

# Introduction to R

Harvard Chan Bioinformatics Core

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

Sponsored by DF/HCC, HSCI, HMS Foundry



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Meeta Mistry



Jihe Liu



Will Gammerdinger



Maria Simoneau



James Billingsley



Sergey Naumenko



Peter Kraft  
*Faculty Advisor*

# Consulting

- Experimental design help
- 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  
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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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# Introductions!



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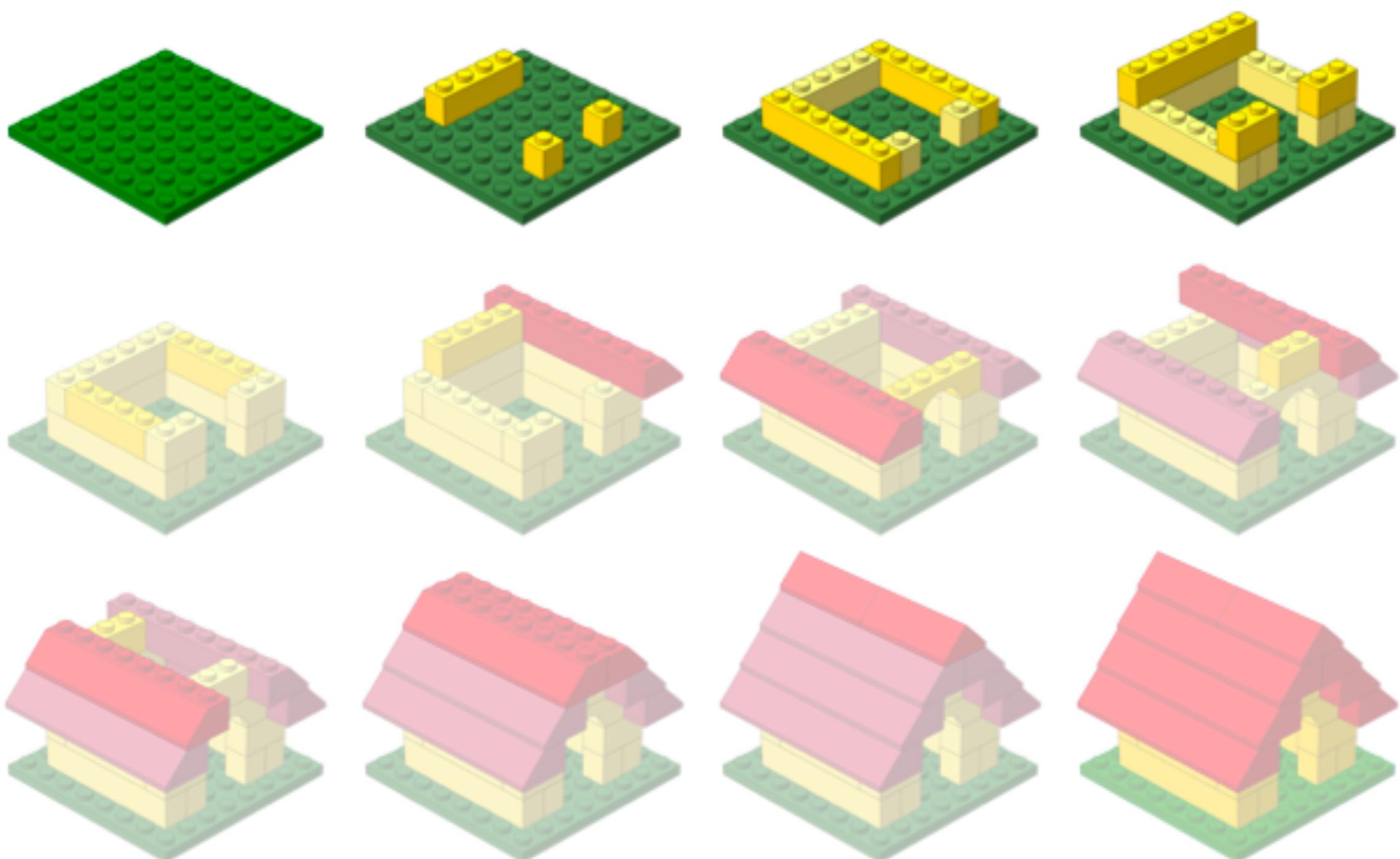


