

Introduction to R

Harvard Chan Bioinformatics Core

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

Sponsored by DF/HCC, HSCI, HMS Foundry



Shannan Ho Sui
Director



John Hutchinson
Associate Director



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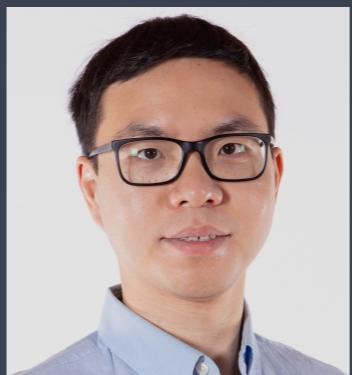
Preetida Bhetariya



Meeta Mistry



Mary Piper
Assoc. Training Director



Jihe Liu



Radhika Khetani
Training Director



Maria Simoneau



James Billingsley



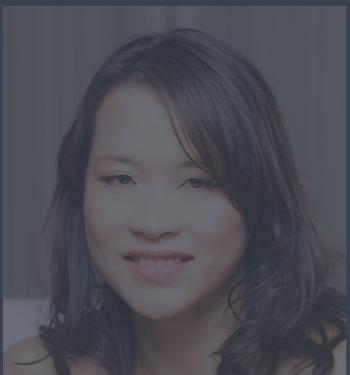
Sergey Naumenko



Joon Yoon



Peter Kraft
Faculty Advisor



Shannan Ho Sui
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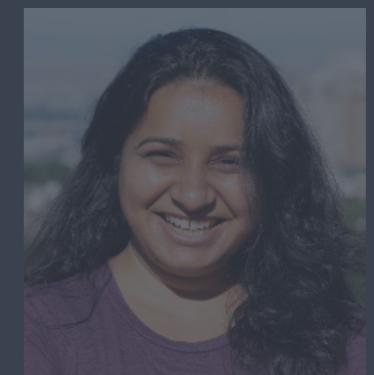
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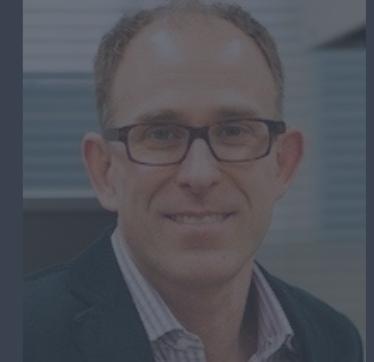
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Consulting

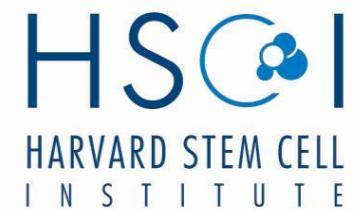
- RNA-seq analysis: bulk, single cell, small RNA
- ChIP-seq and ATAC-seq analysis
- Genome-wide methylation
- WGS, resequencing, exome-seq and CNV studies
- QC & analysis of gene expression arrays
- Functional enrichment analysis
- Grant support

