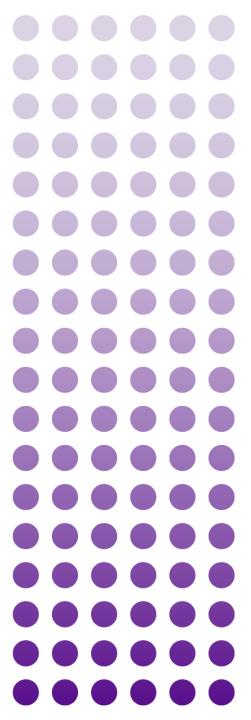


Reproducibility Workshop: Part 2 R Markdown for Reproducible Data Processing and Analysis

Alisa Surkis, PhD, MLS Assistant Director, Research Data and Metrics NYU Health Sciences Library

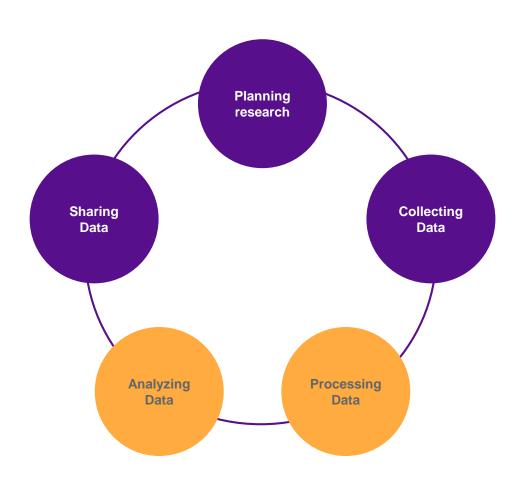


Class Overview

- Why use R?
- Why use R Markdown for Reproducibility?
- Rstudio
- Terminology and Syntax
- Setting up an R Project
- R Basics
- Reproducible Case Study: Data Processing and Analysis



Data Lifecycle





Why use R?

```
notUninsured <- select(filter(AnalysisData, ever_uninsured == 0), anxietySum, difficultyFunctioning)
Uninsured <- select(filter(AnalysisData, ever_uninsured == 1), anxietySum, difficultyFunctioning)
diffAnxiety <- t.test(notUninsured$anxietySum, Uninsured$anxietySum)
diffAnxietyHyp <- ifelse(diffAnxiety$p.value < 0.05, "Rejected", "Accepted")</pre>
```

```
EHRData <- spread(EHRData, key = description, value=value)

EHRData <- select(EHRData, patient_id="PATIENT", date_of_visit = "DATE", ir housing_status = "Housing status", HIV_status = "HIV status in {nominal}")

**To a contract the provided of the participation of the participation
```

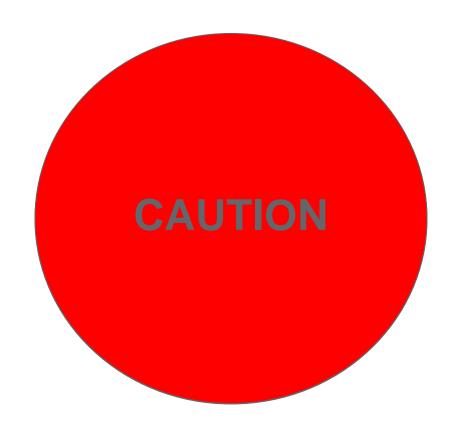
Everything in one places: data processing, analysis, and visualization



Why R?

It's free!

Large user community contributing functionality





Why R Markdown?

Creates formatted documents that integrate:

- Code -- HOW
- Narrative Text -- WHY
- Output -- WHAT

Produces an analysis notebook

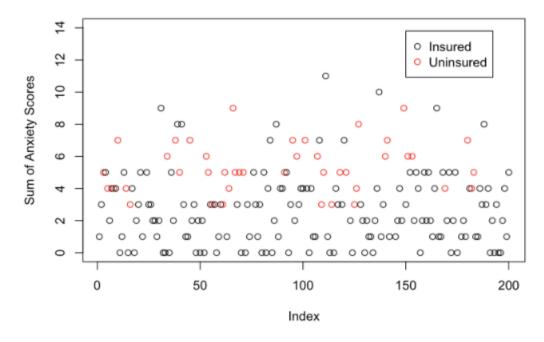


```
analysis$sex <- as.factor(analysis$sex)
```

