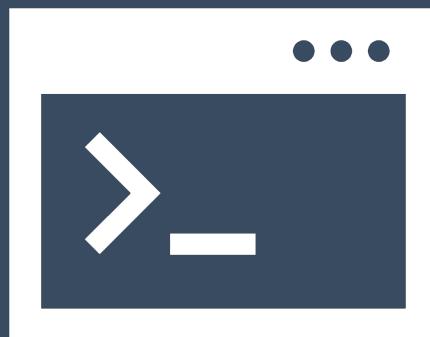




HBC
Harvard Chan Bioinformatics Core

Introduction to Single-cell RNA-seq Analysis

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



Harvard Chan Bioinformatics Core



Introductions!





Shannan Ho Sui
Director



Meeta Mistry
Associate Director



Lorena Pantano
Director of Bioinformatics Platform



John Quackenbush
Faculty Advisor



Upen Bhattacharai



Heather Wick



Will Gammerdinger



Noor Sohail



Elizabeth Partan



Alex Bartlett



Emma Berdan



James Billingsley



Zhu Zhuo



Maria Simoneau



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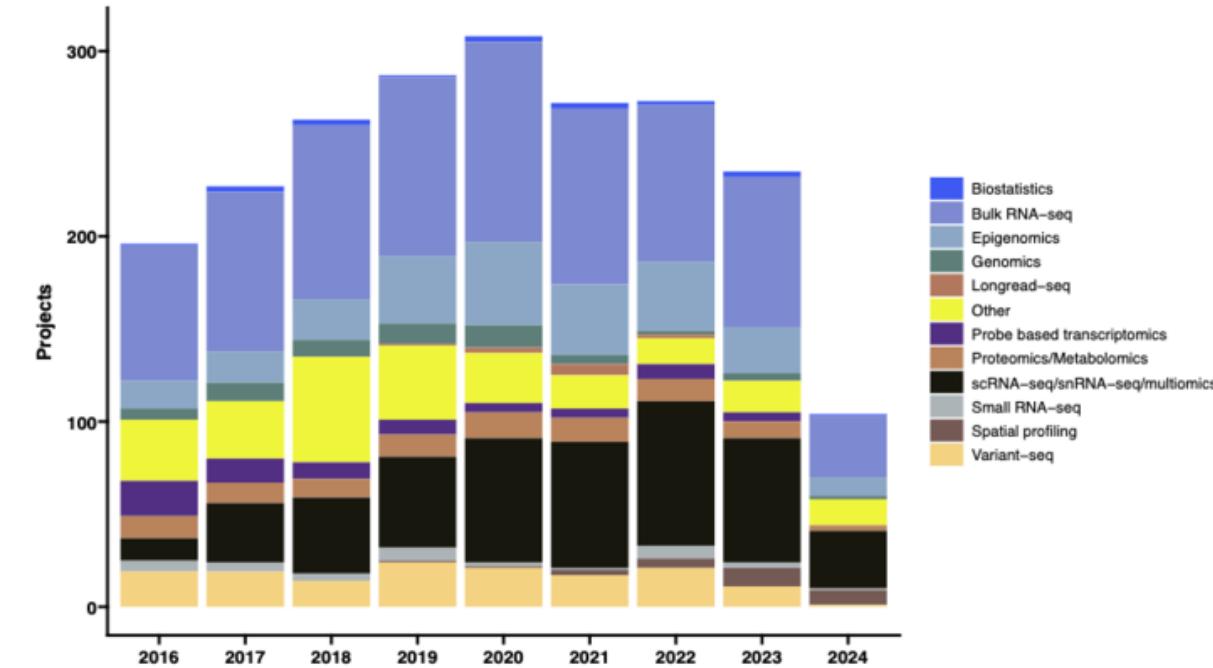
Zhu Zhuo



Maria Simoneau

Consulting

- ❖ Transcriptomics: Bulk, single cell, small RNA
- ❖ Epigenomics: ChIP-seq, CUT&RUN, ATAC-seq, DNA methylation
- ❖ Variant discovery: WGS, resequencing, exome-seq and CNV
- ❖ Multiomics integration
- ❖ Spatial biology
- ❖ Experimental design and grant support



