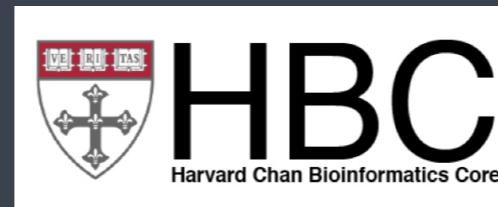


Introduction to Single-cell RNA-seq analysis

Harvard Chan Bioinformatics Core



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



Shannan Ho Sui
Director



John Hutchinson
Associate Director



Victor Barrera



Zhu Zhuo



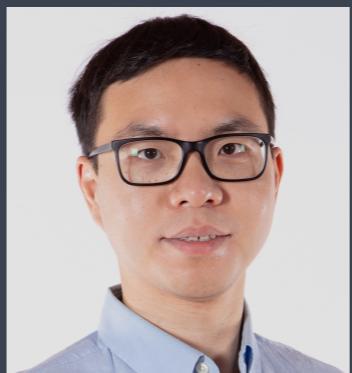
Preetida Bhetariya



Meeta Mistry



Mary Piper
Assoc. Training Director



Jihe Liu



Radhika Khetani
Training Director



Maria Simoneau



James Billingsley



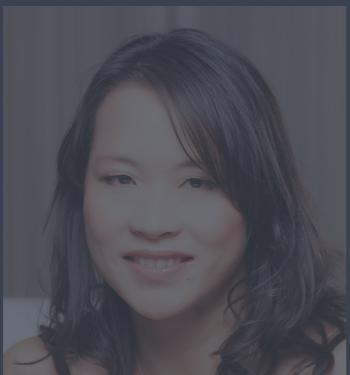
Sergey Naumenko



Joon Yoon



Peter Kraft
Faculty Advisor



Shannan Ho Sui
Director



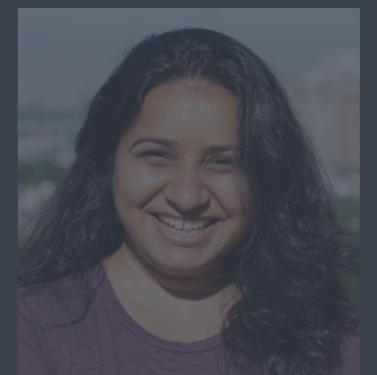
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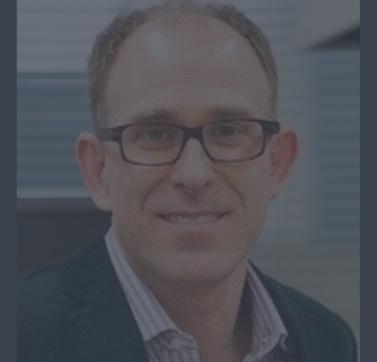
James Billingsley



Sergey Naumenko



Joon Yoon



Peter Kraft
Faculty Advisor

Consulting

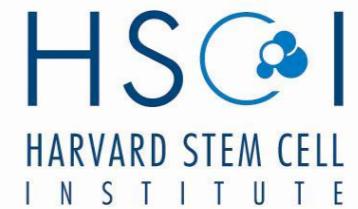
- RNA-seq analysis: bulk, single cell, small RNA
- ChIP-seq and ATAC-seq analysis
- Genome-wide methylation
- WGS, resequencing, exome-seq and CNV studies
- QC & analysis of gene expression arrays
- Functional enrichment analysis
- Grant support

