

R Markdown

from  R Studio®

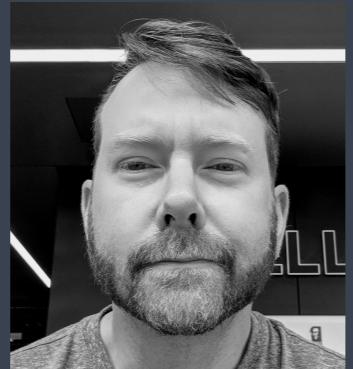
Generating R Analysis Reports with Rmarkdown

Harvard Chan Bioinformatics Core

<https://tinyurl.com/Rmarkdown-reports>



Shannan Ho Sui
Director



John Hutchinson
Associate Director



Victor Barrera



Zhu Zhuo



Preetida Bhetariya



Radhika Khetani
Training Director



Meeta Mistry



Mary Piper
Assoc. Training Director



Jihe Liu



Will Gammerdinger



Maria Simoneau



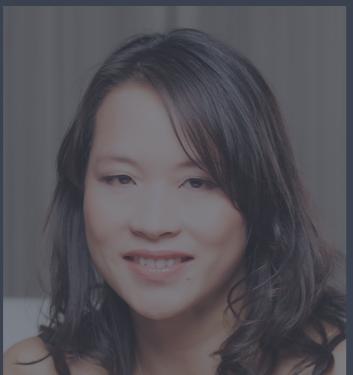
James Billingsley



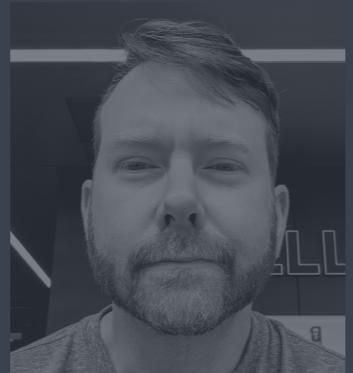
Sergey Naumenko



Peter Kraft
Faculty Advisor



Shannan Ho Sui
Director



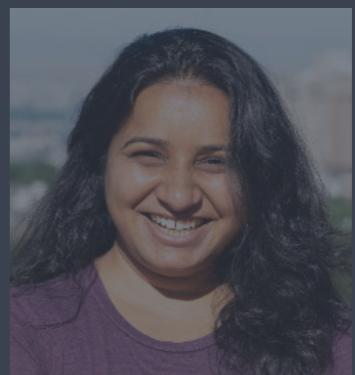
John Hutchinson
Associate Director



Victor Barrera



Zhu Zhuo



Preetida Bhetariya



Radhika Khetani
Training Director



Meeta Mistry



Mary Piper
Assoc. Training Director



Jihe Liu



Will Gammerdinger



Maria Simoneau



James Billingsley



Sergey Naumenko



Peter Kraft
Faculty Advisor

Consulting

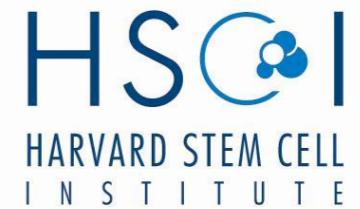
- RNA-seq analysis: bulk, single cell, small RNA
- ChIP-seq and ATAC-seq analysis
- Genome-wide methylation
- WGS, resequencing, exome-seq and CNV studies
- QC & analysis of gene expression arrays
- Functional enrichment analysis
- Grant support

