

Introduction to R

Harvard Chan Bioinformatics Core

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

Sponsored by HMS (TnT) and HSCI



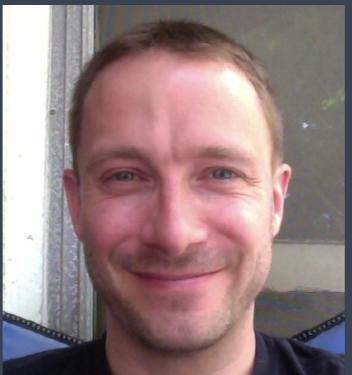
Shannan Ho Sui
Director



John Hutchinson
Associate Director



Victor Barrera



Rory Kirchner



Zhu Zhuo



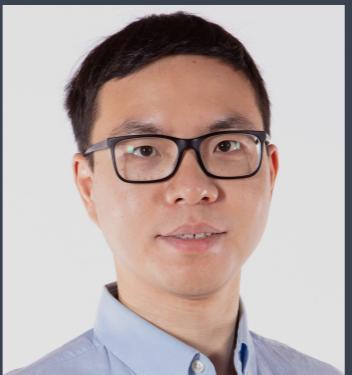
Preetida Bhetariya



Meeta Mistry



Mary Piper



Jihe Liu



Radhika Khetani
Training Director



Ilya Sytchev



James Billingsley



Sergey Naumenko



Joon Yoon

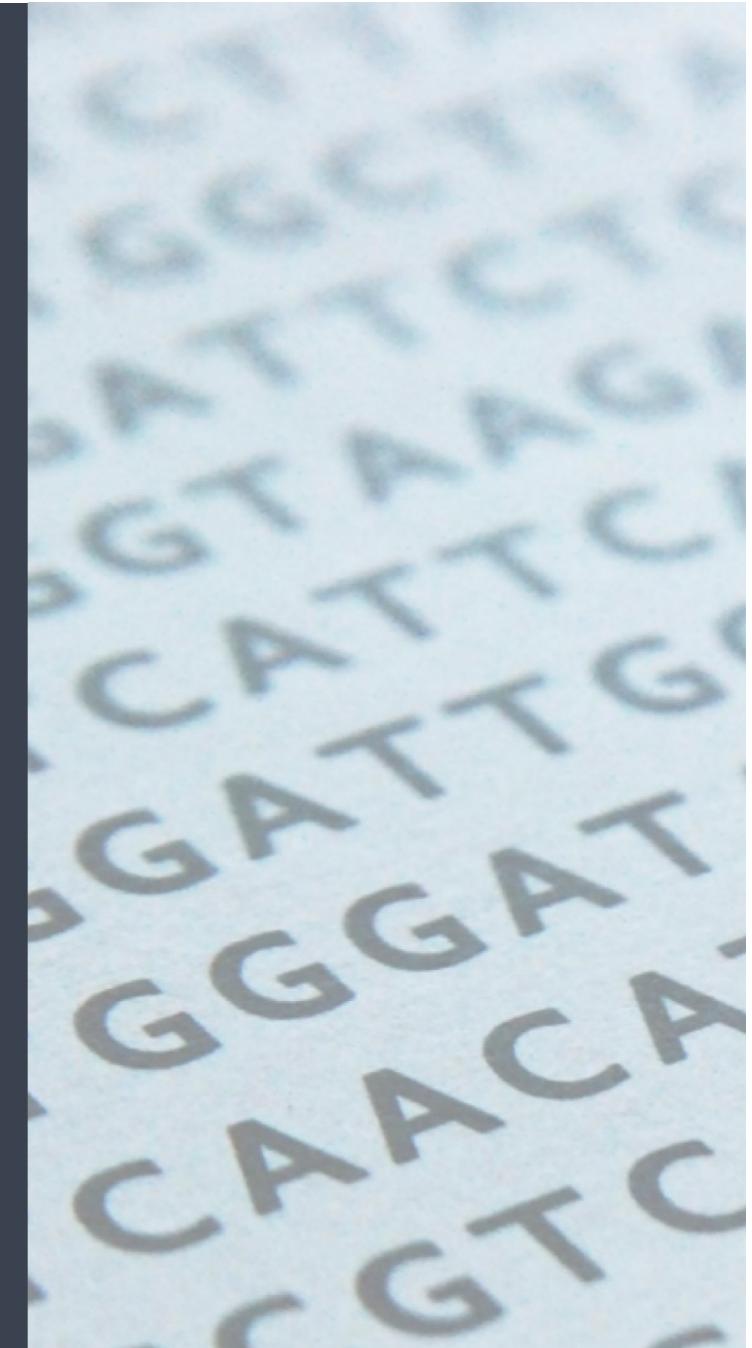


Peter Kraft
Faculty Advisor