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



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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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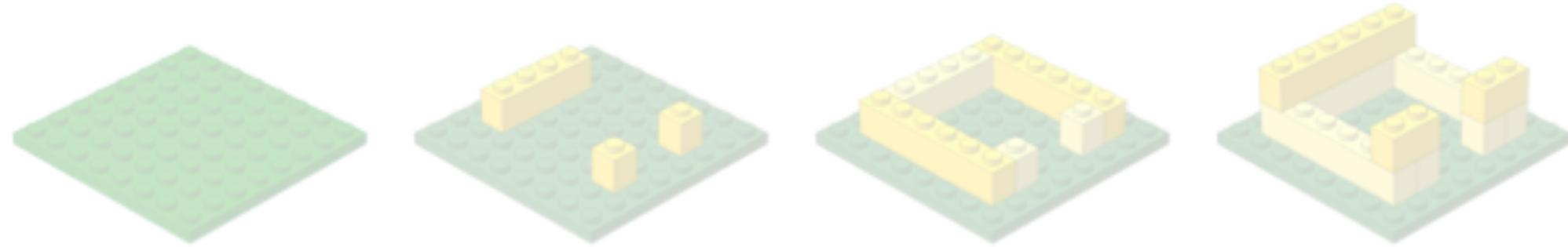
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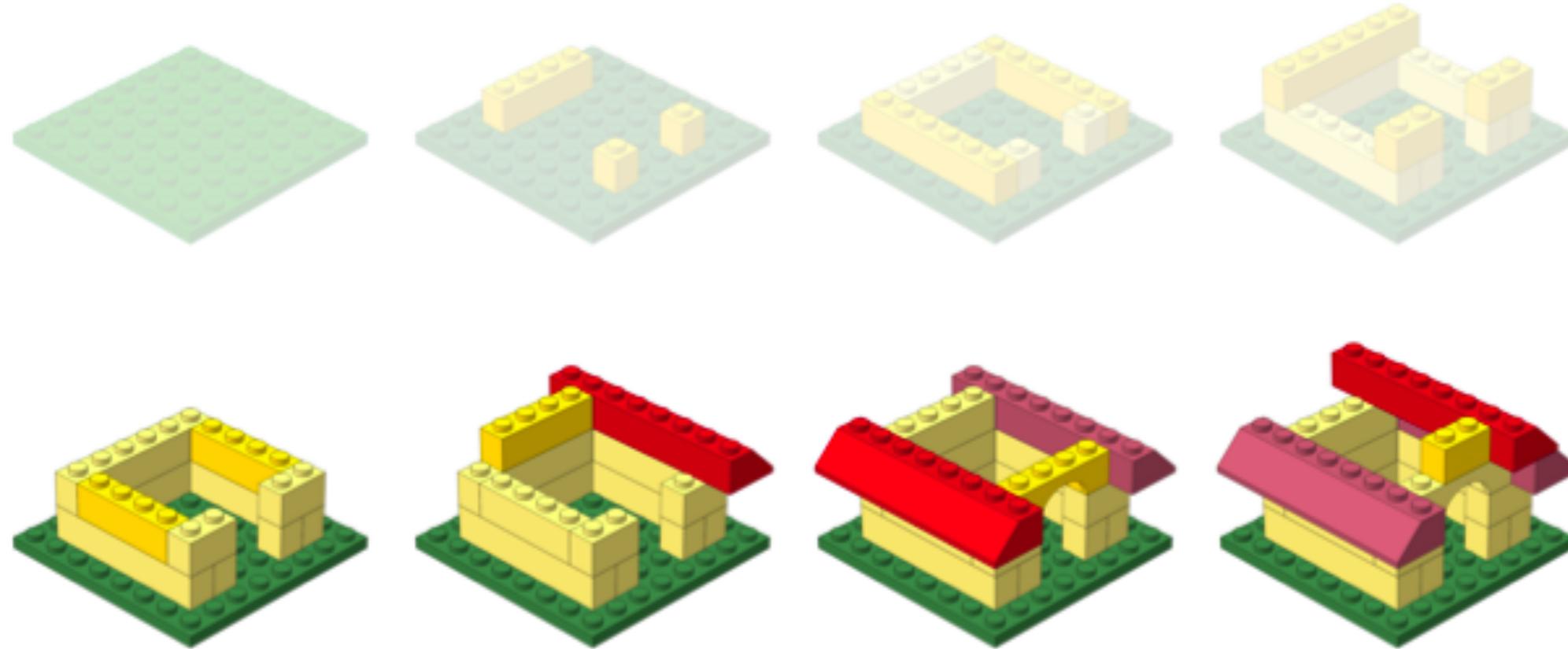