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



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

NIEHS



Training



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

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/>

DF/HCC
DANA-FARBER / HARVARD CANCER CENTER

HSCI
HARVARD STEM CELL
INSTITUTE

 **HARVARD
CATALYST**
THE HARVARD CLINICAL
AND TRANSLATIONAL
SCIENCE CENTER

 **HARVARD
MEDICAL SCHOOL**

Training



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

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/>

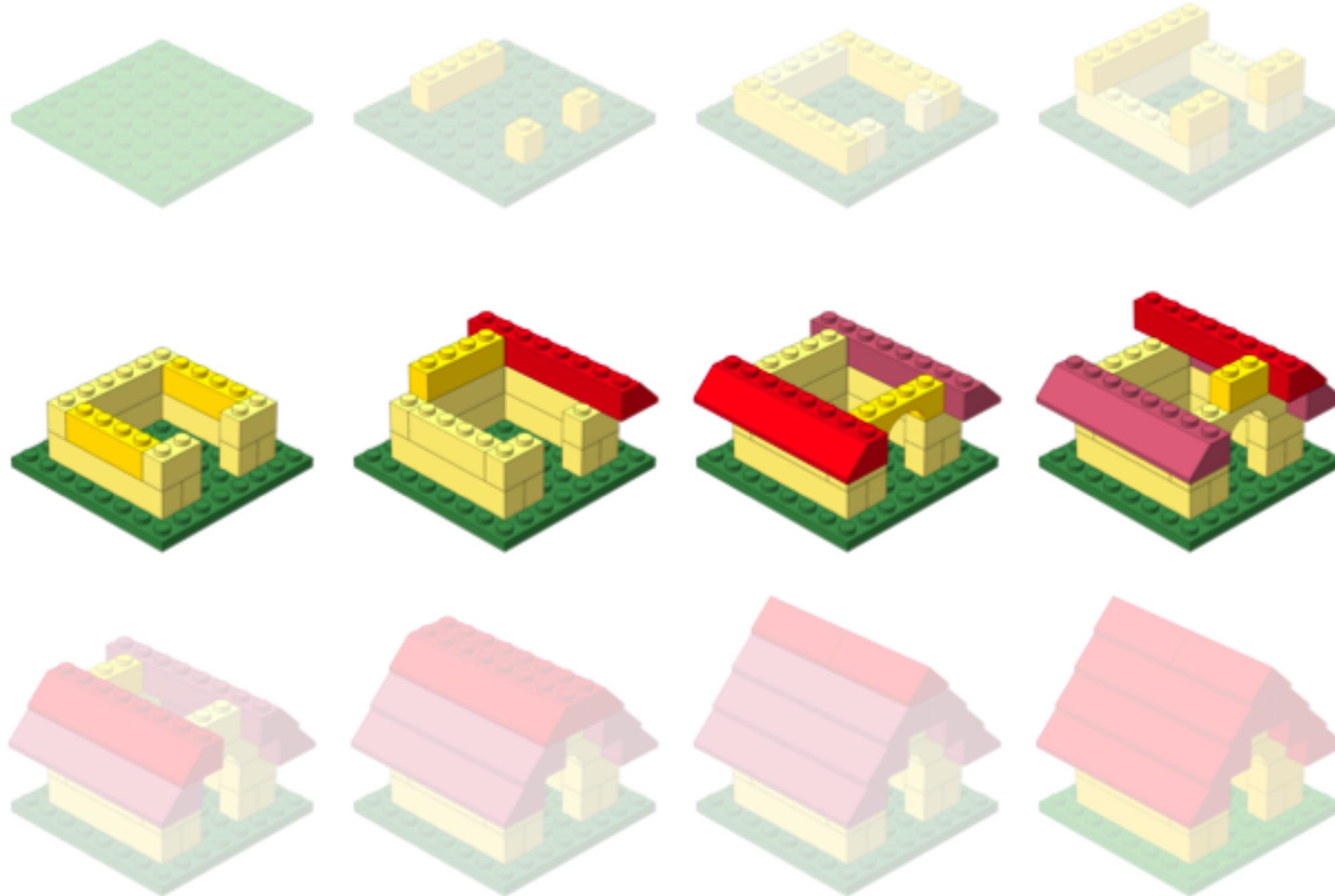
DF/HCC
DANA-FARBER / HARVARD CANCER CENTER