Sergey Naumenko



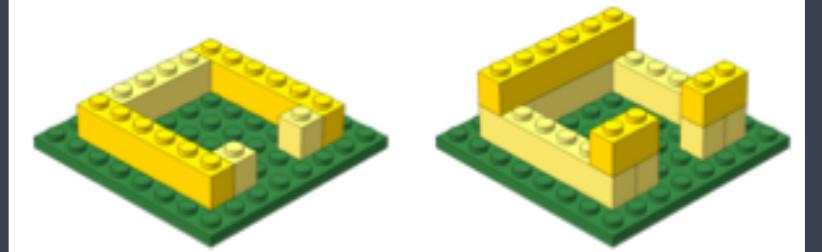
Peter Kraft  
*Faculty Advisor*

# 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](#)

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

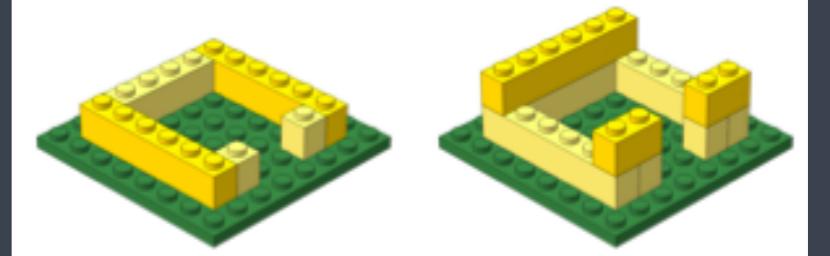
<https://cran.r-project.org/>



- 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](http://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-nanocourse>

# Course schedule online

## Workshop Schedule

### Day 1

Time	Topic	Instructor
10:00 - 10:30	Workshop Introduction	Jihe
10:30 - 11:45	Introduction to R and RStudio	Radhika
11:45 - 12:00	Overview of self-learning materials and homework submission	Mary

### Before the next class:

1. Please **study the contents** and **work through all the code** within the following lessons:
  - o [R Syntax and Data Structure](#)
  - o [Functions and Arguments](#)
  - o [Reading in and inspecting data](#)
2. **Complete the exercises:**
  - o Each lesson above contain exercises; please go through each of them.
  - o **Copy over** your code from the exercises into a text file.
  - o **Upload the saved text file** to [Dropbox](#) the **day before the next class**.