<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/>



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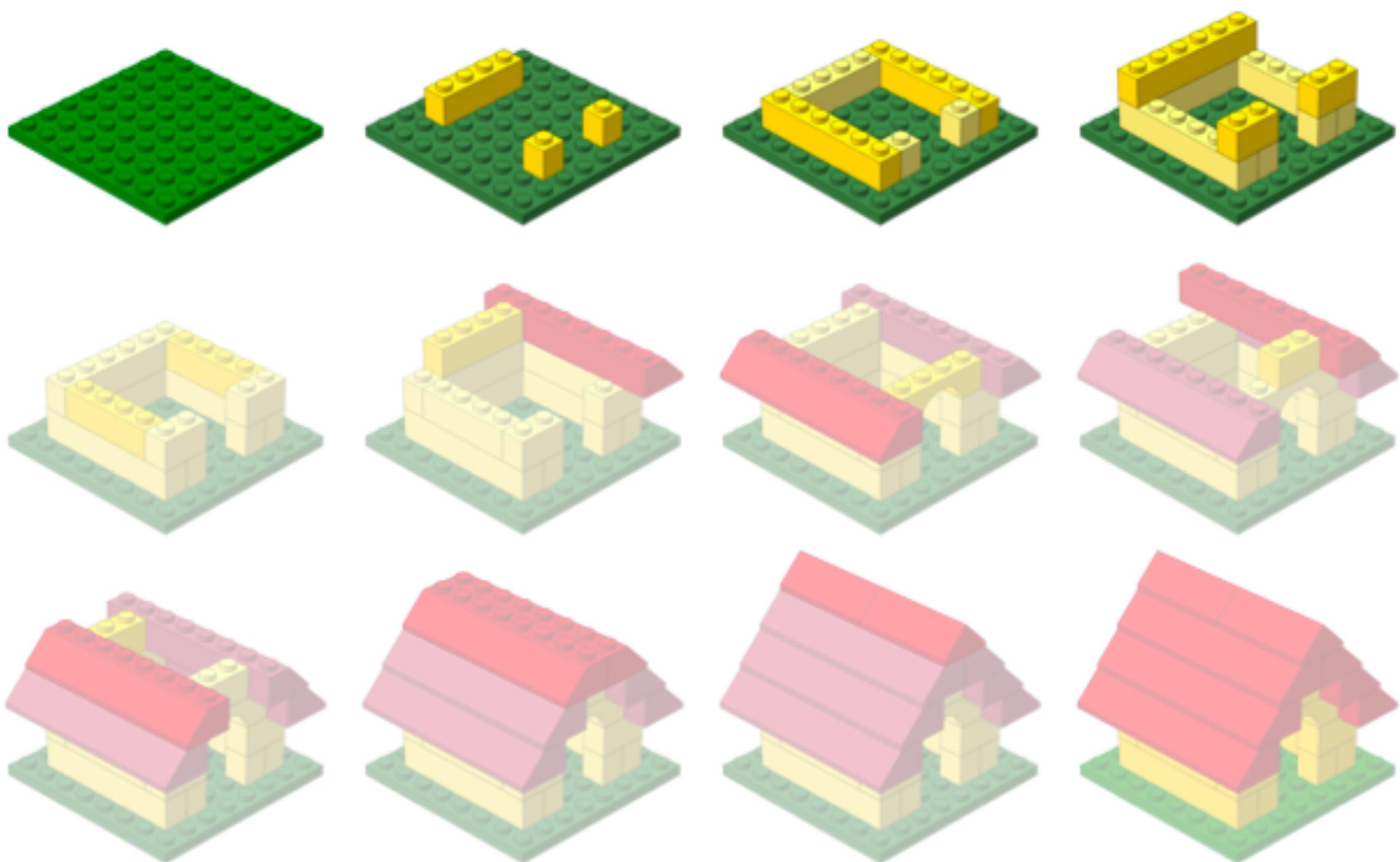
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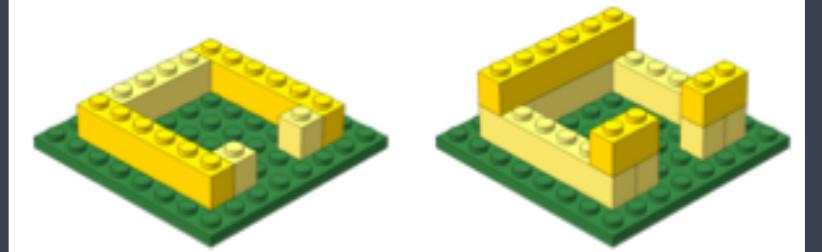
Introductions!

Workshop Scope...



Learning R

Workshop Scope



- ✓ Comfortably use RStudio (a graphical interface for R)
- ✓ Fluently interact with R using RStudio
- ✓ Become familiar with R syntax
- ✓ Understand data structures in R
- ✓ Inspect and manipulate data structures
- ✓ Install packages and use functions in R

CRAN

(Comprehensive R Archive Network)



Available CRAN Packages By Name

[A](#) [B](#) [C](#) [D](#) [E](#) [F](#) [G](#) [H](#) [I](#) [J](#) [K](#) [L](#) [M](#) [N](#) [O](#) [P](#) [Q](#) [R](#) [S](#) [T](#) [U](#) [V](#) [W](#) [X](#) [Y](#) [Z](#)

A3	Accurate, Adaptable, and Accessible Error Metrics for Predictive Models
abbyyR	Access to Abbyy Optical Character Recognition (OCR) API
abc	Tools for Approximate Bayesian Computation (ABC)
ABCanalysis	Computed ABC Analysis
abc.data	Data Only: Tools for Approximate Bayesian Computation (ABC)
abcdeFBA	ABCDE_FBA: A-Biologist-Can-Do-Everything of Flux Balance Analysis with this package
ABCOptim	Implementation of Artificial Bee Colony (ABC) Optimization
ABCp2	Approximate Bayesian Computational Model for Estimating P2
abcrf	Approximate Bayesian Computation via Random Forests