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SCHOOL OF PUBLIC HEALTH

NIEHS



Training

- ❖ Hands-on workshops design to reflect best practices, reproducibility and an emphasis on experimental design
 - ❖ Basic Data Skills
 - ❖ Shell
 - ❖ R
 - ❖ Advanced Topics: Analysis of high-throughput sequencing data
 - ❖ Chromatin Biology
 - ❖ Bulk RNA-seq
 - ❖ Differential Gene Expression
 - ❖ scRNA-seq
 - ❖ Variant Calling
 - ❖ Current Topics in Bioinformatics

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



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

DF/HCC
DANA-FARBER / HARVARD CANCER CENTER



THE HARVARD CLINICAL
AND TRANSLATIONAL
SCIENCE CENTER

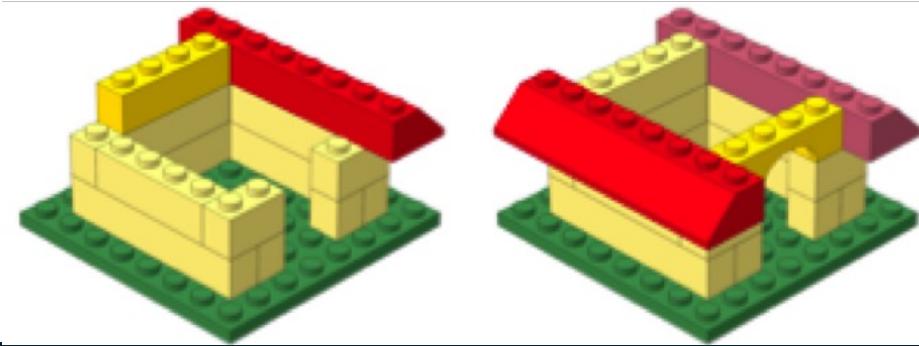
 **HARVARD**
MEDICAL SCHOOL

Workshop scope



Bioinformatic Data Analysis

Workshop Scope



- ❖ 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 schedule

Day 1

Time	Topic	Instructor
09:30 - 09:45	Workshop introduction	Meeta
09:45 - 10:35	Introduction to Single Cell RNA-sequencing: a practical guide	Dr. Arpita Kulkarni
10:35 - 10:40	Break	
10:40 - 11:00	scRNA-seq pre-reading discussion	All
11:00 - 11:45	Quality control set-up	Noor
11:45 - 12:00	Overview of self-learning materials and homework submission	Meeta

