

Introduction to R

Invitation to chat:

What was the most enjoyable part of this past weekend?

Harvard Chan Bioinformatics Core

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

Sponsored by DF/HCC, CFAR, and HMS Foundry

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

<http://bioinformatics.sph.harvard.edu/>



NIEHS

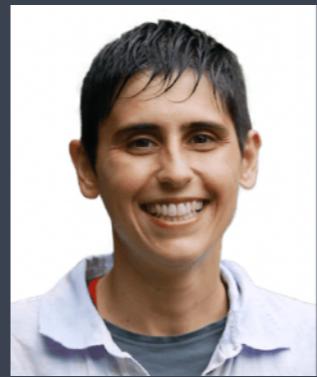




Shannan Ho Sui
Director



Meeta Mistry
Associate Director



Lorena Pantano
Director of Bioinformatics Platform



John Quackenbush
Faculty Advisor



Emma Berdan



Heather Wick



Will Gammerdinger



Noor Sohail



Alex Bartlett



Upendra Bhattacharai



James Billingsley



Zhu Zhuo



Maria Simoneau



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Zhu Zhus



Maria Simoneau

Training

A key component of the HBC's mission is its training initiative. Our dedicated training team holds workshop to help researchers at Harvard better understand analytical methods for NGS data.

HBC's training team is made up of four PhD-level scientists who devote substantial time to material development, training and community building/outreach. All members of the training team also participate in consultations on research projects to ensure they remain up-to-date on current best practices in NGS analysis.

Our hands-on workshops focus on **basic data skills** and **analysis of high-throughput sequencing data**, with an emphasis on **experimental design**, current **best practices** and **reproducibility**. Our workshops are designed for **wet-lab biologists** aiming to independently design sequencing-based experiments and analysing the resulting data.

We offer three types of workshops:

1. Short, 3-hour monthly workshops (*Current topics in bioinformatics*)
2. Basic Data Skills**
3. Advanced Topics: Analysis of high-throughput sequencing (NGS) data**

***The basic data skills workshops serve as the foundation for the advanced workshops.*

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

<https://hbctraining.github.io/main/>

Training

A key component of the HBC's mission is to provide training for researchers at Harvard and beyond.

HBC's training team is made up of experts in training and community based research projects to ensure that our trainees are well prepared for their future careers.

Our hands-on workshops focus on practical skills, with an emphasis on **experimental design** and **bioinformatics**, designed for **wet-lab biologists** aiming to analyse NGS data.

We offer three types of workshops:

1. Short, 3-hour monthly workshops
2. Basic Data Skills**
3. Advanced Topics: Analysis of high-throughput sequencing data

**The basic data skills workshops are designed for researchers who have no prior experience with bioinformatics or NGS data analysis.



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AND TRANSLATIONAL
SCIENCE CENTER



Our dedicated training team holds workshops to help researchers learn how to analyse NGS data.

In addition to devote substantial time to material development, the training team also participate in consultations on best practices in NGS analysis.

Analysis of high-throughput sequencing data, with an emphasis on **experimental design**, **bioinformatics**, and **reproducibility**. Our workshops are designed for wet-lab biologists performing sequencing-based experiments and analysing the resulting data.

bioinformatics)

NGS) data**

or the advanced workshops.

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Our hands-on workshops focus on practical skills, with an emphasis on **experimental design** and **bioinformatics**, for **wet-lab biologists** and **computational biologists**.

We offer three types of workshops:

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2. Basic Data Skills**
3. Advanced Topics: Analysis of high-throughput sequencing data

**The basic data skills workshops are designed for researchers who have no prior experience with bioinformatics or NGS data analysis.



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The training team also devote substantial time to material development, and the training team also participate in consultations on best practices in NGS analysis.

Workshops focus on the analysis of high-throughput sequencing data, with an emphasis on **experimental design**, **bioinformatics**, and **reproducibility**. Our workshops are designed for researchers involved in sequencing-based experiments and analysing the resulting data.

bioinformatics)

bioinformatics (NGS) data**

and **bioinformatics for the advanced workshops**.

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Introductions!