Uninsured analysis

Plot the anxietySum with symbol color determined by if ever uninsured Separate the insured and uninsured and run a t-test

```
plot(analysis$anxietySum, col=analysis$ever_uninsured,ylab="Sum of Anxiety Scores",ylim=c(0,14)) legend(150,13.8,legend=c("Insured","Uninsured"),pch=1,col=1:2)
```

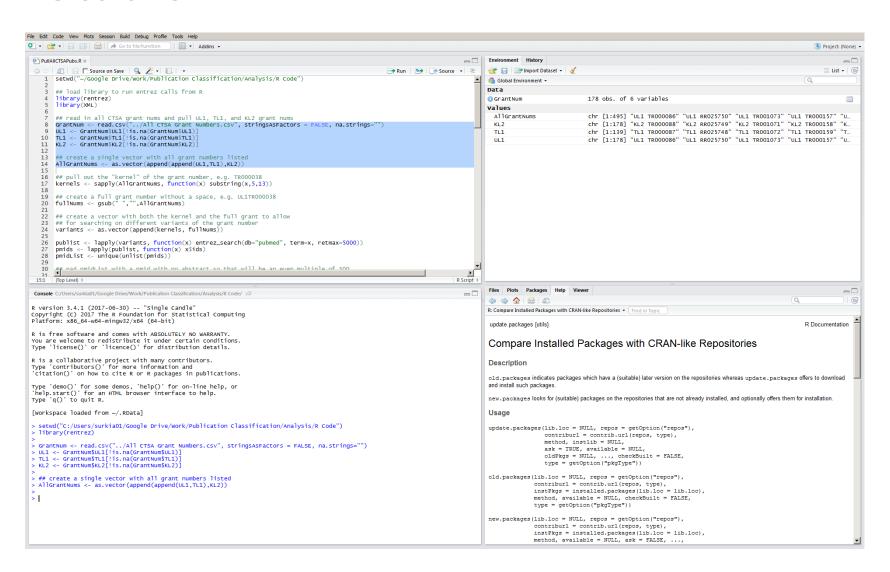


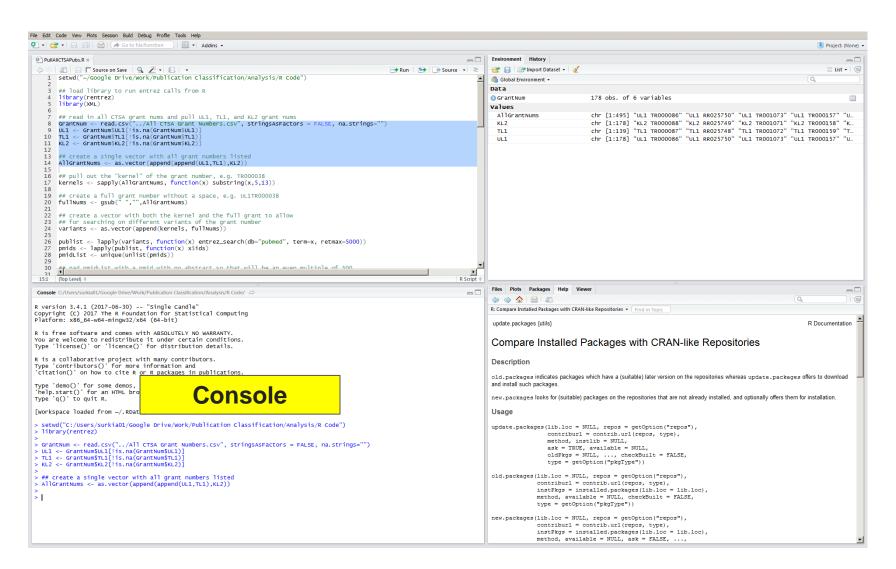
```