Course materials

❖ We continuously update our materials to reflect changes in the field/software

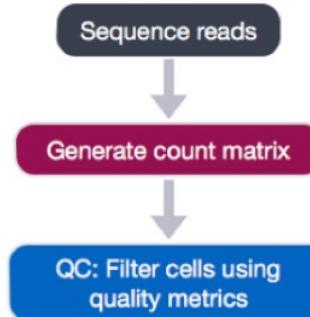


Approximate time: 90 minutes

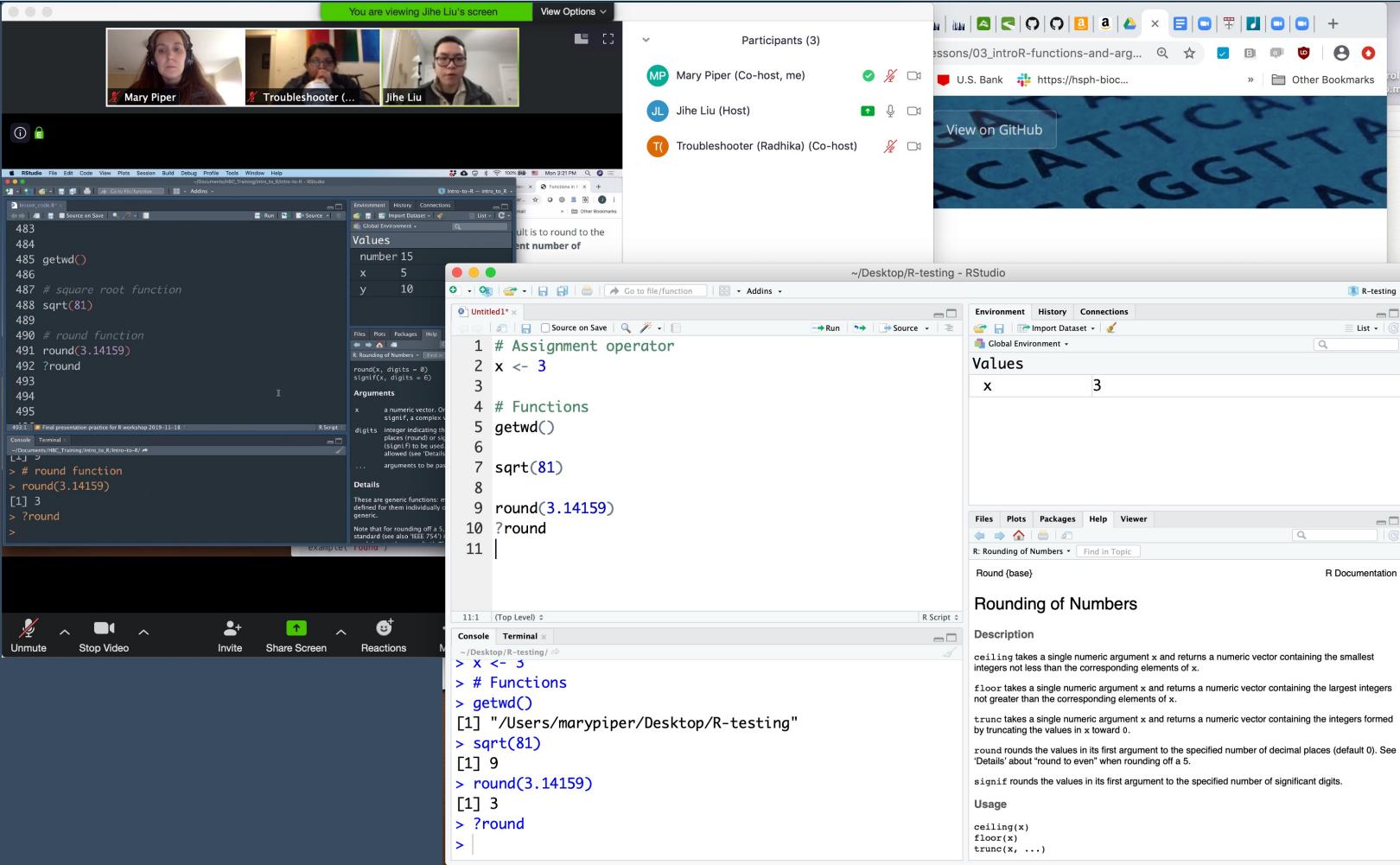
Learning Objectives:

- 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

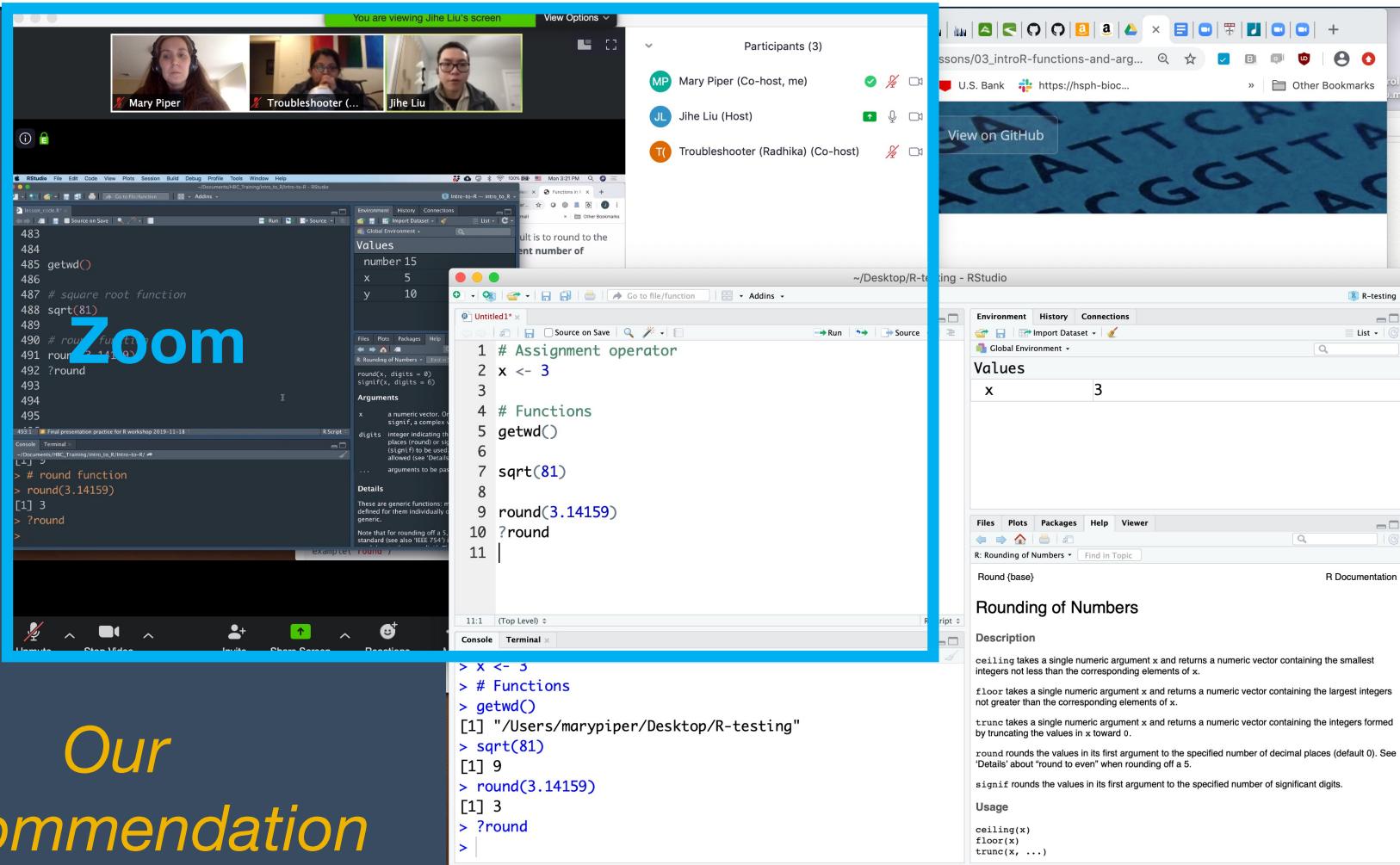
Single-cell RNA-seq: Quality control



