

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



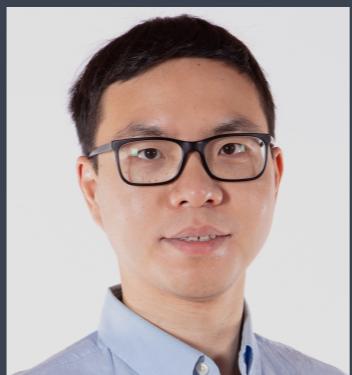
Preetida Bhetariya



Meeta Mistry



Mary Piper
Assoc. Training Director



Jihe Liu



Radhika Khetani
Training Director



Maria Simoneau



James Billingsley



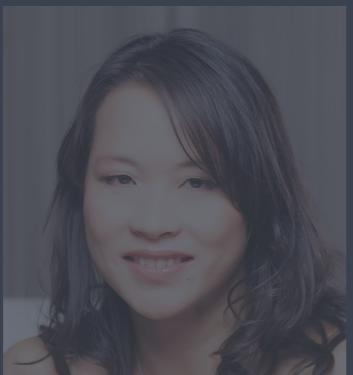
Sergey Naumenko



Joon Yoon



Peter Kraft
Faculty Advisor



Shannan Ho Sui
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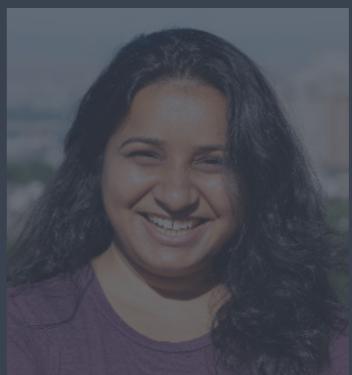
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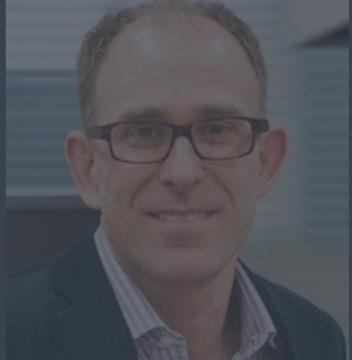
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Consulting