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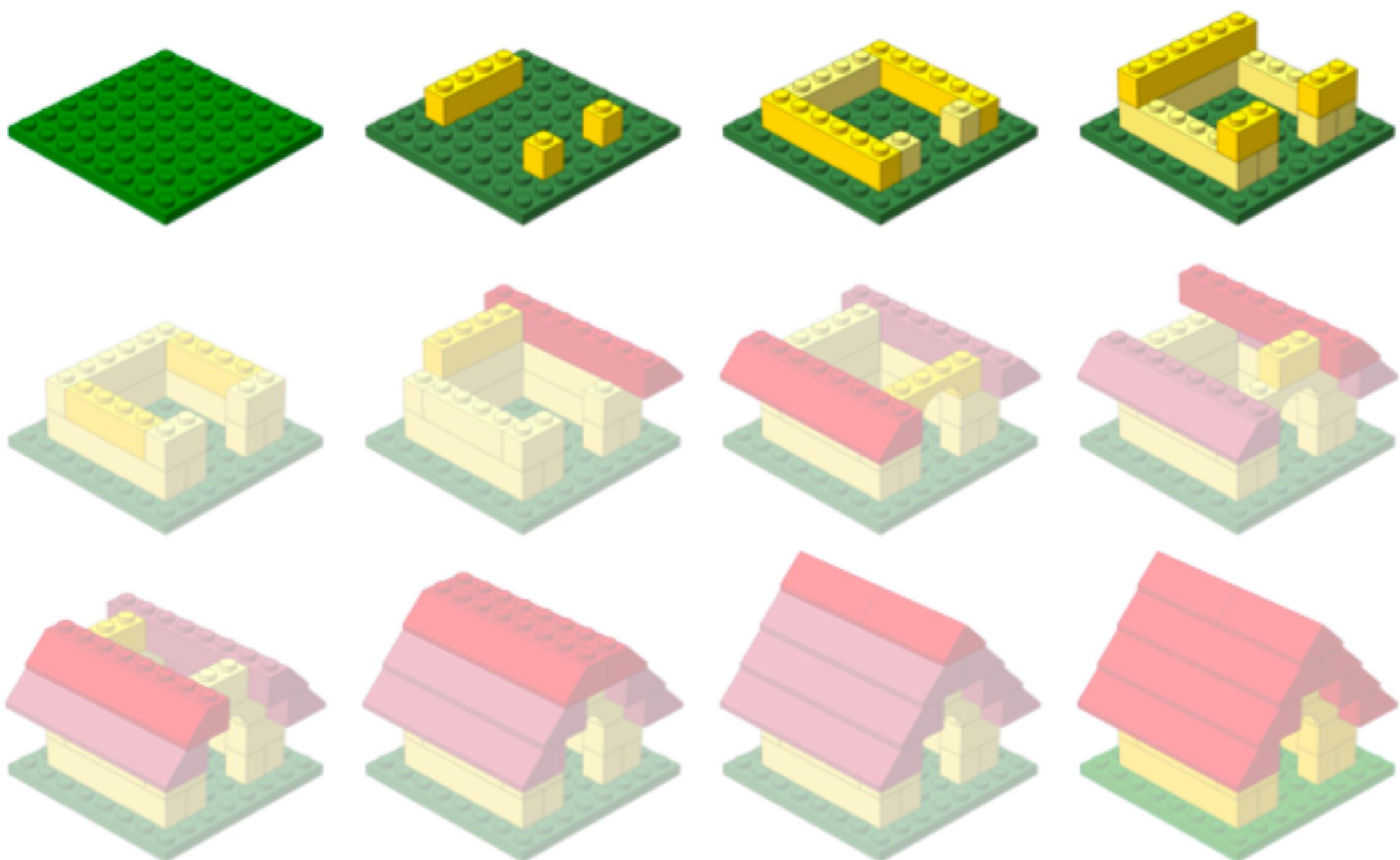