*CRAN
Mirrors
What's new?
Task Views
Search

About R
R Homepage
The R Journal*

- The main repository for R packages
- Easy to install

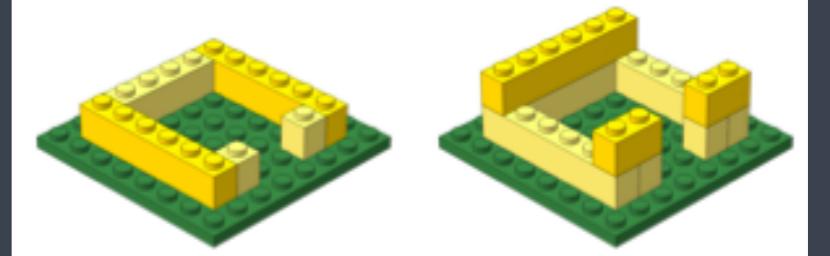
<https://cran.r-project.org/>



- An alternative package repository; “..provides tools for the analysis and comprehension of *high-throughput genomic data*.”
- Includes (but is not limited to) tools for:
 - performing statistical analysis
 - accessing public datasets
- Open source and open development
- Free

www.bioconductor.org

Workshop Scope



- Comfortably use RStudio (a graphical interface for R)
 - Fluently interact with R using RStudio
 - Become familiar with R syntax
 - Understand data structures in R
 - Inspect and manipulate data structures
 - Install packages and use functions in R
- ✓ Visualize data using *ggplot2*
- ✓ Utilize pipes, tibbles and functions from the Tidyverse package suite

Logistics

Course webpage

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

Course schedule online

Workshop Schedule

Day 1

Time	Topic	Instructor
10:00 - 10:30	Workshop Introduction	Radhika
10:30 - 11:15	Introduction to R and RStudio	Radhika
11:15 - 11:30	Overview of self-learning materials and homework submission	Mary

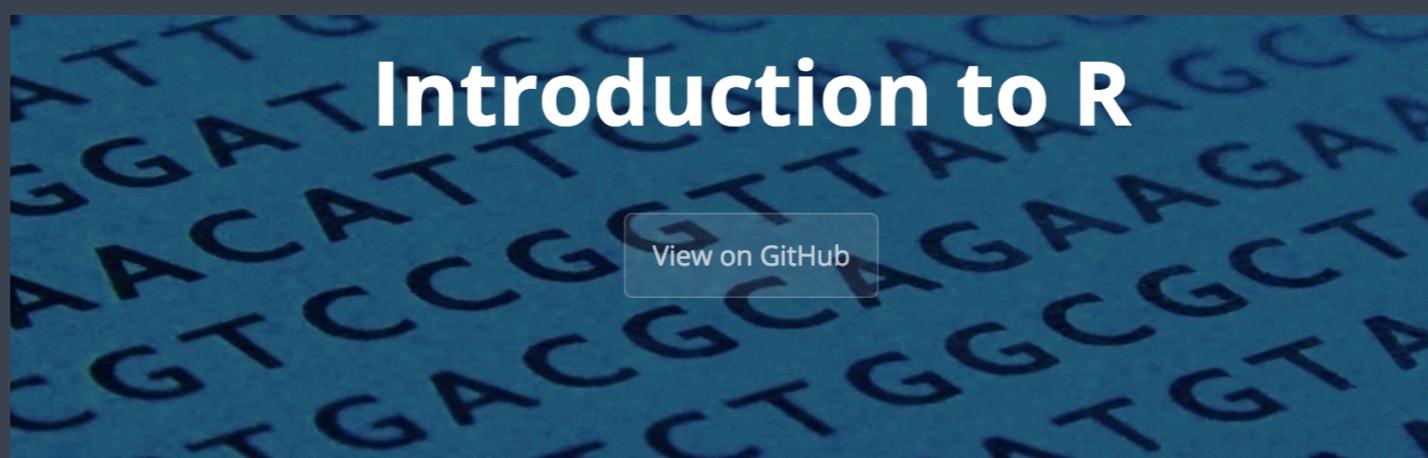
Self-Learning Part 1

1. [R Syntax and Data Structure](#)
2. [Functions and Arguments](#)

Assignment #1

- All exercises from above lessons have been put together in [html format](#) (web access) and [R script format](#) (download for local access).
- Add your solutions to the exercises in the downloaded [.R](#) file and **upload the saved file** to [Dropbox](#) on **Wednesday before the next class**.
- [Email us](#) about questions regarding the homework that you need answered before the next class.
- Post questions that you would like to have reviewed in class [here](#).

