

# A whirlwind tour of Rstudio, R, and Rmarkdown Magic for behavioral and brain scientists

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# The big outline

- ▶ Part 0: Background and Community
- ▶ Part 1: Rstudio
- ▶ Part 2: Project and environment setup
- ▶ Part 3: R (et al., eg Python)
- ▶ Part 4: Rmarkdown
- ▶ Part 5: Advanced R and beyond
- ▶ Part 6: A few of our favorite things

## Part 0: Background and Community

- ▶ What this is & isn't; a bunch of things we aren't covering but you should be aware of
  - ▶ This is a taste and to bring you into a bigger world
- ▶ Centralization, standards
- ▶ Help
- ▶ Including rigor & reproducibility of packages
- ▶ The “tidyverse”
  - ▶ Learn it. But don't learn *only* the tidyverse; you'll be lost in base R

## R Background

- ▶ Created in 1992 by Gentleman & Ihaka

*[we] considered the problem of obtaining decent statistical software for our undergraduate Macintosh lab. After considering the options, we decided that the most satisfactory alternative was to write our own. [...] Finally we added some syntactic sugar to make it look somewhat like S. We call the result “R”.*

## What is R?

- ▶ R is for stats and general purpose programming
- ▶ R is a functional language
  - ▶ Turing complete – can do anything other languages can do
- ▶ R is an environment to interface with the language
  - ▶ Console based
  - ▶ Type in commands
  - ▶ No point-and-click
- ▶ R is a collection of tools
  - ▶ Pre-packaged software at your disposal
- ▶ R is free (as in beer and speech)
  - ▶ No cost, no restrictions

# R is a bit ugly

The screenshot shows the RGui (64-bit) interface. The R Console window displays the R startup message and basic usage instructions. The script editor window shows a R script with code for merging datasets and modifying variable classes.

```
R version 3.3.1 (2016-06-21) -- "Bug in Your Hair"
Copyright (C) 2016 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'licence()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> citation()

To cite R in publications use:

R Core Team (2016). R: A language and environment for statist
computing. R Foundation for Statistical Computing, Vienna, Au

## Load and clean data
#####
### 0.1 Specify the column names and participants you want (ie, baseline visit f
adni.cols <- c("RID", "VISCODE", "DX", "AGE", "PTGENDER", "PTEDUCAT", 'PTETHCAT'
adni.rows <- c(adnimerge$VISCODE=="1" & adnimerge$MOCA>=16)
merge_subset <- adnimerge[adni.rows,adni.cols]

### remove participants with missing data
merge_subset <- merge_subset[complete.cases(merge_subset),]

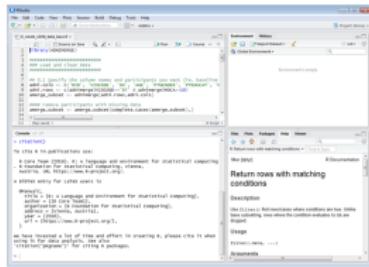
## 0.2 Bring in modified hachinksi
merge_subset$HMSCORE <- modhach$HMSCORE[match(merge_subset$RID, modhach$RID)]

## 0.3 Manually change variable classes (remove class 'labelled')
merge_subset$RID <- as.character(merge_subset$RID)
merge_subset$VISCODE <- as.character(merge_subset$VISCODE)
merge_subset$DX <- as.character(merge_subset$DX)
merge_subset$AGE <- as.numeric(merge_subset$AGE)
merge_subset$PTGENDER <- as.character(merge_subset$PTGENDER)
merge_subset$PTEDUCAT <- as.numeric(merge_subset$PTEDUCAT)
merge_subset$PTETHCAT <- as.character(merge_subset$PTETHCAT)
```

# But R has many interfaces

- ▶ Today we focus on RStudio (MatLab-like)
- ▶ But see also Deducer, RCommander (SPSS-like)

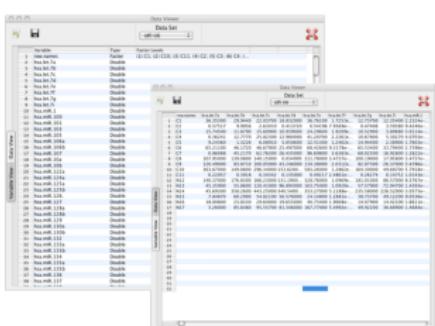
RStudio



RCommander



Deducer



## R is a community (actually many communities!)

- ▶ Help and resources
- ▶ Package development and distribution

## R: Help!

- ▶ <https://www.statmethods.net/>
- ▶ Online forums (Stack Exchange, r-lists)
- ▶ SpringerLink
  - ▶ All R books for free (pdf format) or for minimal cost (printed)
- ▶ Vignettes
  - ▶ step-by-step instruction guides for packages