Zhu Zhus



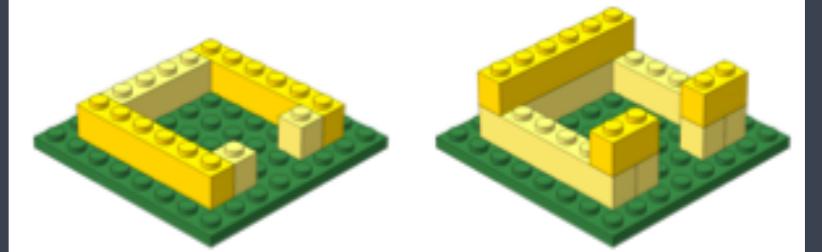
Maria Simoneau

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

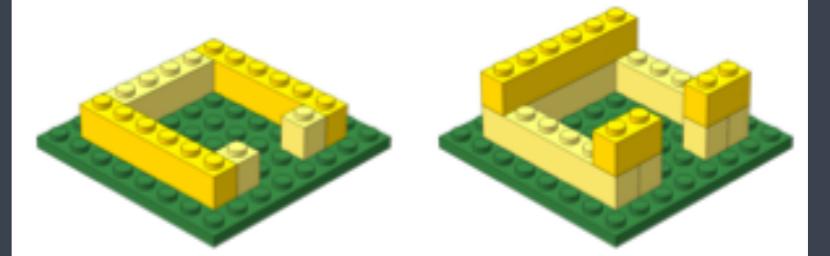
<https://cran.r-project.org/>



- 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 webpage

Introduction to DGE

[View on GitHub](#)

Approximate time: 60 minutes

Learning Objectives

- Explore different types of normalization methods
- Become familiar with the `DESeqDataSet` object
- Understand how to normalize counts using DESeq2

Normalization

The first step in the DE analysis workflow is count normalization, which is necessary to make accurate comparisons of gene expression between samples.

```
graph TD; A["Pseudocounts with  
Kallisto, Sailfish, Salmon"] --> B["Read counts  
associated with genes"]; B --> C["Normalization"]; C --> D["Unsupervised clustering analyses"]; C --> E["Quality control"]
```

The flowchart illustrates the DE analysis workflow. It begins with 'Pseudocounts with Kallisto, Sailfish, Salmon', followed by 'Read counts associated with genes'. This leads to 'Normalization', which then branches into 'Unsupervised clustering analyses' and 'Quality control'.