HSCI
HARVARD STEM CELL
INSTITUTE

 **HARVARD
CATALYST**
THE HARVARD CLINICAL
AND TRANSLATIONAL
SCIENCE CENTER

 **HARVARD
MEDICAL SCHOOL**

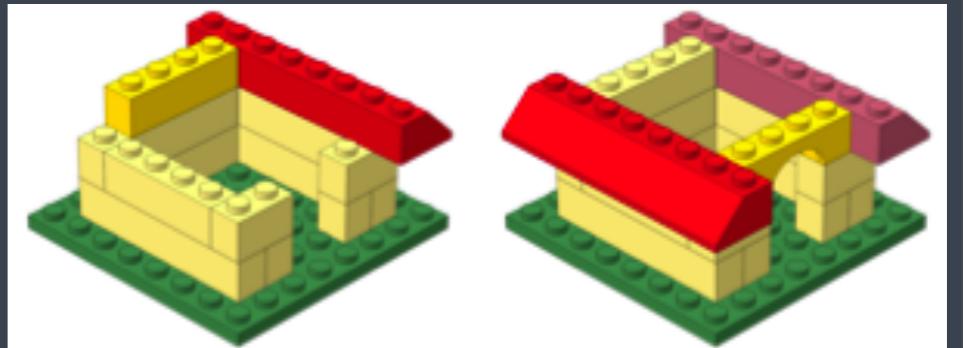
Workshop scope



<http://anoved.net/tag/lego/page/3/>

Bioinformatics data analysis

Learning Objectives



- ✓ Understand Rmarkdown syntax
- ✓ Utilize the **knitr** package to ‘knit’ together Rmarkdown analysis reports into html documents
- ✓ Practice altering the **knitr** options to customize the content presented in the reports

Logistics

Course webpage

<https://tinyurl.com/Rmarkdown-reports>

Course schedule online

Tools for Reproducible Research

[View on GitHub](#)

Workshop Schedule

Day 1

Time	Topic	Instructor
09:30 - 10:10	Workshop Introduction	Radhika
10:10 - 10:55	RMarkdown Basics	TBD
10:55 - 11:00	Break	
11:00 - 11:45	RMarkdown Intermediate	TBD
11:45 - 12:00	Assignment review	Jihe

Assignment #1

- [Practice with RMarkdown](#)
- Upload the files requested in the above exercise to [Dropbox](#) day before the next class.

Course materials online



Learning Objectives

- Use code chunk options to customize the report
- Describe how to add figures and tables to an RMarkdown
- Describe how to specify the output format for RMarkdown