notUninsured <- filter(analysis, ever_uninsured == FALSE)
Uninsured <- filter(analysis, ever_uninsured == TRUE)

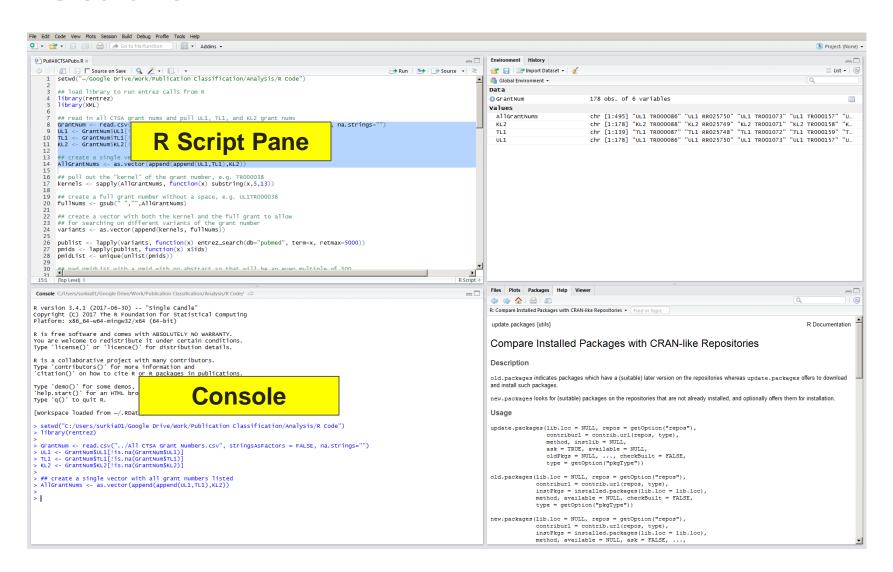
diffAnxiety <- t.test(notUninsured$anxietySum, Uninsured$anxietySum)
diffAnxietyHyp <- ifelse(diffAnxiety$p.value < 0.05, "Rejected", "Accepted")
```

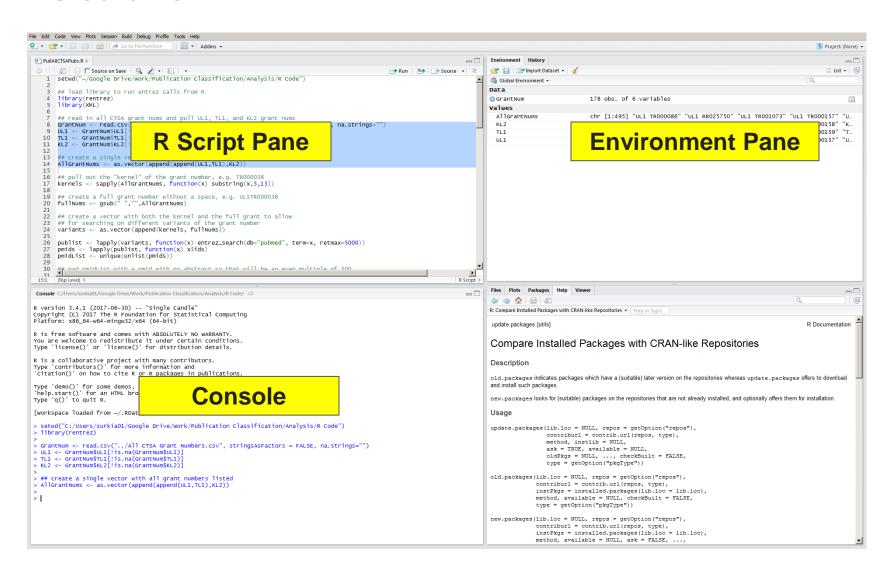
Results of analysis with uninsured vs insured populations