Workshop scope



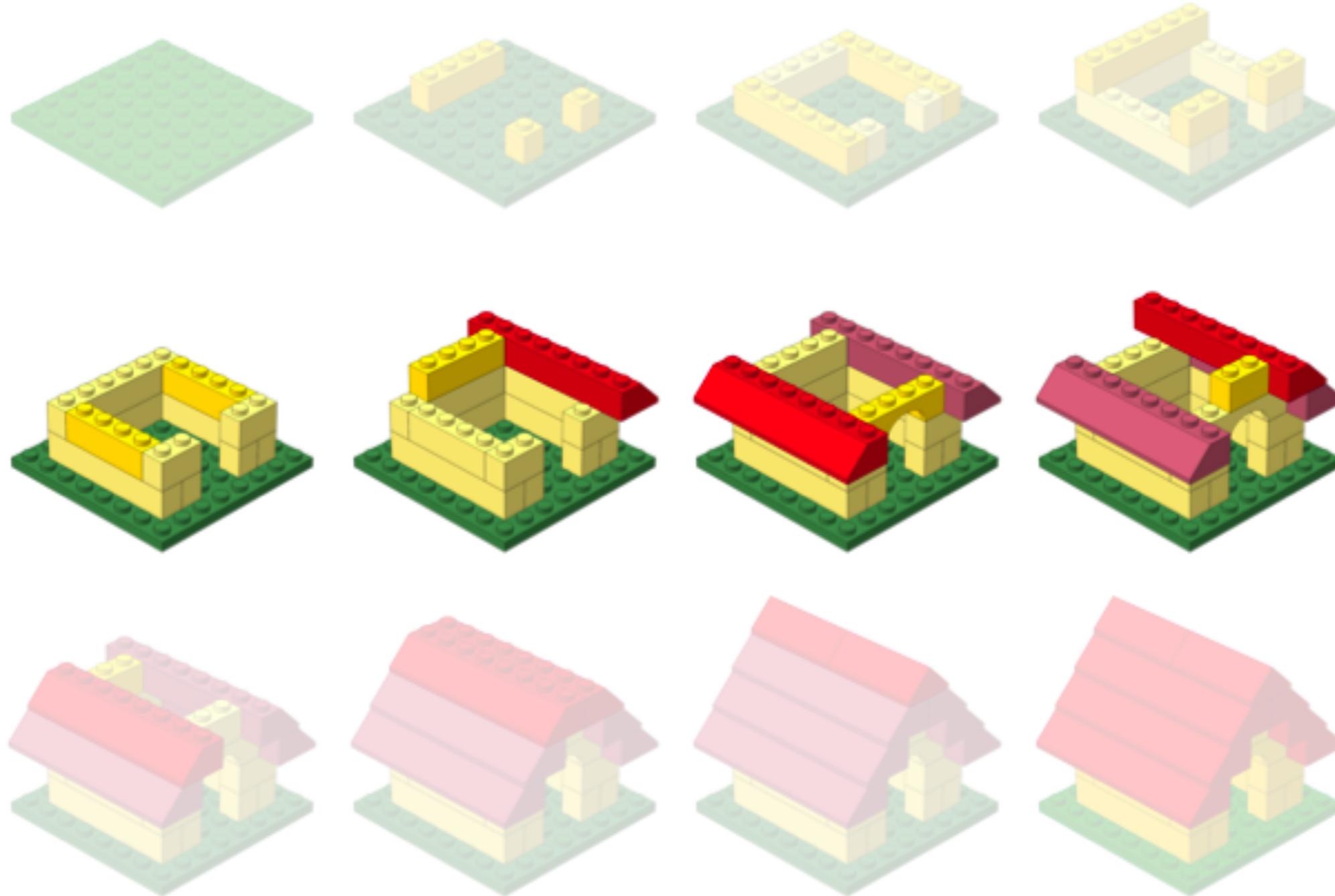
<http://anoved.net/tag/lego/page/3/>

Bioinformatics data analysis



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

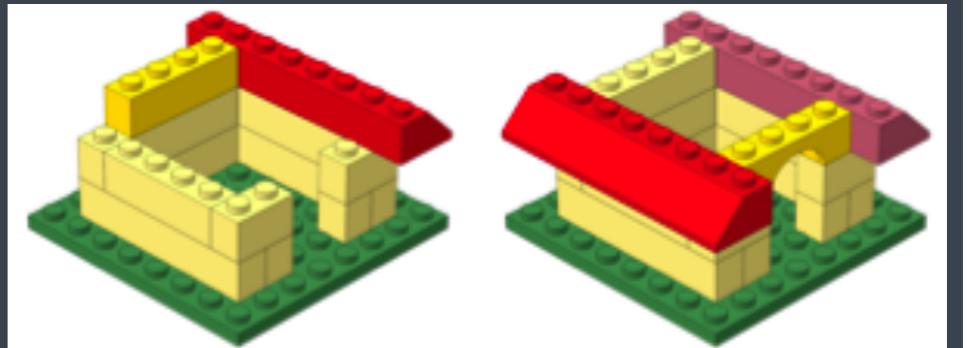
Bioinformatics data analysis



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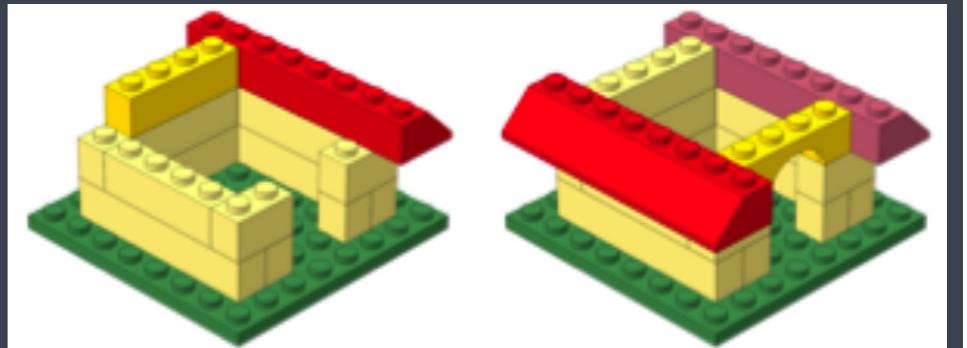
Bioinformatics data analysis