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/>



Training

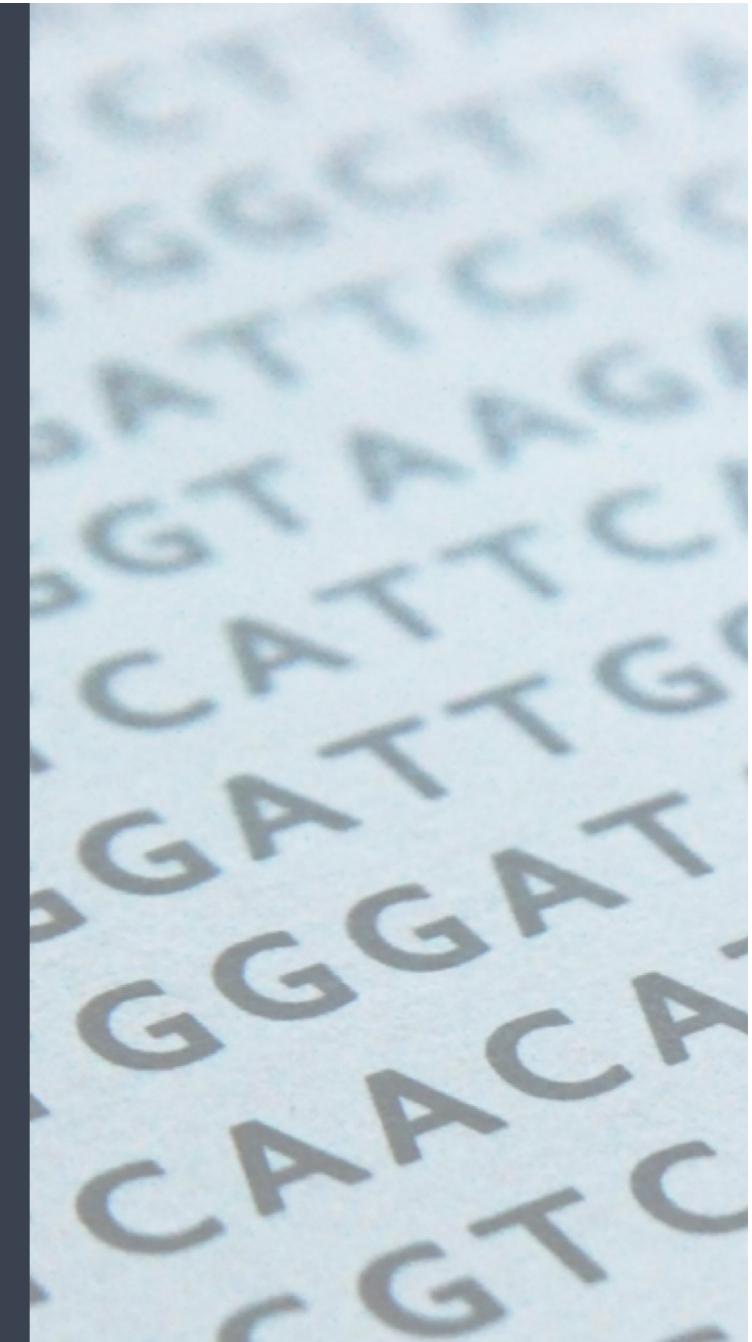
We have divided our short workshops into 2 categories:

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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NIEHS / CFAR
Bioinformatics
Core

HSCI
HARVARD STEM CELL
INSTITUTE

Center for Stem
Cell
Bioinformatics

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Consulting

HMS
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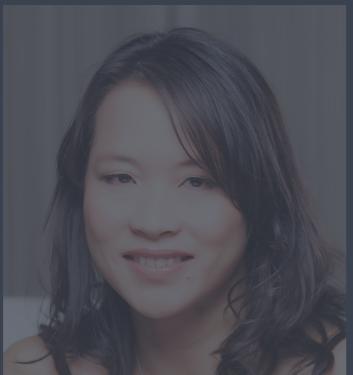
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Introductions!