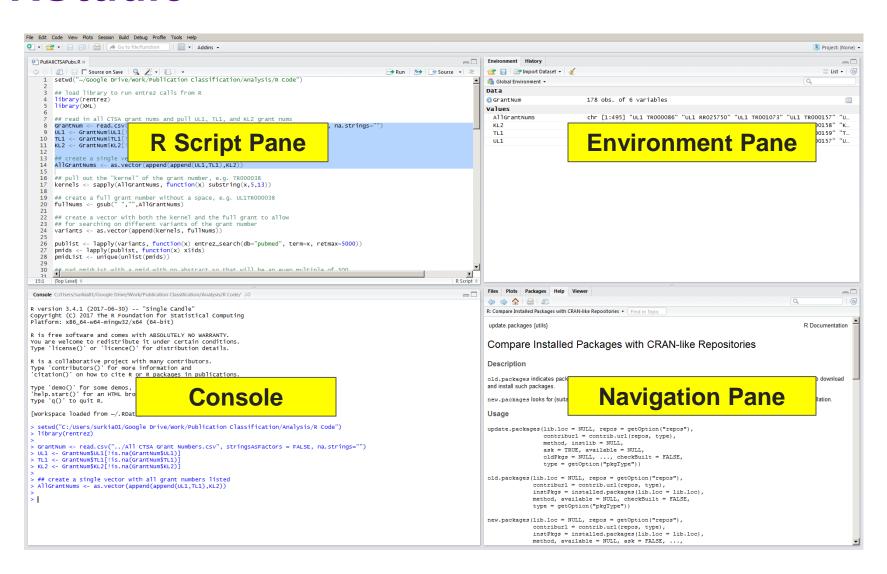
The hypothesis that there is no difference between the insured and uninsured populations in their total anxiety is Rejected with p-value of 9.038641710^{-14}



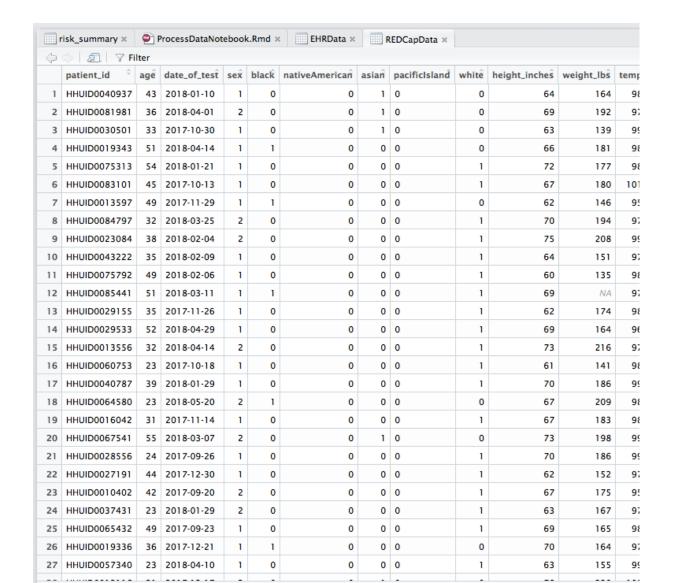






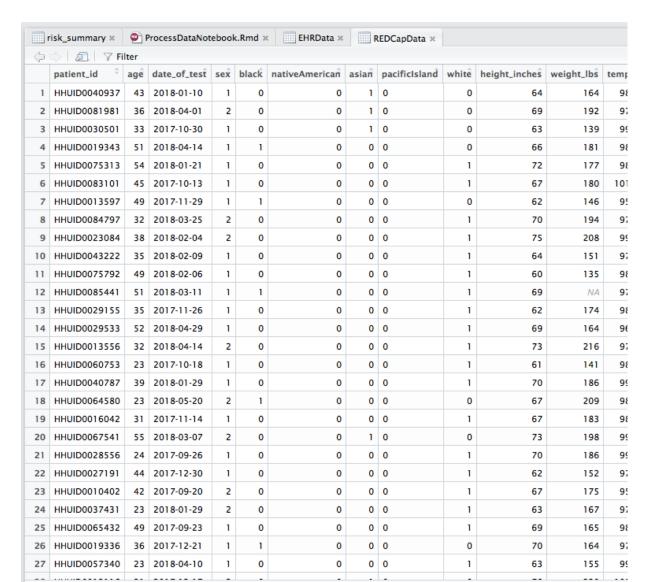


- Integrated development environment for R, which means one window with access to:
 - Variables
 - Help window
 - Plots
 - Scripting
- Convenience -- Tab Completion
- Reproducibility -- Integration with R Markdown