Course schedule online

Workshop Schedule

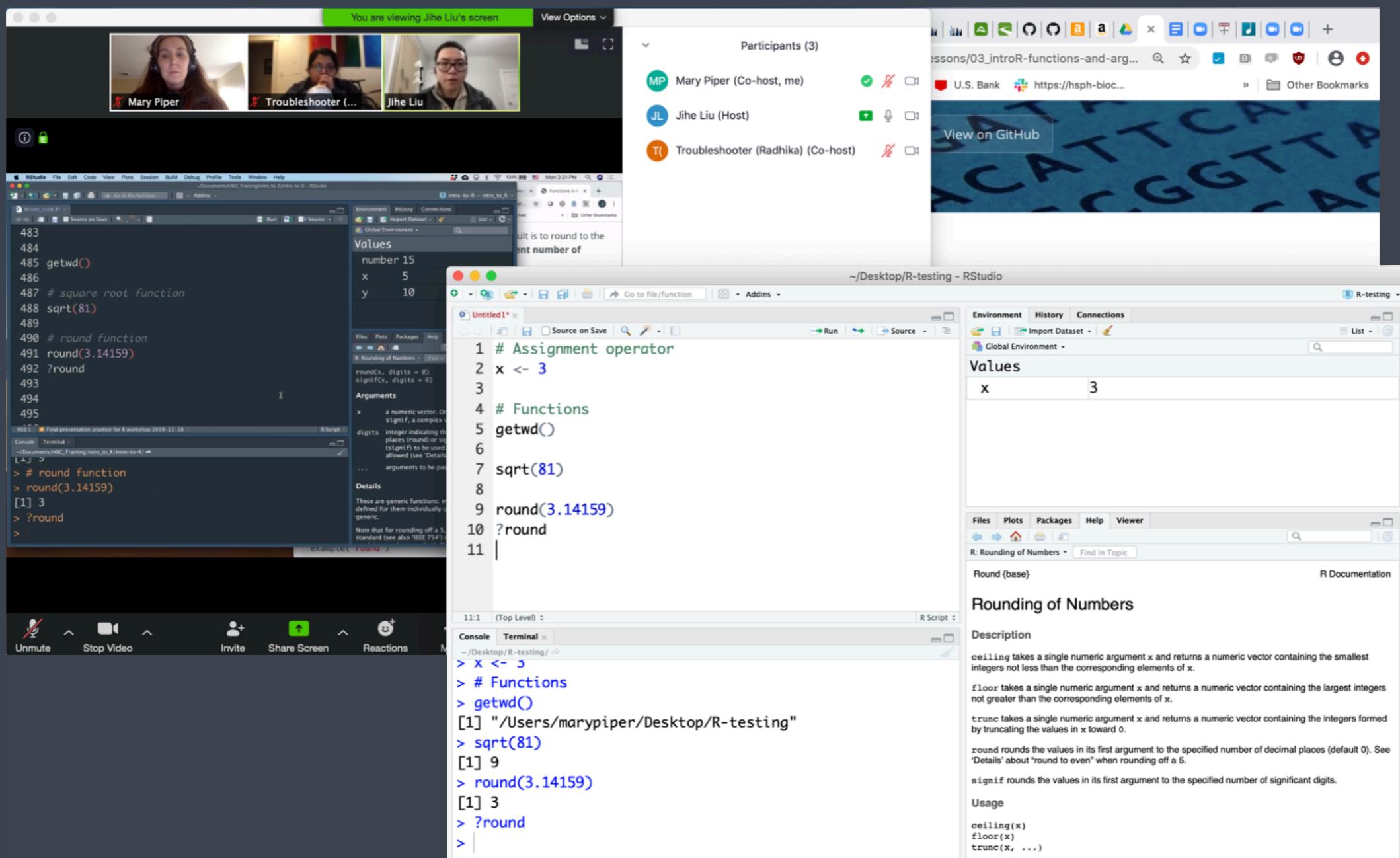
Day 1

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

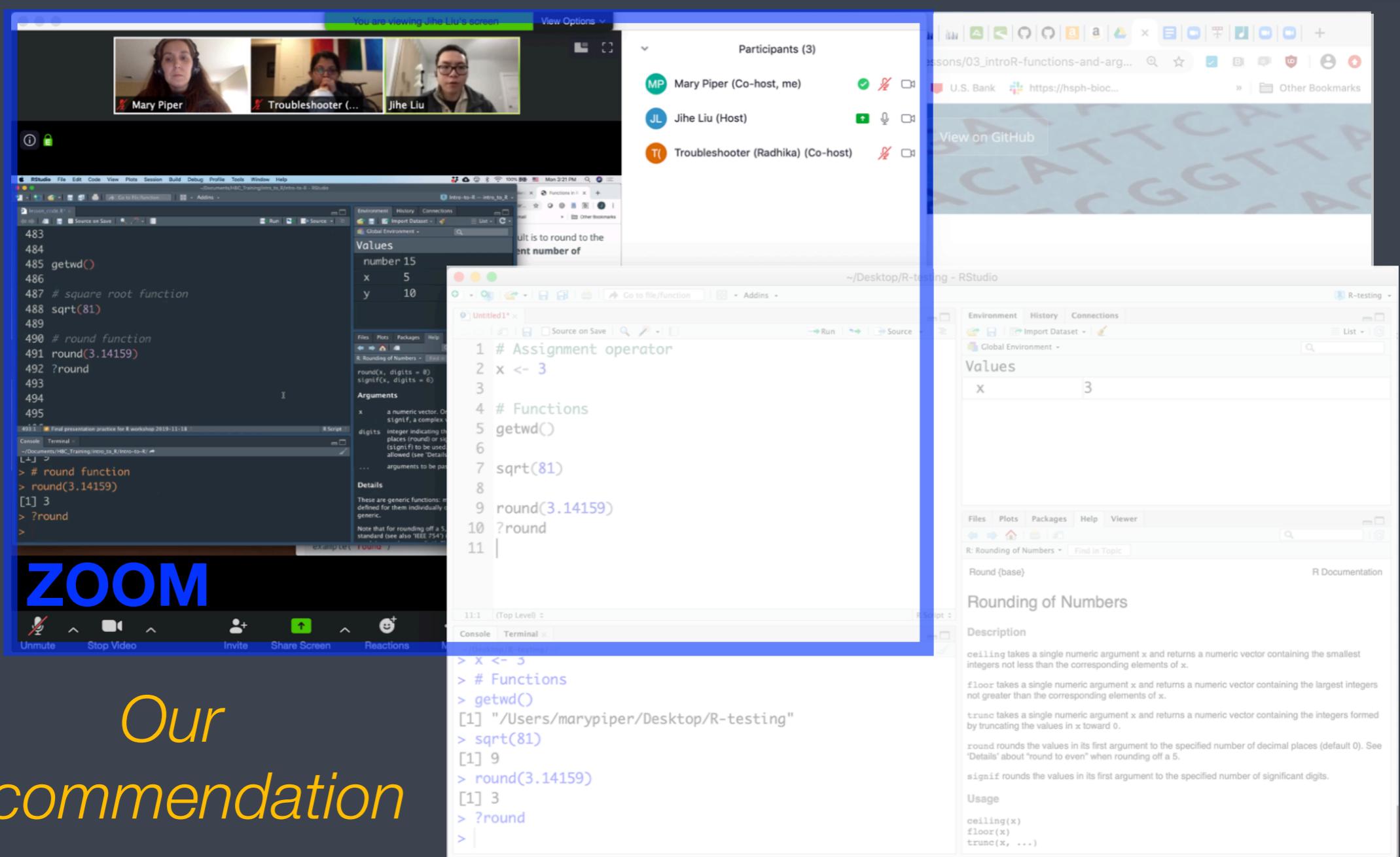
Before the next class:

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**.

Single screen & 3 windows?

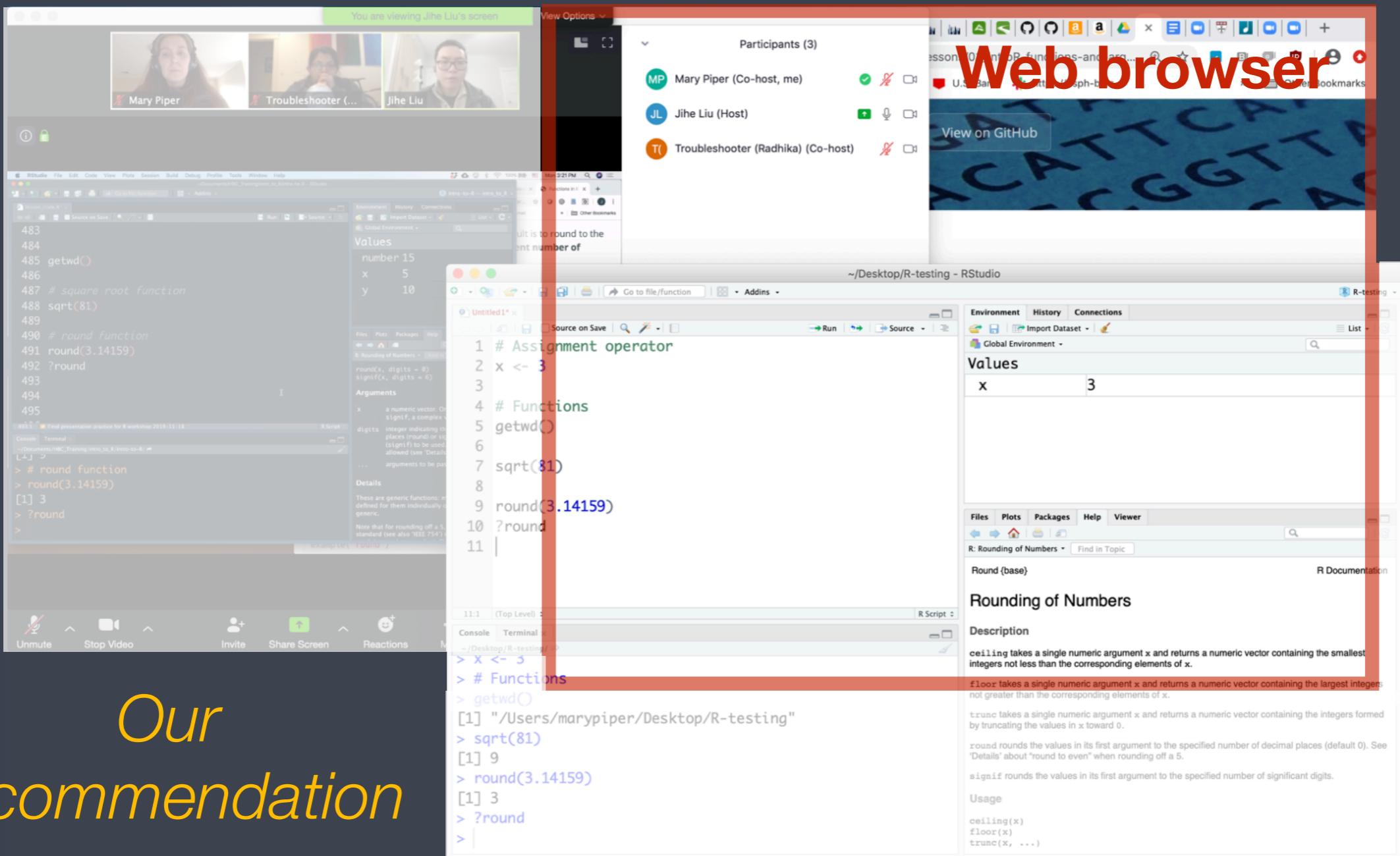


Single screen & 3 windows?