# 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.

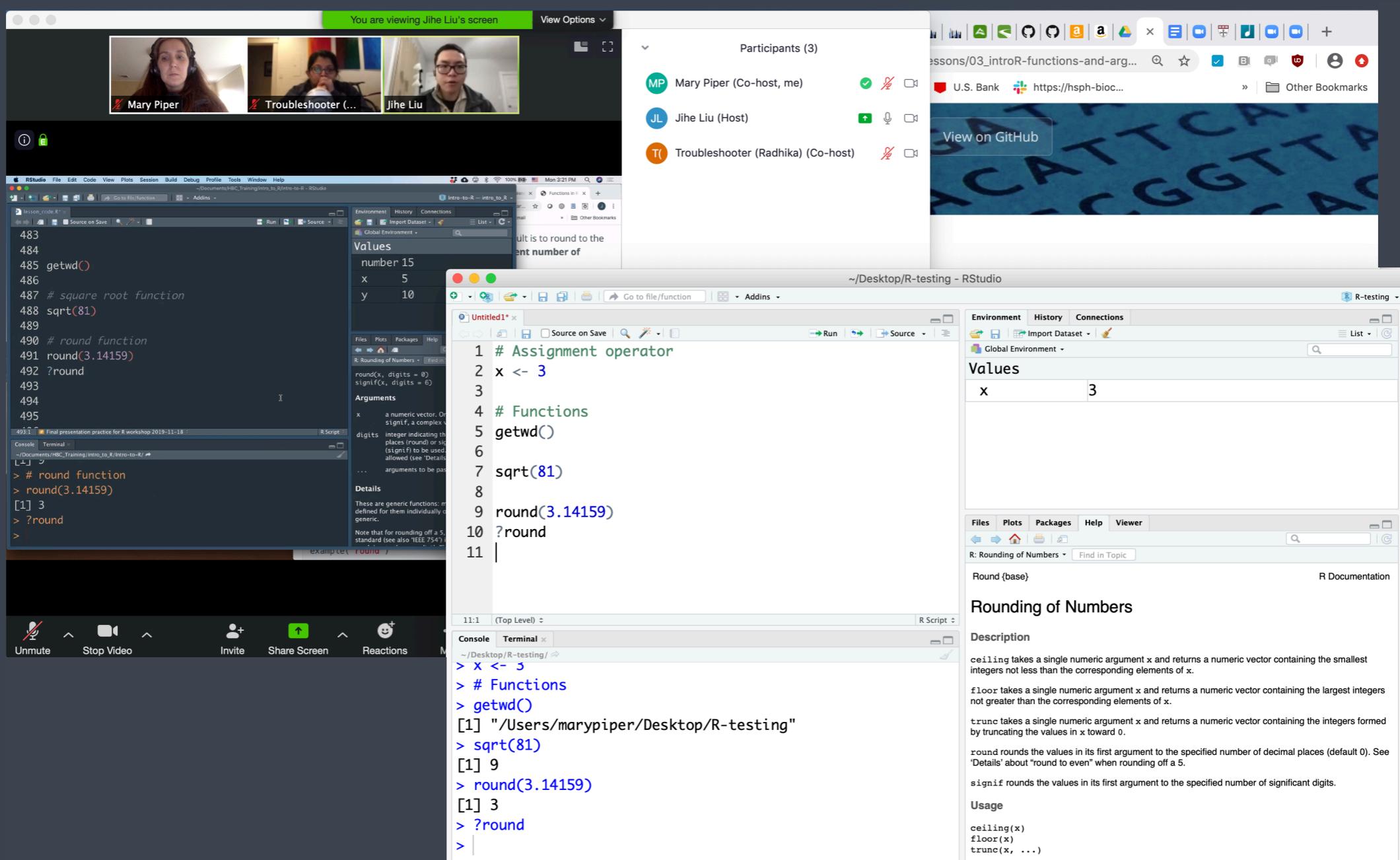
### The R syntax

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.

