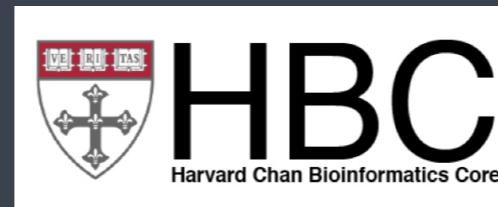


# Introduction to Single-cell RNA-seq analysis

Harvard Chan Bioinformatics Core



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



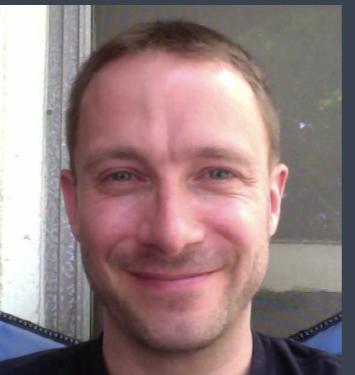
Shannan Ho Sui  
*Director*



John Hutchinson  
*Associate Director*



Victor Barrera



Rory Kirchner



Zhu Zhuo



Preetida Bhetariya



Meeta Mistry



Mary Piper  
*Assoc. Training Director*



Jihe Liu



Radhika Khetani  
*Training Director*



Maria Simoneau  
*Project coordinator*



James Billingsley



Sergey Naumenko



Joon Yoon



Peter Kraft  
*Faculty Advisor*



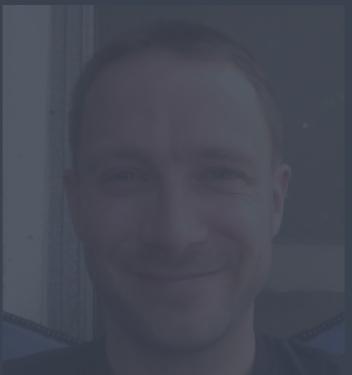
Shannan Ho Sui  
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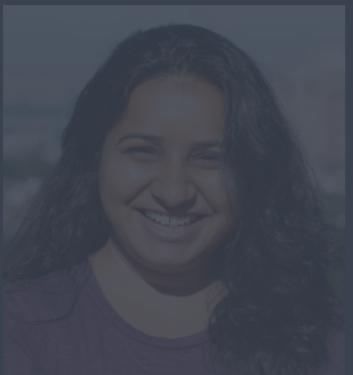
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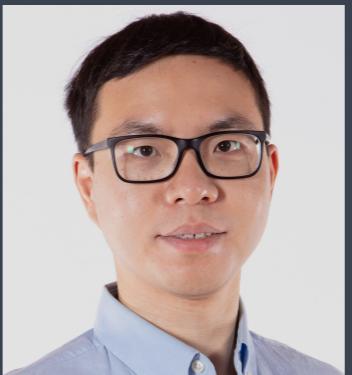
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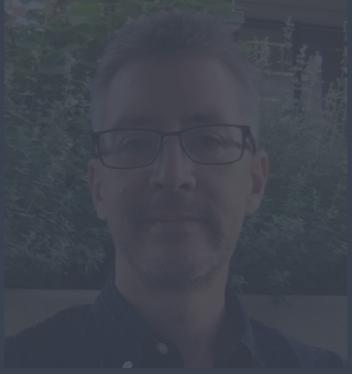
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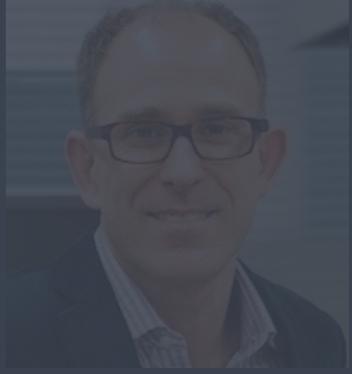
James Billingsley