## R Packages

- ▶ Packages are bundles of code made by someone (or many people) for everyone to use
  - ▶ If you can think of a stats problem, there is a package for it
- ▶ Available primarily on CRAN
  - ▶ But also github, r-forge

# Tidyverse

- ▶ something here about tidy

## Part 1: RStudio

- ▶ Settings, a quit tour through stuff, features
- ▶ Examples on getting setup

# RStudio Environment

The screenshot shows the RStudio interface with several windows open:

- Code Editor:** The main window displays R code for creating an ADNI data subset. The code includes library imports, data loading, cleaning, and merging steps. It also handles missing data and manually changes variable classes.
- Console:** A red box highlights the console output area. It shows statistical summaries for various variables like APOE4, FDG, AV45, CDRSB, ADAS13, and MOCA across different brain regions (Wholebrain, Hippocampus, Midtemp, nPACCtailB, and MSMScore).
- File Browser:** The right-hand sidebar shows the project structure for "2019\_Rstudio\_Magic". It includes files for R environment, R scripts, and other project components.

```
library(ADNImerger)
#####
## Load and clean data
#####
## 0.1 Specify the column names and participants you want (ie, baseline visit for all participants with MOCA>=1
admin.cols <- c("RID", "VISCODE", "DX", "AGE", "PTGENDER", "PTEDUCAT", "PTETHCAT", "PTRACCAT", "APOE4", "FDG", "ADAS13", "CDRSB", "MOCA")
admin.rows <- c(adminmerge$VISCODE=="b1" & adminmerge$MOCA>=16)
admin_subset <- adminmerge[admin.rows, admin.cols]
#####
## remove participants with missing data
admin_subset <- admin_subset[complete.cases(admin_subset),]
#####
## 0.2 Bring in modified hachkins
admin_subset$MSMScore <- modhach$MSMScore[match(admin_subset$RID, modhach$RID)]
#####
## 0.3 Manually change variable classes (remove class 'labelled')
admin_subset <- as.data.frame(admin_subset)
```

CONSOLE

Variable	Wholebrain	Hippocampus	Midtemp	nPACCtailB	MSMScore
Mean	:71.92	:71.92	:71.92	:71.92	:71.92
Min.	:0.0000	.Min. :0.6983	.Min. :0.8385	.Min. :0.0000	.Min. :16.36
3rd Qu.	:76.60	:76.60	:76.60	:76.60	:76.60
Max.	:89.60	:89.60	:89.60	:89.60	:89.60
APOE4	FDG	AV45	CDRSB	ADAS13	MOCA
Min.	:0.0000	Min. :0.6983	Min. :0.8385	Min. :0.0000	Min. :16.00
1st Qu.	:0.0000	1st Qu.:1.1800	1st Qu.:1.1800	1st Qu.:0.0000	1st Qu.:22.00
Median	:0.0000	Median :1.2802	Median :1.1105	Median :0.0000	Median :25.00
Mean	:1.5248	Mean :1.2682	Mean :1.1989	Mean :1.202	Mean :13.8
3rd Qu.	:1.0000	3rd Qu.:1.3620	3rd Qu.:1.3714	3rd Qu.:1.2000	3rd Qu.:18.00
Max.	:2.0000	Max. :1.7013	Max. :1.2056	Max. :15.5000	Max. :46.0

# RStudio Environment

The screenshot shows the RStudio interface with several windows open:

- Script Editor:** Displays the R script `create_ADNI_data.R`. The code performs the following steps:
  - Imports required packages: `tidyverse`, `lapply`, `data.table`, and `stringr`.
  - Creates a function `PTRACCAT` that takes a list of data frames and merges them into a single data frame.
  - Specifies column names for the merged data frame.
  - Loads and cleans data from `ADNI_data`.
  - Specifies column names and participants for baseline visit.
  - Creates `adni.cols` and `adni.rows` based on `PTCODE` and `MOCA`.
  - Removes participants with missing data.
  - Merges the cleaned data with the baseline visit data.
  - Changes variable classes (removing `labelled` class).
- Console:** Shows statistical summaries for various variables like APOE4, FDG, AV45, CDRSB, ADAS13, MOCA, Hippocampus, and MHTemp across different brain regions.
- Environment:** Shows the global environment with objects like `merge_subset` (665 obs. of 17 variables), `ids` (chr vector), and `MOCA` (num vector).
- Plots:** A scatter plot titled "FILEs, PLOTS, HELP" is shown, with the plot area highlighted by a red box.
- File Browser:** Shows the project structure with files like `README.md`, `script.R`, `output`, and `external`.