Course materials online



Introduction to R

[View on GitHub](#)

Approximate time: 70 min

Learning Objectives

- Employ variables in R.
- Describe the various data types used in R.
- Construct data structures to store data.

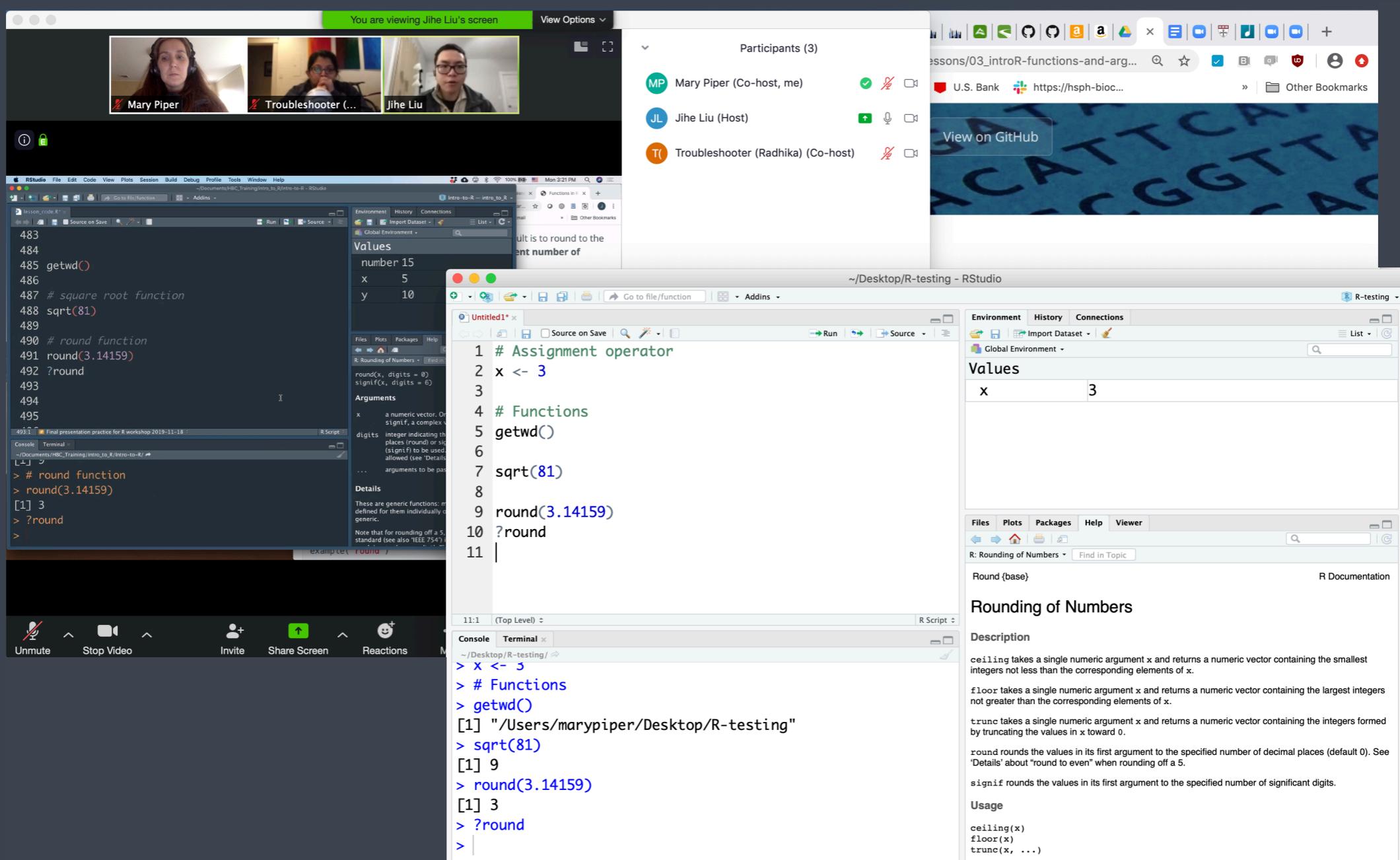
The R syntax

Now that we know how to talk with R via the script editor or the console, we want to use R for something more than adding numbers. To do this, we need to know more about the R syntax.