Sergey Naumenko



Joon Yoon



Peter Kraft  
*Faculty Advisor*

# Consulting

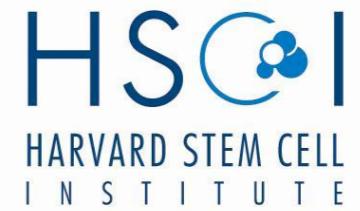
- RNA-seq analysis: bulk, single cell, small RNA
- ChIP-seq and ATAC-seq analysis
- Genome-wide methylation
- WGS, resequencing, exome-seq and CNV studies
- QC & analysis of gene expression arrays
- Functional enrichment analysis
- Grant support

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



**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/>



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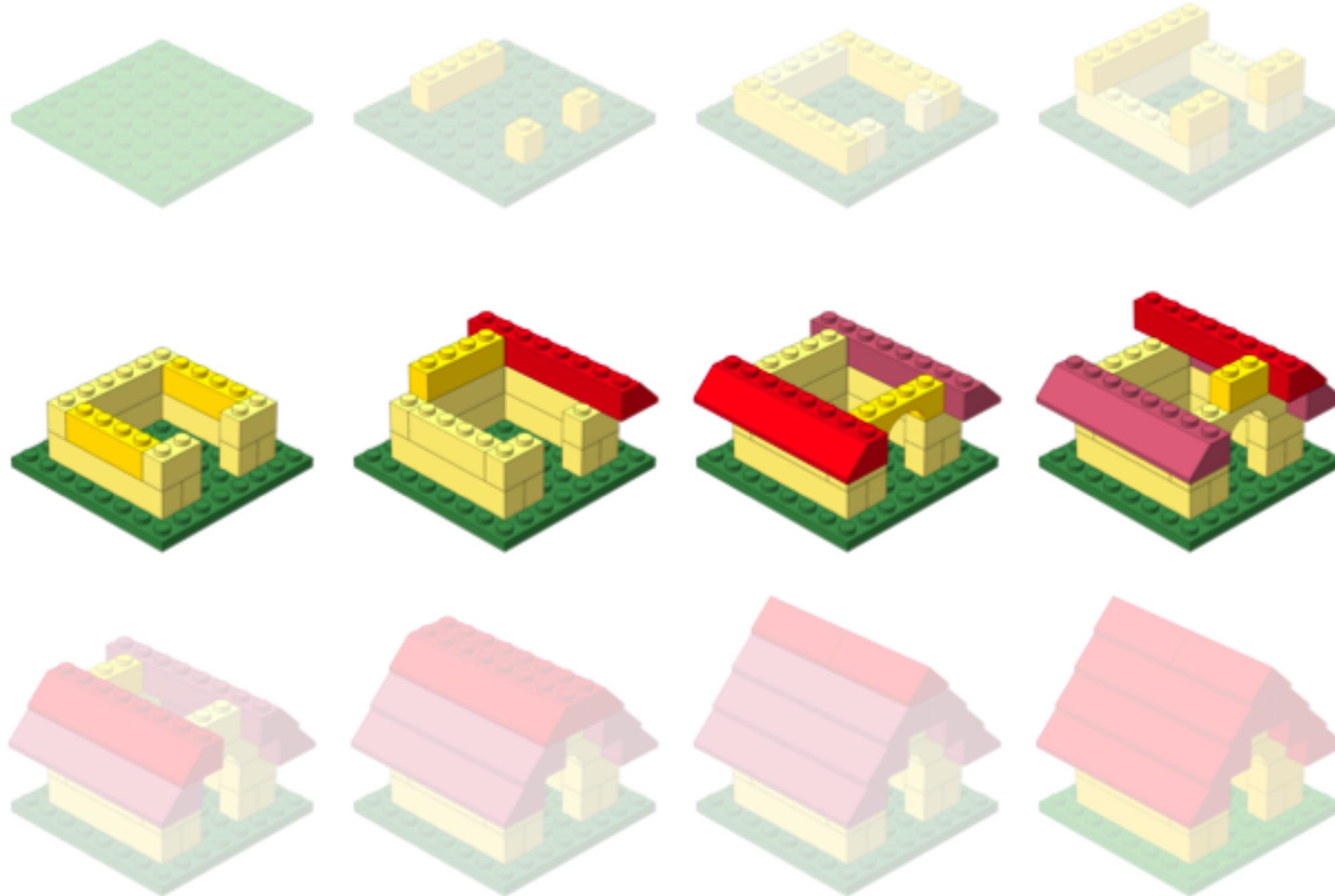
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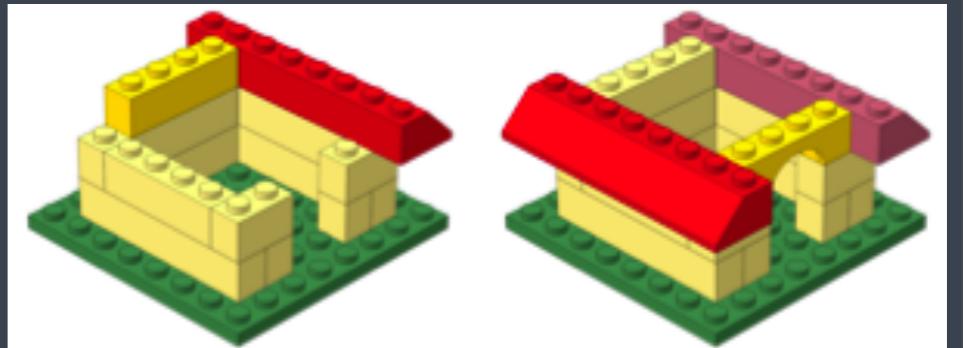
# Workshop scope