- 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

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/>



Training

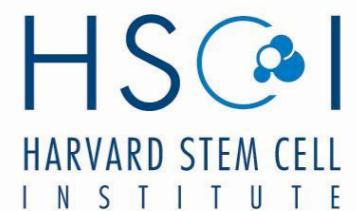
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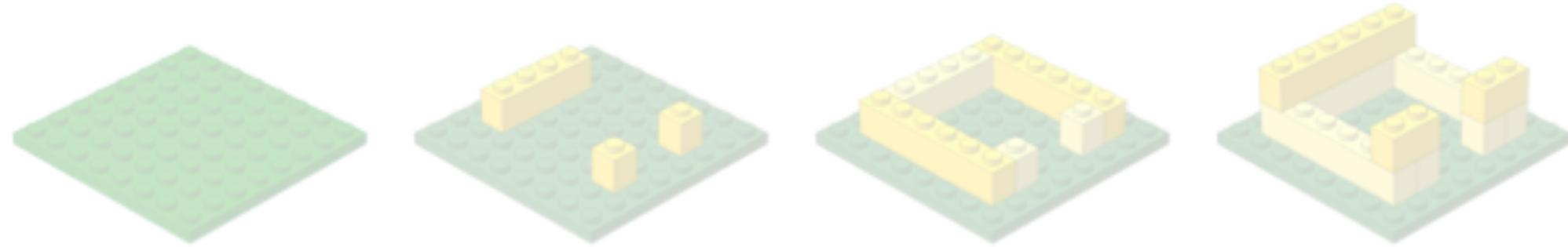
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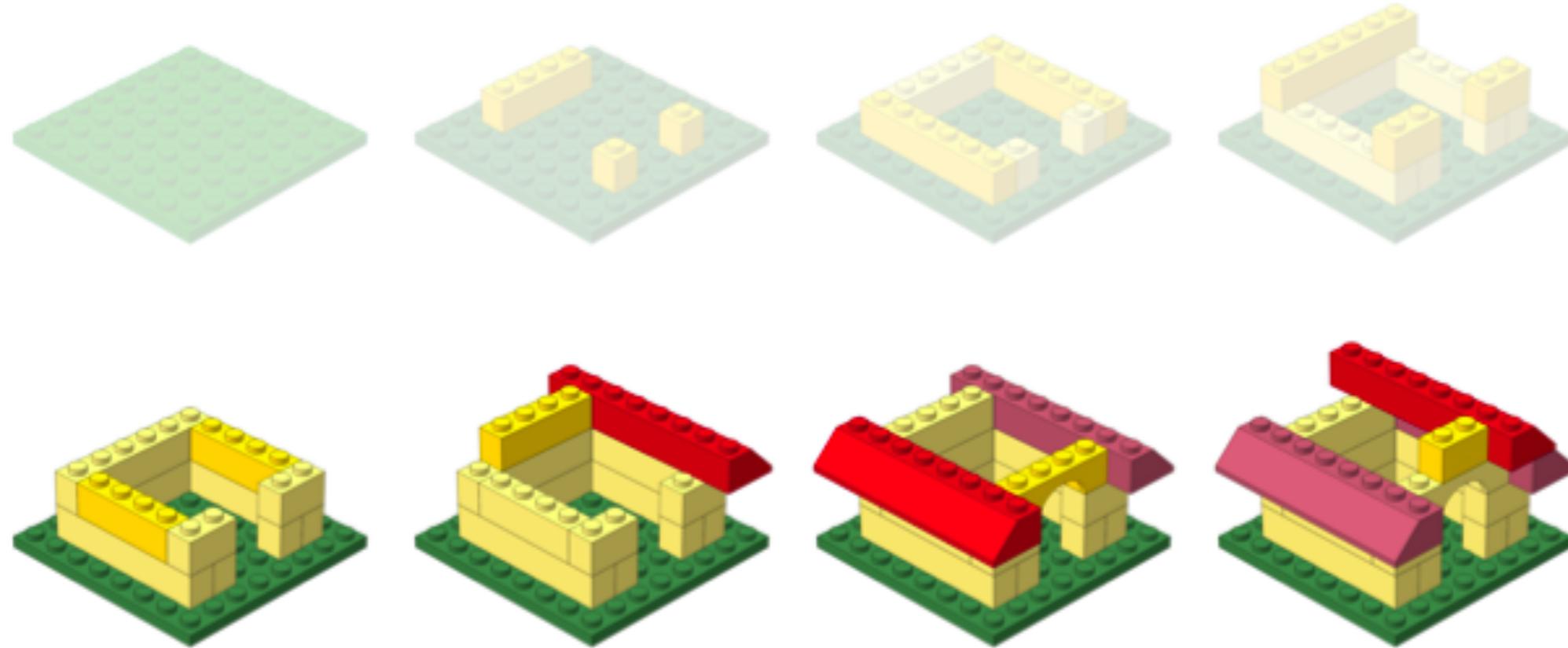


Workshop scope



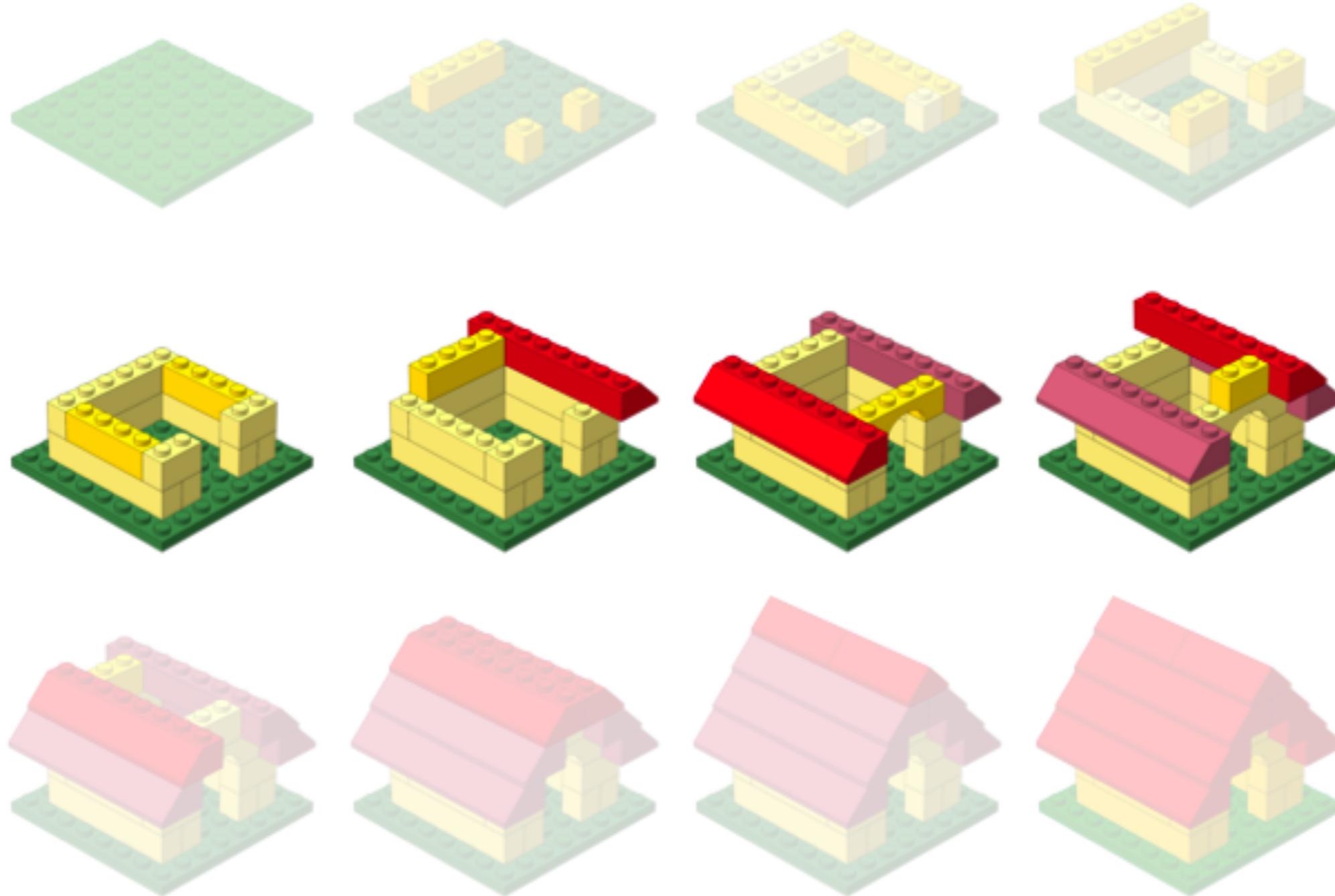
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Bioinformatics data analysis