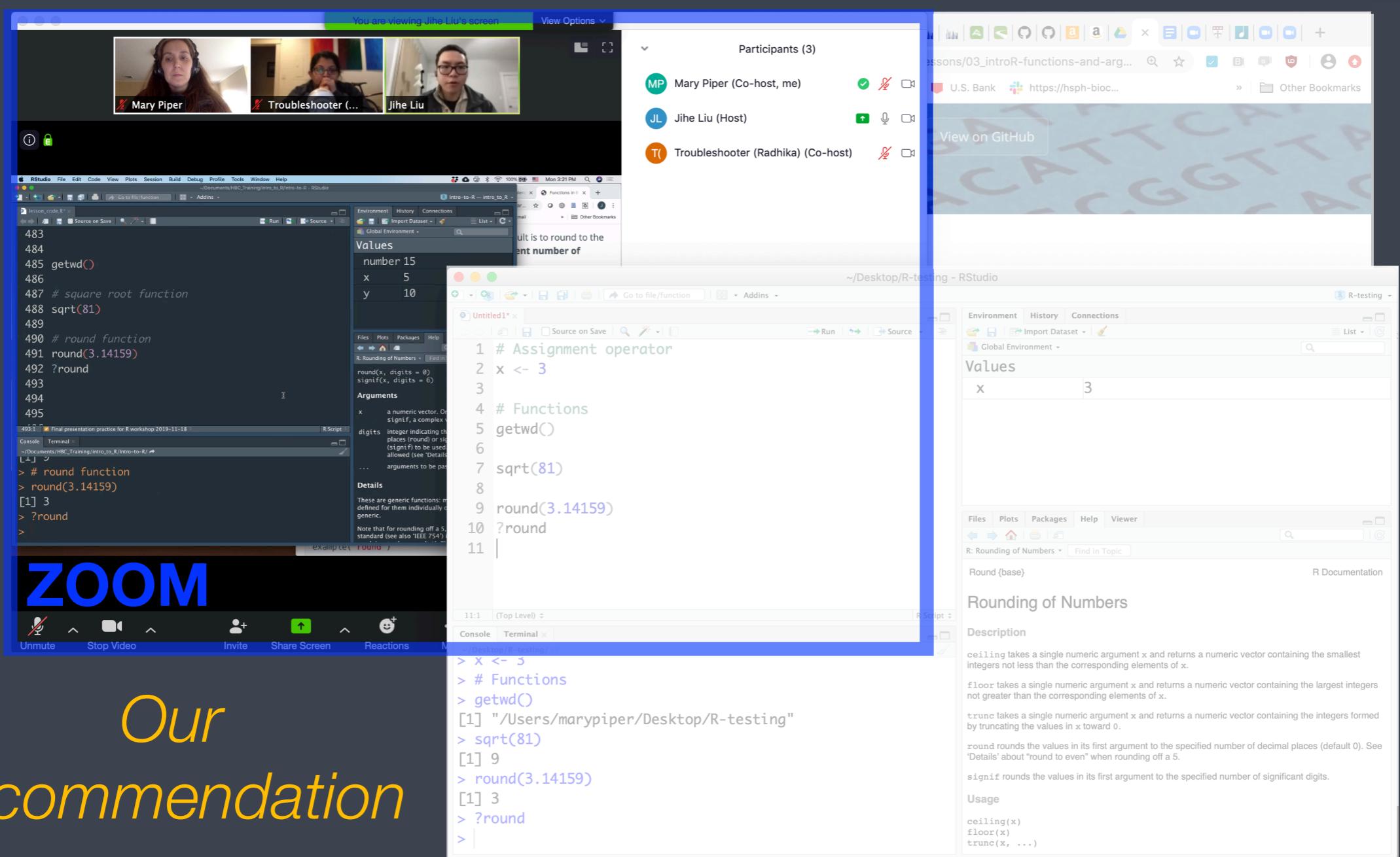
Below is an example script highlighting the many different “parts of speech” for R (syntax):