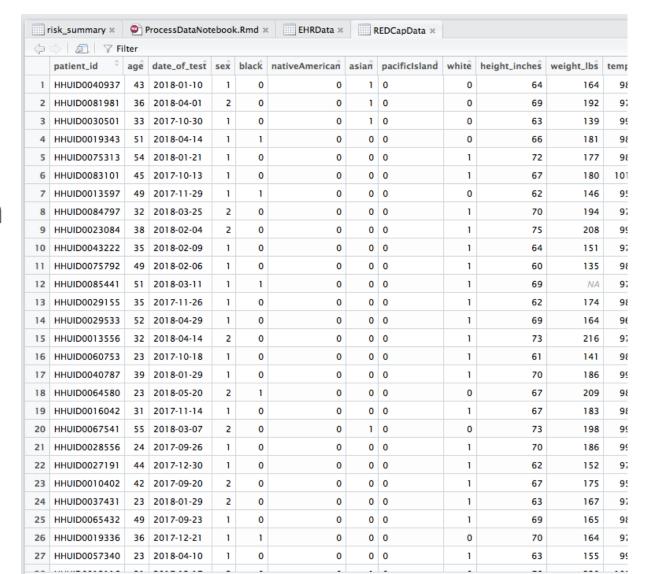
Each column is a different variable





Each column is a different variable

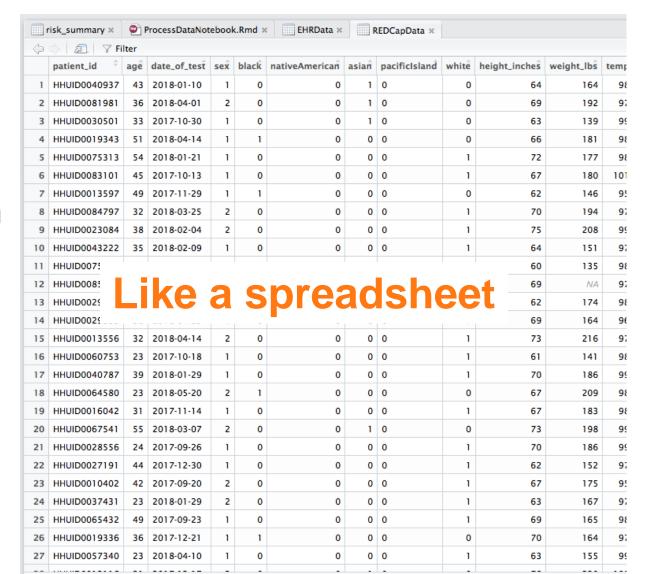
Each row is an observation





Each column is a different variable

Each row is an observation





• Numeric variable = *numeric* or *integer*

Ex: 1, 1.5, 200000, 3.14159



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• Text variable = *character*

Ex: a, b, hello, 3b



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Categorical variable = factor

Ex: cat, dog, pig, rhino, horse



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• Text variable = *character*

Ex: a, b, hello, 3b

Categorical variable = factor

Ex: cat, dog, pig, rhino, horse

Ordered categorical variable = ordered factor

Ex: xsmall, small, medium, large, xlarge



• Numeric variable = *numeric* or *integer*

Ex: 1, 1.5, 200000, 3.14159

Text variable = character

Ex: a, b, hello, 3b

Categorical variable = factor

Ex: cat, dog, pig, rhino, horse

Ordered categorical variable = ordered factor

Ex: xsmall, small, medium, large, xlarge

True/false = logical

Ex: TRUE, FALSE



Talking to R

Function calls

- how to tell R what to do
- always followed by ()

getwd()



Functions: Output

```
dat <- read.csv(file = "allFound.csv", header = TRUE)</pre>
```

Assignment operator (<-): assigns the output of the function to a name that you can then refer back to



Functions: Input

```
dat <- read.csv(file = "allFound.csv", header = TRUE)</pre>
```



Arguments: instructions that specify how a function should be run. Not always required, may be more than one, they are separated by commas, and they all go in the ()



Functions: Input

Argument: instructions that specify how a function should be run. Not always required, may be more than one, they are separated by commas, and they all go in the ()