FILEs, PLOTS, HELP

# RStudio Environment

The screenshot shows the RStudio interface with several windows open:

- Code Editor:** Shows R code for creating an ADNI data subset. The code includes library imports, data loading, merging, and subset selection. A red box highlights the final command: `> view(merge_subset)`.
- Environment:** Shows the `merge_subset` object, which is a data frame with 665 observations and 17 variables. It lists columns like `ADAS13`, `CDRSB`, `MOCA`, and `PTEDUCAT`.
- File Browser:** Shows the project structure under `workshops > 2019_Rstudio_Magic`. It includes files like `README.md`, `environment.Rproj`, and `output`.
- Text Overlay:** A large red text overlay in the center-right area reads "VARIABLES, HISTORY, VERSION CONTROL".

# RStudio Environment

The screenshot displays the RStudio interface with several panes:

- Code pane:** Shows R code for creating an ADNI data subset. The code includes library imports, data loading, cleaning, and subset selection. It uses functions like `library`, `read.csv`, `subset`, and `complete.cases`.
- Console pane:** Displays statistical summaries for variables like APOE4, FDG, AV45, CDRSB, ADAS13, and MOCA. For example, APOE4 has a mean of 71.92 and a median of 70.00. The FDG variable has a range from 89.60 to 208.00.
- Environment pane:** Shows the global environment with objects like `anmerge\_subset` (665 obs., 17 variables), `variable\_type\_map`, and `Values` (e.g., `MOCA` with values 28-30).
- File browser pane:** Lists files in the 'workshops' directory, including 'README.md' (modified May 12, 2019, 11:29 AM) and various Rmd files (modified May 12, 2019, 11:33 AM and 11:30 PM).

```
library(ADNImerGE)
#####
## Load and clean data
#####
## 0.1 Specify the column names and participants you want (ie, baseline visit for all participants with MOCA>=1
admin.cols <- c("RID", "VISCODE", "DX", "AGE", "PTGENDER", "PTEDUCAT", "PTETHCAT", "PTRACCAT", "APOE4", "FDG", "AV45", "CDRSB", "ADAS13", "MOCA")
admin.rows <- c(adminmerge$VISCODE=="b1" & adminmerge$MOCA>=16)
anmerge_subset <- adminmerge[admin.rows,admin.cols]
#####
## remove participants with missing data
anmerge_subset <- anmerge_subset[complete.cases(anmerge_subset),]

## 0.2 Bring in modified hachkins
anmerge_subset$MSMSCORE <- modhach$MSMSCORE[match(anmerge_subset$RID, modhach$RID)]
####

## 0.3 Manually change variable classes (remove class 'labelled')
anmerge_subset$FDG <- as.numeric(as.character(anmerge_subset$FDG))
anmerge_subset$AV45 <- as.numeric(as.character(anmerge_subset$AV45))
anmerge_subset$CDRSB <- as.numeric(as.character(anmerge_subset$CDRSB))
anmerge_subset$ADAS13 <- as.numeric(as.character(anmerge_subset$ADAS13))
anmerge_subset$MOCA <- as.numeric(as.character(anmerge_subset$MOCA))

# Whole brain
anmerge_subset$Hippocampus <- as.numeric(as.character(anmerge_subset$Hippocampus))
anmerge_subset$Midtemp <- as.numeric(as.character(anmerge_subset$Midtemp))
anmerge_subset$pACCtrailsB <- as.numeric(as.character(anmerge_subset$pACCtrailsB))
anmerge_subset$MSMSCORE <- as.numeric(as.character(anmerge_subset$MSMSCORE))

# Individual brain regions
anmerge_subset$Lhipp <- as.numeric(as.character(anmerge_subset$Lhipp))
anmerge_subset$Rhipp <- as.numeric(as.character(anmerge_subset$Rhipp))
anmerge_subset$LMtemp <- as.numeric(as.character(anmerge_subset$LMtemp))
anmerge_subset$RMtemp <- as.numeric(as.character(anmerge_subset$RMtemp))
anmerge_subset$Lamygd <- as.numeric(as.character(anmerge_subset$Lamygd))
anmerge_subset$Ramygd <- as.numeric(as.character(anmerge_subset$Ramygd))
anmerge_subset$Lhipp <- as.numeric(as.character(anmerge_subset$Lhipp))
anmerge_subset$Rhipp <- as.numeric(as.character(anmerge_subset$Rhipp))
anmerge_subset$LMtemp <- as.numeric(as.character(anmerge_subset$LMtemp))
anmerge_subset$RMtemp <- as.numeric(as.character(anmerge_subset$RMtemp))
anmerge_subset$Lamygd <- as.numeric(as.character(anmerge_subset$Lamygd))
anmerge_subset$Ramygd <- as.numeric(as.character(anmerge_subset$Ramygd))
```