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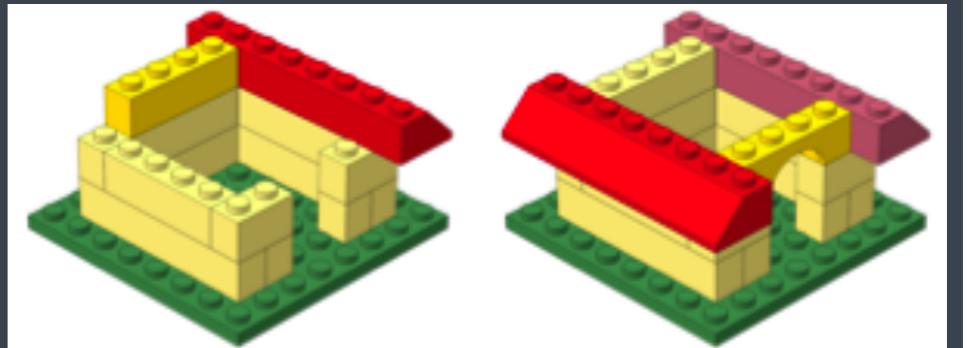
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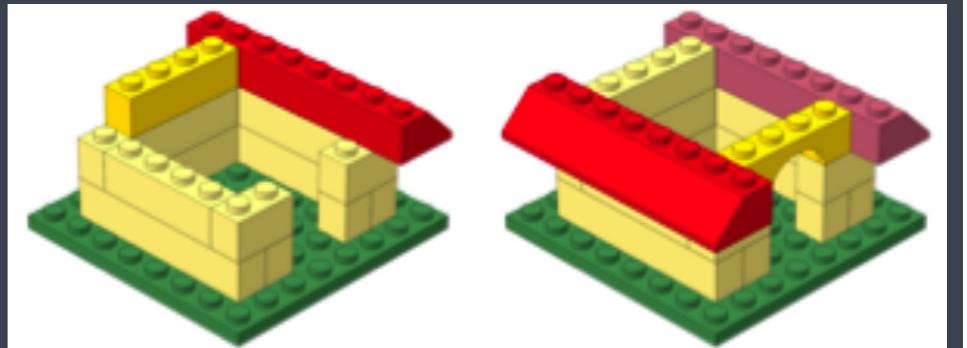
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Learning Objectives