<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
- ✓ Understand practical considerations for performing scRNA-seq, rather than in-depth exploration of algorithm theory

# 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

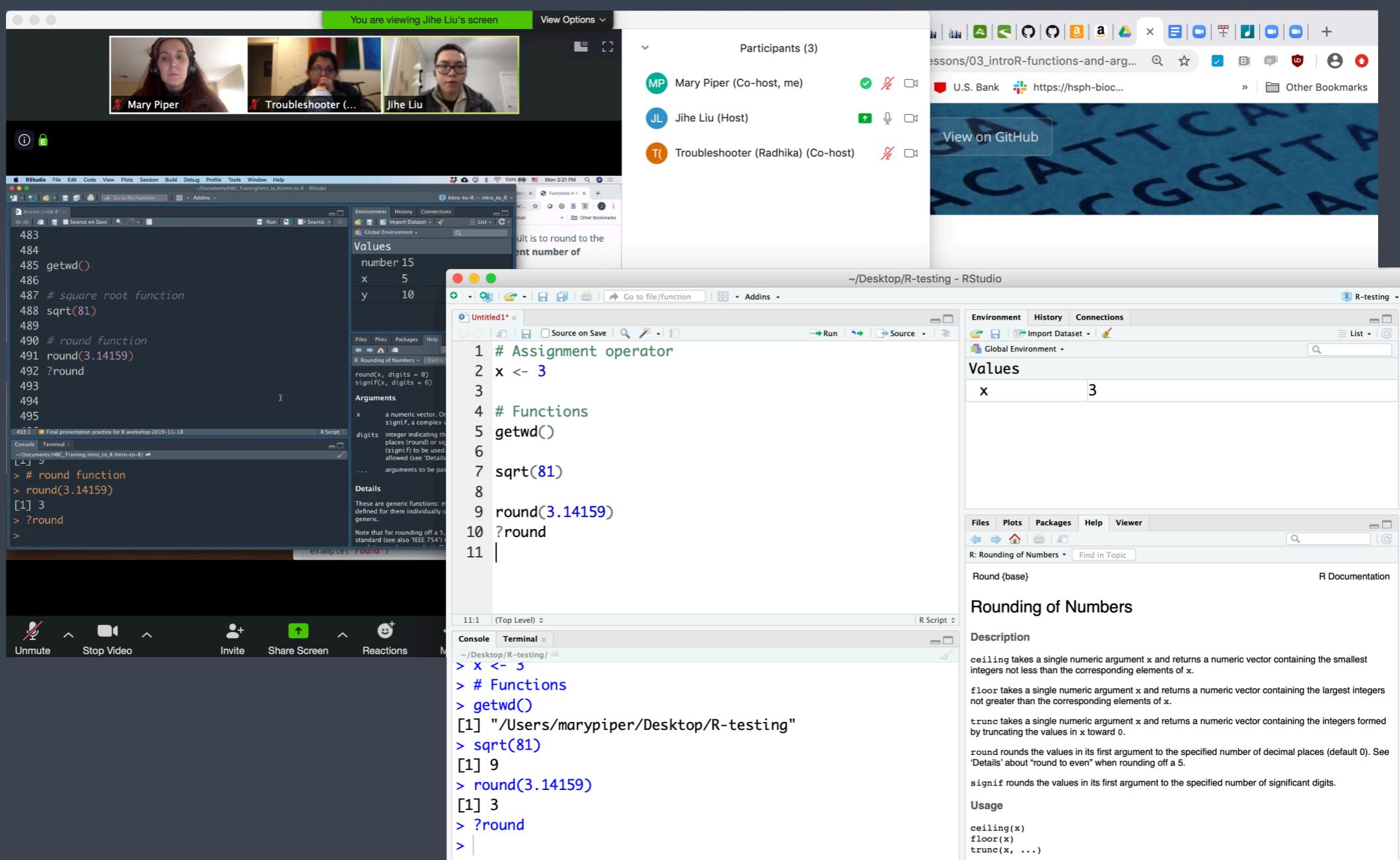
**Learning Objectives:**

- 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

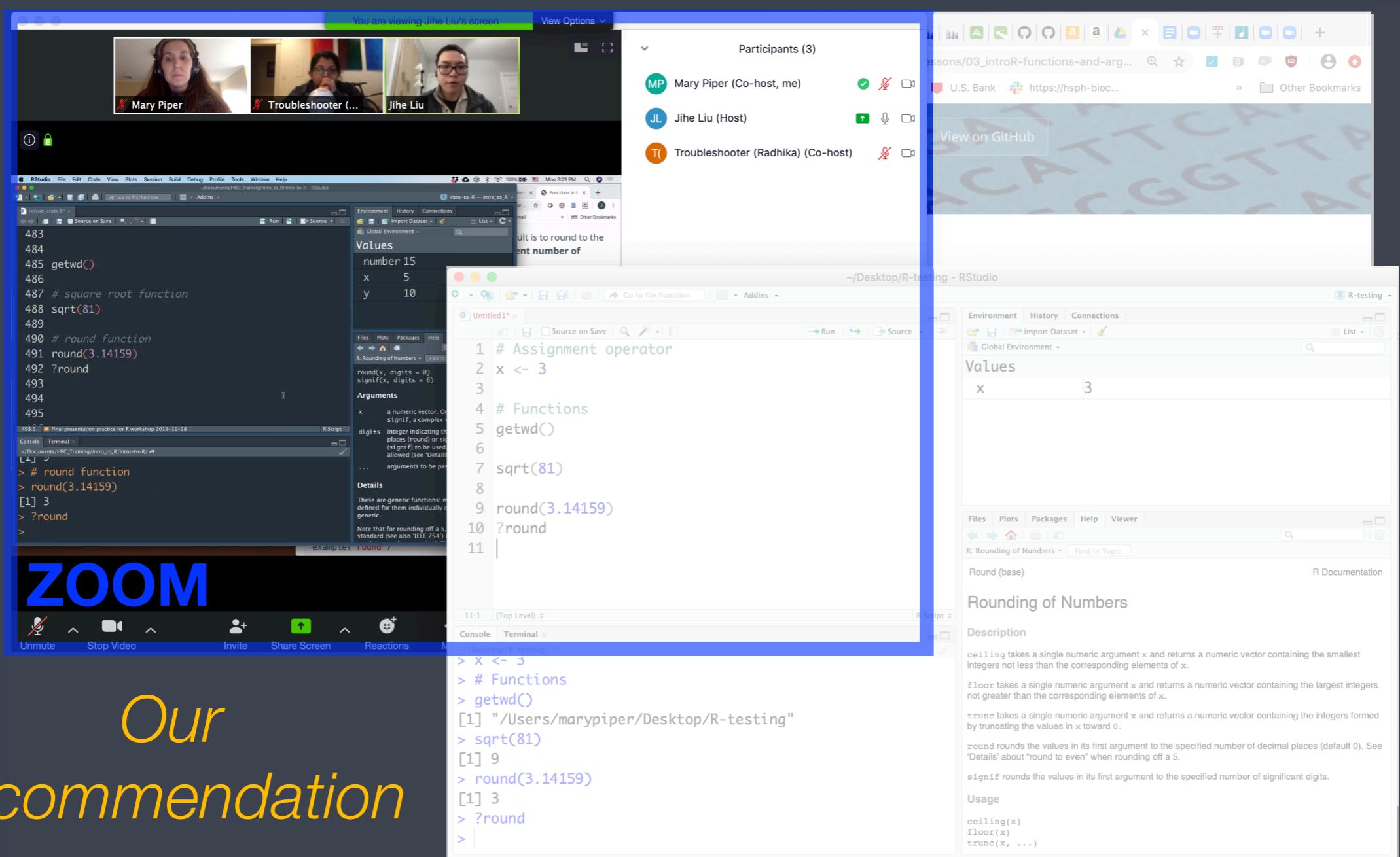
**Single-cell RNA-seq: Quality control**