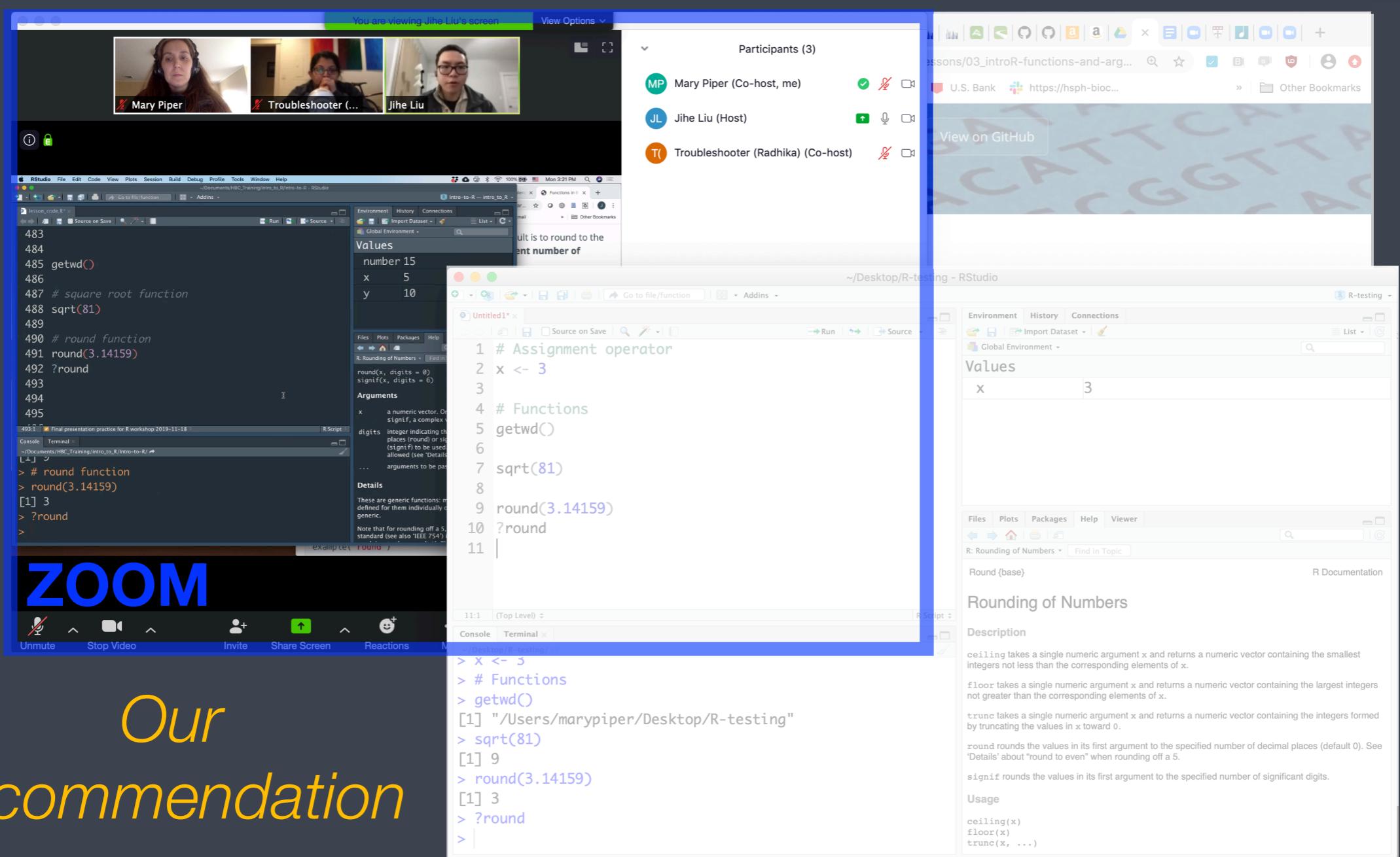
Below is an example script highlighting the many different “parts of speech” for R (syntax):

- the **comments** `#` and how they are used to document function and its content
- **variables and functions**
- the **assignment operator** `<-`

Single screen & 3 windows?

