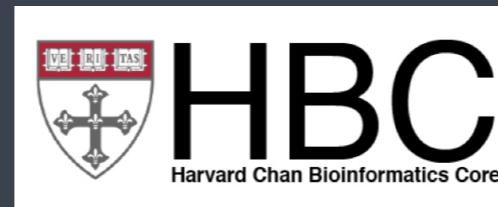


Introduction to Single-cell RNA-seq analysis

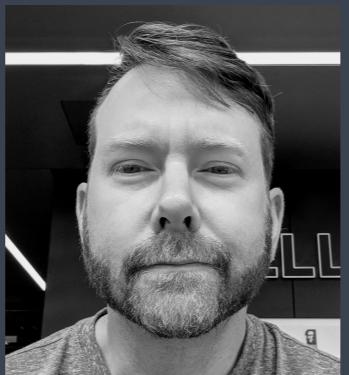
Harvard Chan Bioinformatics Core



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



Shannan Ho Sui
Director



John Hutchinson
Associate Director



Victor Barrera



Rory Kirchner



Zhu Zhuo



Preetida Bhetariya



Meeta Mistry



Mary Piper



Jihe Liu



Radhika Khetani
Training Director



Ilya Sytchev



James Billingsley



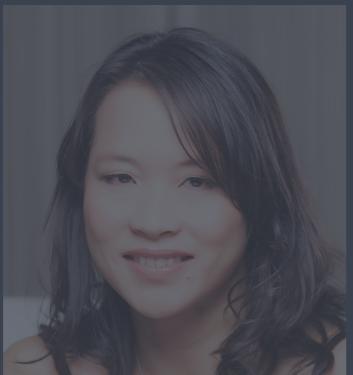
Sergey Naumenko



Joon Yoon



Peter Kraft
Faculty Advisor



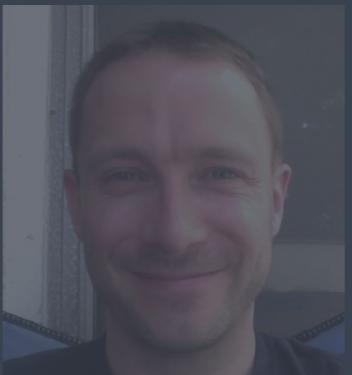
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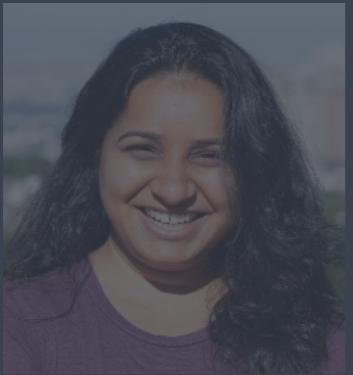
Victor Barrera



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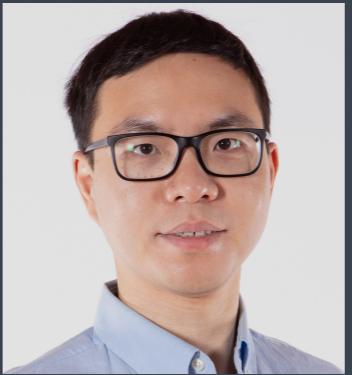
Preetida Bhetariya



Meeta Mistry



Mary Piper



Jihe Liu



Radhika Khetani
Training Director



Ilya Sytchev



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/>



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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/>