Learning Objectives



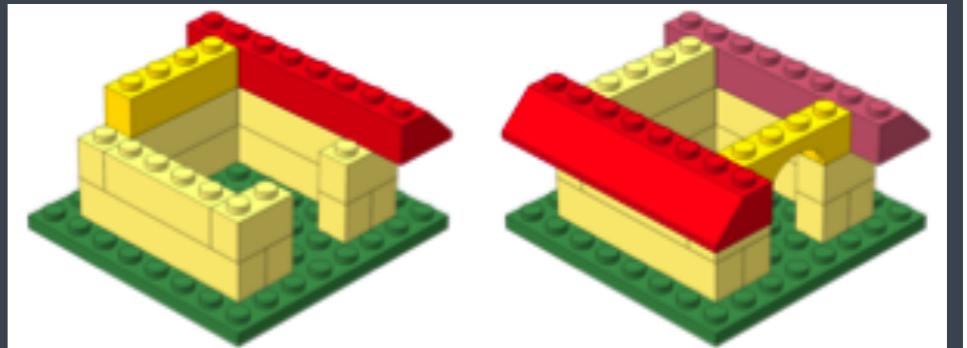
- ✓ Describe best practices for designing a single-cell RNA-seq experiment
- ✓ Describe steps in a single-cell RNA-seq analysis workflow
- ✓ Use Seurat and associated tools to perform analysis of single-cell expression data, including data filtering, QC, integration, clustering, and marker identification
- ✓ Understand practical considerations for performing scRNA-seq, rather than in-depth exploration of algorithm theory

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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

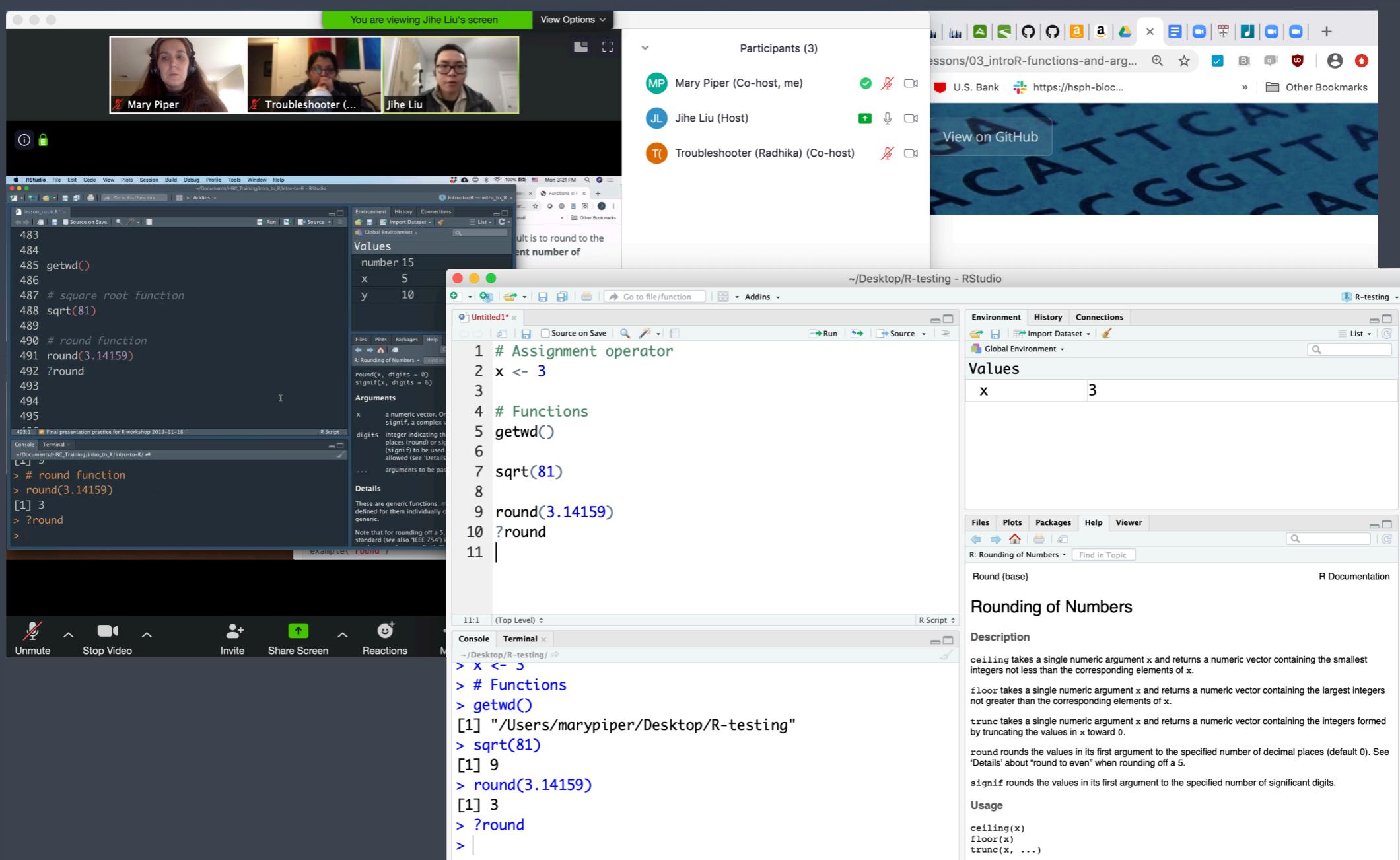
Learning Objectives:

- 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

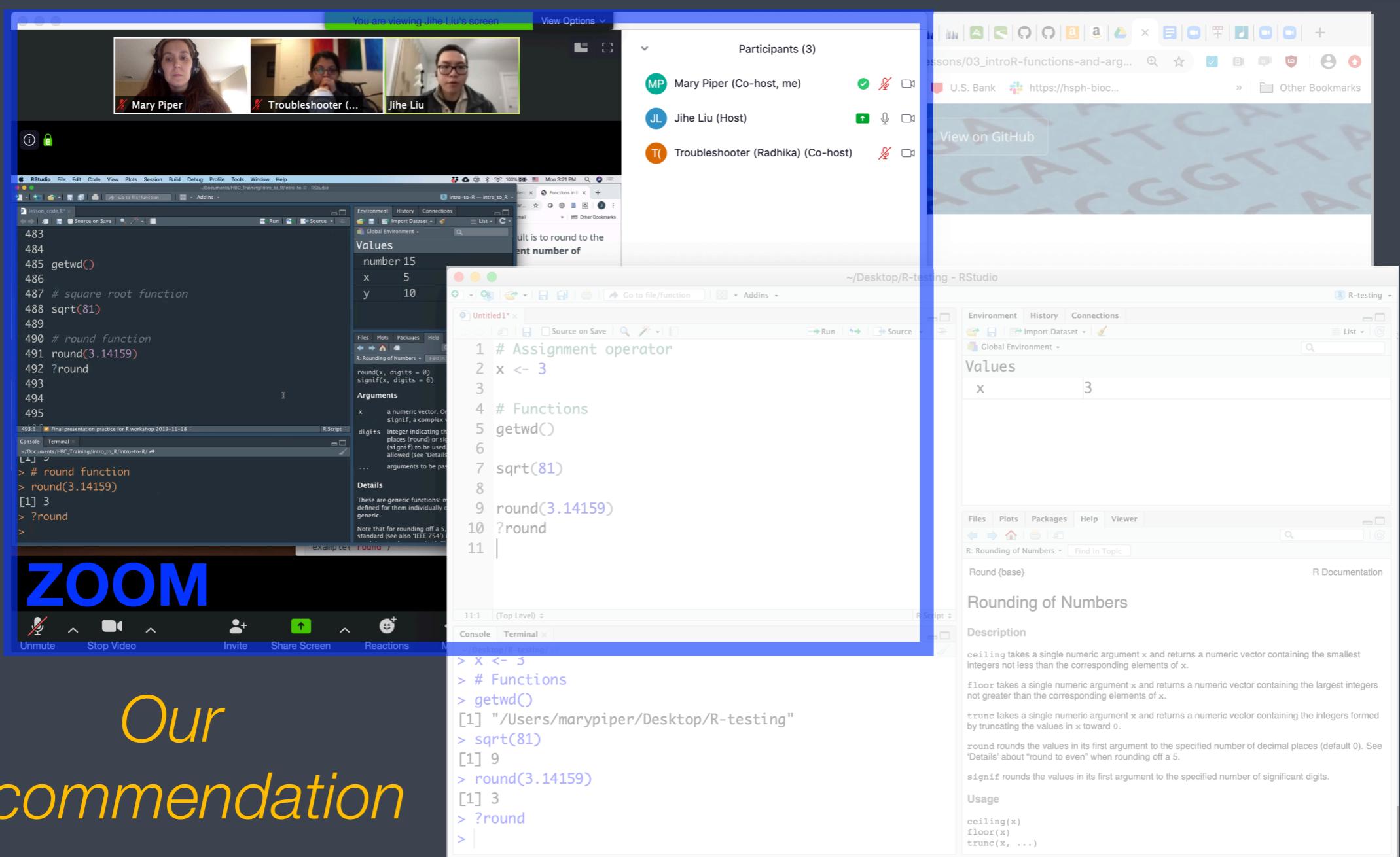
Single-cell RNA-seq: Quality control

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

Single screen & 3 windows?

