

CogLab: Visualize Data

WEEK 8

recap: Oct 12, 2023

- what we covered:
 - reviewing data analysis plan
 - R 101
- your to-do's were:
 - *prep*: Visualization Basics primer from posit
 - *prep*: work on project milestone #5
 - *prep*: work on formative milestone #1 resubmission

today's agenda

- packages in R
- graphing data

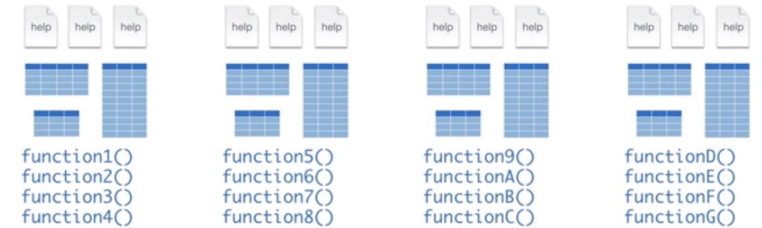
open your RStudio project

- open the project and your .Rmd file

packages in R

- packages contain functions
- before we can use them, we need to **install** packages
 - installation only happens once
- inside your notebook, delete everything after the last ---
- create a new heading **# install packages**
- create a new code chunk using command + option + I
 - or use the green C icon
- install **tidyverse**
- run the chunk:
 - command + shift + enter OR green play button
- comment (#) the install line after installation is complete (we will not need to do this again)

Packages



```
first-R-notebook.Rmd x
Preview on Save
Preview
Source Visual
1 ---
2 title: "R Notebook"
3 output: html_notebook
4 editor_options:
5   chunk_output_type: inline
6 ---
7
8 |
```

```
8 # install packages
9
10 ```{r}
11 install.packages("tidyverse", "ggplot2")
12 ```
```

install packages

```
```{r}
#install.packages("tidyverse", "ggplot2")
```
```

tidyverse

- a package of **packages**, which contain their own **functions**
- extremely flexible ways of manipulating and plotting data



loading packages in R

- we must always load the packages when we want to run code that uses functions from those packages
- create a new heading
`# load packages`
- create a new code chunk
- load tidyverse
- run the chunk
- save your notebook

```
# load packages
```

```
```{r}  
library(tidyverse)
```
```

```
Registered S3 methods overwritten by 'dbplyr':
```

```
  method      from  
  print.tbl_lazy  
  print.tbl_sql
```

```
— Attaching packages —
```

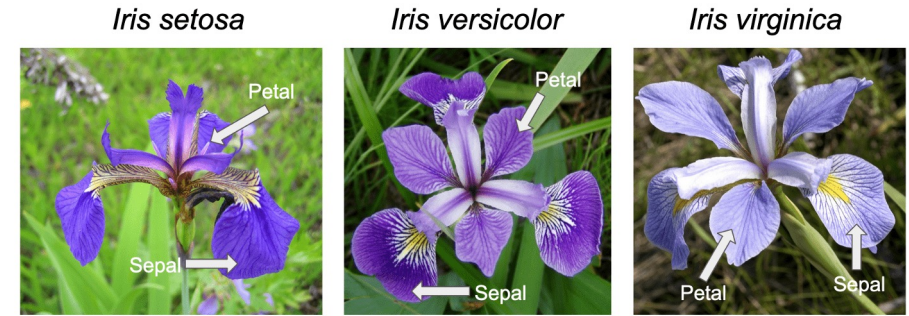
```
ggplot2 3.4.0      ✓ purrr   1.0.1  
✓ tibble 3.1.8      ✓ dplyr   1.0.10  
✓ tidyr  1.3.0      ✓ stringr 1.5.0  
✓ readr  2.1.3      ✓ forcats 0.5.2 — Conflicts
```

```
tidyverse
```

```
* dplyr::filter() masks stats::filter()  
* dplyr::lag()    masks stats::lag()
```