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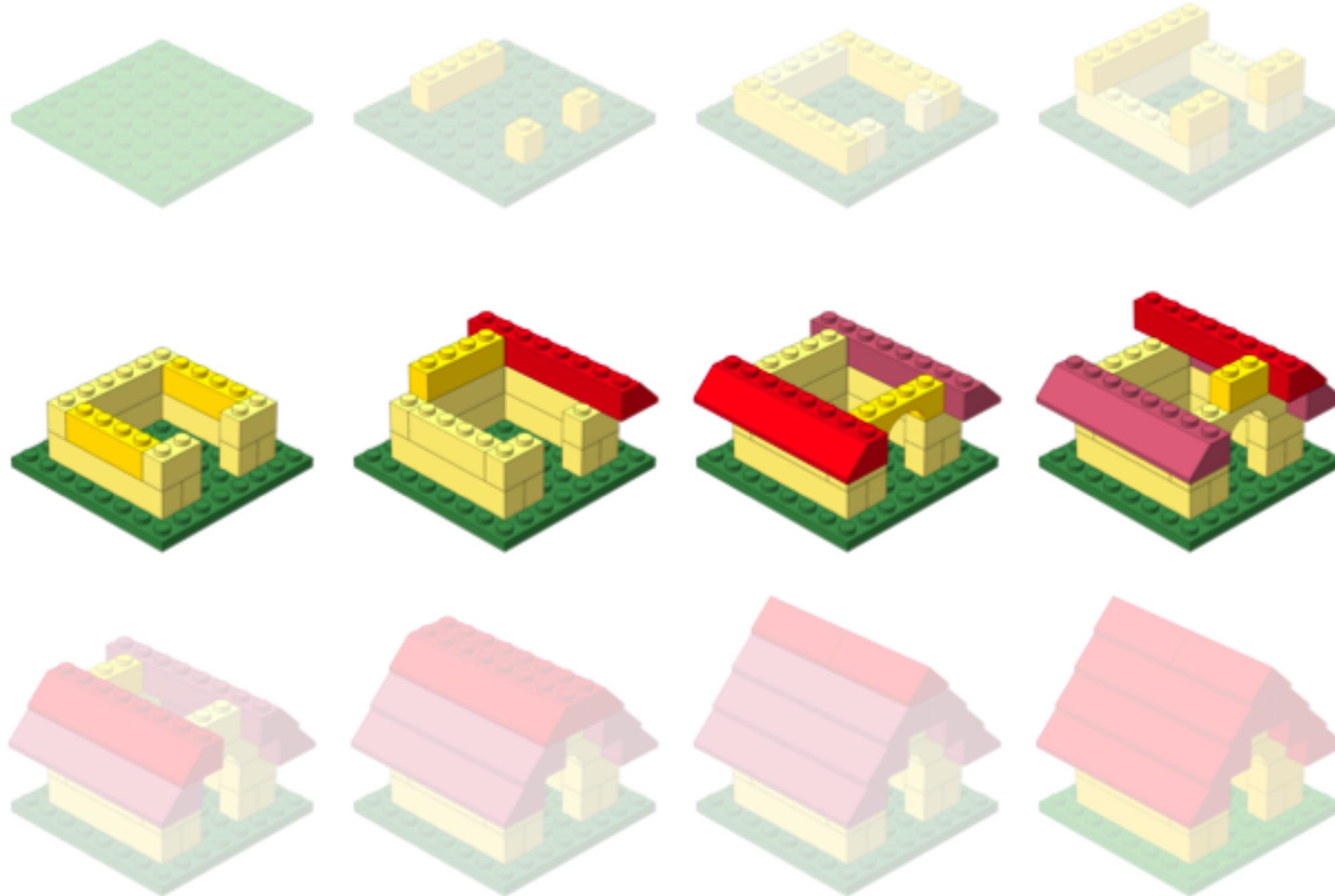
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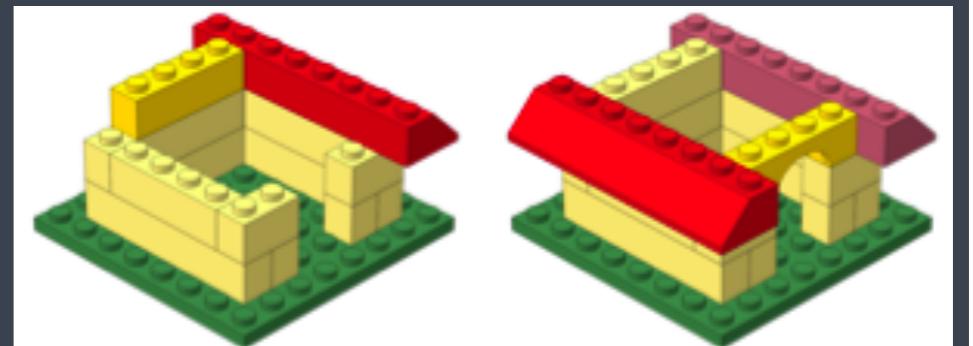
Workshop scope