Functions: Output

Data frame

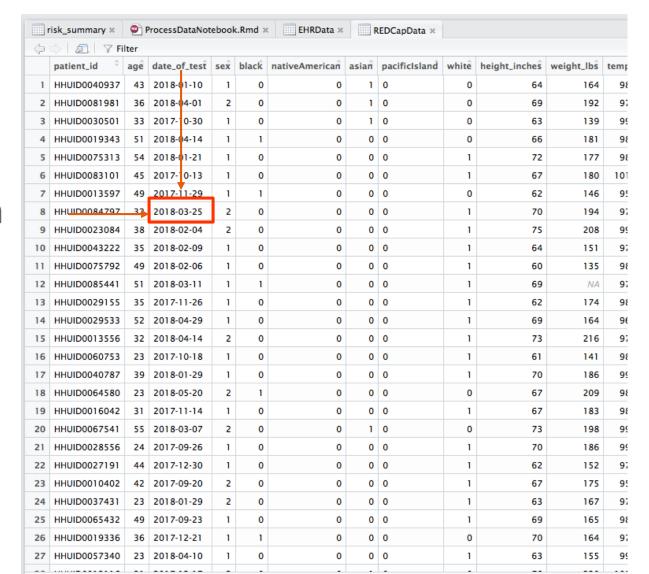
```
dat <- read.csv(file = "allFound.csv", header = TRUE)</pre>
```



Data frames: Accessing elements

Each column is a different variable

Each row is an observation





Data frames: Accessing elements

Each column is a different variable

Each row is an observation

dat[rows, columns]



Data frames: Accessing elements

Each column is a different variable

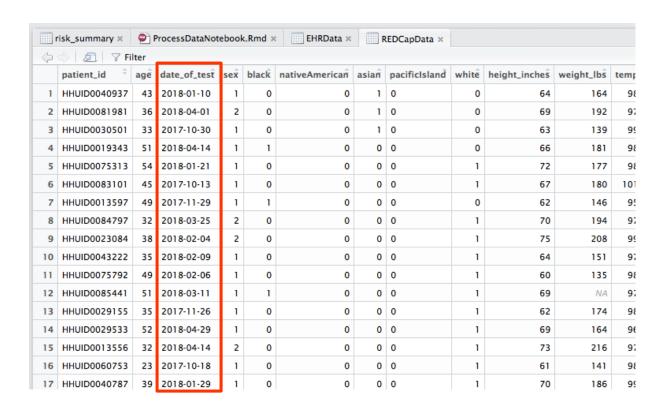
Each row is an observation

dat[rows, columns]

dat[observations, variables]



Data Frames: Accessing variables



dat\$date_of_test



R Projects

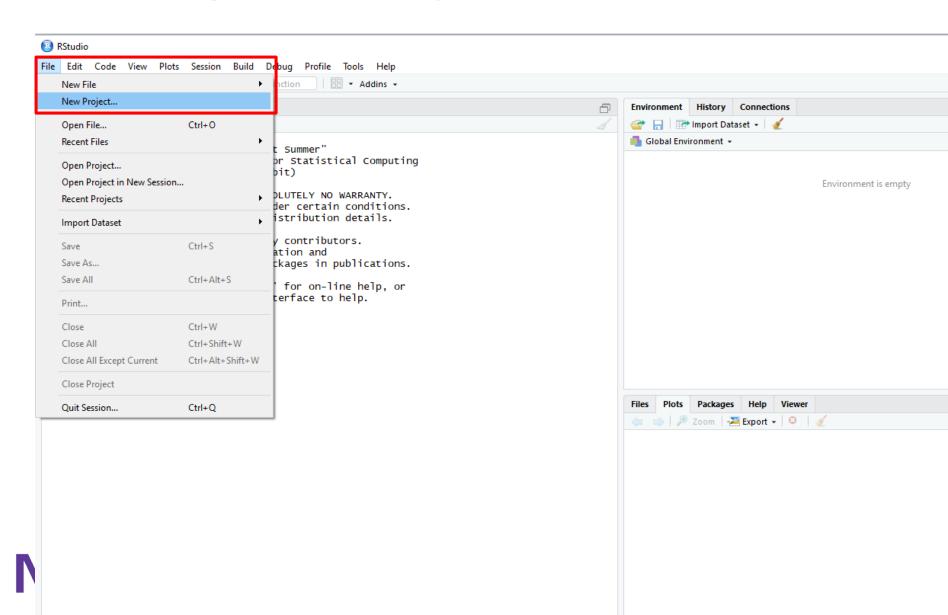
- An R Project has its own
 - Working directory
 - Workspace
 - History
 - Source documents
- Convenience of starting where you left off
- Helps with organization