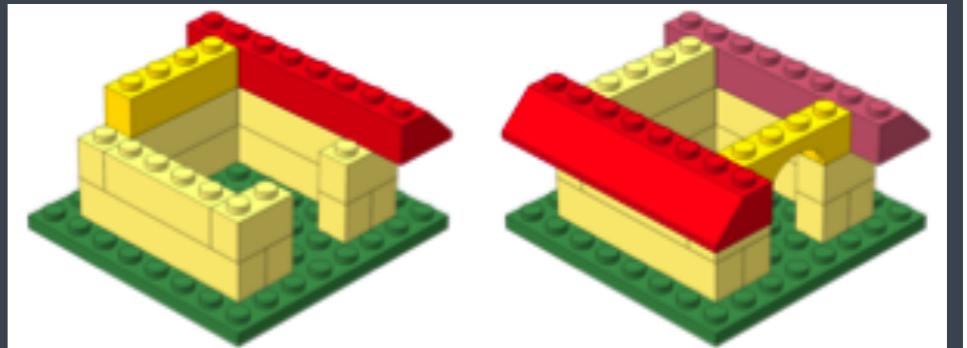
- ✓ Describe best practices for designing a single-cell RNA-seq experiment
- ✓ Describe steps in a single-cell RNA-seq analysis workflow
- ✓ Use Seurat and associated tools to perform analysis of single-cell expression data, including data filtering, QC, integration, clustering, and marker identification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

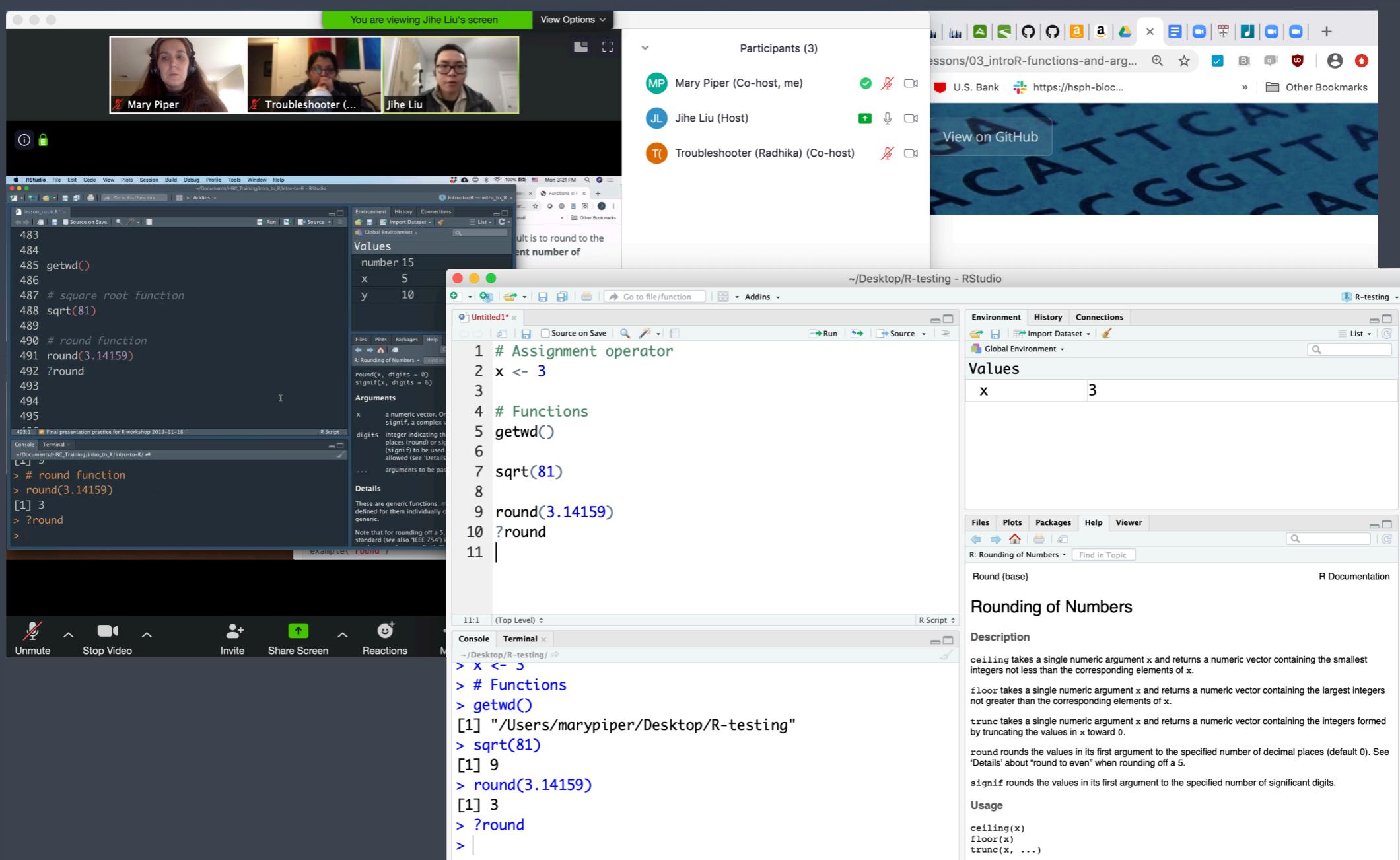
Learning Objectives:

- 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

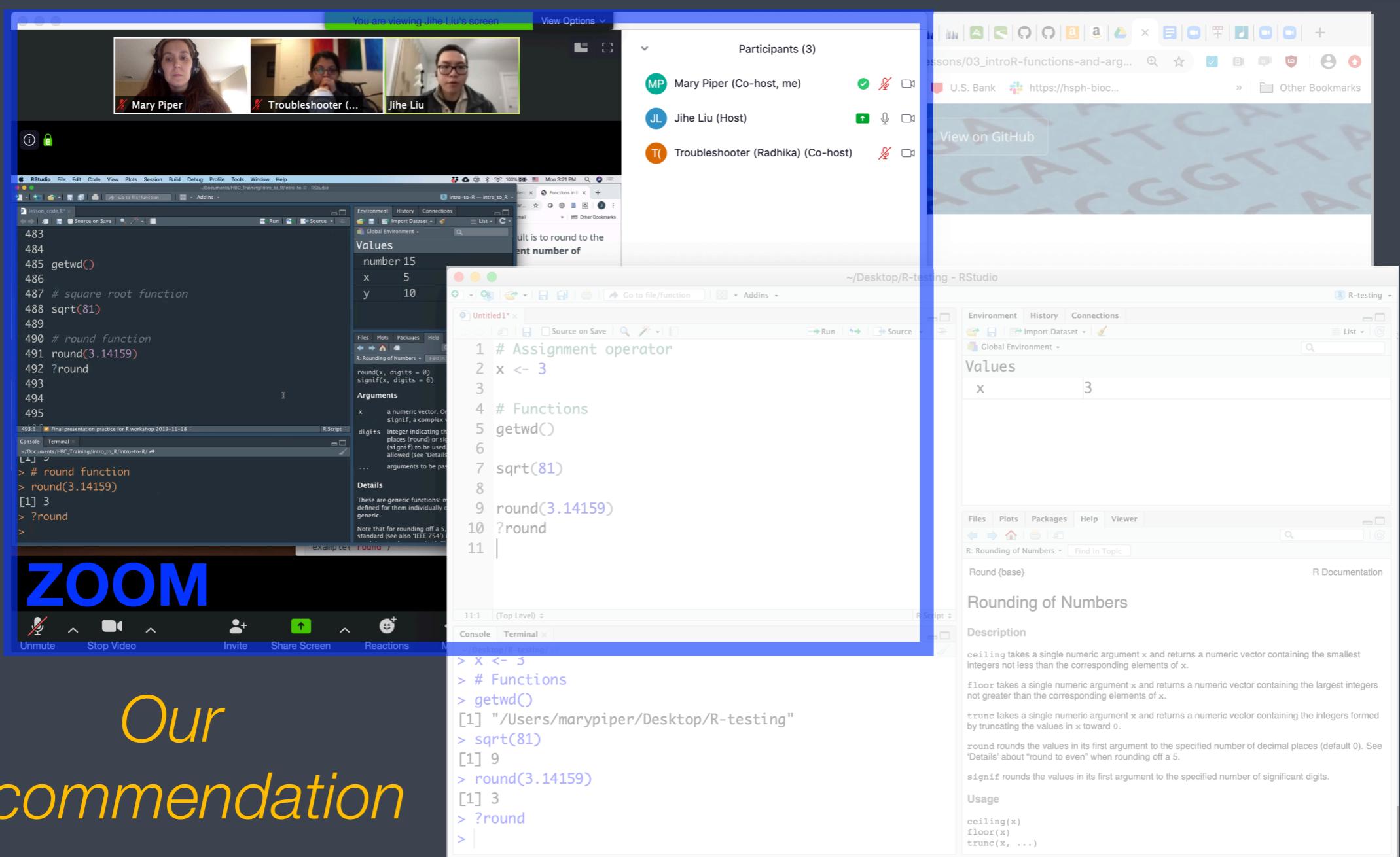
Single-cell RNA-seq: Quality control

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

Single screen & 3 windows?