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

Bioinformatics data analysis

Learning Objectives



- ✓ Describe best practices for designing a Single-cell RNA-seq experiment
- ✓ Describe steps in a Single-cell RNA-seq analysis workflow.
- ✓ Use Seurat and associated tools to perform analysis of single-cell expression data, including data filtering, QC, integration, clustering, and marker identification

Logistics

Course webpage

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

Course materials online

Introduction to Single-cell RNA-seq

[View on GitHub](#)

Approximate time: 90 minutes

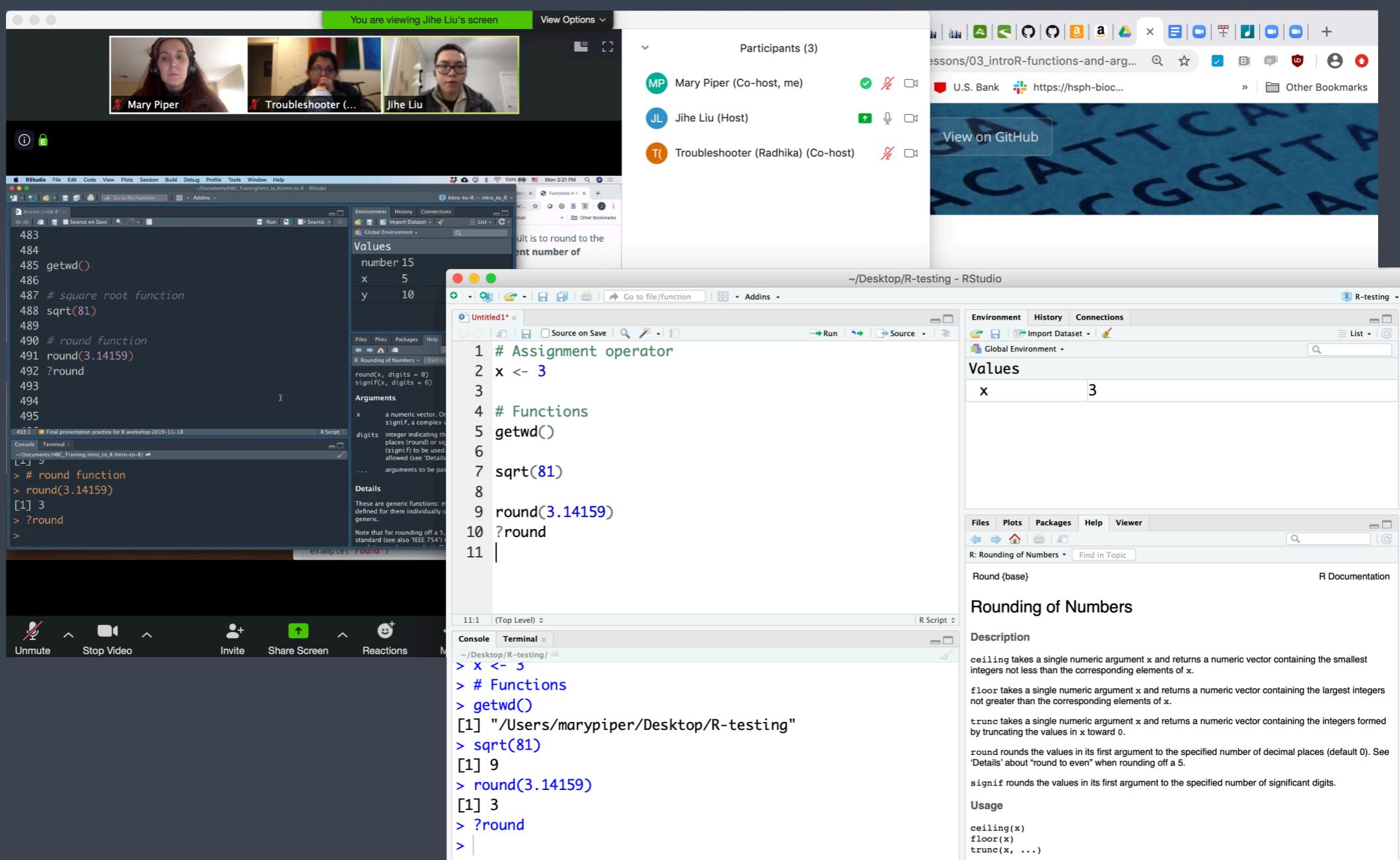
Learning Objectives:

- Understand how to bring in data from single-cell RNA-seq experiments
- Construct QC metrics and associated plots to visually explore the quality of the data
- Evaluate the QC metrics and set filters to remove low quality cells

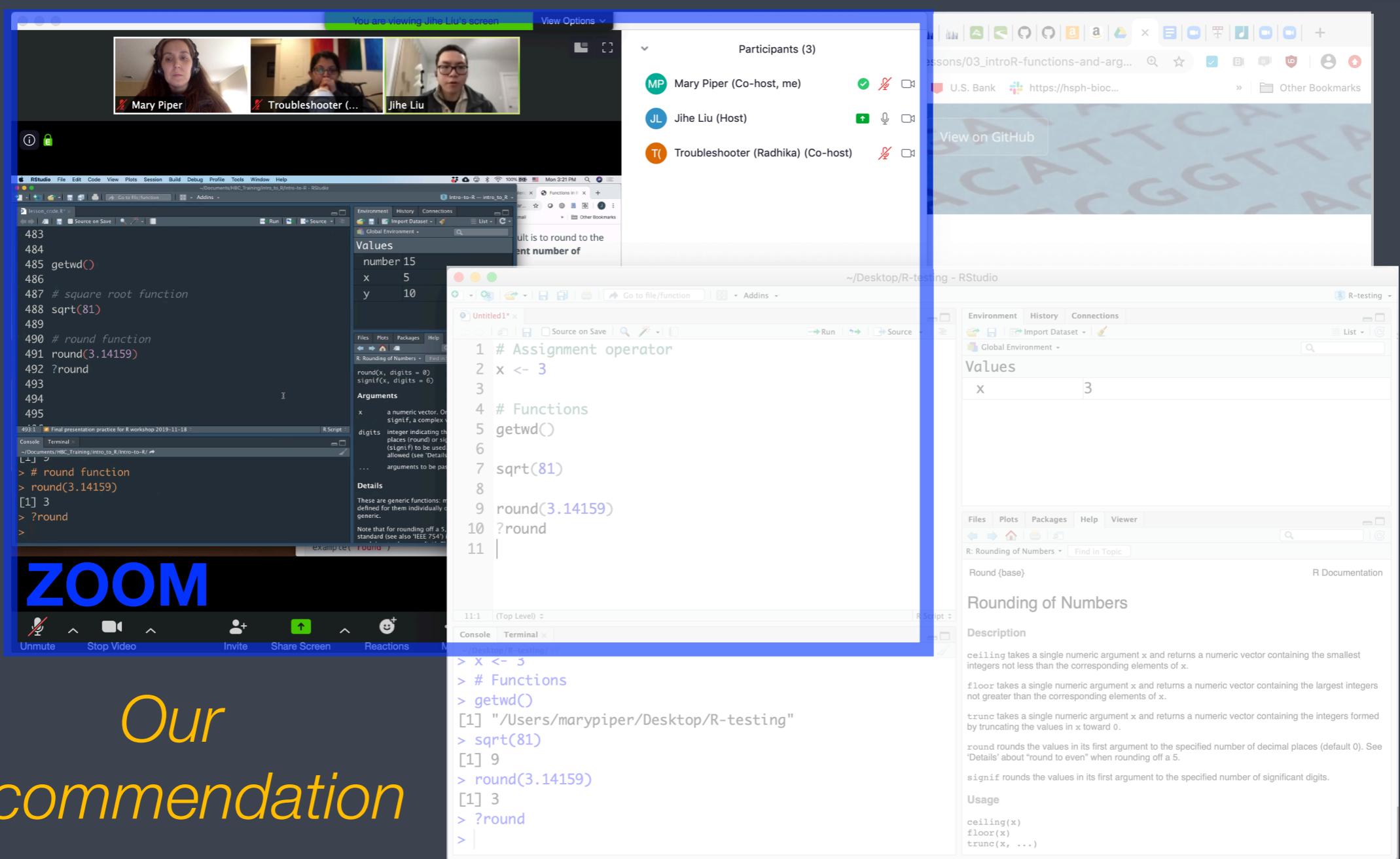
Single-cell RNA-seq: Quality control

```
graph TD; A[Sequence reads] --> B[Generate count matrix]; B --> C["QC: Filter cells using quality metrics"]
```