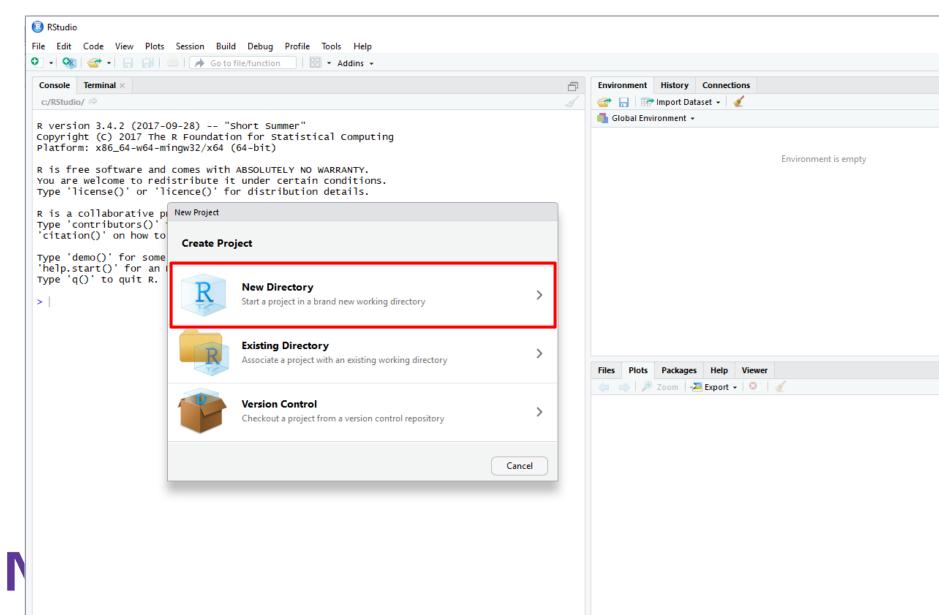


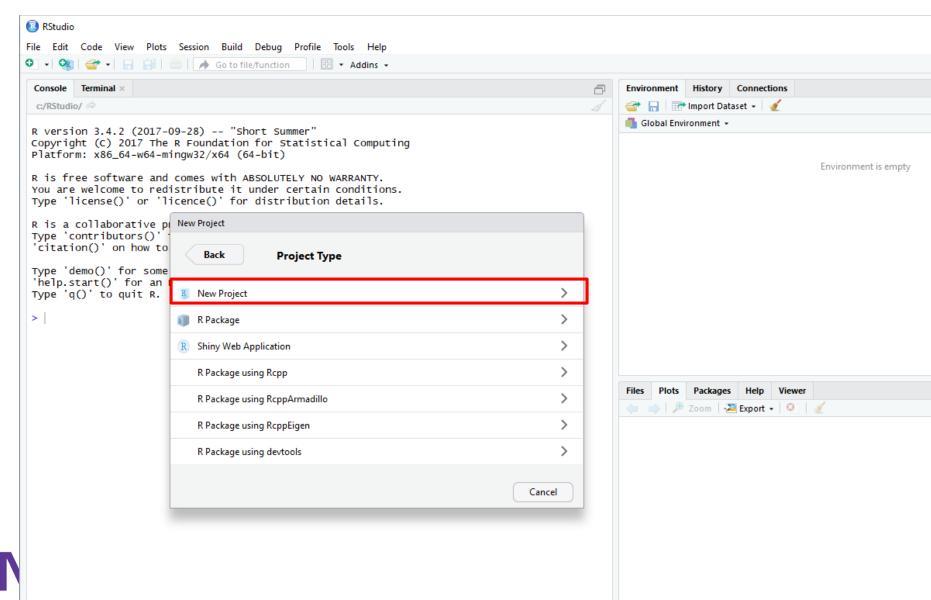
Creating your R Project

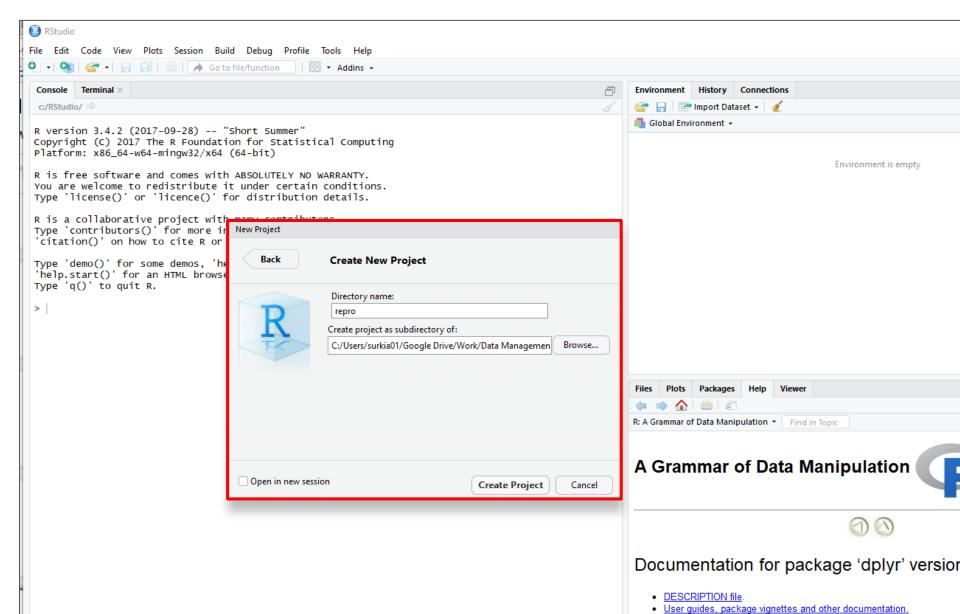
- Open R Studio
- Select New Project from the File menu











Structuring your project

Create the following folders within your repro folder:

- code
- raw_data
- processed_data
- results

Name	Date modified	Туре	Size
.Rproj.user	7/2/2018 3:03 PM	File folder	
code	7/2/2018 3:04 PM	File folder	
processed_data	7/2/2018 3:04 PM	File folder	
raw_data	7/2/2018 3:04 PM	File folder	
results	7/2/2018 3:04 PM	File folder	
desktop.ini	7/2/2018 3:03 PM	Configuration sett	1 KB
📵 repro.Rproj	7/2/2018 3:03 PM	RPROJ File	1 KB



Data files

Drag and drop the following two files into the code folder that is inside your repro folder:

- EHRData.csv
- REDCapData_Export.csv



Good Enough Practices for Scientific Computing: Data Management

- Save the raw data
- Record all steps for processing data
 - Do all processing within R
- Each project in its own directory
 - Directory named after project
- Each document type in its own sub-directory
- All files with names that reflect their content/function



GO TO HANDOUT



Documentation

☐ Is it clear where to begin? (e.g., can someone picking a project up see where to start running it)
☐ Can you determine which file(s) was/were used as input in a process that produced a derived file?
☐ Is there documentation about every result?
☐ Have you noted the exact version of every external application used in the process?
☐ For analyses that include randomness, have you noted the underlying random seed(s)?



Organization

- Which is the most recent data file/code?
- ☐ Which folders can I safely delete?
- ☐ Have you stored the raw data behind each plot?
- ☐ Do you run backups on all files associated with your analysis?



Automation

- ☐ Are there lots of manual data manipulation steps are there?
- ☐ Are all custom scripts under version control?
- ☐ Is your writing (content) under version control?



Publication

- ☐ Have you archived the exact version of every external application used in your process(es)?
- ☐ Are textual statements connected/linked to the supporting results or data?
- ☐ Did you archived preprints of resulting papers in a public repository?
- ☐ Did you release the underlying code at the time of publishing a paper?
- ☐ Are you providing public access to your scripts, runs, and results?