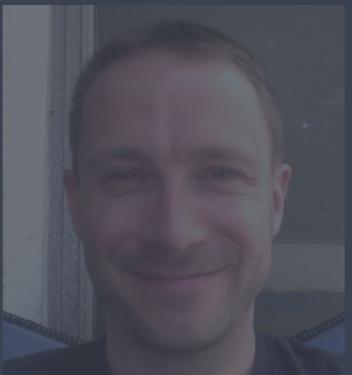
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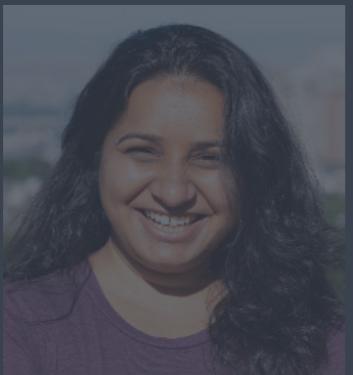
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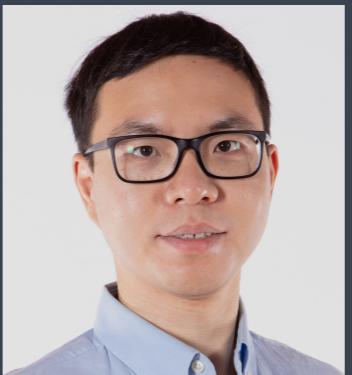
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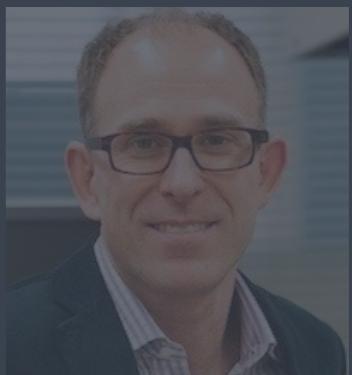
James Billingsley