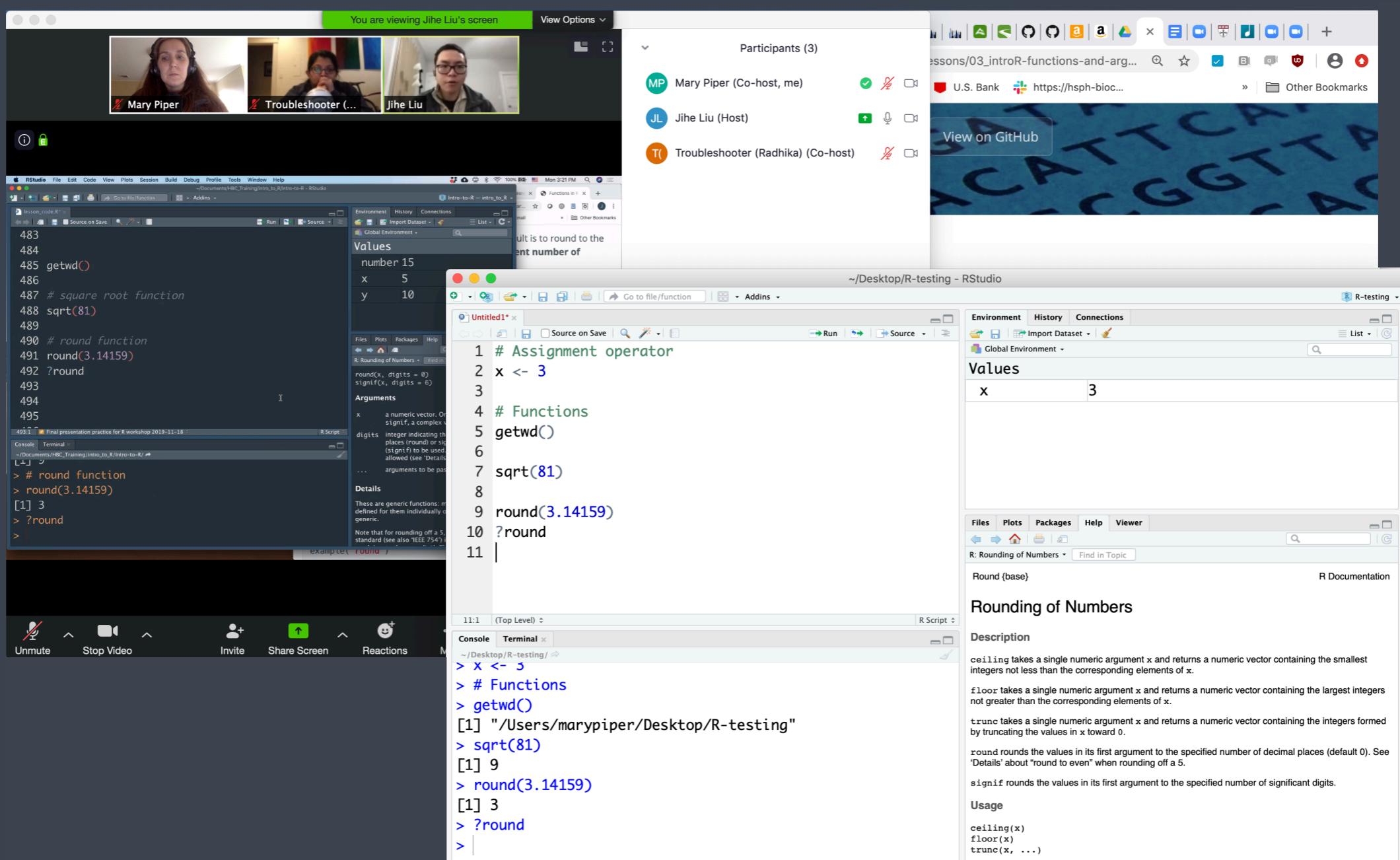
More about Code chunks

By this point, we have mentioned the word “knit” quite a few times, and you have installed and loaded the `knitr` package too. But, we have not yet fully defined what it is. `knitr` is an R package, developed by Yihui Xie, designed to convert RMarkdown and a couple of other file formats