	Min.	Q1	Median	Q3	Max.
APOE4	0.0000	0.6983	0.8385	0.8835	208.00
FDG	89.60	176.60	189.00	200.00	208.00
AV45	0.0000	0.0000	0.0000	0.0000	0.0000
CDRSB	0.0000	0.0000	0.0000	0.0000	0.0000
ADAS13	0.0000	0.0000	0.0000	0.0000	0.0000
MOCA	0.0000	0.0000	0.0000	0.0000	0.0000
Hippocampus	11.2421	11.5111	11.2213	11.6883	11.0000
Midtemp	98.8410	101.6510	101.0535	101.0501	101.0000
pACCtrailsB	105.1621	105.2223	105.2086	105.2520	105.1000
MSMSCORE	105.7026	110.5000	110.5714	110.6882	110.5888
Lhipp	112.0570	112.0570	112.0570	112.0570	112.0570
Rhipp	148.6036	148.6036	148.6036	148.6036	148.6036
LMtemp	106.002	106.002	106.002	106.002	106.002
RMtemp	32.189	32.189	32.189	32.189	32.189
Lamygd	5.3540	5.3540	5.3540	5.3540	5.3540
RAMygd	3.0000	3.0000	3.0000	3.0000	3.0000

# RStudio Environment

~\workshops\2019\_RStudio\_Magic - master - RStudio

File Edit Code View Plots Session Build Debug Profile Tools Help

o 0\_create\_ADNI\_data.RData 1\_create\_ADNI\_data\_tidyverse.R amerge\_subset

DATA VIEWER

DX	AGE	PTGENDER	PTEDUCAT	PTRECAT	PTRACCAT	APOE4	FDG	AV45	CDRSB	ADAS13	MOCA	WholeBrain	
2002	MCI	64.0	Male	18	Not Hisp/Latino	White	0	1.2091938	0.9754323	2.5	4	28	1135568.8
2003	MCI	63.6	Female	18	Not Hisp/Latino	White	0	1.2889628	1.1645374	2.0	11	24	1070369.3
2007	MCI	85.4	Female	20	Hisp/Latino	White	0	1.305182	1.4495259	2.5	9	23	920710.1
2010	MCI	62.9	Female	20	Not Hisp/Latino	Other	1	1.3121151	1.1472844	0.5	6	27	966402.9
2011	MCI	69.9	Female	14	Not Hisp/Latino	White	0	1.4571991	1.0579399	1.5	7	25	987823.5
2018	MCI	76.4	Female	18	Not Hisp/Latino	White	0	1.3148491	1.052191	1.5	10	26	1004817.0
2022	MCI	66.0	Male	18	Not Hisp/Latino	Other	1	1.2031270	1.3135914	1.5	6	25	1173068.2
2027	MCI	61.9	Female	14	Not Hisp/Latino	White	0	1.4000448	1.0297671	1.0	6	24	969957.1
2031	MCI	72.5	Male	16	Not Hisp/Latino	White	0	1.3404430	0.9939887	2.0	10	24	1059879.5
2036	MCI	66.7	Female	14	Not Hisp/Latino	White	0	1.2959310	1.0307979	1.0	5	30	1019101.0
2037	MCI	75.8	Male	16	Not Hisp/Latino	White	1	1.3074956	1.4389912	0.5	20	20	1104797.3
2042	MCI	68.5	Male	20	Not Hisp/Latino	White	0	1.2081130	1.0555841	1.5	18	23	1061388.8
2043	MCI	72.2	Female	20	Not Hisp/Latino	White	1	1.3761158	1.2040191	2.0	8	27	1039110.3