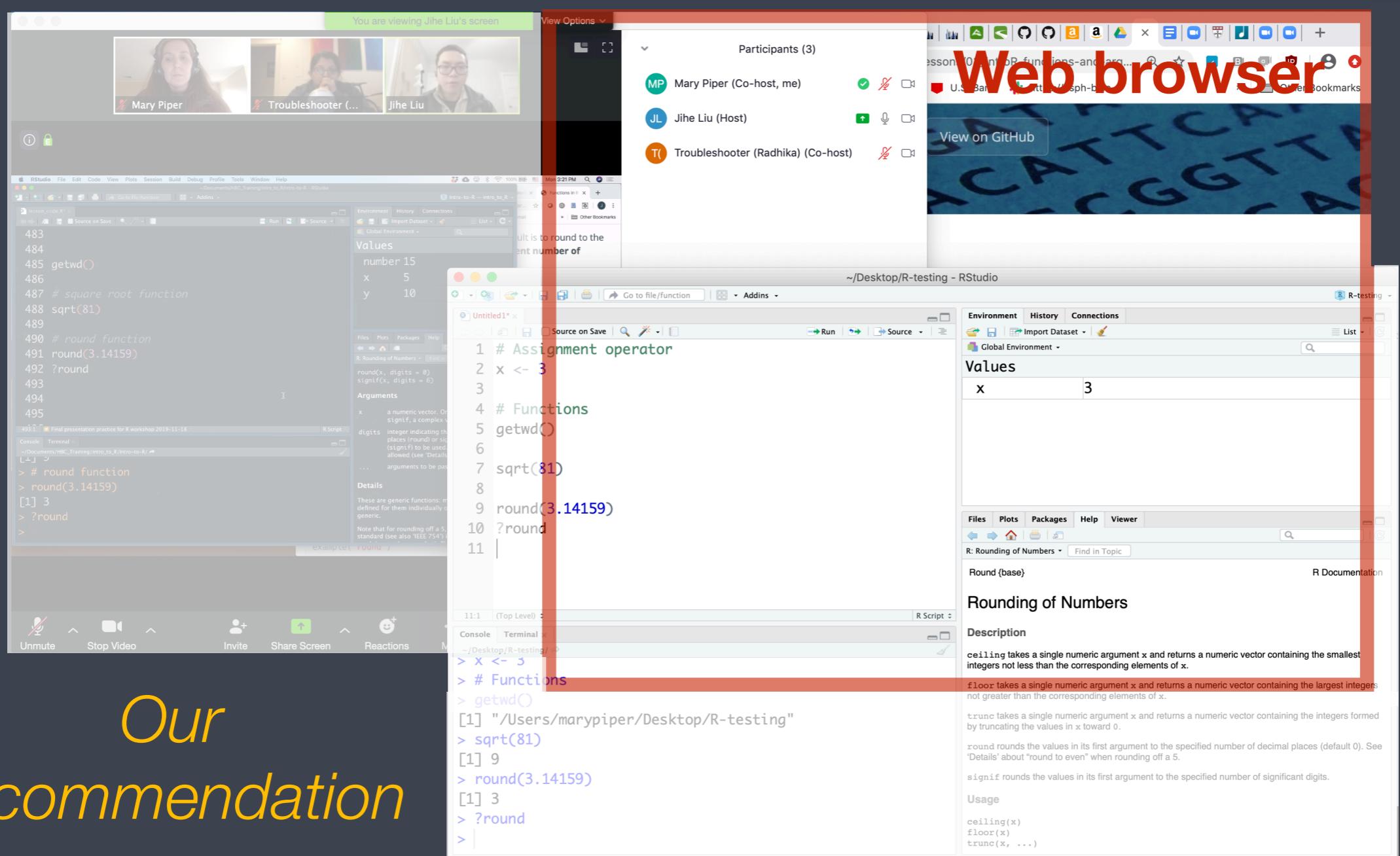


Single screen & 3 windows?