examining a dataframe

- view the iris dataset
- how many rows and columns?
- what are the column names?
- **research question**: how are the species different from each other?
- first we plot, then we analyze



| | Sepal.Length | Sepal.Width | Petal.Length | Petal.Width | Species |
|----|--------------|-------------|--------------|-------------|---------|
| 1 | 5.1 | 3.5 | 1.4 | 0.2 | setosa |
| 2 | 4.9 | 3.0 | 1.4 | 0.2 | setosa |
| 3 | 4.7 | 3.2 | 1.3 | 0.2 | setosa |
| 4 | 4.6 | 3.1 | 1.5 | 0.2 | setosa |
| 5 | 5.0 | 3.6 | 1.4 | 0.2 | setosa |
| 6 | 5.4 | 3.9 | 1.7 | 0.4 | setosa |
| 7 | 4.6 | 3.4 | 1.4 | 0.3 | setosa |
| 8 | 5.0 | 3.4 | 1.5 | 0.2 | setosa |
| 9 | 4.4 | 2.9 | 1.4 | 0.2 | setosa |
| 10 | 4.9 | 3.1 | 1.5 | 0.1 | setosa |

```
> nrow(iris)
[1] 150
> ncol(iris)
[1] 5
> colnames(iris)
[1] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width" "Species"
```


the grammar of graphics

- converting data to a visual display
- `ggplot()` is a function from the `ggplot2` package, which is included in the `tidyverse`
- three key steps to use `ggplot()`:
 - select a dataset
 - pick a geometric object
 - specify aesthetics