Single Screen & 3 Windows

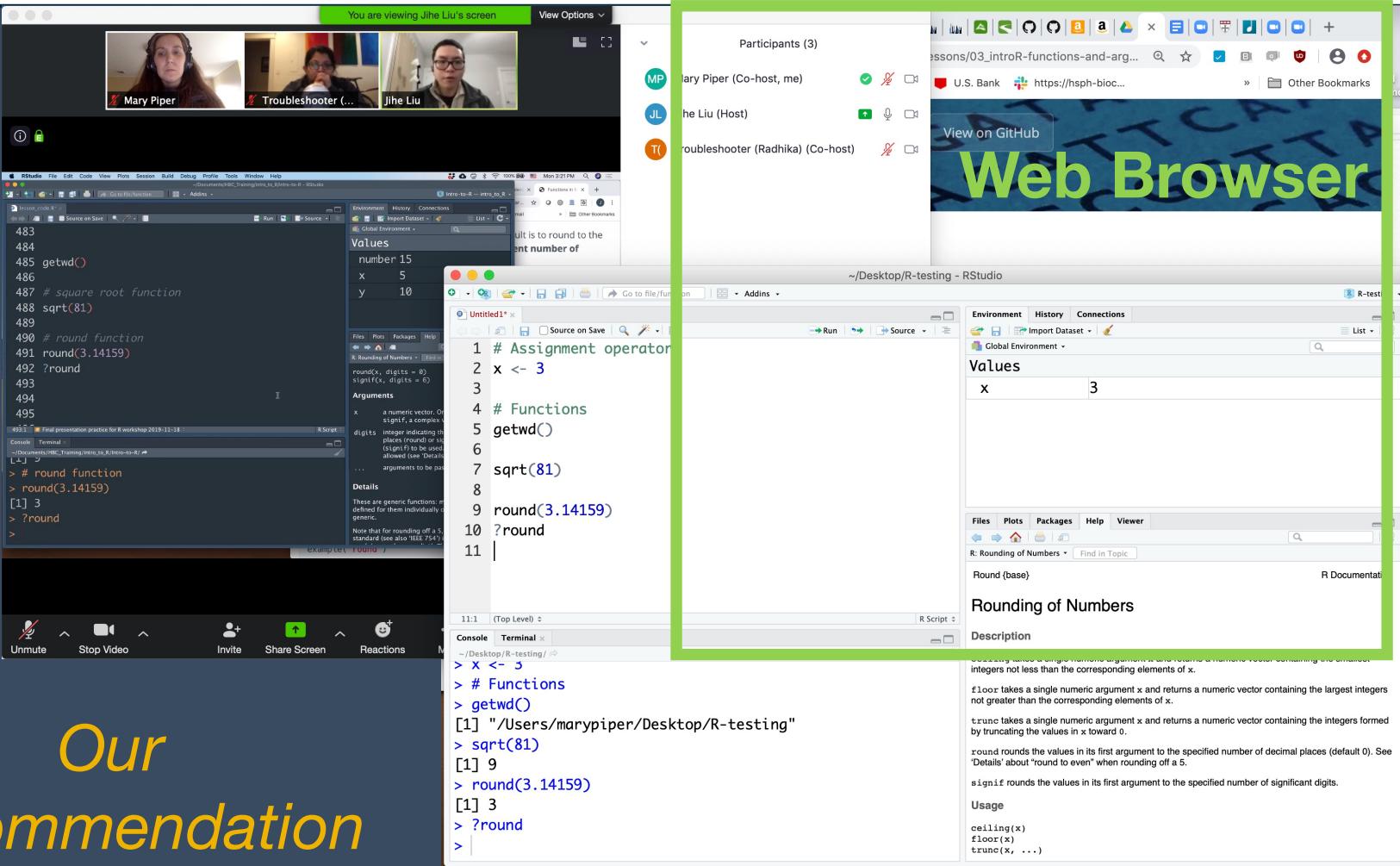


Single Screen & 3 Windows



*Our
Recommendation*

Single Screen & 3 Windows