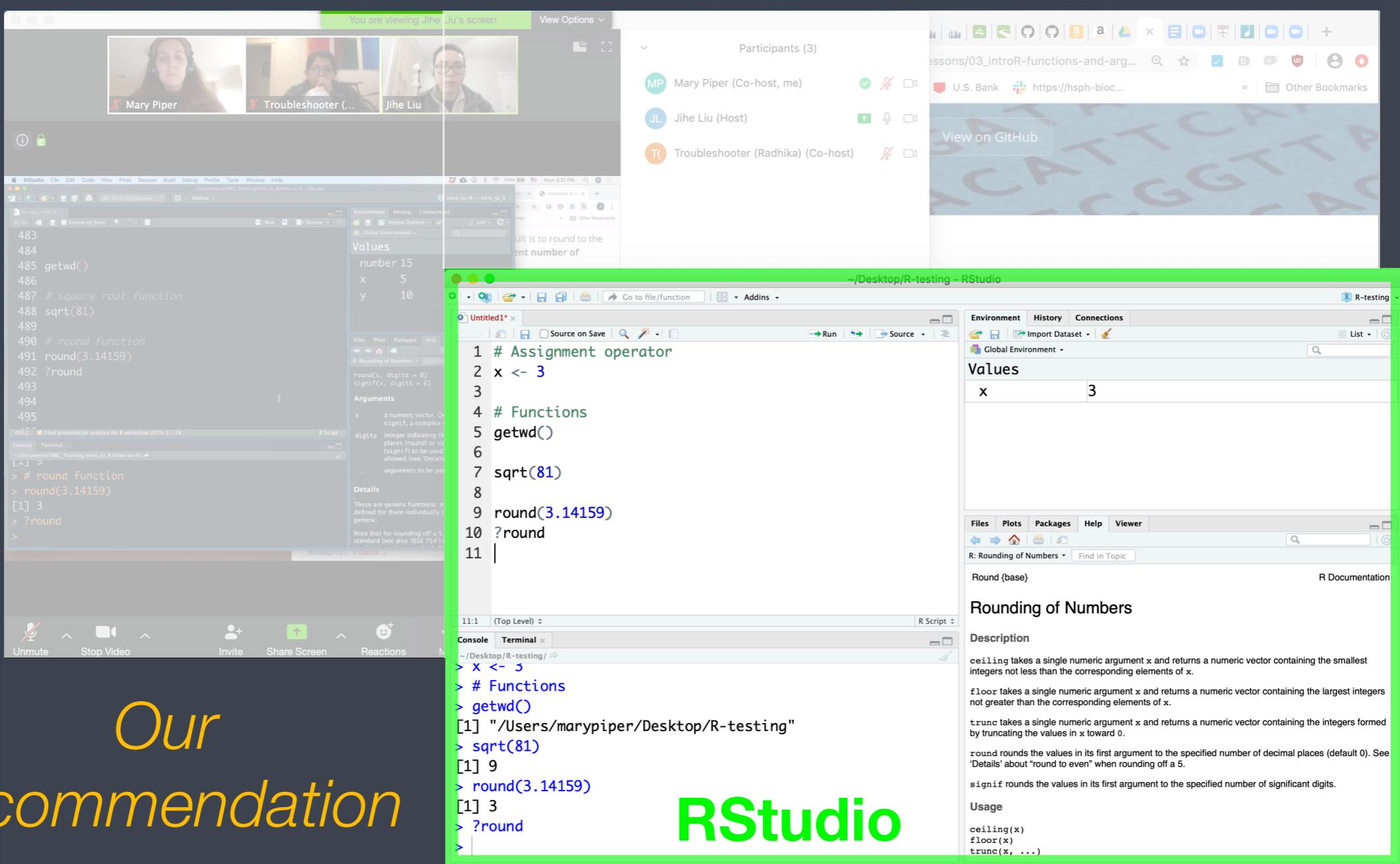
*Our
recommendation*

Single screen & 3 windows?