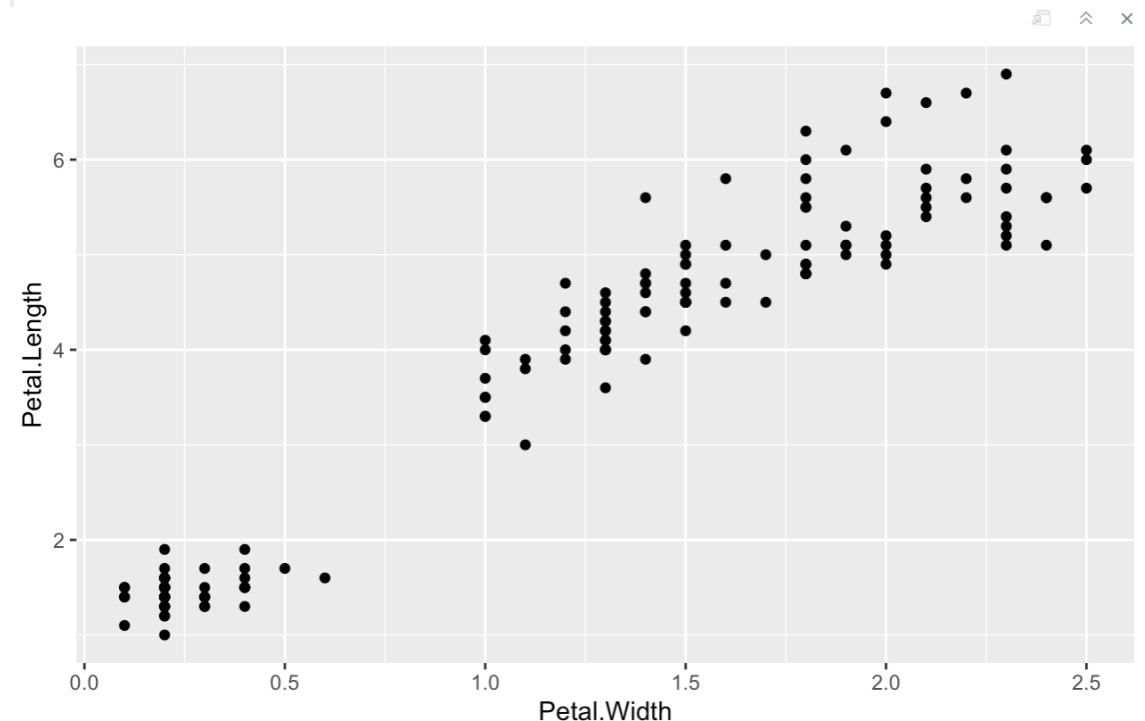


ggplot basic structure

- plot the **petal width** (x) and **length** (y) from the iris dataset
- `ggplot()` specifies the **dataset** and creates an empty graph
- `geom_point()` adds a layer of points to this empty graph
- **mapping** specifies how to map the data to the points

```
# plot iris
```

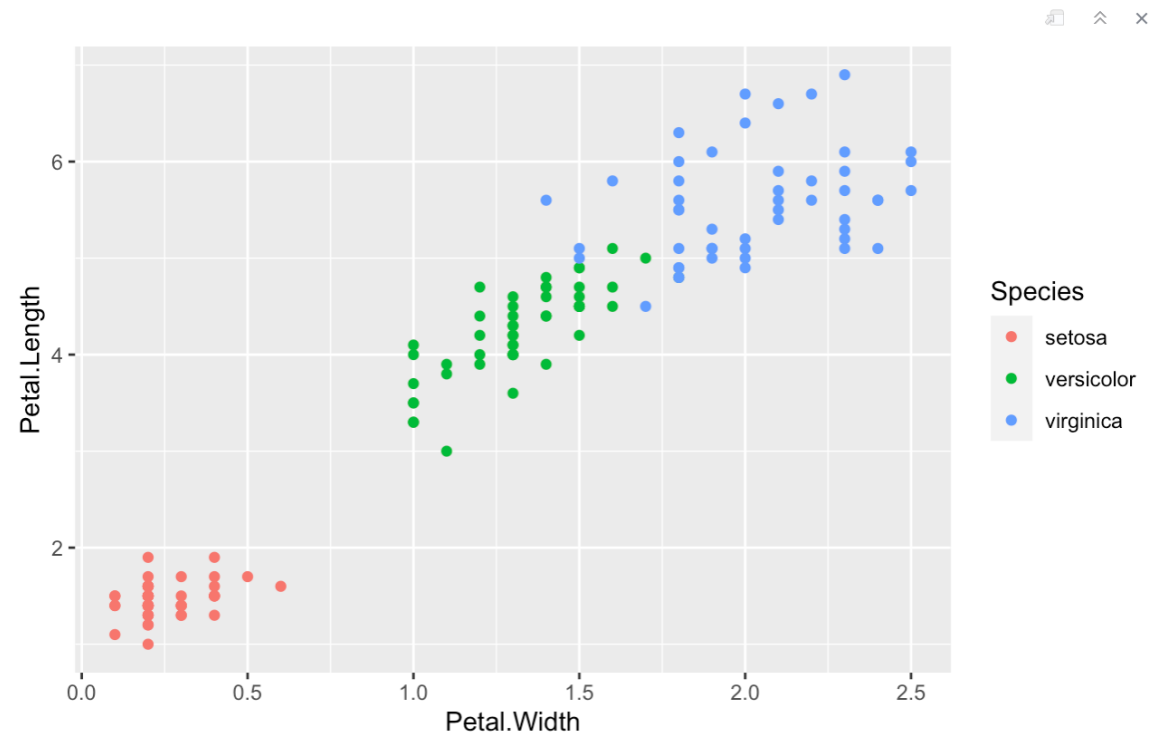
```
```${r}  
ggplot(data = iris)+
 geom_point(mapping = aes(x = Petal.Width, y = Petal.Length))
````
```



aesthetics

- aesthetics define **visual properties** of objects in the plot
- allow us to include a third variable in a 2-d plot using properties like size, shape, color, etc.
- map the **color** of the points to **species**