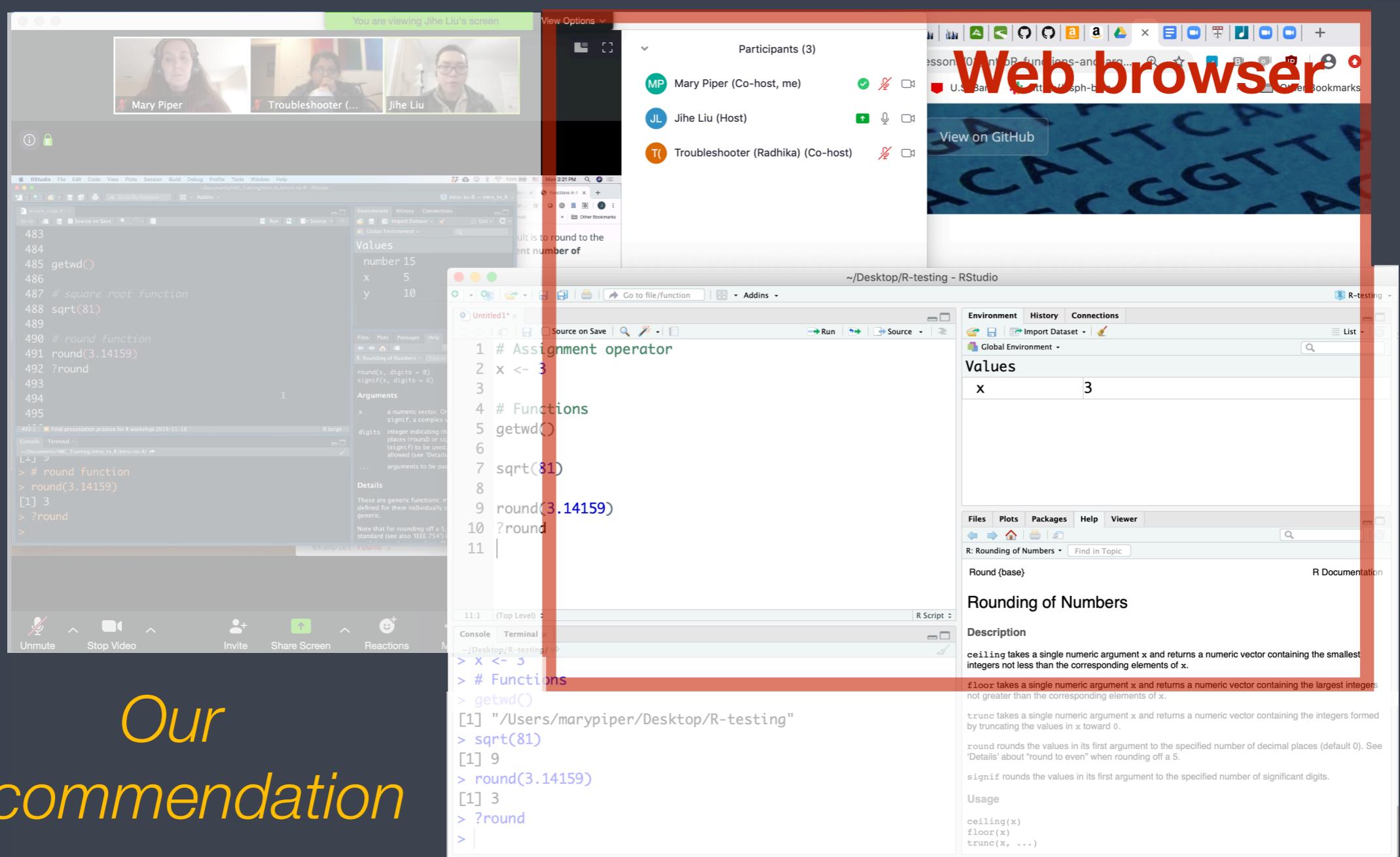


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