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

# Single screen & 3 windows?

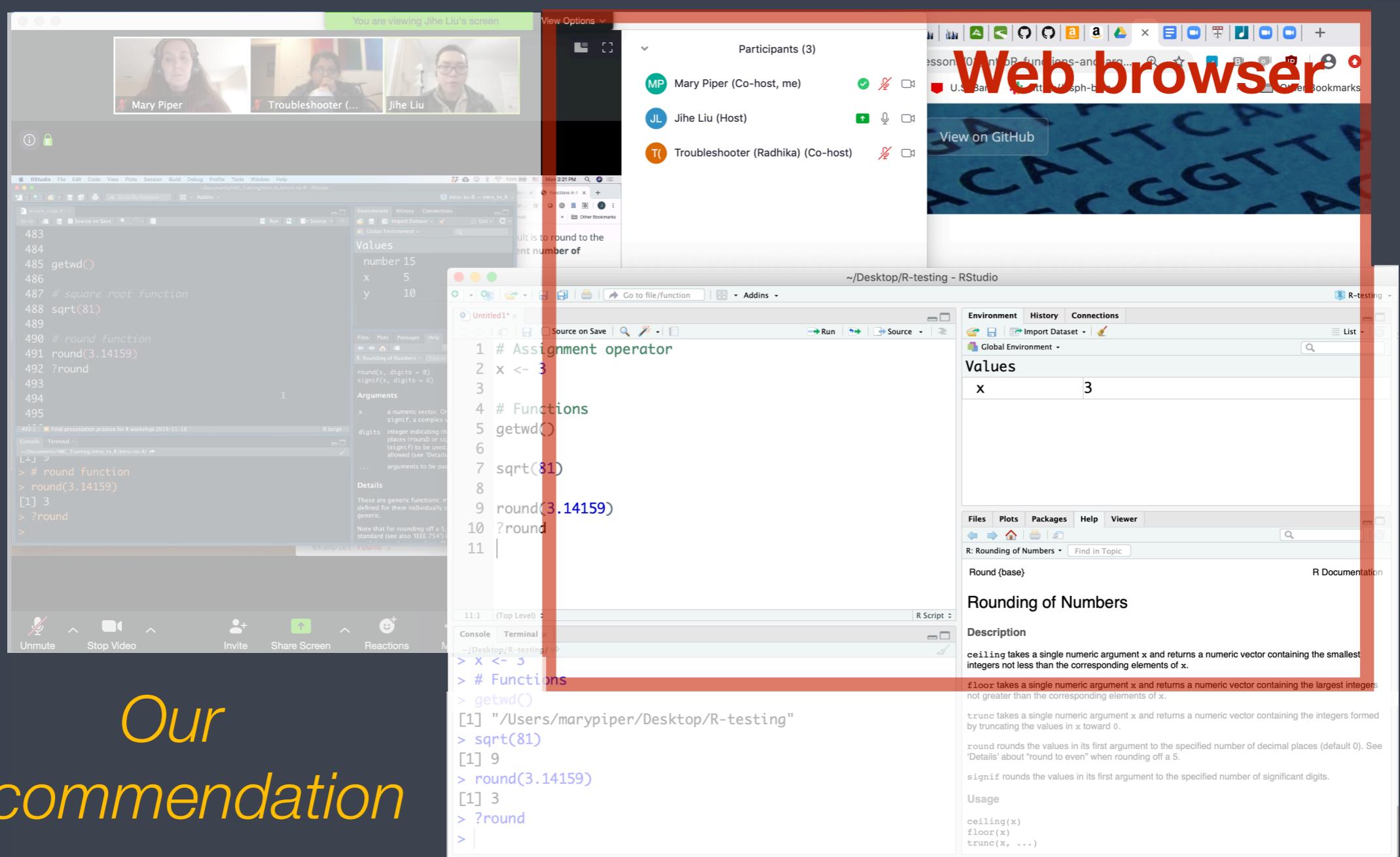


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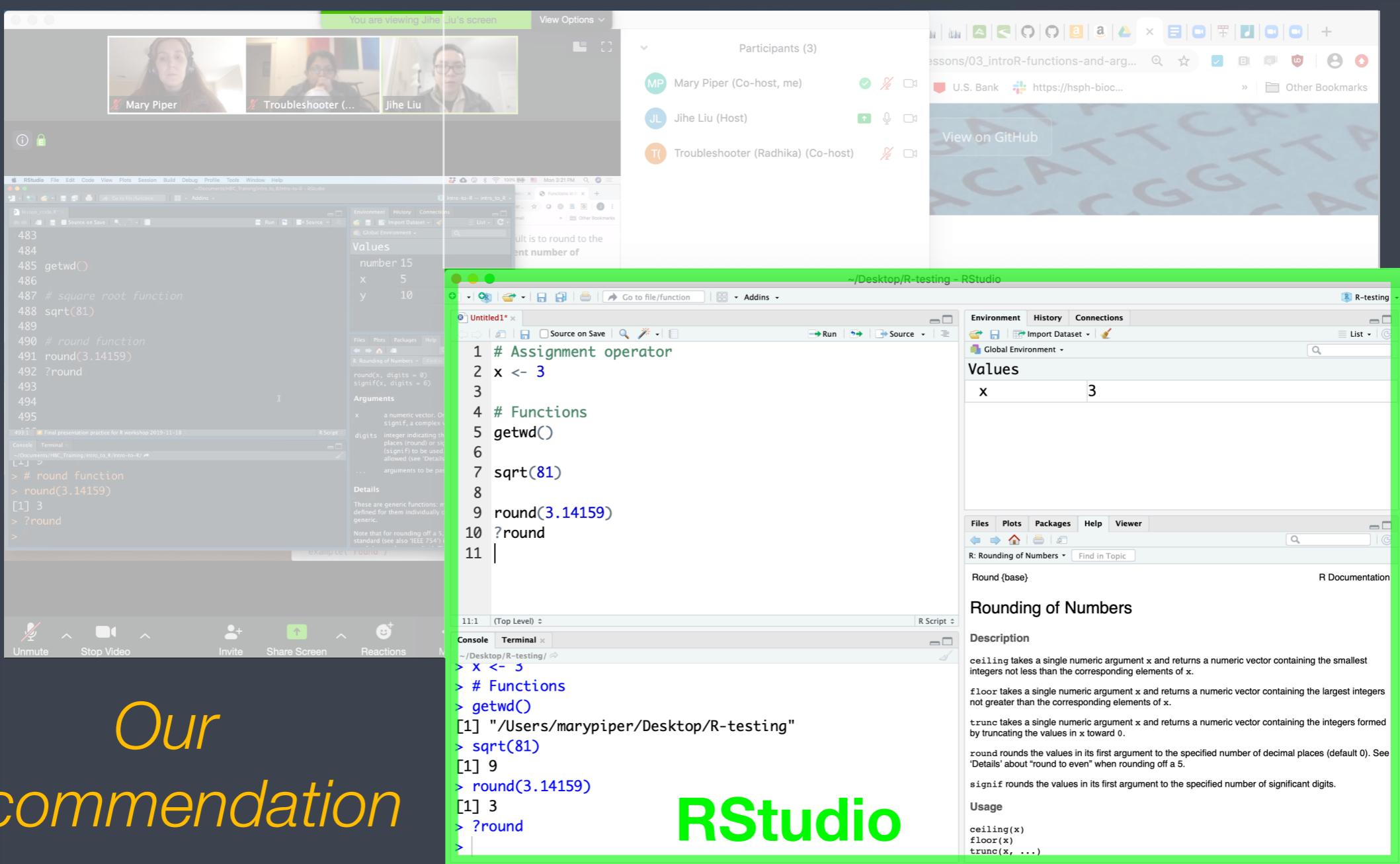