Showing 10 of 15 1665 entries

Console Terminal Jobs

~\workshops\2019\_RStudio\_Magic

```
Mean : 71.92 Mean : 16.36
3rd Qu.: 76.60 3rd Qu.: 18.00
Max. : 89.60 Max. : 20.00

APOE4 FDG AV45 CDRSB ADAS13 MOCA
Min. : 0.0000 Min. : 0.6983 Min. : 0.8385 Min. : 0.0000 Min. : 0.0 Min. : 16.00
1st Qu.: 0.0000 1st Qu.: 1.0000 1st Qu.: 1.1000 1st Qu.: 0.0000 1st Qu.: 8.0 1st Qu.: 22.00
Median : 0.0000 Median : 1.2802 Median : 1.1105 Median : 0.0000 Median : 10.0 Median : 25.00
Mean : 0.5248 Mean : 1.2682 Mean : 1.1989 Mean : 0.1200 Mean : 13.8 Mean : 23.89
3rd Qu.: 1.0000 3rd Qu.: 1.3620 3rd Qu.: 1.3714 3rd Qu.: 2.0000 3rd Qu.: 18.0 3rd Qu.: 26.00
Max. : 2.0000 Max. : 1.7012 Max. : 2.0256 Max. : 15.5000 Max. : 46.0 Max. : 30.00

WholeBrain Hippocampus MidTemp nPACCtrailsB HMSCore
Min. : 114.421 Min. : 1.011 Min. : 12213 Min. : -18.6883 Min. : 0.0000
1st Qu.: 984410 1st Qu.: 6510 1st Qu.: 2535 1st Qu.: -1.051 1st Qu.: 0.0000
Median : 1051621 Median : 7223 Median : 20186 Median : -2.5250 Median : 1.0000
Mean : 1057026 Mean : 7150 Mean : 20302 Mean : -3.6882 Mean : 0.5888
3rd Qu.: 1120570 3rd Qu.: 7834 3rd Qu.: 22088 3rd Qu.: -0.3482 3rd Qu.: 1.0000
Max. : 1486036 Max. : 10602 Max. : 32189 Max. : 5.3540 Max. : 3.0000
> view(amerge_subset)
> |
```

Environment History Connections Git

Global Environment

anmerge\_subset 665 obs. of 17 variables  
variable\_type\_map num [1:17] "0 0 0 0 0 0 0 1 0 ...  
ids chr [1:665] "2002" "2003" "2007" "2010" "2011" "2012" ...  
MOCA num [1:665] 28 24 23 27 25 26 25 24 24 30 ...  
Functions scatterplotter function (x, y, x.lim = NA, y.lim = NA, x.lab = "...") {

Files Plots Packages Help Viewer

Home workshops : 2019\_RStudio\_Magic

Name	Size	Modified
Renviron	52 B	May 12, 2019, 11:33 AM
2019_RStudio_Magic.Rproj	210 B	May 12, 2019, 6:30 PM
external		
mice		
output		
R		
README.md	42 B	May 12, 2019, 11:29 AM
Rmd		

# Benefits of RStudio

- ▶ Built-in integration with version control (git or SVN)
- ▶ Package and documentation generation
- ▶ Reproducible science!
  - ▶ R Markdown documents
    - ▶ Save and execute code
    - ▶ Generate high quality reports that can be shared
  - ▶ Create presentations (like this one!)
  - ▶ Even write papers

# RStudio Resources

The screenshot shows the RStudio website homepage. At the top, there's a navigation bar with links for Products, Resources, Pricing, About Us, Blogs, and a search icon. Below the navigation is a decorative banner featuring a colorful, abstract graphic of overlapping colored bands.

**RStudio**: A screenshot of the RStudio IDE interface, showing the code editor, workspace, and plots.

**Shiny**: An image of a map of the United States with a "ZIP explorer" interface overlaid.

**R Packages**: Icons for several popular R packages: `markdown`, `Shiny`, `tidyverse`, `knitr`, and `ggplot2`.

**RStudio** description: RStudio makes R easier to use. It includes a code editor, debugging & visualization tools.

**Shiny** description: Shiny helps you make interactive web applications for visualizing data. Bring R data analysis to life.

**R Packages** description: Our developers create popular packages to expand the features of R. Includes `ggplot2`, `dplyr`, `R Markdown` & more.

At the bottom, there are download and learn more buttons for each section, and a horizontal orange progress bar.

# RStudio Resources

Online Learning - RStudio

https://www.rstudio.com/online-learning/

R Studio

Products Resources Pricing About Us Blogs

## Online learning

A wealth of tutorials, articles, and examples exist to help you learn R and its extensions. Scroll down or click a link below for a curated guide to learning R and its extensions.