Sergey Naumenko

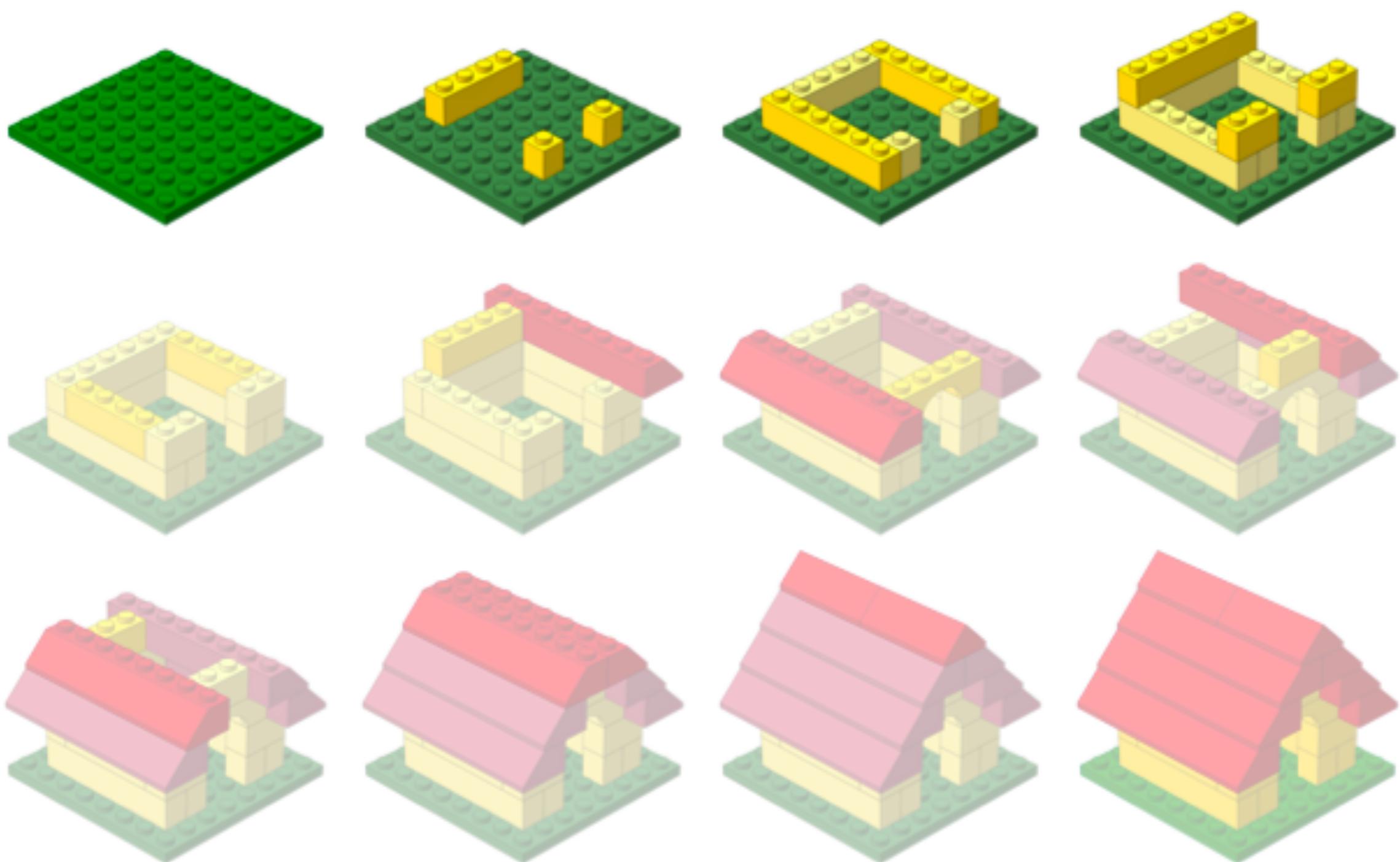


Joon Yoon



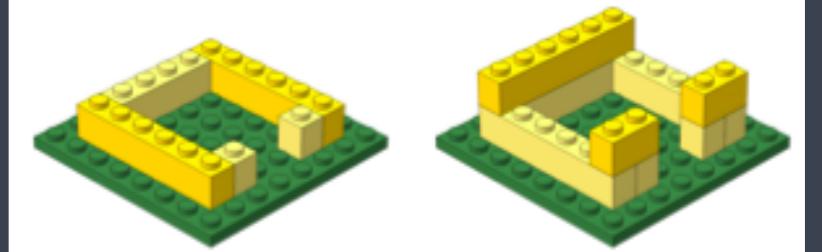
Peter Kraft
Faculty Advisor

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](#)

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

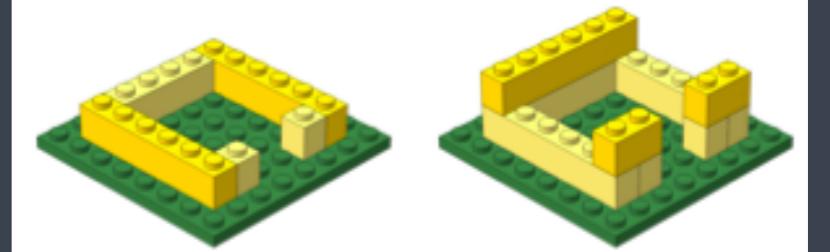
<https://cran.r-project.org/>



- 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.