*Our  
recommendation*

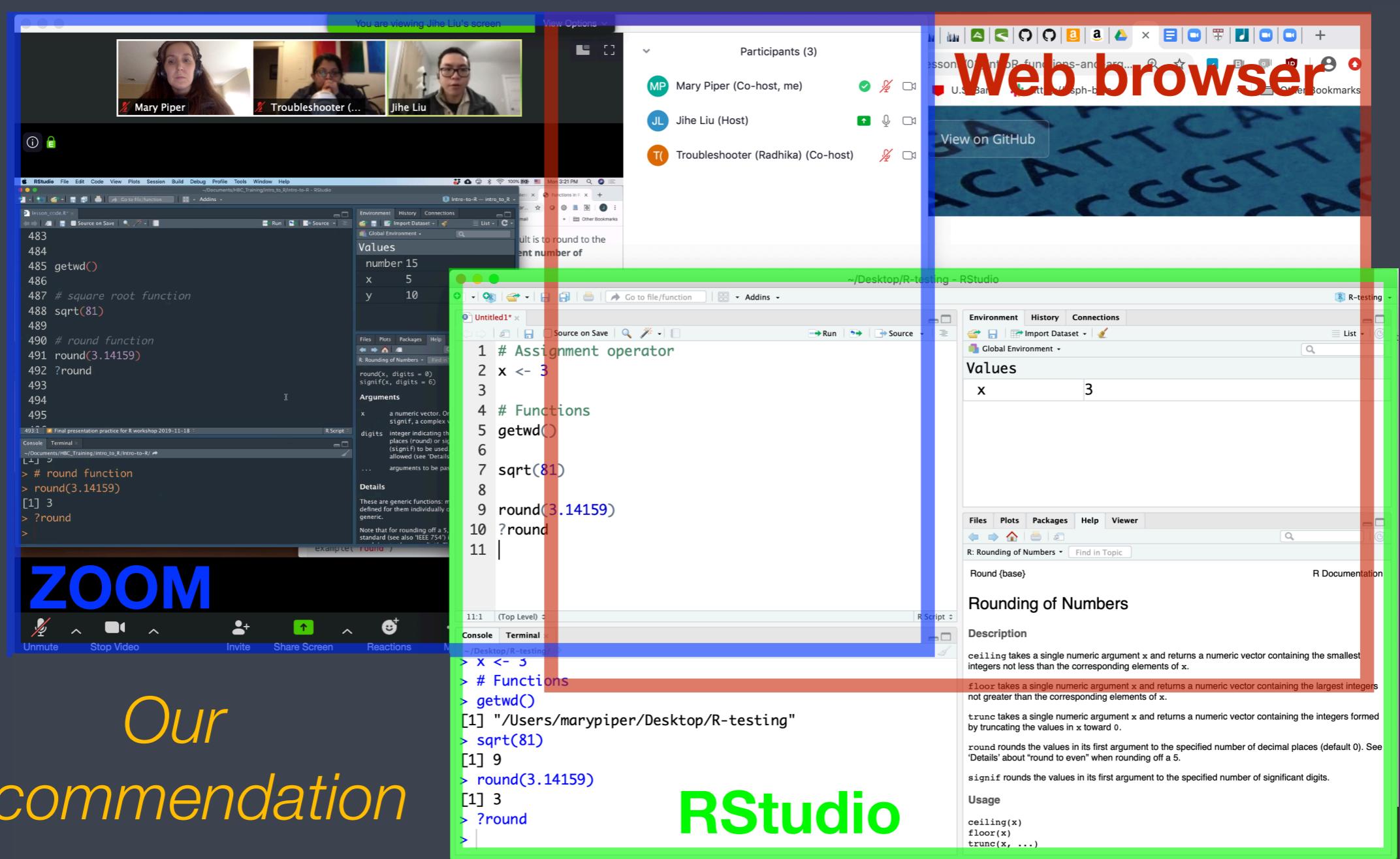
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# Single screen & 3 windows?