- R Programming
- Shiny
- R Markdown
- Data Science
- Books

R Programming  
Read More >

Shiny  
Read More >

R Markdown  
Read More >

Data Science  
Read More >

# RStudio Resources

Cheatsheets - RStudio x + - □ x

https://www.rstudio.com/resources/cheatsheets/

R Studio Products Resources Pricing About Us Blogs Q

## RStudio Cheat Sheets

The cheat sheets below make it easy to learn about and use some of our favorite packages. From time to time, we will add new cheat sheets to the gallery. If you'd like us to drop you an email when we do, let us know by clicking the button to the right.

SUBSCRIBE TO CHEAT SHEET UPDATES HERE

- RStudio IDE
- R Markdown
- Shiny
- Package Development
- Data Import
- Data Transformation with dplyr
- Data Visualization with ggplot2
- Apply functions with purrr
- Deep Learning with Keras
- Data Science in Spark with Sparklyr
- String manipulation with stringr
- Dates and times with lubridate

### Python with R and Reticulate Cheat Sheet

The reticulate package provides a comprehensive set of tools for interoperability between Python and R. With reticulate, you can call Python from R in a variety of ways including importing Python modules into R scripts, writing R Markdown Python chunks, sourcing Python scripts, and using Python interactively within the RStudio IDE. This cheatsheet will remind you how.  
Updated 4/19.

Use Python with R with reticulate :: CHEAT SHEET

The reticulate package makes it easy to have and use Python in R. It's a Python interface, just like R itself.

Python in R Markdown

Object Conversion

Helpers



## Part 2: Project and Environment Setup

- ▶ Hidden files & whatnot
- ▶ Have a structure ready to go on Github
- ▶ Explain/walk through
- ▶ Discuss the helpful packages above

# RStudio Setup

- ▶ Download R and Rstudio
- ▶ Add-on packages

```
#to install from CRAN
install.packages('devtools', dependencies = TRUE)
#to install from a file
install.packages('/mypath/to/package/ADNIMERGE.tar.gz',
                 type='source', repos=NULL)
#to install from a git  (requires the devtools package)
dev.tools::install_github(Gibbsdavid/CatterPlots)
```

- ▶ See <https://jennybc.github.io/2014-05-12-ubc/r-setup.html> for a detailed guide

# Rstudio Setup: Projects & Git

- ▶ Download git and link to RStudio

Options

The screenshot shows the 'Options' dialog in RStudio, specifically the 'Git/SVN' tab. On the left is a sidebar with icons for General, Code Editing, Appearance, Pane Layout, Packages, Sweave, and Spelling. The 'Git/SVN' icon at the bottom is highlighted with a blue background.

Enable version control interface for RStudio projects

Git executable:  
C:/Program Files (x86)/Git/bin/git.exe

Use Git Bash as shell for Git projects

SVN executable:  
(Not Found)

SSH RSA Key:  
(None)

[? Using Version Control with RStudio](#)

# Rstudio Setup: Projects & Git

- ▶ Create a new project File

New Project

**Create Project**

---

 **New Directory**  
Start a project in a brand new working directory >

---

 **Existing Directory**  
Associate a project with an existing working directory >

---

 **Version Control**  
Checkout a project from a version control repository >

---

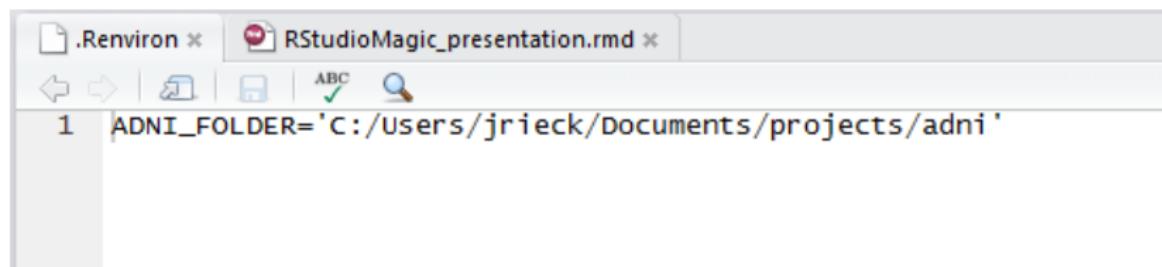
**Cancel**

## Format .gitignore

- ▶ File types to ignore:
  - ▶ `.Rproj.user`
  - ▶ `.Rhistory`
  - ▶ `.Ruserdata`
  - ▶ `.Renviron`
  - ▶ `.rda` & `.Rdata` (to avoid pushing potentially sensitive data files to git)
  - ▶ `**` before each extention will match directories anywhere in the repo

