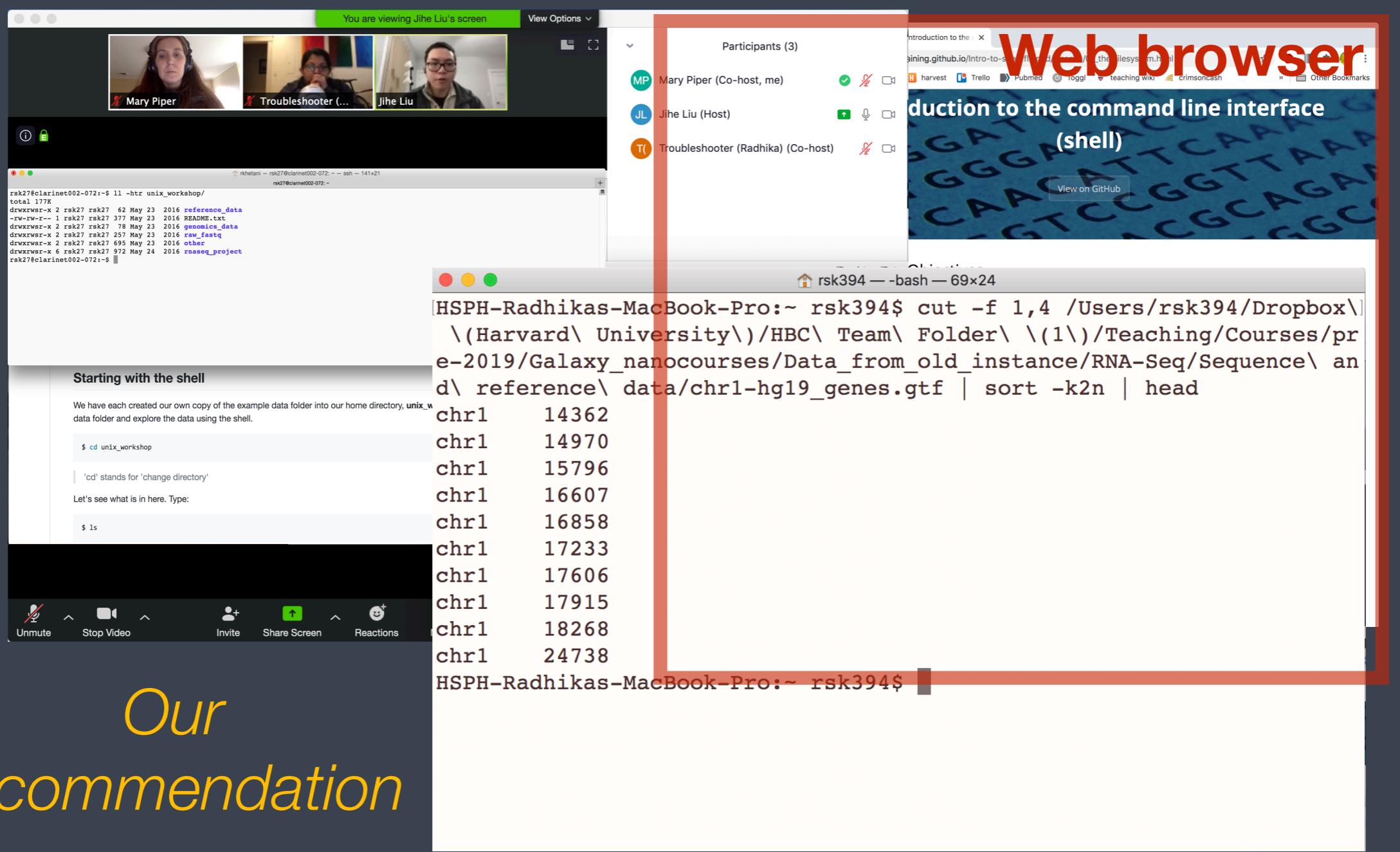
# Single screen & 3 windows?