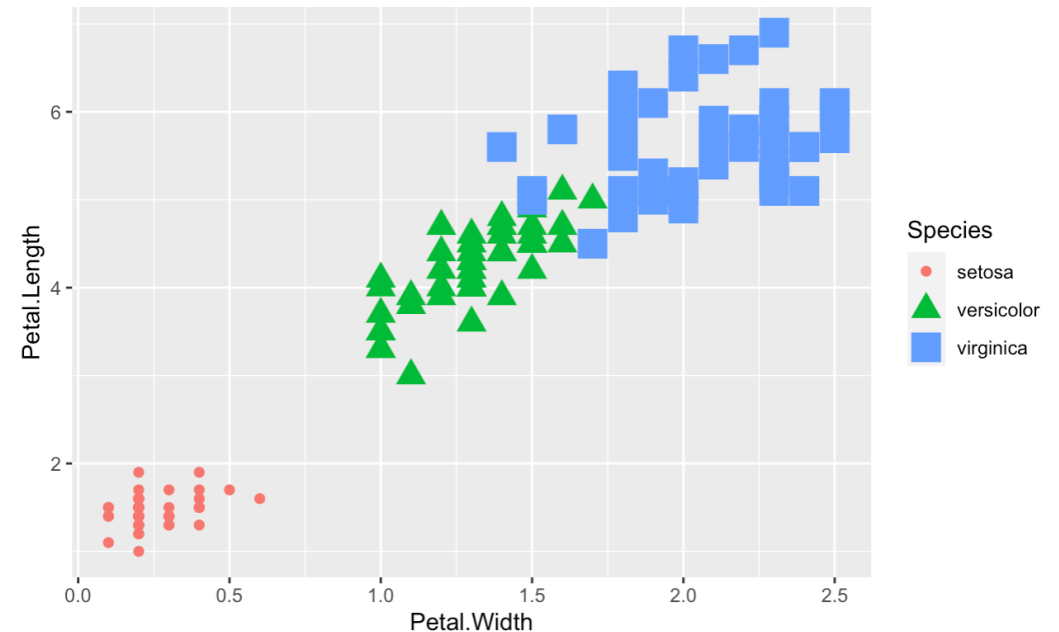
```
```\r}\nggplot(data = iris)+\n  geom_point(mapping = aes(x = Petal.Width, y = Petal.Length, color = Species))\n```\n
```



# other aesthetics

- map **size** and **shape** to the **species** as well
- is petal information helpful is distinguishing the species?

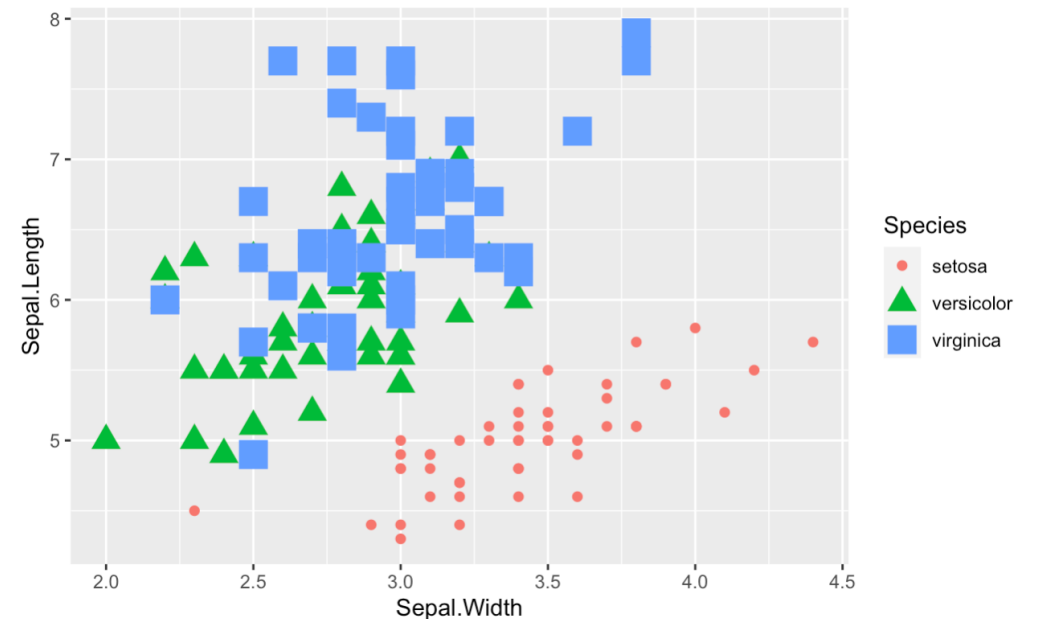
```
ggplot(data = iris)+
 geom_point(mapping = aes(x = Petal.Width, y = Petal.Length,
 color = Species, size = Species,
 shape = Species))
 ...
```



# exercise

- plot **sepal width** and **length** for the three species