Single screen & 3 windows?

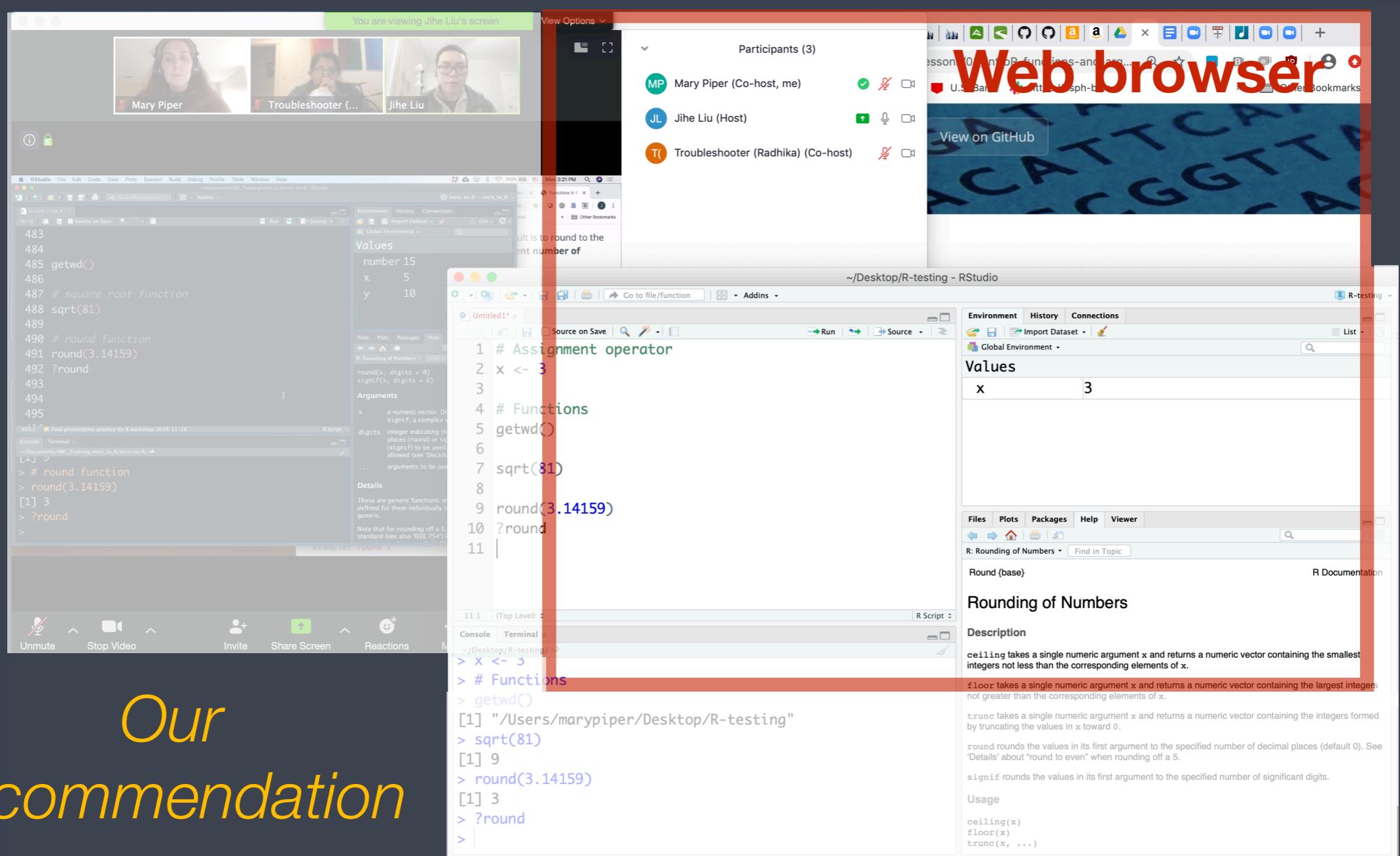


Single screen & 3 windows?



*Our
recommendation*

Single screen & 3 windows?



*Our
recommendation*

Single screen & 3 windows?

The screenshot shows a video conference interface with three windows:

- Top Left Window:** A video feed showing three participants: Mary Piper, Troubleshooter (Radhika), and Jihe Liu.
- Middle Left Window:** An RStudio session titled "intro_to_R -- intro_to_R". It contains the following R code:

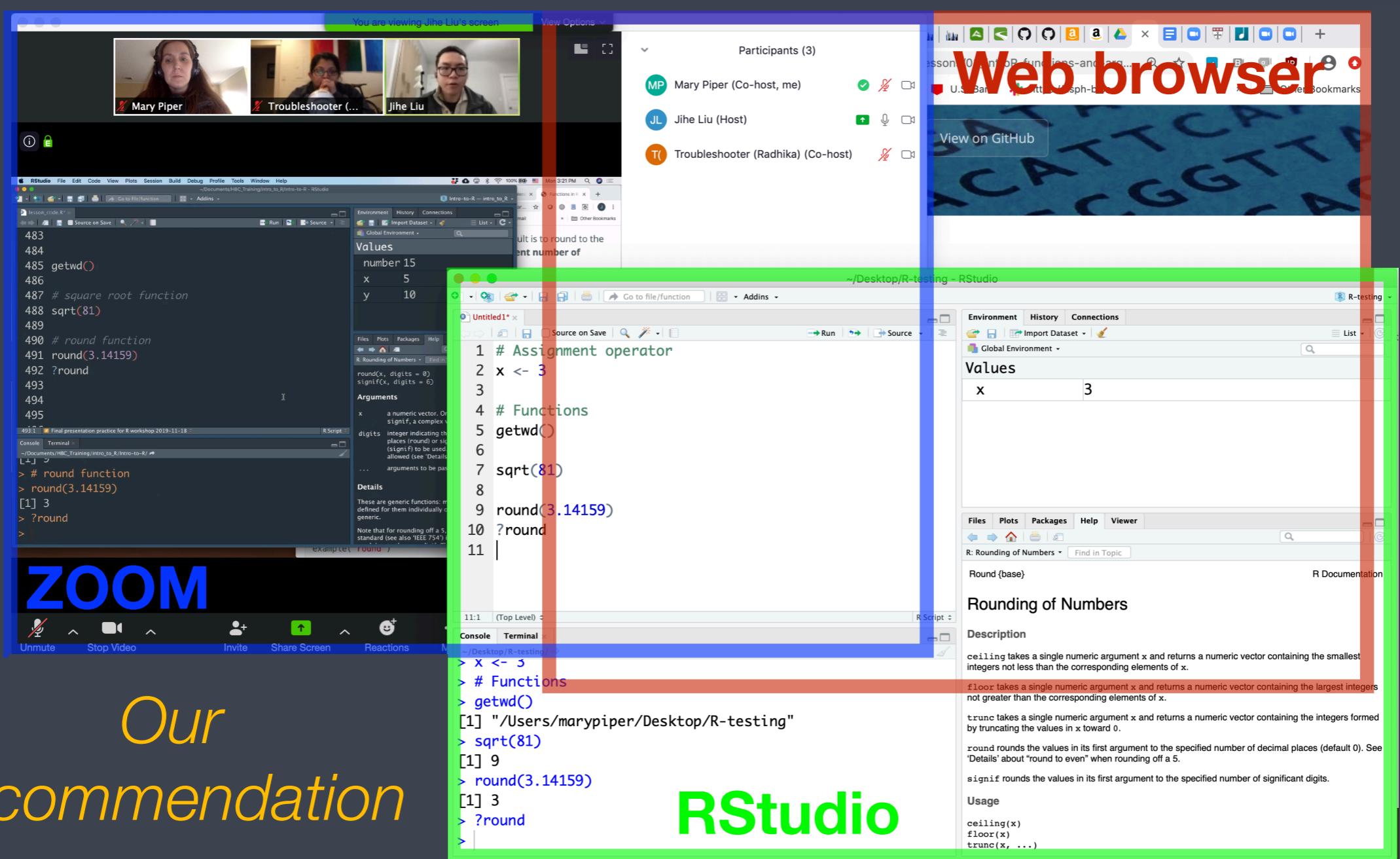
```
483  
484  
485 getwd()  
486  
487 # square root function  
488 sqrt(81)  
489  
490 # round function  
491 round(3.14159)  
492 ?round  
493  
494  
495
```
- Bottom Left Window:** An RStudio session titled "Untitled1*". It contains the following R code:

```
1 # Assignment operator  
2 x <- 3  
3  
4 # Functions  
5 getwd()  
6  
7 sqrt(81)  
8  
9 round(3.14159)  
10 ?round  
11
```
- Top Right Window:** A web browser window showing a GitHub page for "introR-functions-and-args".
- Middle Right Window:** An RStudio session titled "~/Desktop/R-testing - RStudio". It contains the following R code:

```
11:1 (Top Level) >  
Console Terminal x  
~/Desktop/R-testing/ >  
> x <- 3  
> # Functions  
> getwd()  
[1] "/Users/marypiper/Desktop/R-testing"  
> sqrt(81)  
[1] 9  
> round(3.14159)  
[1] 3  
> ?round  
>
```
- Bottom Right Window:** A detailed view of the "round" function documentation from the R documentation website.