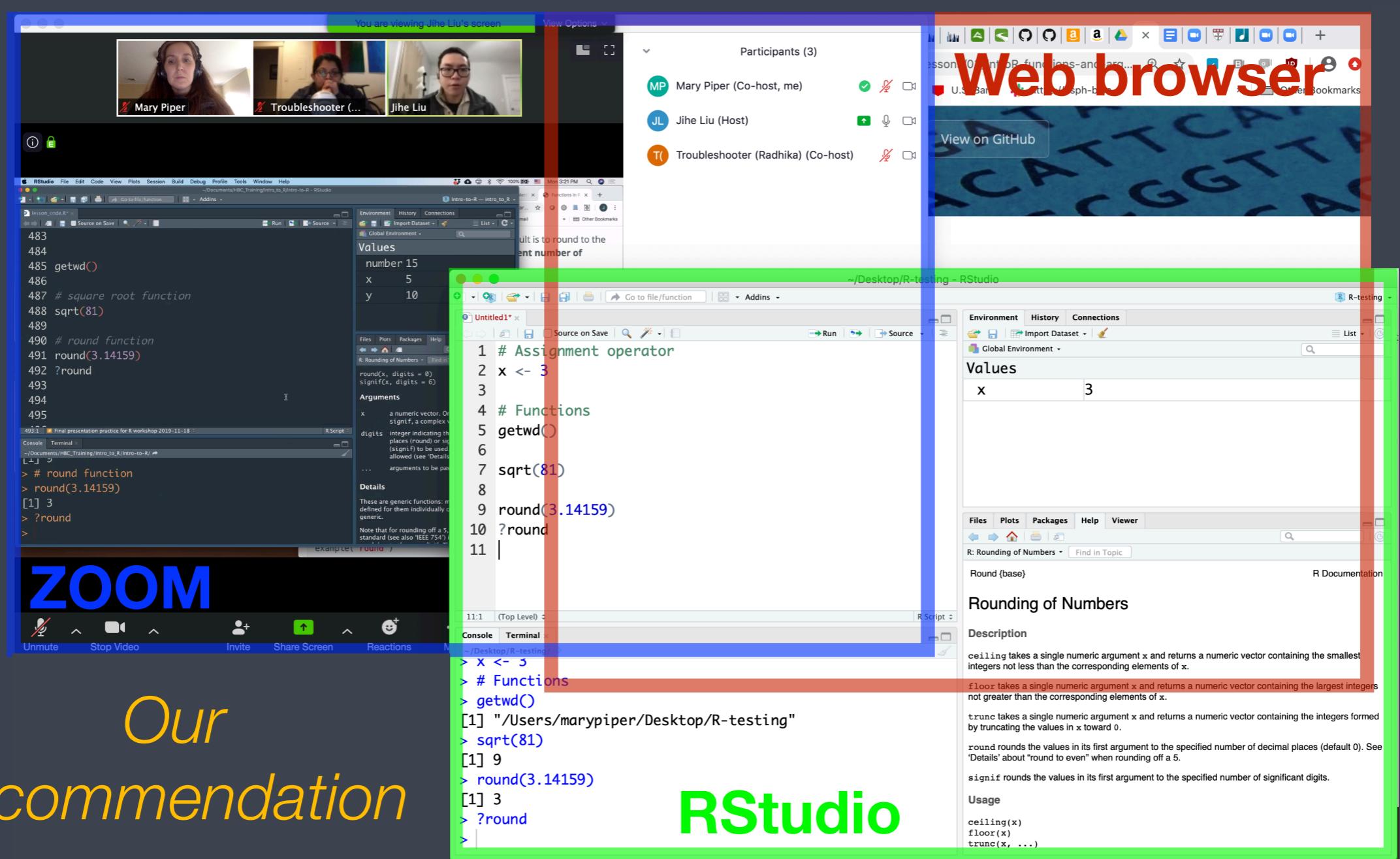


*Our
recommendation*

Single screen & 3 windows?



Single screen & 3 windows?

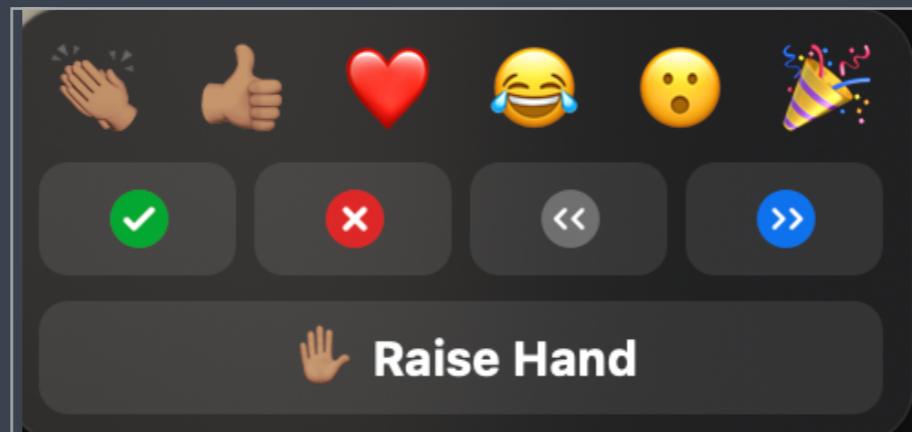


Odds and Ends

- ❖ 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 (2/2)

- ❖ Questions for the presenter?
 - Post the question in the Chat window OR
 -  **Raise 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)