- is sepal information helpful is distinguishing the species?

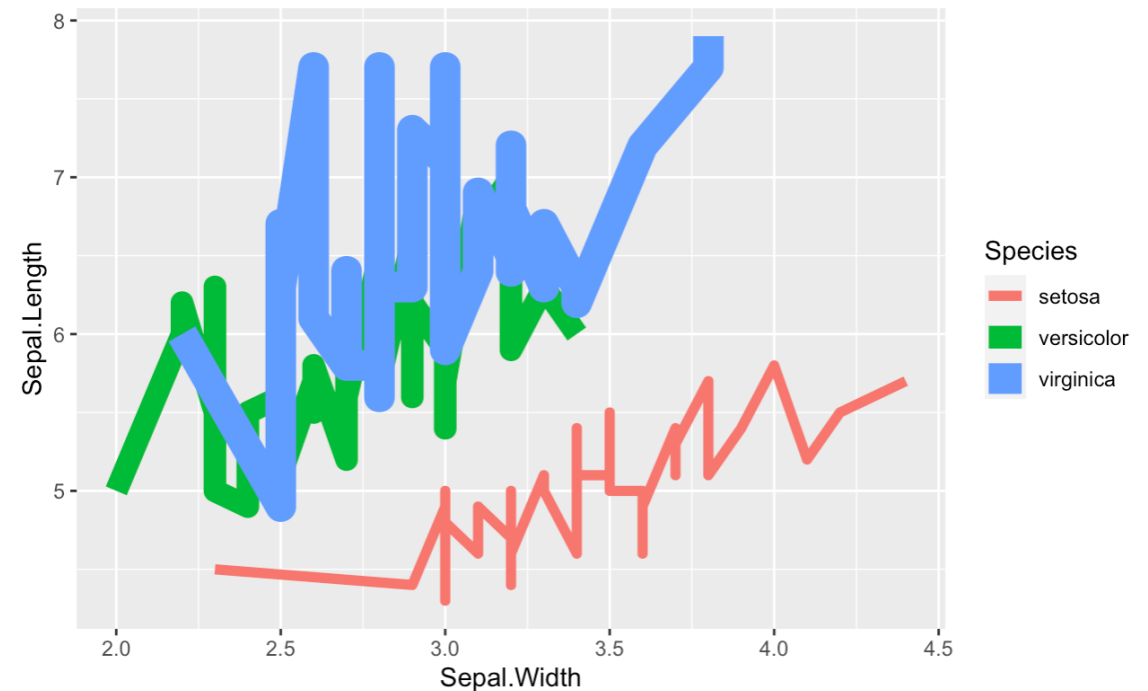
```
ggplot(data = iris)+
 geom_point(mapping = aes(x = Sepal.Width, y = Sepal.Length,
 color = Species, size = Species,
 shape = Species))
† ...
```



# geometric objects

- geoms specify **the type of visual object** that will be used to display the data
  - scatterplots: `geom_point()`
  - histograms: `geom_histogram()`
  - density plots: `geom_density()`
  - bar plots: `geom_bar()` / `geom_col()`
  - line plots: `geom_line()`
  - curves: `geom_smooth()`
  - boxplots: `geom_boxplot()`