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

# Single screen & 3 windows?

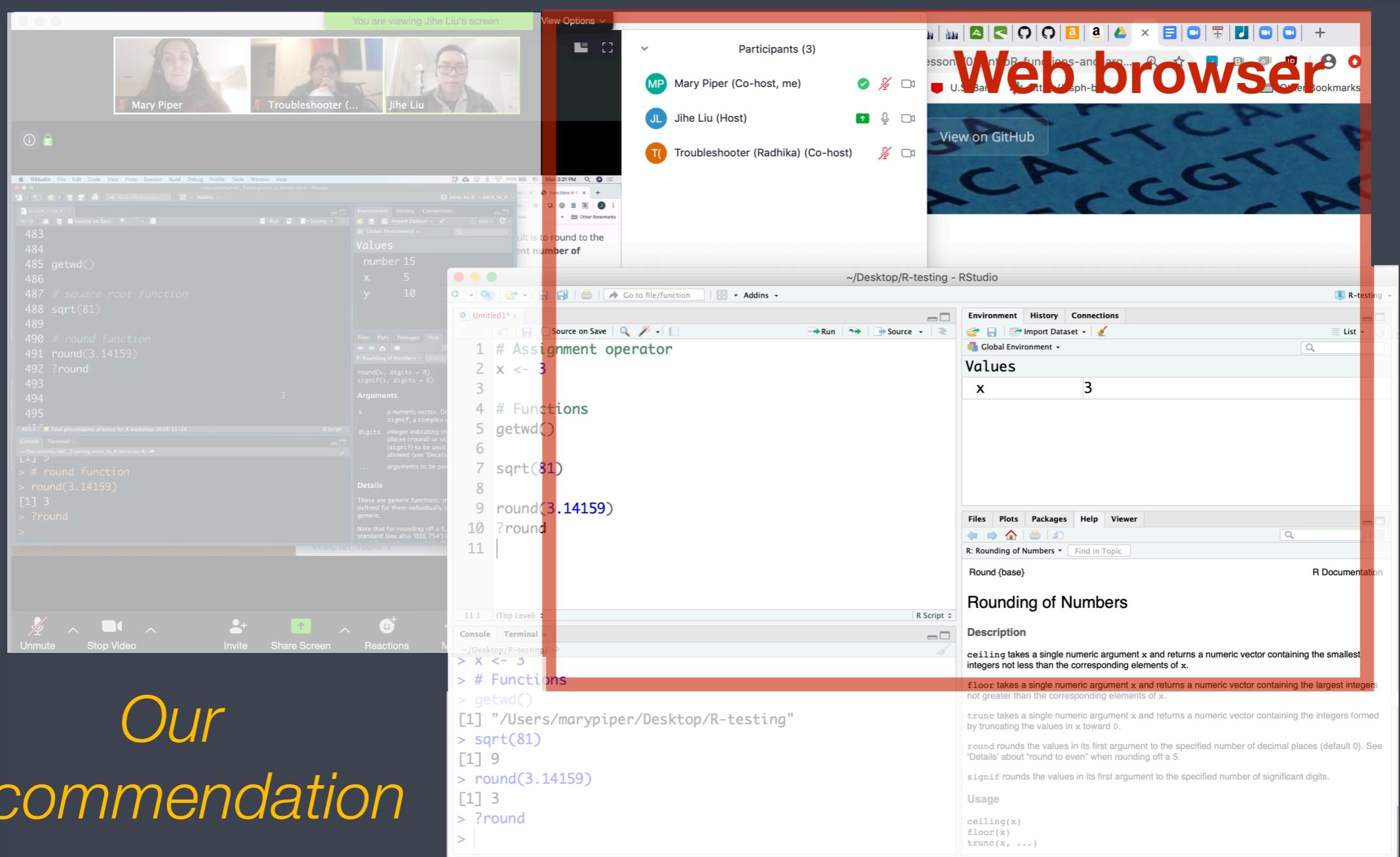


# Single screen & 3 windows?



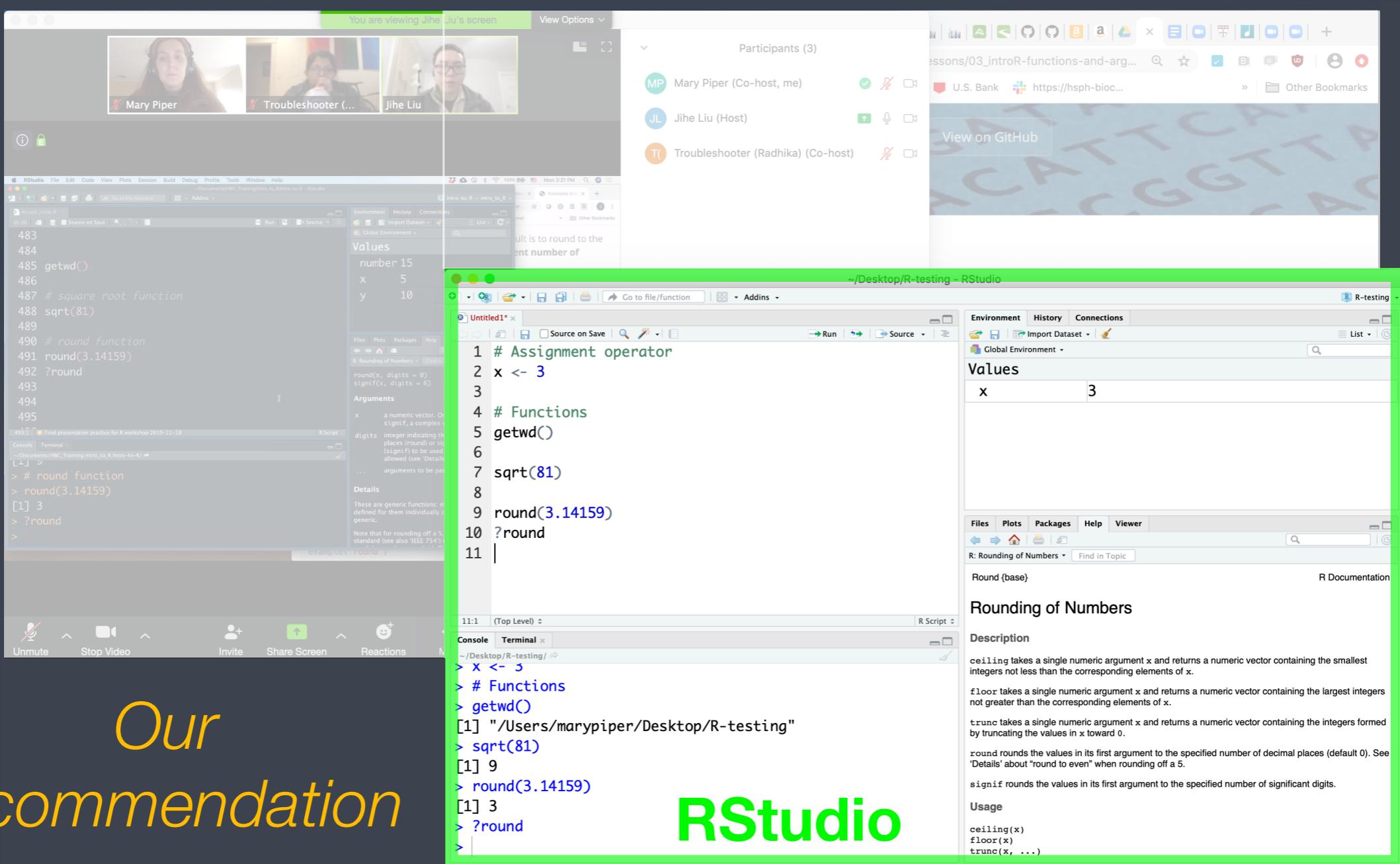
*Our  
recommendation*