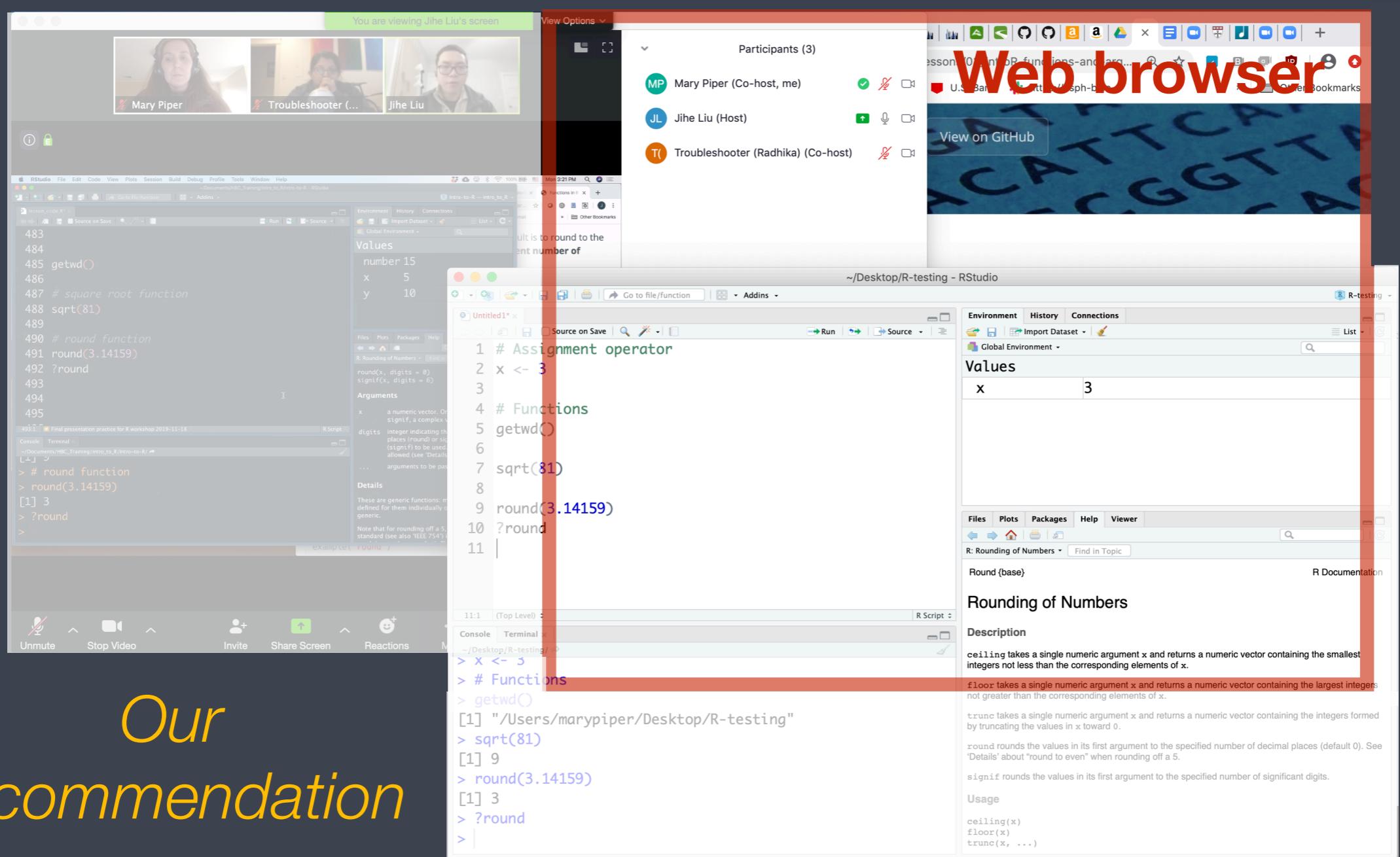


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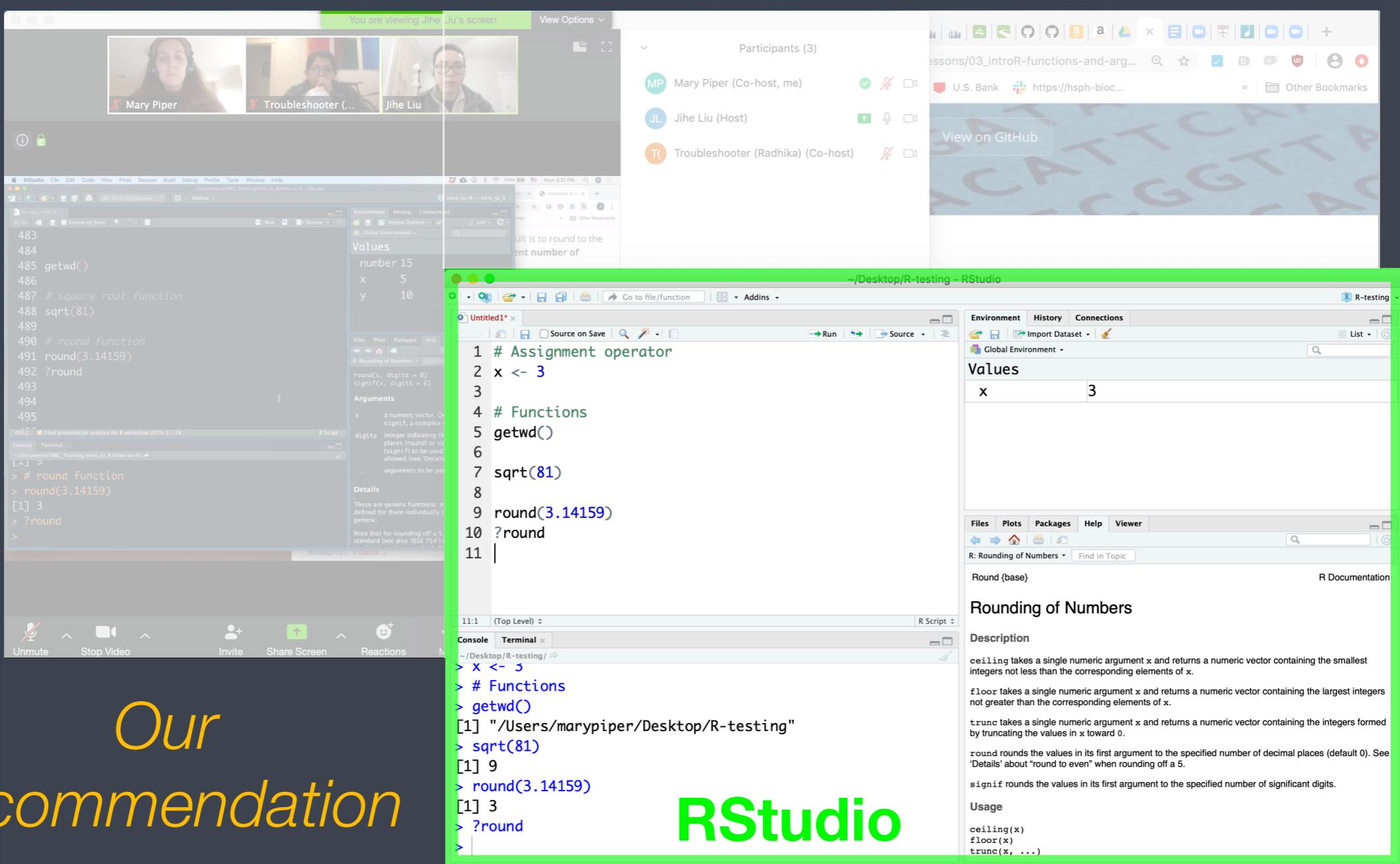