- change `geom_point()` to `geom_line()` in the sepal plot

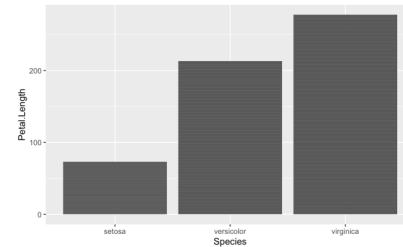
```
ggplot(data = iris)+
 geom_line(mapping = aes(x = Sepal.Width, y = Sepal.Length,
 color = Species, size = Species,
 shape = Species))
```



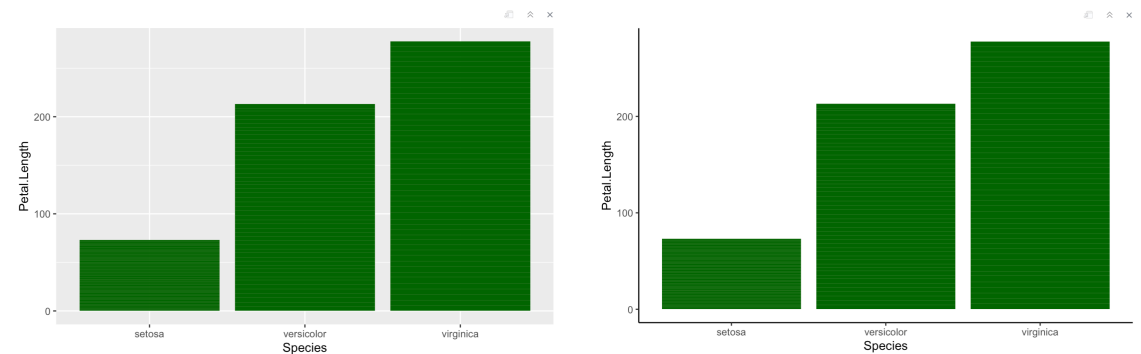
# displaying aggregate information

- if you simply wanted to display the aggregate information, [bar/column plots](#) are more suitable
- use `geom_col()` to display the petal lengths as a function of species
- fill the plot with any color you want ([colors in R](#))
- add a theme to the plot ([ggplot2 themes](#))