# Single screen & 3 windows?

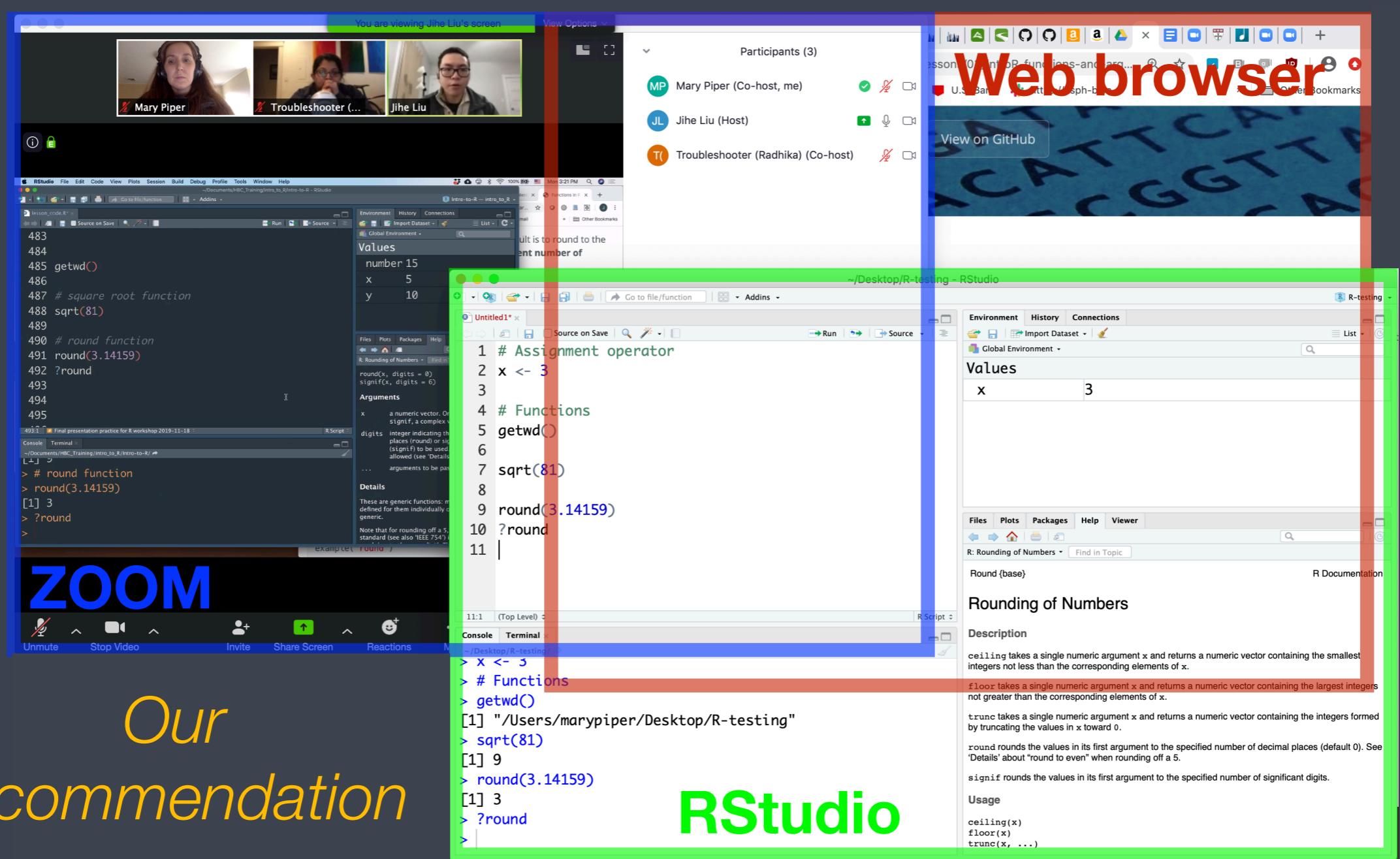


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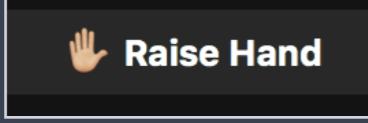


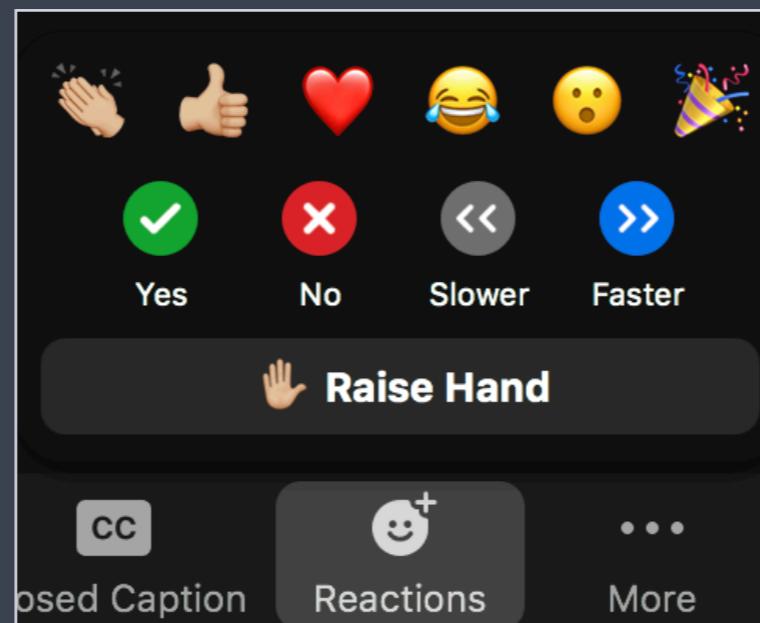
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# Odds and Ends

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

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  -  = "agree", "I'm all set" (equivalent to a **green post-it**)
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  - Type “X” in chat = "disagree", "I'm not ready" (equivalent to a **red post-it**)
- ❖ Questions for the presenter?
  - Post the question in the Chat window OR
  - Let the moderator know you have a question for the speaker