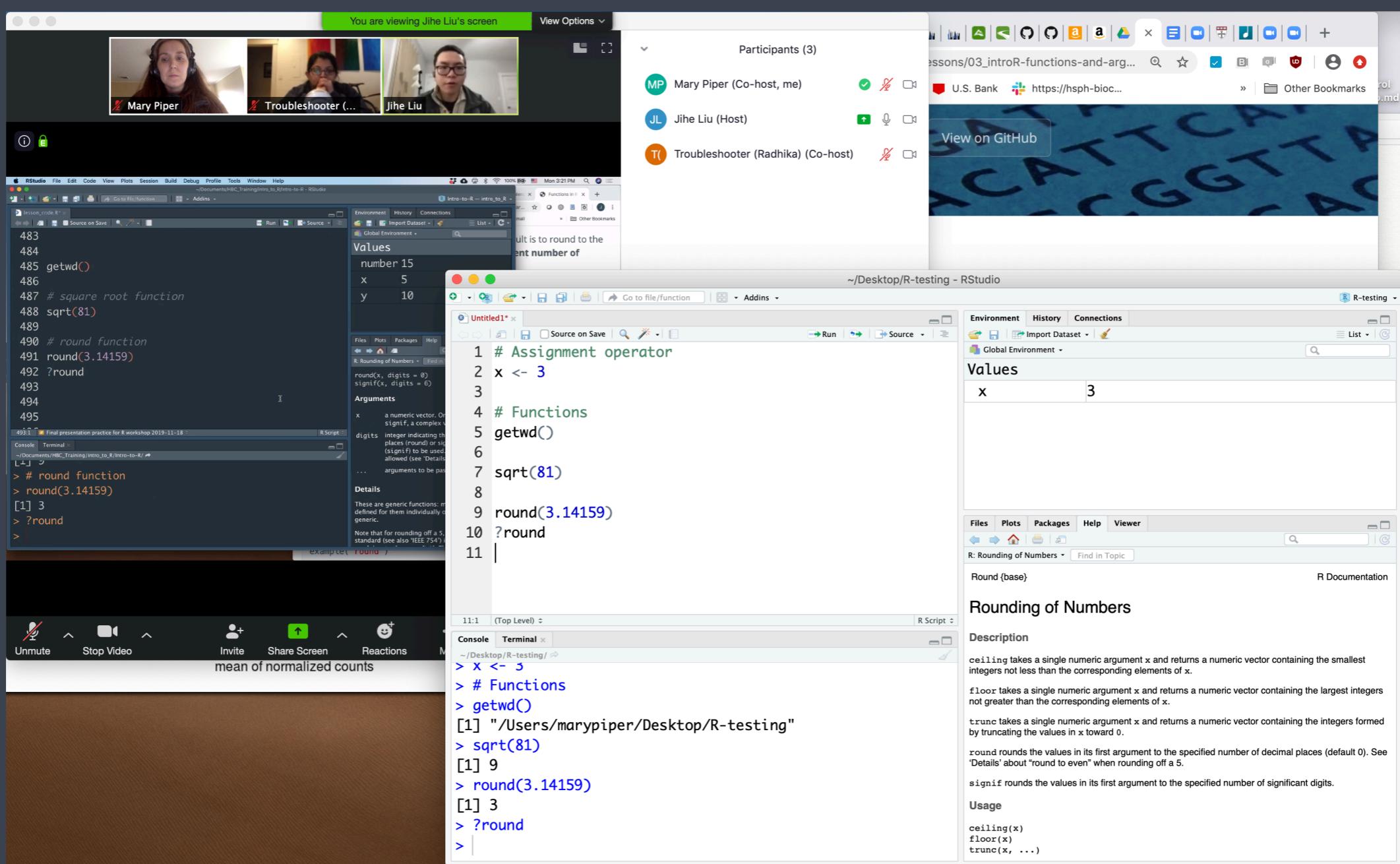
The R syntax

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.

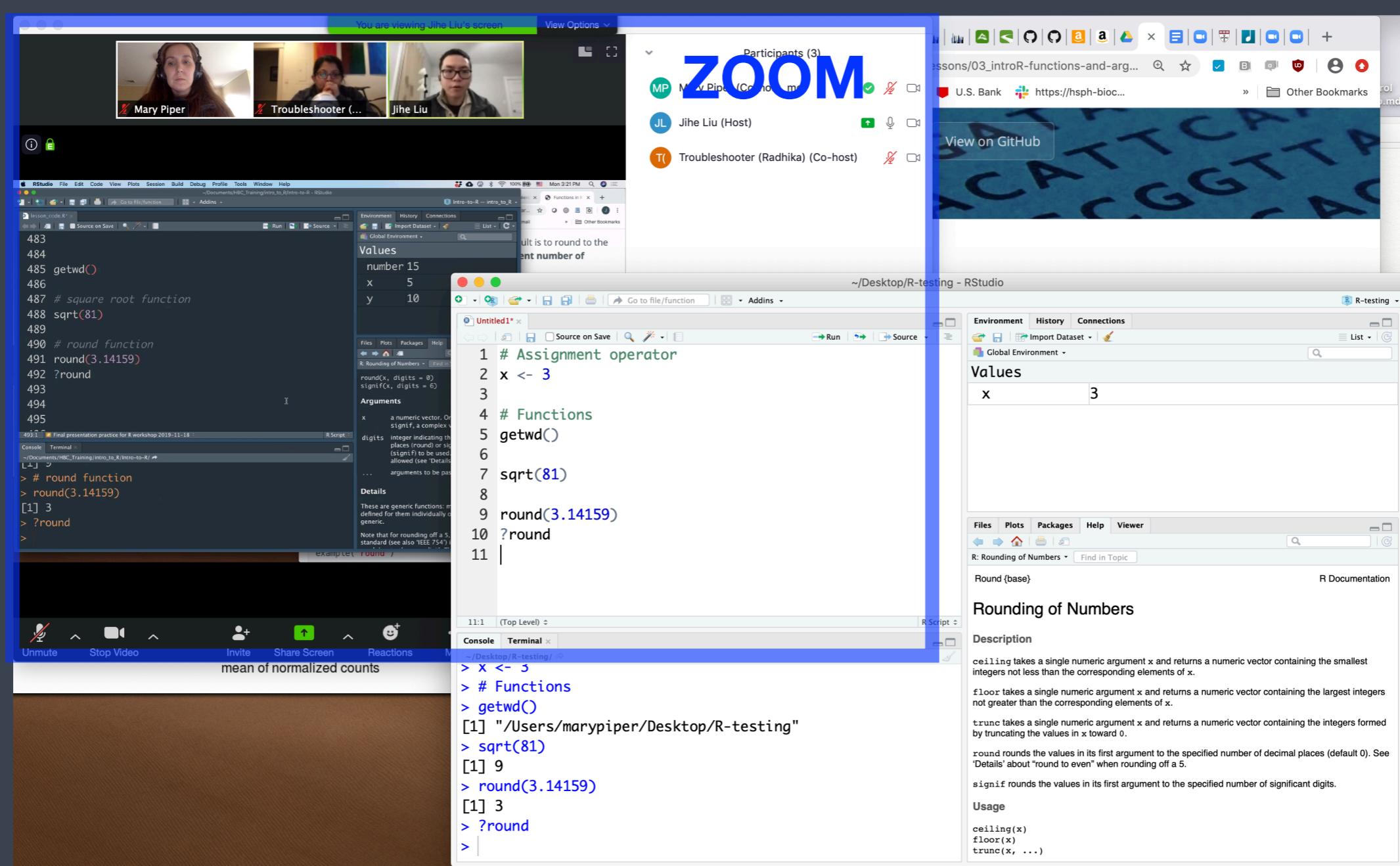
Below is an example script highlighting the many different “parts of speech” for R (syntax):