into a final report document in HTML or PDF or other formats.

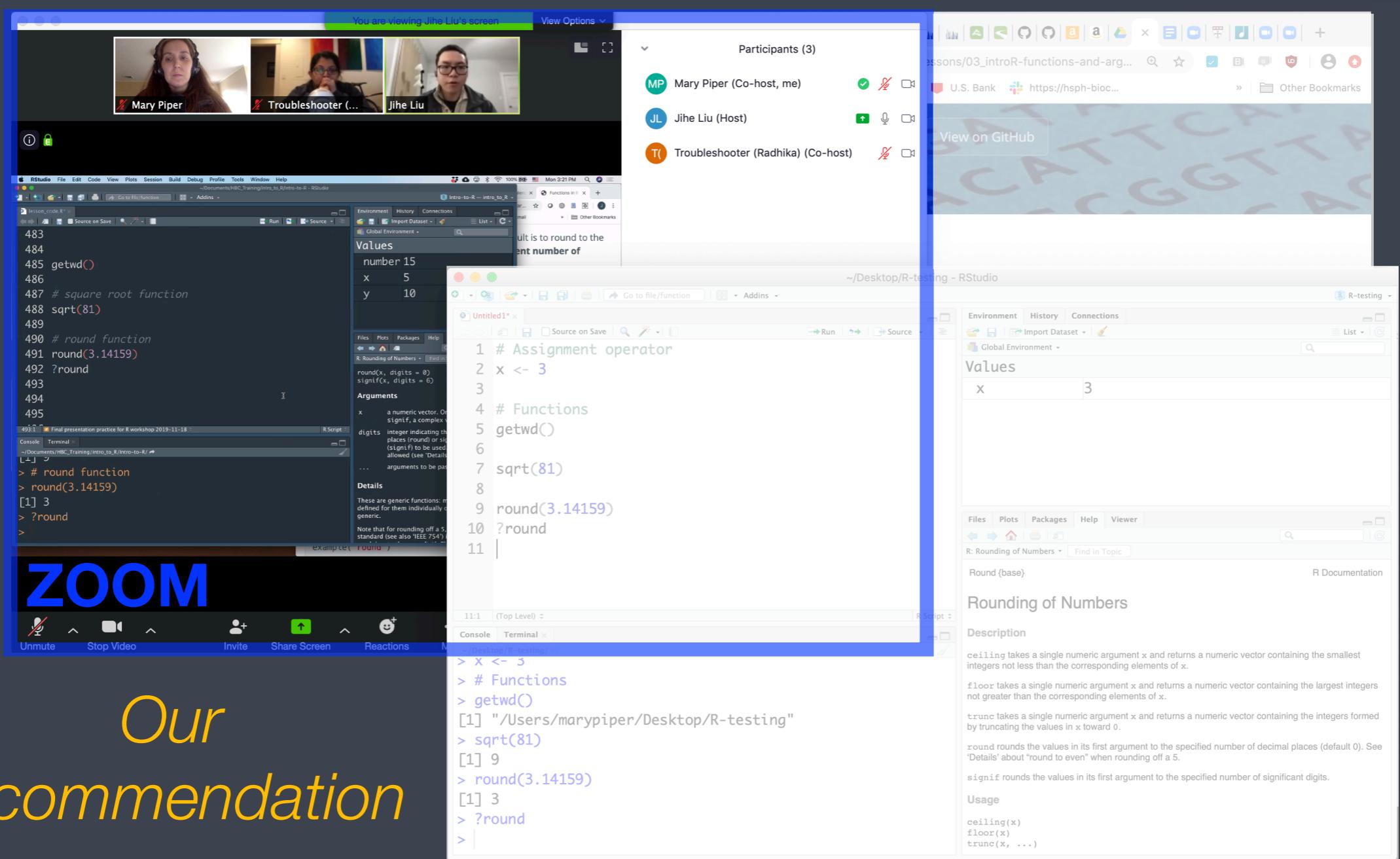
The `knitr` package provides a lot of customization options for code chunks embedded within the file. These options are written in the form of `tag=value`.

```
```{r chunk-name, echo=FALSE, warning=FALSE, message=FALSE}
x <- 4
y <- 2
x + y
```
```