*Our
recommendation*

Single screen & 3 windows?



Single screen & 3 windows?

The image shows a video conference interface with three windows:

- Top Left Window:** A video feed showing three participants: Mary Piper, Troubleshooter (Radhika), and Jihe Liu.
- Middle Left Window:** An RStudio session titled "Untitled1". It contains the following R code:

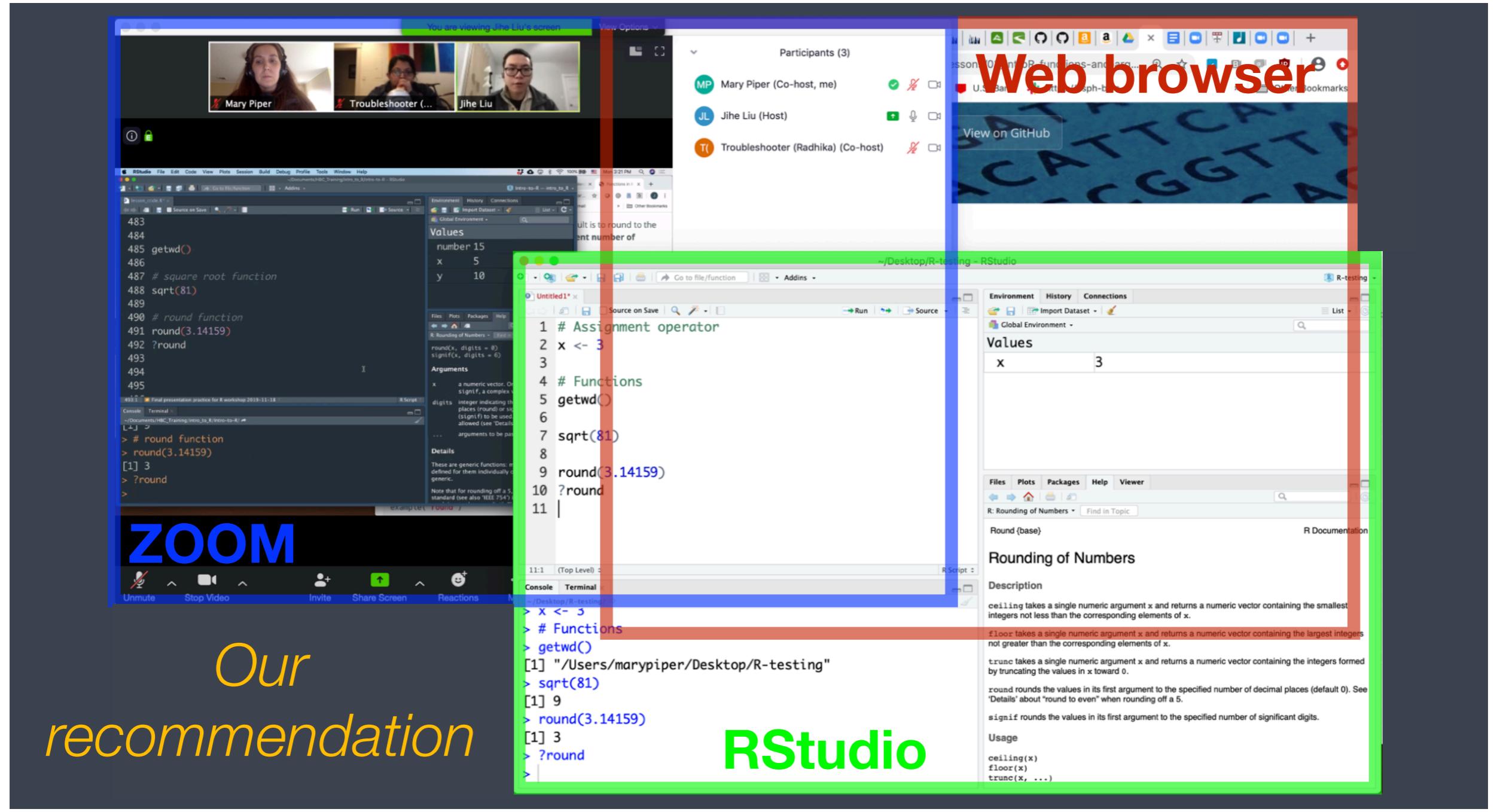
```
1 # Assignment operator
2 x <- 3
3
4 # Functions
5 getwd()
6
7 sqrt(81)
8
9 round(3.14159)
10 ?round
11
```
- Bottom Left Window:** A terminal window showing the same R code being run.

```
> x <- 3
> # Functions
> getwd()
[1] "/Users/marypiper/Desktop/R-testing"
> sqrt(81)
[1] 9
> round(3.14159)
[1] 3
> ?round
>
```
- Top Right Window:** A web browser window showing a GitHub page for a presentation script titled "03_introR-functions-and-args.Rmd".
- Middle Right Window:** Another RStudio session titled "R-testing". It shows the variable `x` assigned the value 3. Below it is a "Rounding of Numbers" documentation page from R Documentation.