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

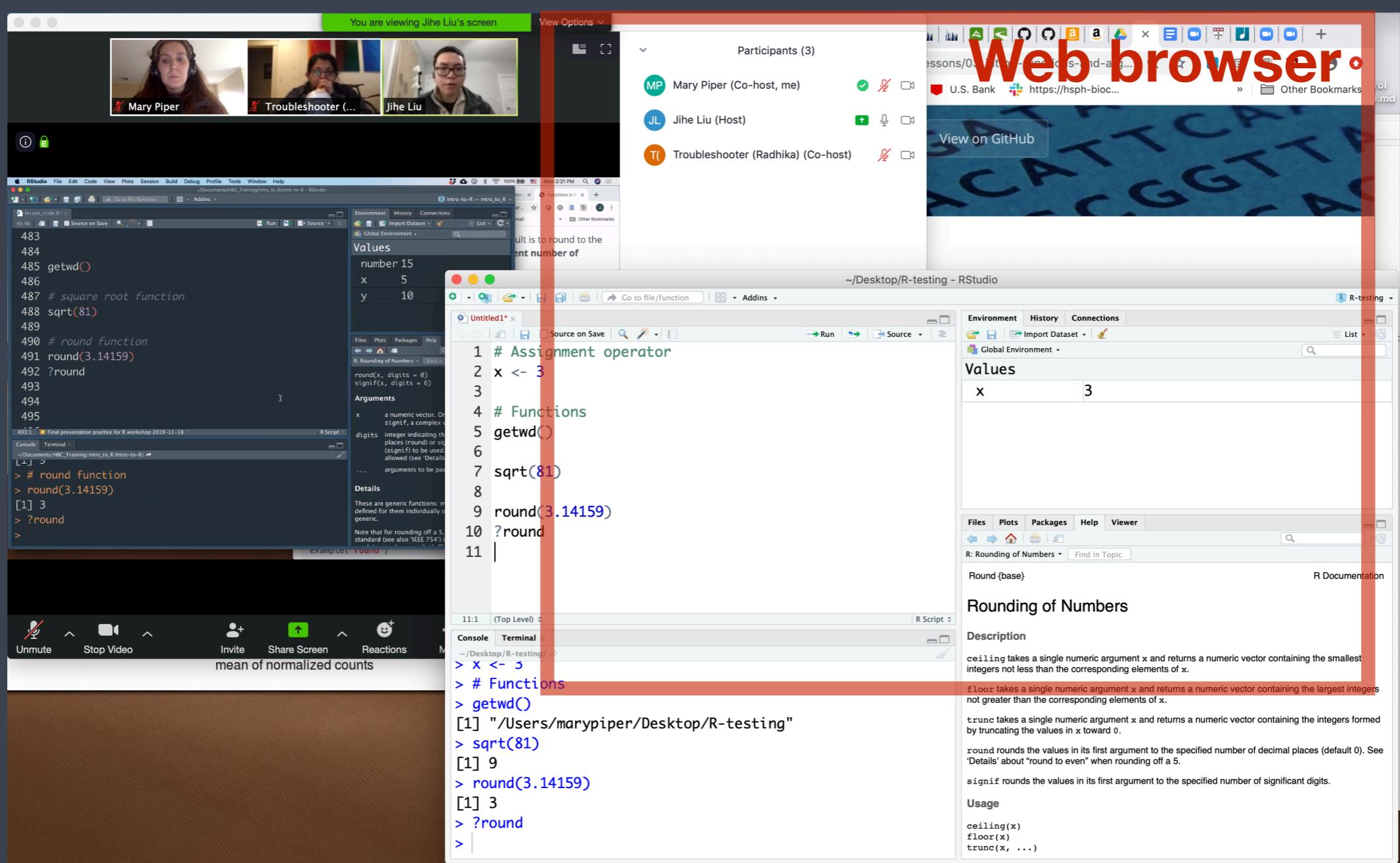
The 3 Window problem...