## Format environmental variables

- ▶ Set environmental variables (ie, directory location of data) to make code generalizable across computers
  - ▶ In your project folder create a `.Renvironment` file and define variables



The screenshot shows the RStudio interface with the .Renvironment file open. The title bar displays two tabs: ".Renvironment" and "RStudioMagic\_presentation.rmd". Below the title bar is a toolbar with icons for back, forward, file operations, and search. The main editor area contains the following text:

```
1 ADNI_FOLDER='C:/Users/jrieck/Documents/projects/adni'
```

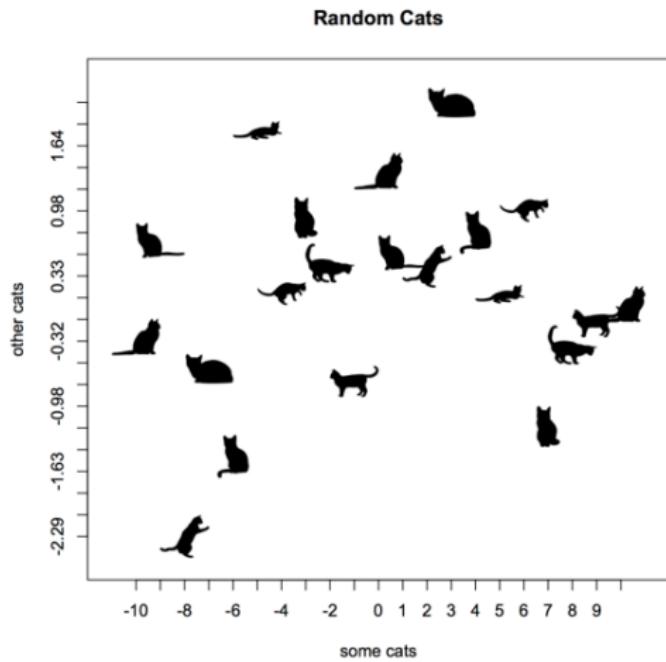
## Part 6: A few of our favorite things

- ▶ Fun R do-dads

# CatterPlot for feline based graphics:

- ▶ <https://github.com/Gibbsdavidl/CatterPlots>

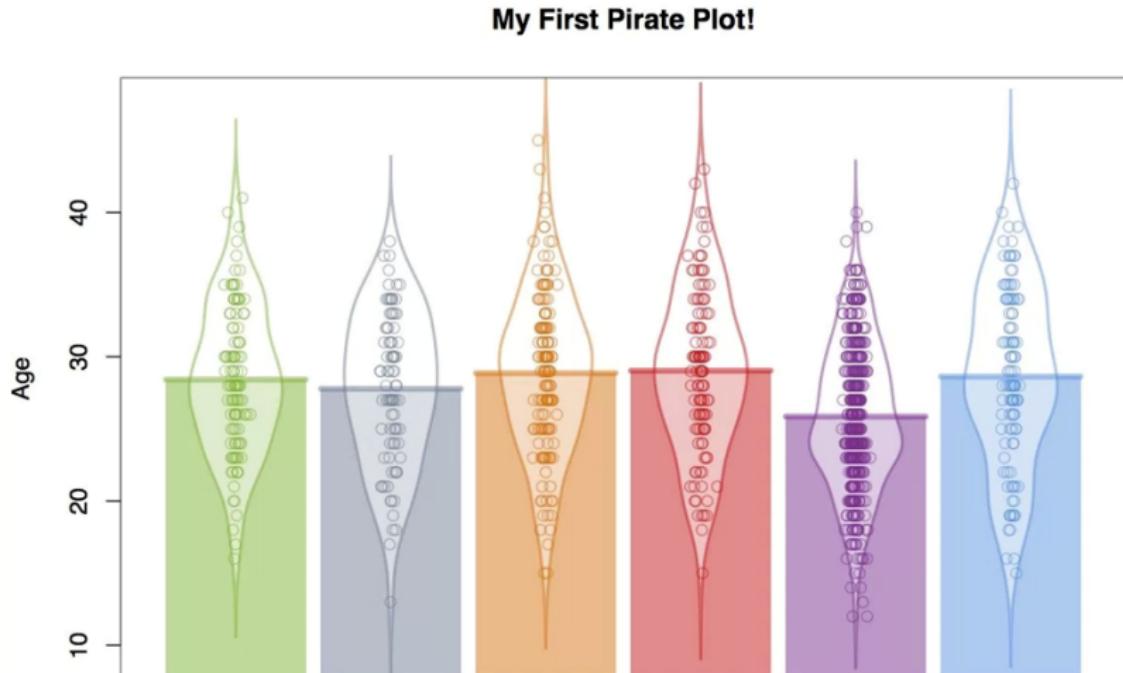
```
dev.tools:::install_github(Gibbsdavidl/CatterPlots)
```