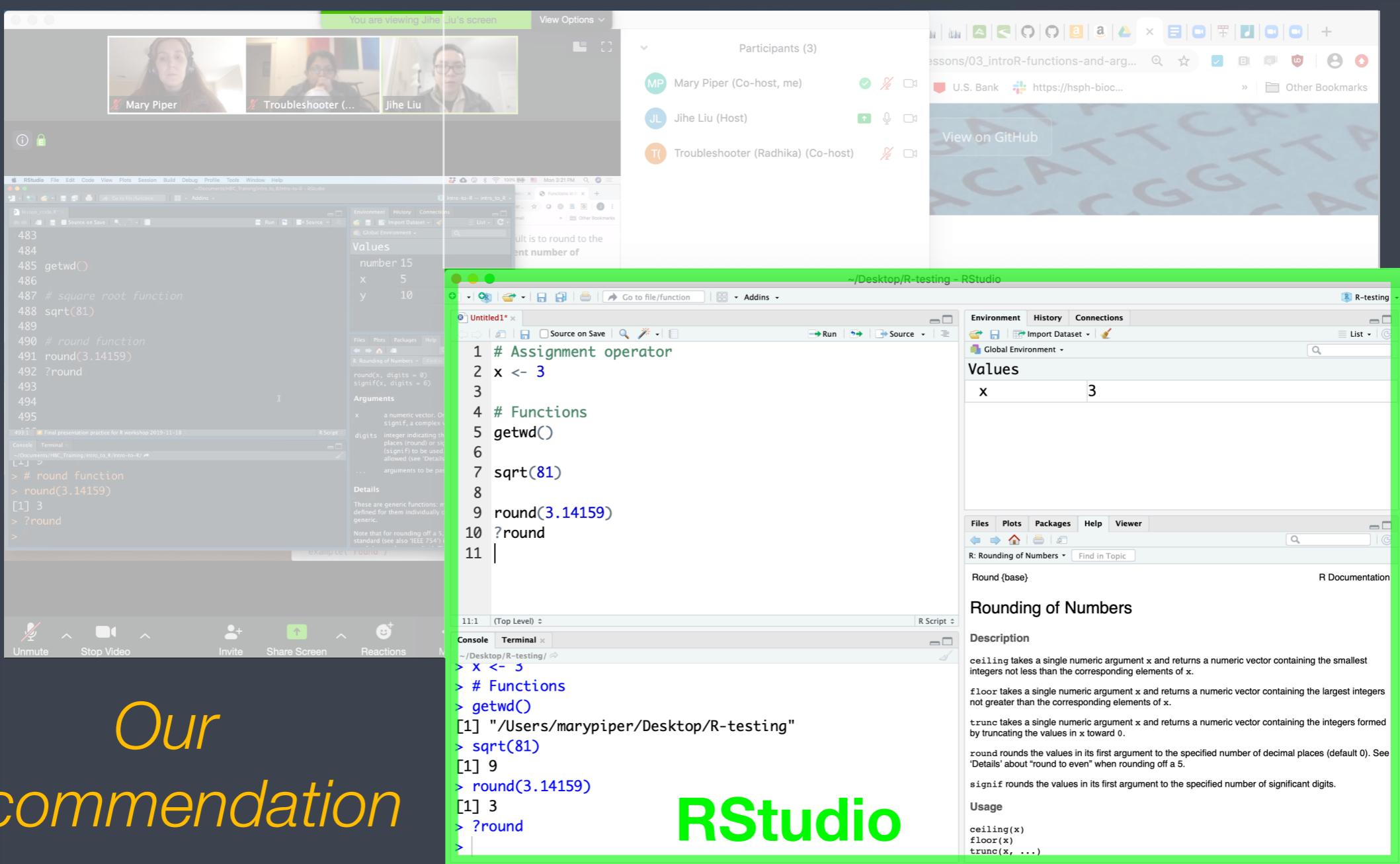