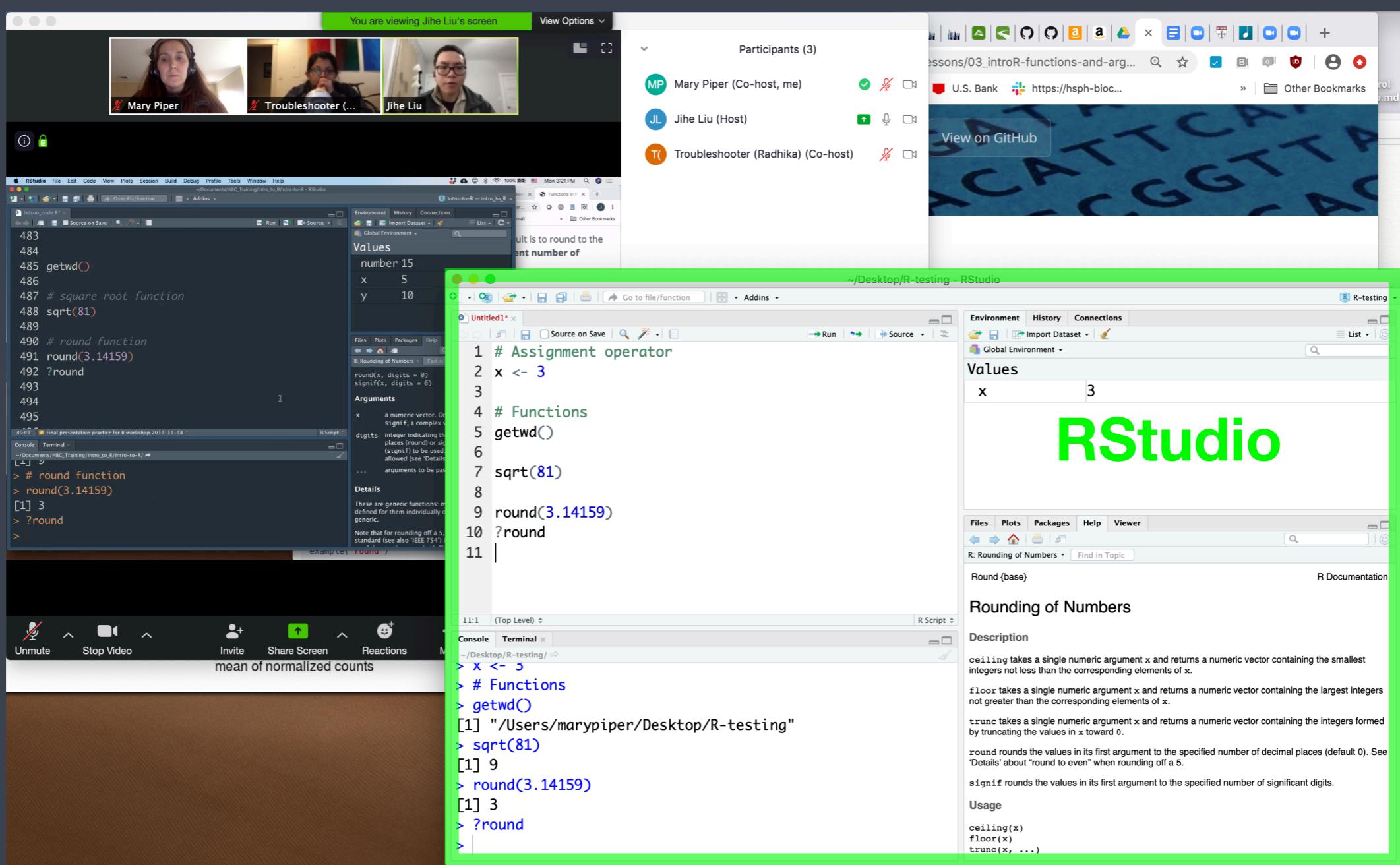
The 3 Window problem....