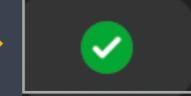
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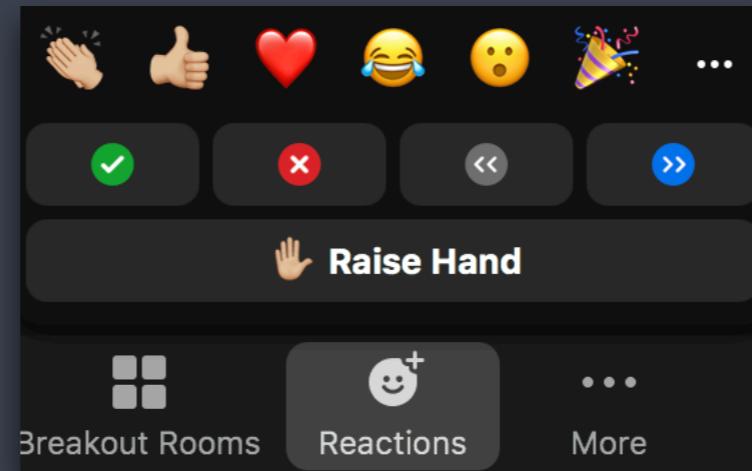


# Odds and Ends

- ❖ Quit/minimize all applications that are not required for class
- ❖ Captioning is available upon request

# Odds and Ends (1/2)

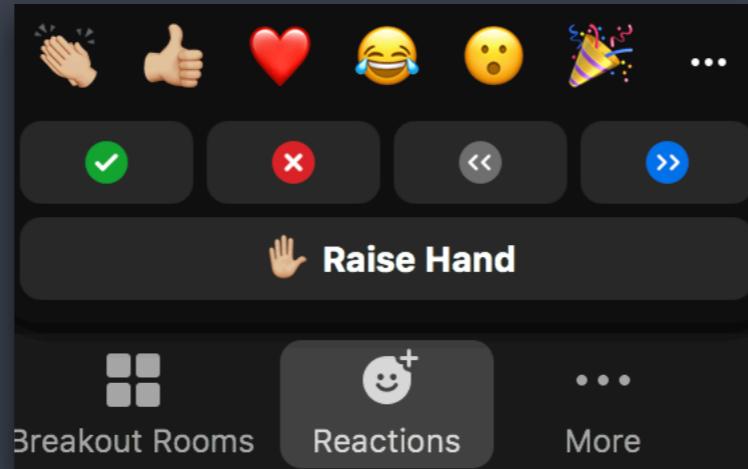
- ❖ Quit/minimize all applications that are not required for class
- ❖ Captioning is available upon request
- ❖ Are you all set?
  - ▶  = "agree", "I'm all set" (equivalent to a **green post-it**)
  - ▶  = "disagree", "I need help" (equivalent to a **red post-it**)



# Odds and Ends (2/2)

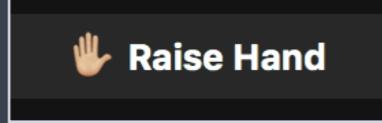
- ❖ Questions for the presenter?

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



# Odds and Ends (2/2)

- ❖ Questions for the presenter?

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

- ❖ Technical difficulties with RStudio or R?

- Start a private chat with the Troubleshooter with a description of the problem.

# Contact us!

*HBC training team:* [hbctraining@hsph.harvard.edu](mailto:hbctraining@hsph.harvard.edu)

*HBC consulting:* [bioinformatics@hsph.harvard.edu](mailto:bioinformatics@hsph.harvard.edu)

Twitter

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