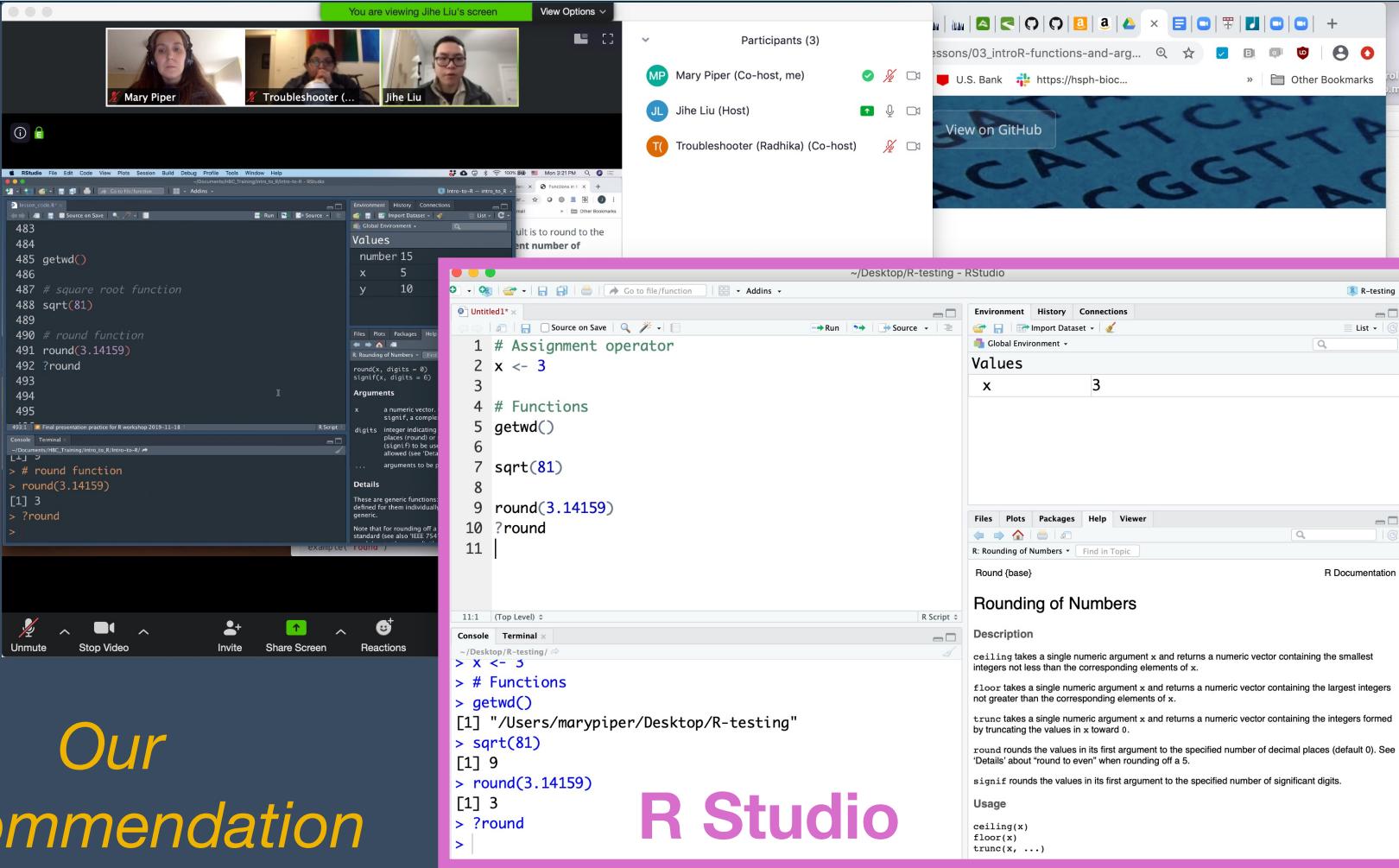


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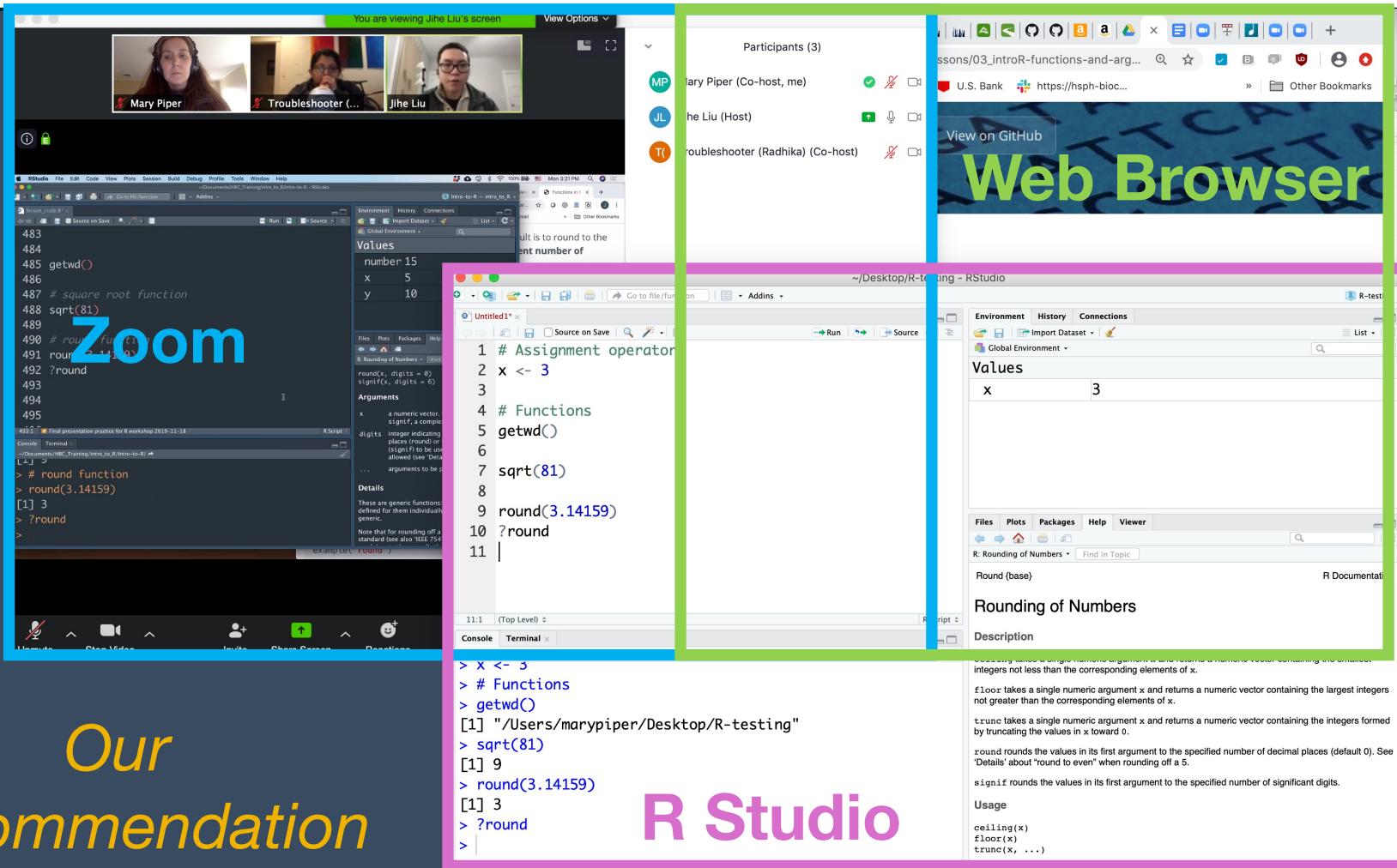
Single Screen & 3 Windows