Single screen & 3 windows?

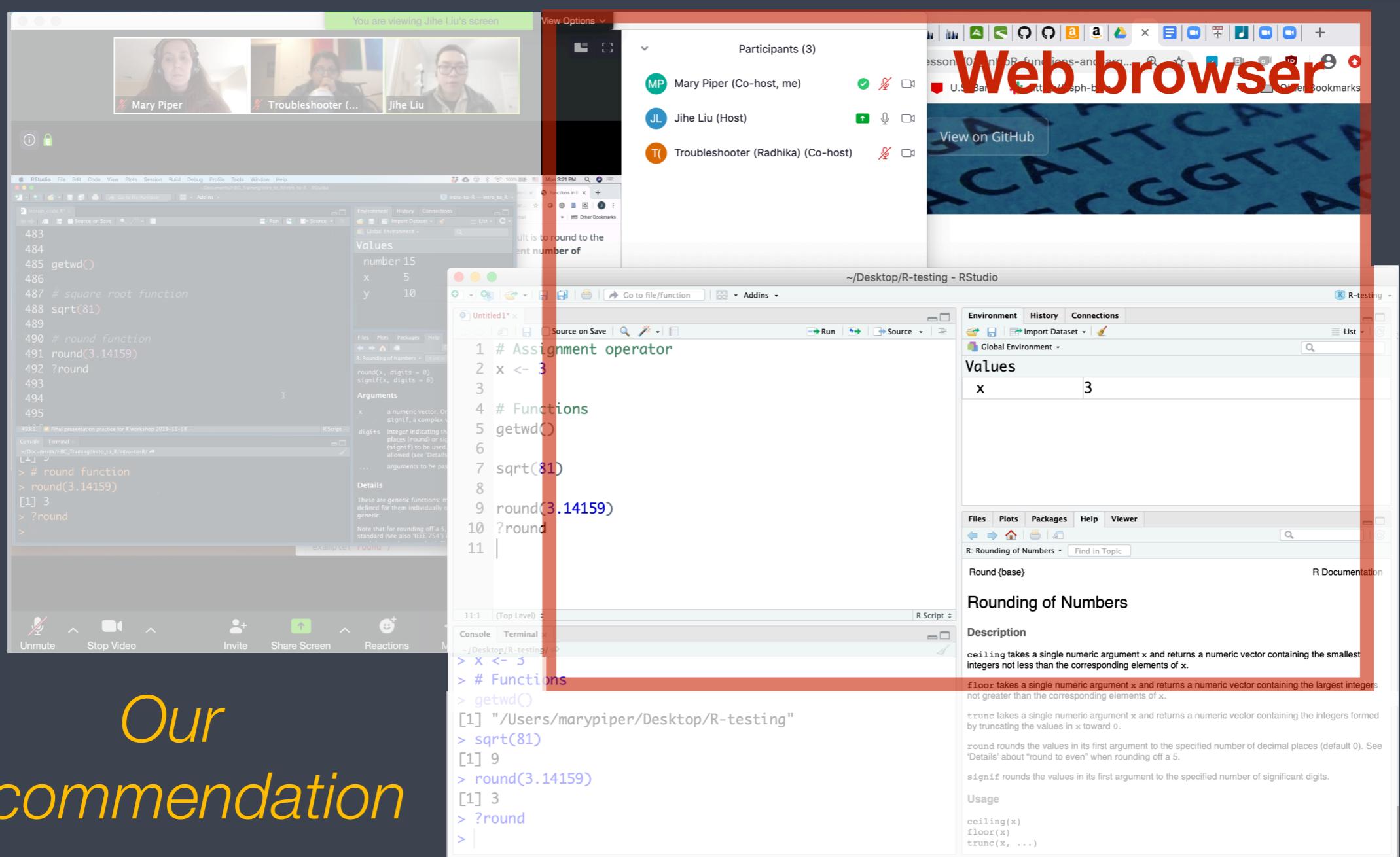


Single screen & 3 windows?