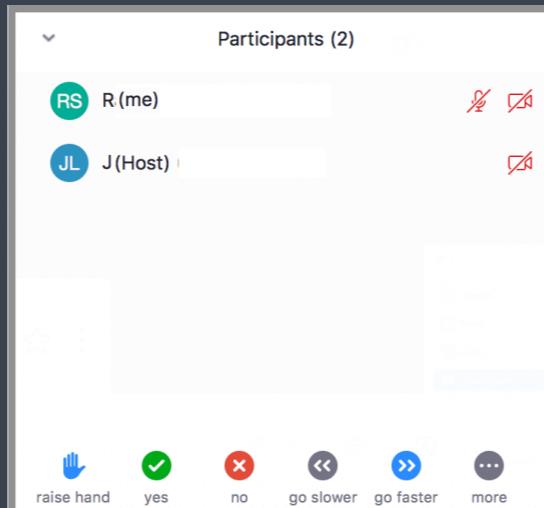
Our recommendation: RStudio

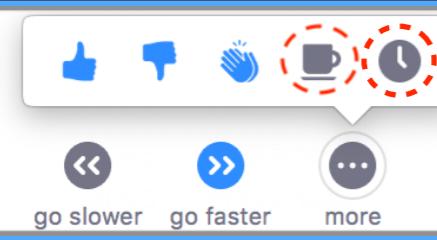
Single screen & 3 windows?



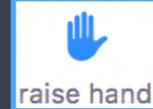
Odds and Ends (1/2)

- ❖ Quit/minimize all applications that are not required for class
- ❖ Click on “Participants” to open that panel in Zoom



- ▶  = "agree", "I'm all set" (equivalent to a **green post-it**)
- ▶  = "disagree", "I need help" (equivalent to a **red post-it**)
- ▶  If you are away from the computer use the coffee cup or clock icon

Odds and Ends (2/2)

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

Contact us!

Training team  : hbctraining@hsph.harvard.edu

Consulting  : bioinformatics@hsph.harvard.edu

 [@bioinfocore](https://twitter.com/bioinfocore)