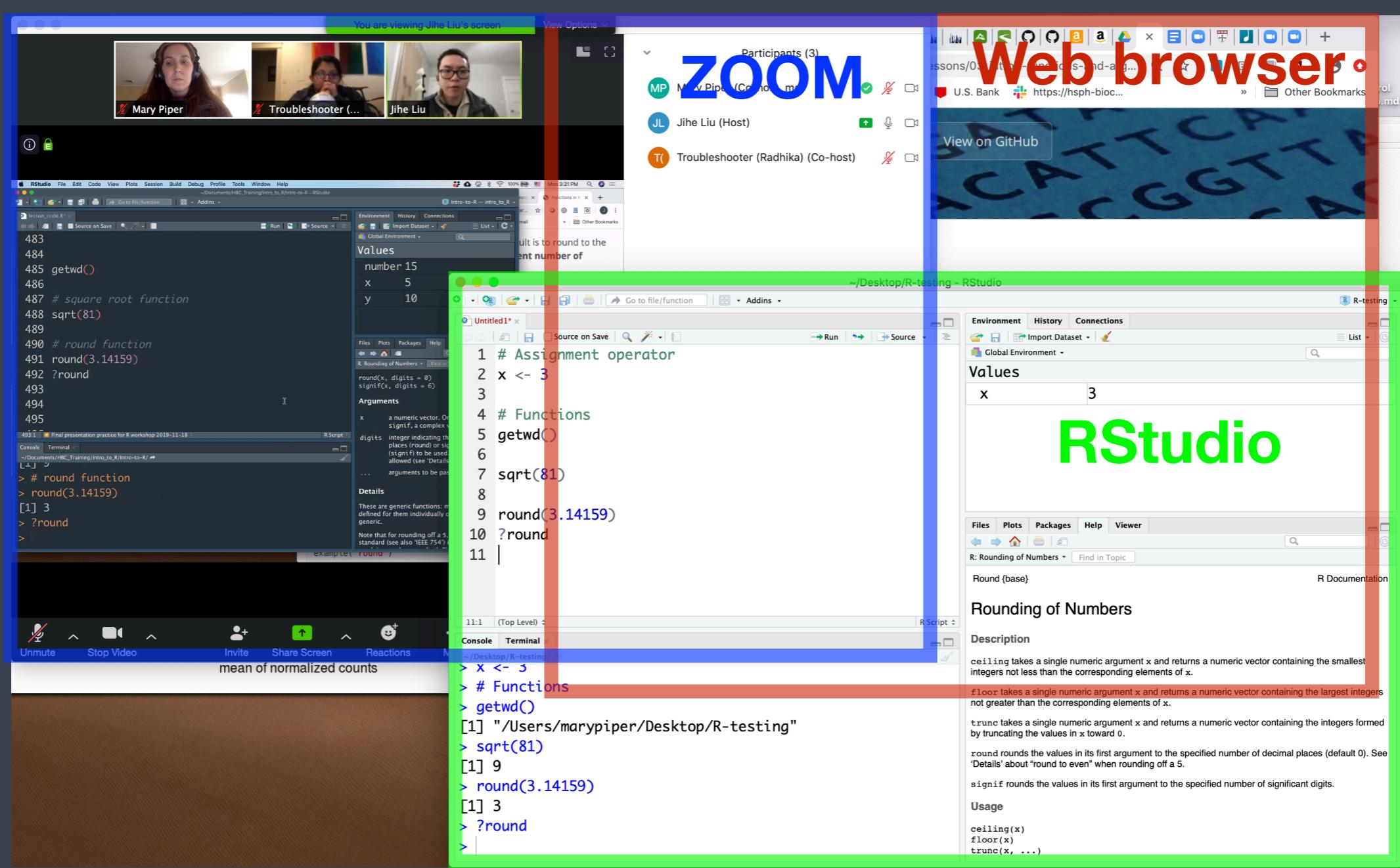
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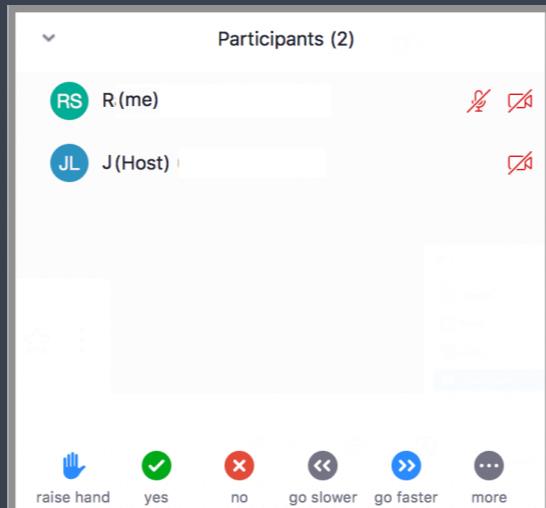


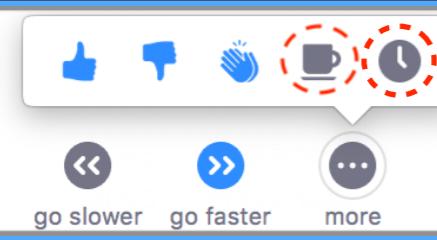
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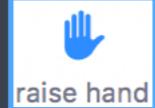
Odds and Ends (1/2)

- ❖ Quit/minimize all applications that are not required for class
- ❖ Click on “Participants” to open that panel in Zoom



- ▶  = "agree", "I'm all set" (equivalent to a **green post-it**)
- ▶  = "disagree", "I need help" (equivalent to a **red post-it**)
- ▶  If you are away from the computer use the coffee cup or clock icon

Odds and Ends (2/2)

- ❖ Questions for the presenter?
 - Post the question in the Chat window OR
 - Post the question in Poll everywhere at <https://pollev.com/hbctraining945> OR
 - Raise your 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!

HBC training team: hbctraining@hsph.harvard.edu

HBC consulting: bioinformatics@hsph.harvard.edu

Twitter

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