# Single screen & 3 windows?



# Single screen & 3 windows?



# Single screen & 3 windows?

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

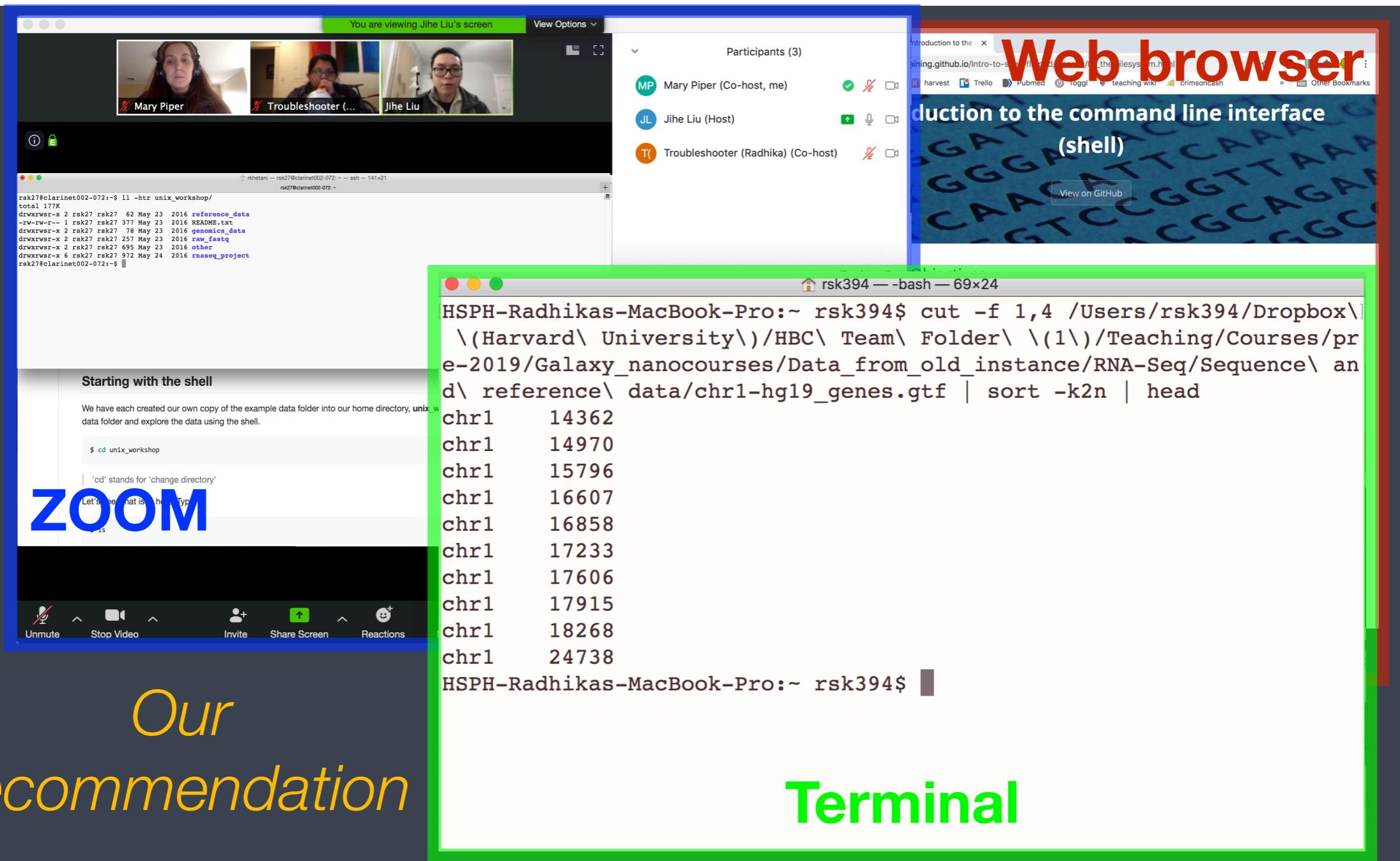
- Video Feed:** Shows three participants: Mary Piper, Troubleshooter (Radhika), and Jihe Liu.
- Participants List:** Shows three participants: Mary Piper (Co-host, me), Jihe Liu (Host), and Troubleshooter (Radhika) (Co-host).
- Terminal Session:** A green-highlighted window showing a command-line interface. The command run is:

```
rsk394 — bash — 69x24
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/chr1-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
```