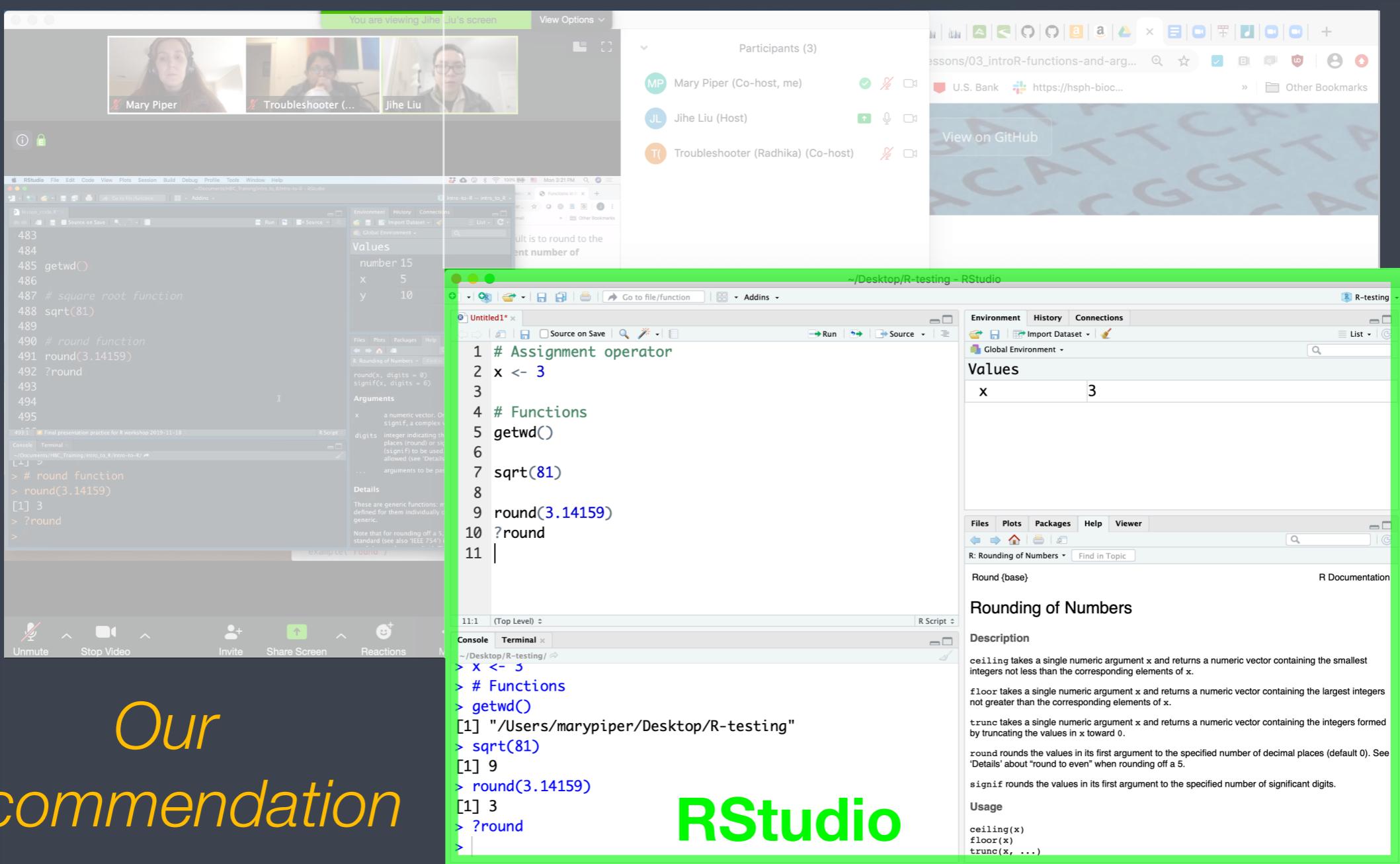


*Our
recommendation*

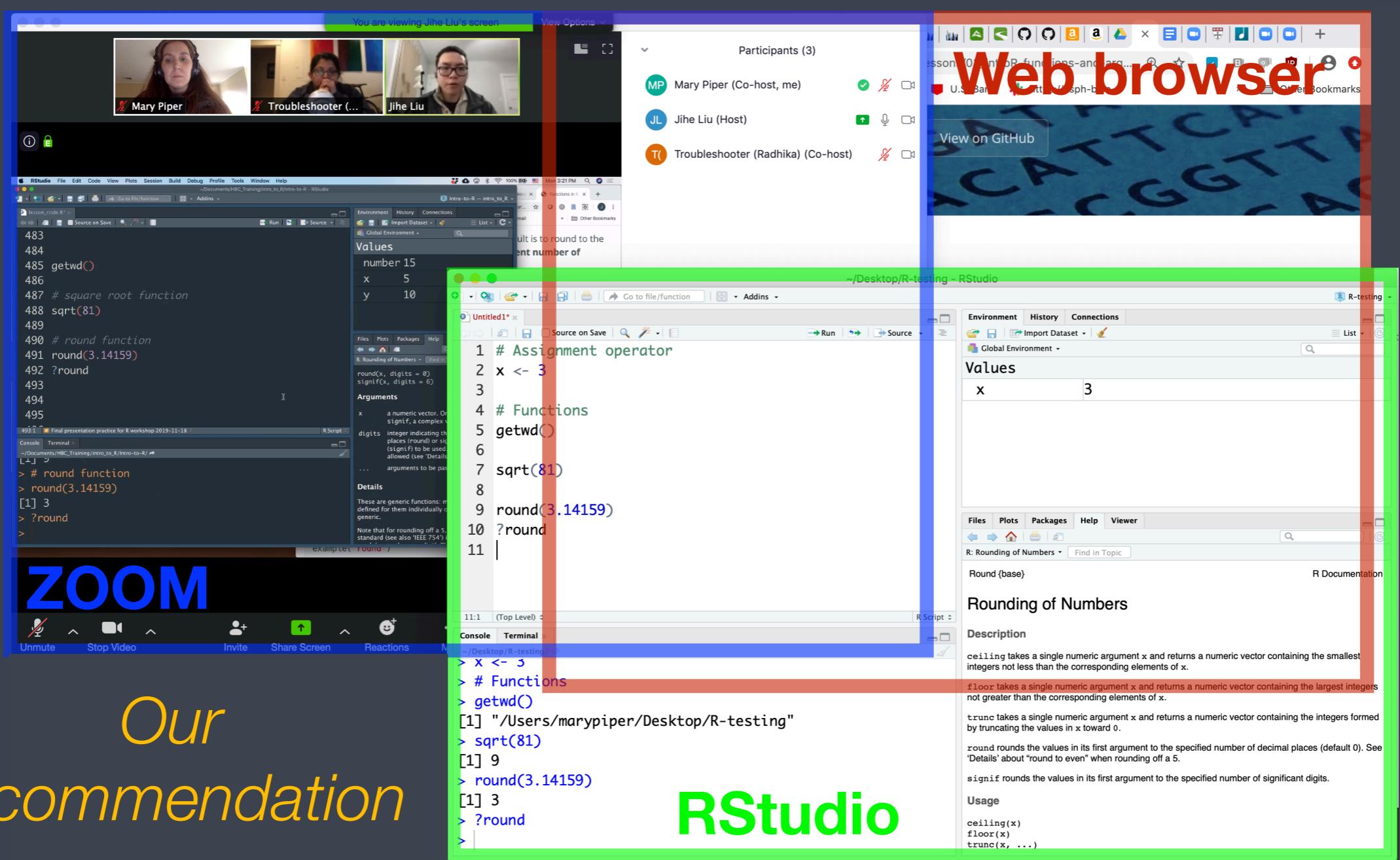
Single screen & 3 windows?