```
ggplot(data = iris)+
 geom_col(mapping = aes(x = Species, y = Petal.Length))
```



```
ggplot(data = iris)+
 geom_col(mapping = aes(x = Species, y = Petal.Length), fill = "darkgreen")
```










```
ggplot(data = iris)+
 geom_col(mapping = aes(x = Species, y = Petal.Length), fill = "darkgreen")+
 theme_classic()
```

# class data

- create a new heading  
# load class data
- read in class data via  
read\_csv
- save and run the chunk
- view the data

```
load class data
```

```
```{r}  
savic = read_csv("class_data.csv")  
```
```

| Environment                                                                                                                                                             | History                                                                                                  | Connections                                                                                   | Git                                                                                 | Tutorial |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|----------|
|   |  Import Dataset ▾     |  304 MiB ▾ |  |          |
| R ▾                                                                                                                                                                     |  Global Environment ▾ |                                                                                               |                                                                                     |          |
| Data                                                                                                                                                                    |                                                                                                          |                                                                                               |                                                                                     |          |
|  savic                                                                             | 27089 obs. of 40 variables                                                                               |                                                                                               |                                                                                     |          |

```
View(savic)
```



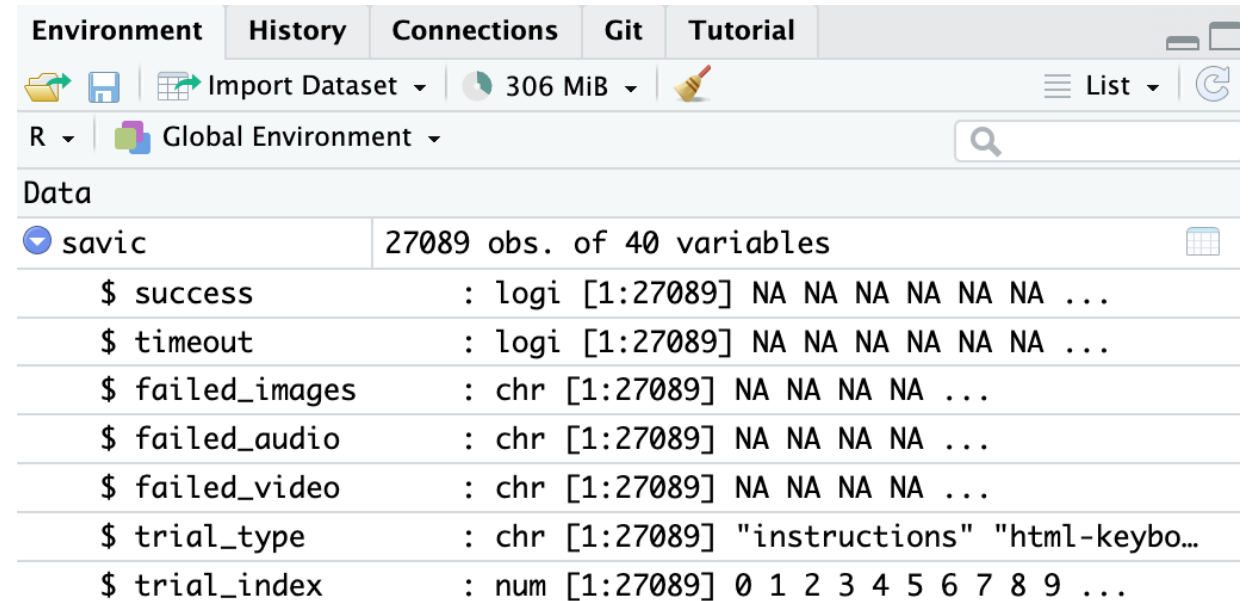
# class data

- how many rows?
- how many columns?
- what are the column names?
- research question?

```
basic info
`` `{r}
nrow(savic)
ncol(savic)
colnames(savic)
`` `
```

# exploring data types

- look at the default data types assigned to these columns in our dataframe
- ID
- rt
- typeoftrial
- relatedness
- type

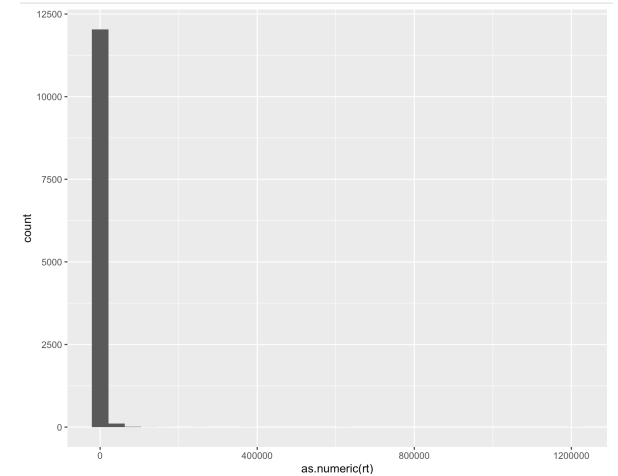


The screenshot shows the RStudio interface with the 'Data' pane open. The dataframe 'savic' is selected, showing 27089 observations and 40 variables. The following table displays the data types for the first seven variables:

| Variable         | Data Type      | Sample Values                  |
|------------------|----------------|--------------------------------|
| \$ success       | logi [1:27089] | NA NA NA NA NA NA ...          |
| \$ timeout       | logi [1:27089] | NA NA NA NA NA NA ...          |
| \$ failed_images | chr [1:27089]  | NA NA NA NA ...                |
| \$ failed_audio  | chr [1:27089]  | NA NA NA NA ...                |
| \$ failed_video  | chr [1:27089]  | NA NA NA NA ...                |
| \$ trial_type    | chr [1:27089]  | "instructions" "html-keybo..." |
| \$ trial_index   | num [1:27089]  | 0 1 2 3 4 5 6 7 8 9 ...        |

# histogram of reaction time

- create a new chunk titled  
# histogram of RT
- use ggplot to plot response time from the dataframe
- an error may be returned if R does not recognize RT as a number
- we can change the type of the column