*Our recommendation*

**Terminal**

# Single screen & 3 windows?

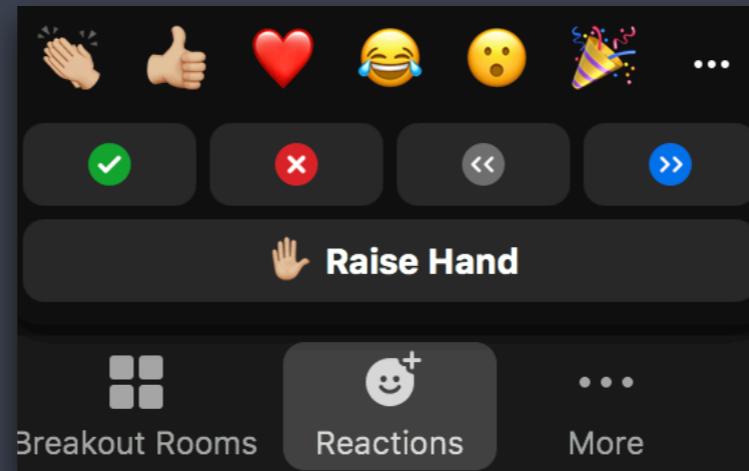


# Odds and Ends (1/2)

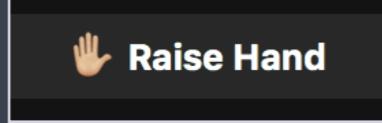
- ❖ Quit/minimize all applications that are not required for class

# 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**)

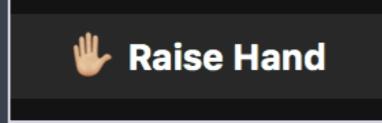


# Odds and Ends (2/2)

- ❖ Questions for the presenter?
  - Post the question in the Chat window OR
  -  when the presenter asks for questions
  - Let the Moderator know

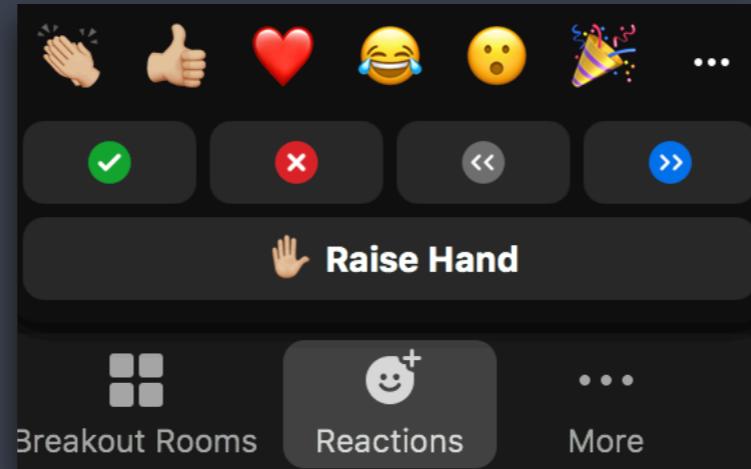
# Odds and Ends (2/2)

- ❖ 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 private chat with the Troubleshooter with a description of the problem.



# Thanks!

- Kathleen Keating and Andy Bergman from HMS-RC
- [Data Carpentry](#)

*These materials have been developed by members of the teaching team at the [Harvard Chan Bioinformatics Core \(HBC\)](#). These are open access materials distributed under the terms of the [Creative Commons Attribution license \(CC BY 4.0\)](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.*



# Contact us!

*HBC training team:* [hbctraining@hsph.harvard.edu](mailto:hbctraining@hsph.harvard.edu)

*O2 (HMS-RC):* [rchelp@hms.harvard.edu](mailto:rchelp@hms.harvard.edu)

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

## Twitter

*HBC:* @bioinfocore

*HMS-RC:* @hms\_rc