Single screen & 3 windows?



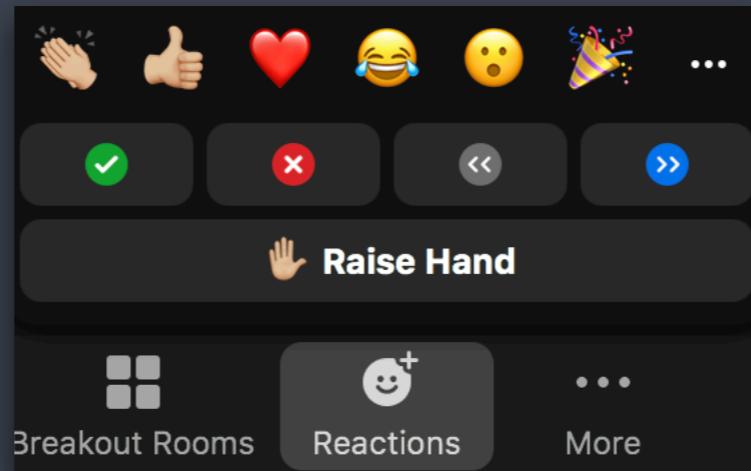
Single screen & 3 windows?



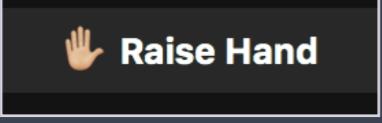
*Our
recommendation*

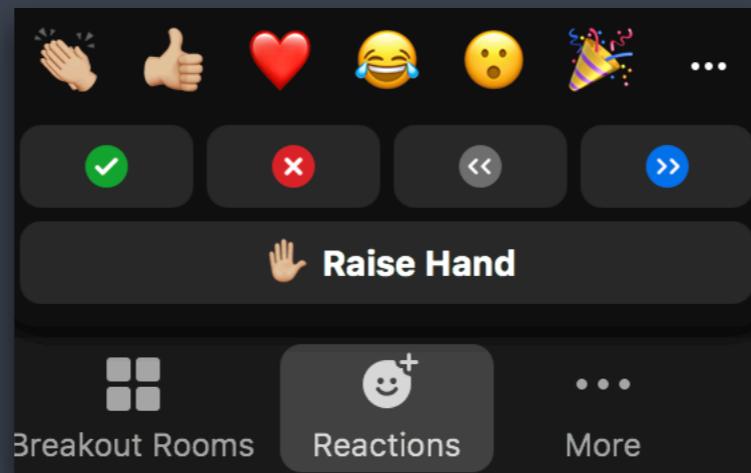
Odds and Ends

- ❖ 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**)
 - ▶  = "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
- ❖ 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

HBC: @bioinfocore