Bottom Left Text: Our recommendation

Bottom Right Text: RStudio

Single screen & 3 windows?



Course participation

- ▶ Please keep your videos on, we would love to see your faces!
- ▶ 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!



Homework and Expectations

- ❖ 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

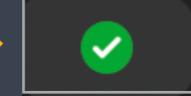
Odds and Ends (1/2)

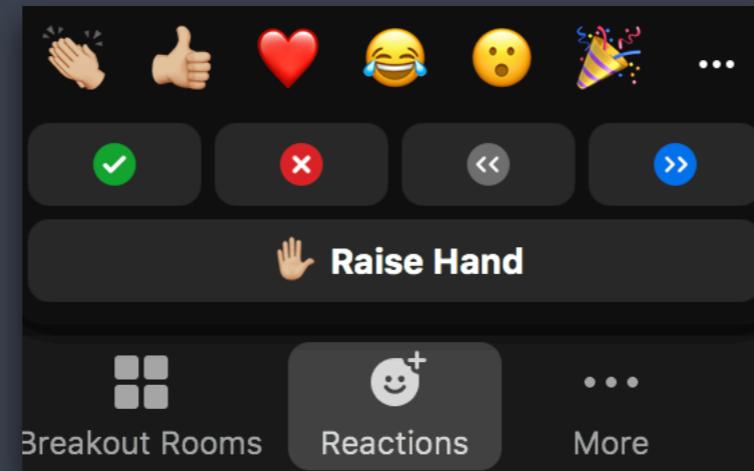
- ❖ Quit/minimize all applications that are not required for class

Odds and Ends (1/2)

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

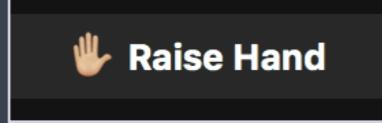
Odds and Ends (1/2)

- ❖ 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**)



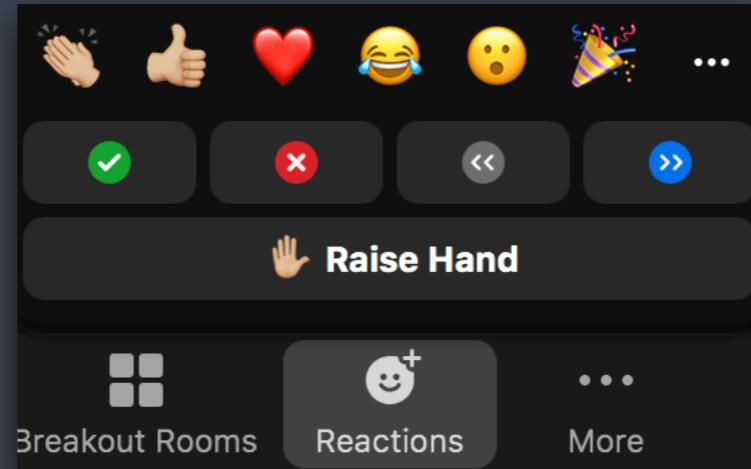
Odds and Ends (2/2)

- ❖ Questions for the presenter?

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

- ❖ 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

Twitter

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