*Our
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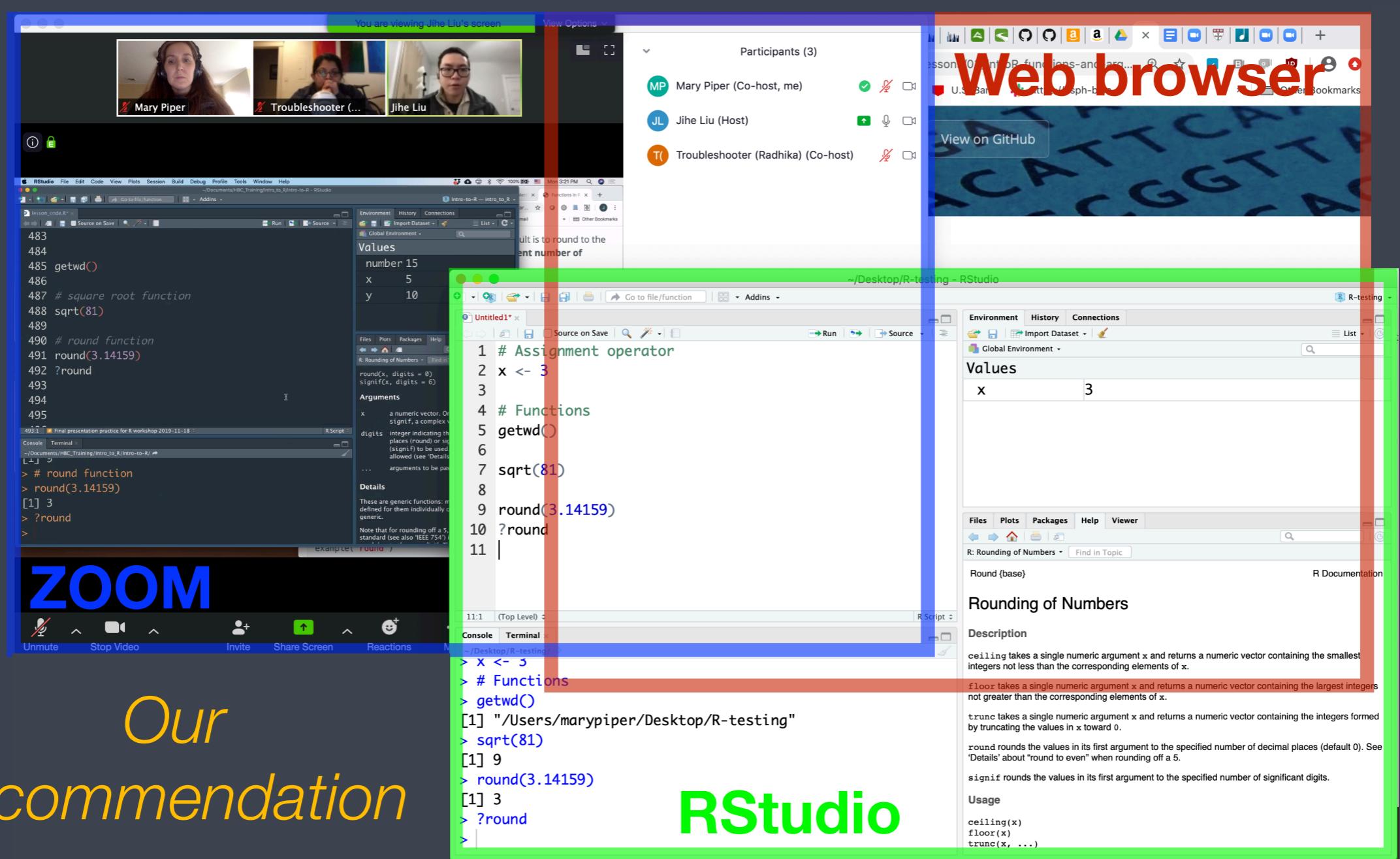