```
histogram of RT
```

```
```{r}
ggplot(data = savic) +
  geom_histogram(mapping = aes(x= rt))
```
```

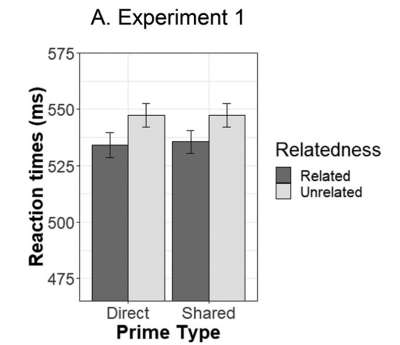
```
histogram of RT
```

```
```{r}
ggplot(data = savic) +
  geom_histogram(mapping = aes(x= as.numeric(rt)))
```
```

# what kind of plots do we want?

- think about each piece of data we will analyze
- which kind of plot will best capture those data?

# analysis preview



| phase       | measure                                                              | type                                      | exclusion criteria                                                                           |
|-------------|----------------------------------------------------------------------|-------------------------------------------|----------------------------------------------------------------------------------------------|
| attention   | accuracy                                                             | descriptive                               | < 0.75                                                                                       |
| association | proportion of correct/congruent responses + direct/shared responding | descriptive                               |                                                                                              |
| priming     | $RT_{related}$ vs. $RT_{unrelated}$ for direct and shared pairs      | inferential (mixed effects model / ANOVA) | RT < 200 ms and RT > 1500 ms<br>correct responses related/unrelated and direct/shared trials |

# HW: fixing accuracy

| AB                                                                 | AC               | AD       | AE     | AF        | AG        | AH      | AI              | AJ  |
|--------------------------------------------------------------------|------------------|----------|--------|-----------|-----------|---------|-----------------|-----|
| response                                                           | revised_response | sentence | novel1 | novel2    | novel3    | correct | revised_correct | cue |
|                                                                    |                  |          |        |           |           |         |                 |     |
| sh it were easier to get a foobly mipp. Sometimes I wis foobly     |                  |          |        | mipp      | NOT_FOUND |         |                 |     |
| cided I'd go looking for a foobly apple. In the end, I deci foobly |                  |          |        | NOT_FOUND | NOT_FOUND |         |                 |     |
| et there told me they saw a foobly app The people I me foobly      |                  |          |        | NOT_FOUND | NOT_FOUND |         |                 |     |
| I would like a dodish horse better. I am not sure if I dodish      |                  |          |        | NOT_FOUND | NOT_FOUND |         |                 |     |

- go to revised\_class\_data on drive
- group task: fix the data!
  - **Semantic Snakes**: fix the attention check **responses + accuracy**
  - **Berries**: fix association responses, IDs 275998227- 276772242
  - **Nellaphen**: fix association responses, IDs 823472278 – 988749039
- complete before Tuesday (Oct 24)

# next class

- **before** class

- *prep*: Work with Data primer
- *try*: HW, fix the data!
- *apply*: Week 8 Quiz
- *apply*: formative milestone # 1 resubmission
- *apply*: project milestone 5 (full experiment)

- **during** class

- manipulating data