# What's a pirate's favorite programming language?

- ▶ <https://cran.r-project.org/web/packages/yarrr/vignettes/pirateplot.html>

```
install.packages('yarrr')
```



# Color palettes to fit your mood

- ▶ <https://github.com/karthik/wesanderson>

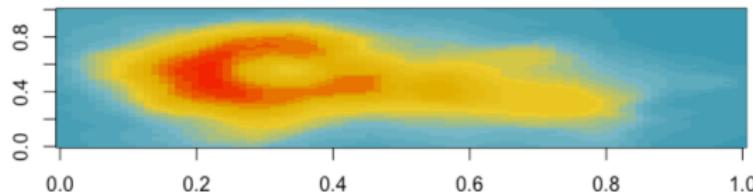
```
devtools::install_github(karthik/wesanderson)
```

The Life Aquatic with Steve Zissou (2004)

```
wes_palette("Zissou1")
```

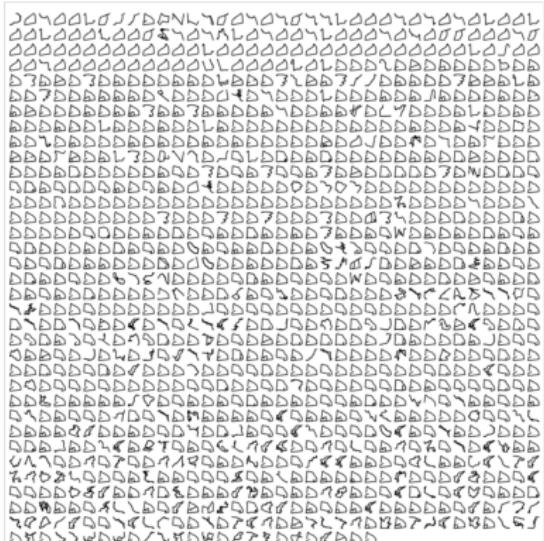


```
pal <- wes_palette("Zissou1", 21, type = "continuous")
image(volcano, col = pal)
```



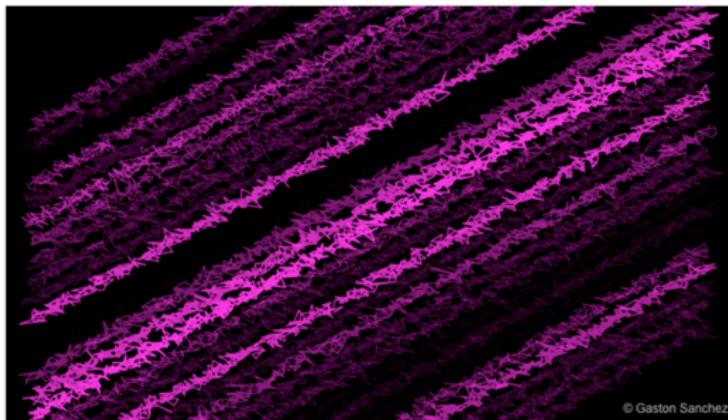
# Mapping your Strava routes

- ▶ <https://www.r-bloggers.com/strava-rides-map-in-r/>
- ▶ ALSO <https://marcusvolz.com/?p=4068>
  - ▶ `dev.tools::install_github(marcusvolz/strava)`



# Make aRt!

- ▶ R Graph Gallery
  - ▶ <http://www.r-graph-gallery.com/>
- ▶ Rtist: Gaston Sanchez
  - ▶ <http://gastonsanchez.com/Rtist/>



```
# -----
# Pink Barbs
# -----
# generate points x-y values
x <- seq(0, 100, length = 1000)
y <- x + rnorm(1000)

# -----
# Pink Barbs
# -----
# see graphical parameters
op <- par(bg = "black", mar = rep(0, 4))
# plot
plot(x, y, type = "n")
for (i in seq(-80, 70, by = 5))
{
  lines(x + rnorm(1000), x + i + rnorm(1000, 2), pch = 19,
        lwd = 2, col = have[2, i], lty = runif(1000),
        lwd = sample(seq(0.1, 2, length = 20), 1))
}
# signature
legend("bottomright", legend = "@ Gaston Sanchez", bty = "n",
       text.col = "gray75")
# reset par
par(op)
dev.off()
```