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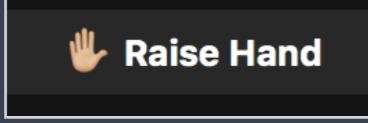


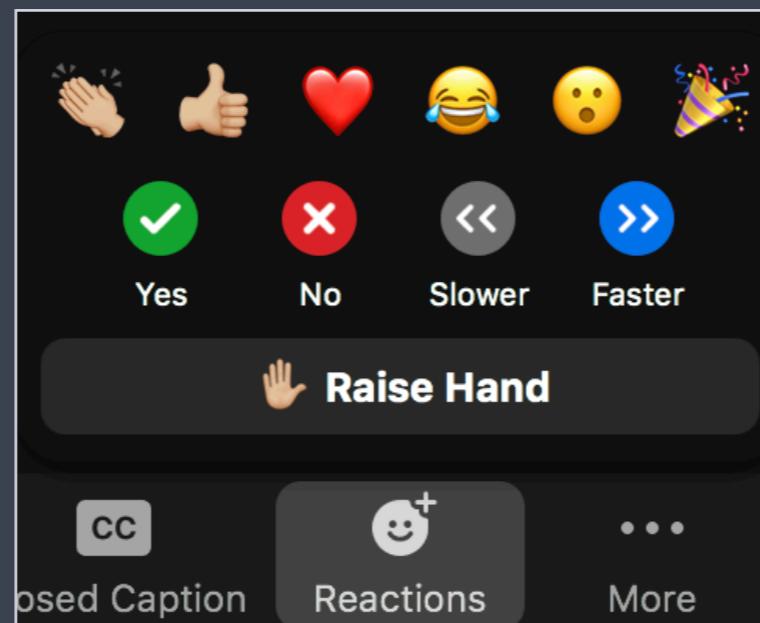
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Odds and Ends

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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

Contact us!

Training team  : hbctraining@hsph.harvard.edu

Consulting  : bioinformatics@hsph.harvard.edu

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