Our Recommendation

R Studio



Single Screen & 3 Windows



Course participation

- ❖ Mandatory review of self-learning lessons and assignments
- ❖ Attendance required for all classes
- ❖ Your questions and active participation drive learning
- ❖ **We look forward to all of your questions!**



Course participation

- ❖ At-home lessons and exercises after each session
- ❖ Cover material not previously discussed
- ❖ Provides us feedback to help pace the course appropriately
- ❖ 3-5 hours to complete
- ❖ Homework load is heavier in the beginning of this workshop series and tapers off

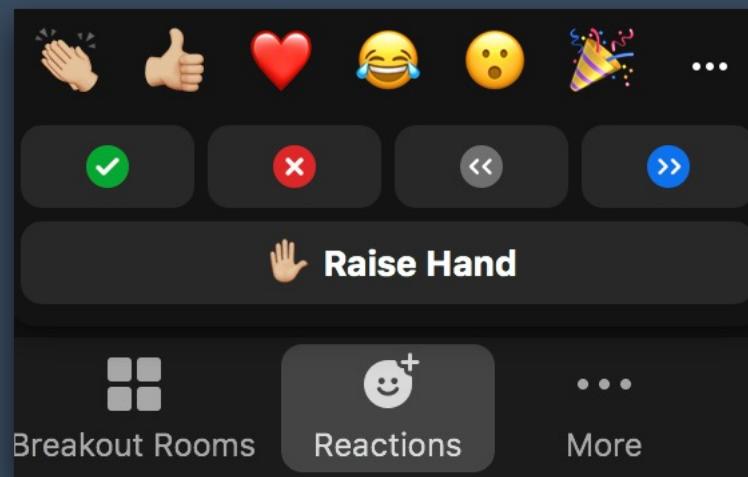
Using AI for Assignments

- ❖ Do
 - ❖ Try to resolve error messages with it
 - ❖ Test code written by AI on a dataset where you have expected results
 - ❖ Take the time to review the generated code line-by-line
- ❖ Don't
 - ❖ Implement it in replacement to learning
 - ❖ Write code that you don't understand
 - ❖ Assume the output from an AI process is correct

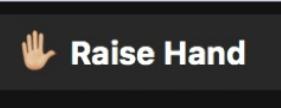
Odds & Ends

- ❖ Quit/minimize all applications that are not required for class
- ❖ Are you all set?

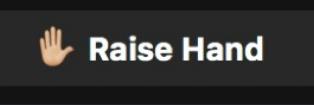
- ❖  = "agree", "I'm all set"
- ❖  = "disagree", "I need help"



Odds & Ends

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

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 - ❖  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

Contact Us

- ❖ *HBC training team:* hbctraining@hsph.harvard.edu
- ❖ *HBC consulting:* bioinformatics@hsph.harvard.edu