*Our
recommendation*

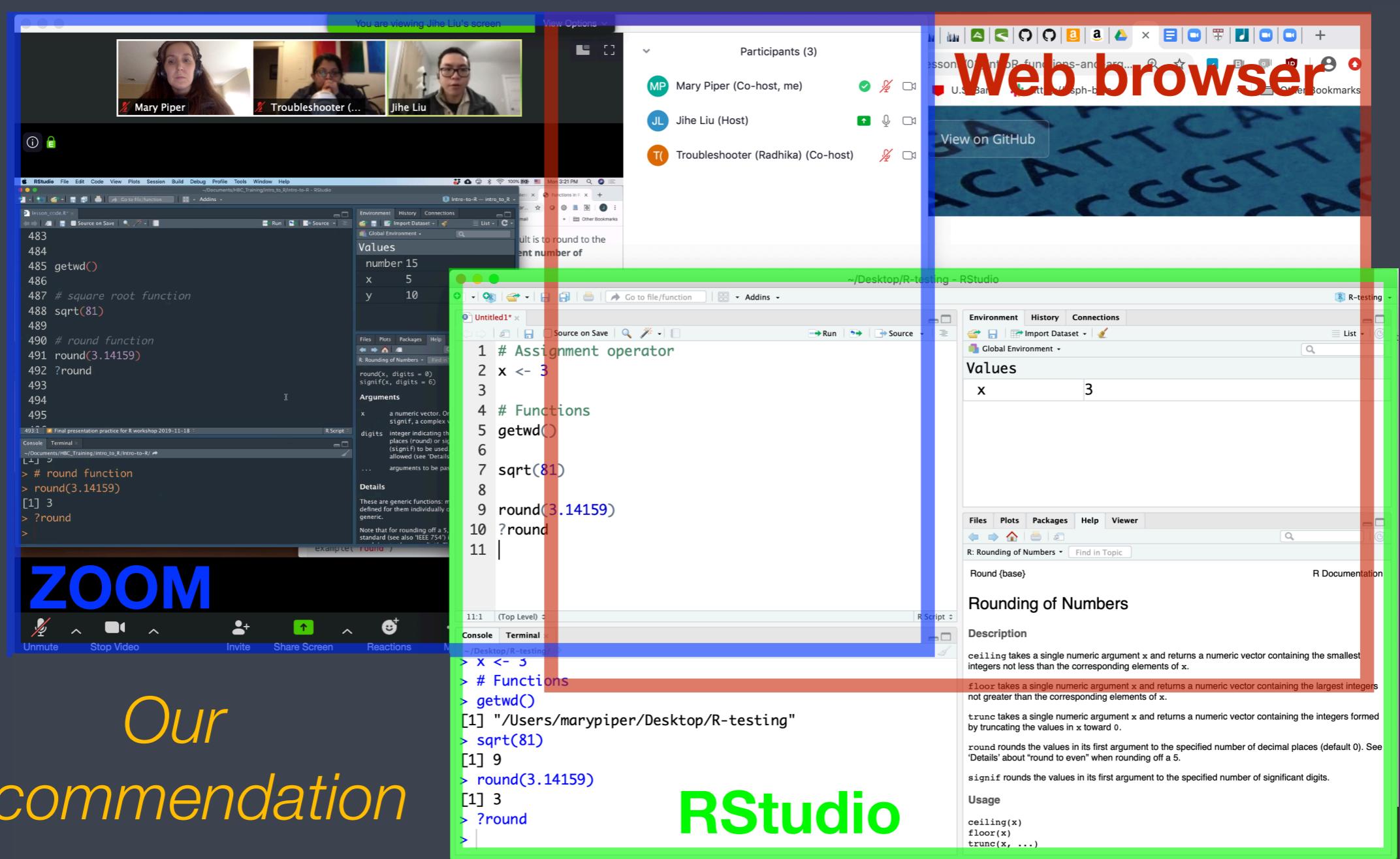
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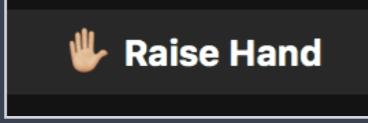


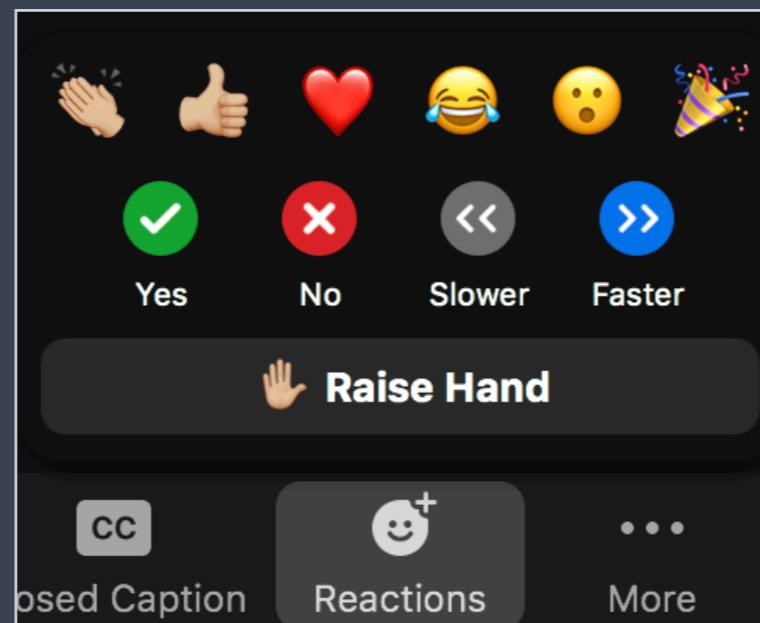
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Odds and Ends

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

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- ❖ Are you all set?
 -  = "agree", "I'm all set" (equivalent to a **green post-it**)
 - Type “X” in chat = "disagree", “I’m not ready” (equivalent to a **red post-it**)



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**)
 - 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

Odds and Ends

- ❖ Quit/minimize all applications that are not required for class
- ❖ Are you all set?
 -  **Raise Hand** = "agree", "I'm all set" (equivalent to a **green post-it**)
 - 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
- ❖ Technical difficulties with R or RStudio?
 - 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

Twitter

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