Lab 01b: BMI 5/625

Introducing ggplot

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R Basics

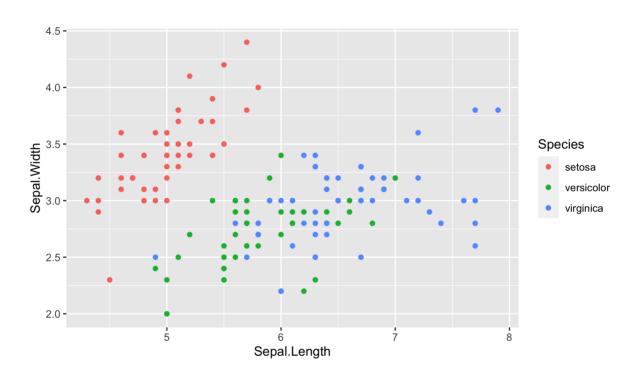
- R is an interpreter (>)
- Name objects in R (i_like_snake_case ←) asdf
- Know your object types (typeof())
- Case matters (my_names ≠ My_names)
- Use comments! (# use the hashtag symbol)
- Functions (fun!)
- Use packages ("install once per machine, load once per R session")
- Use the %>% ("dataframe first, dataframe once")

Introducing ggplot

- Goal for this session: a very quick ggplot refresher
- Meet our dataset:
 - Palmer Penguins

```
glimpse(penguins)
```

Sidebar: Why not Fisher's Irises?



- Hint: The original citation for that data is:
 - R. A. Fisher (1936) "The use of multiple measurements in taxonomic problems." Annals of Eugenics 7(2): 179-188



So: Penguins!

```
glimpse(penguins)
```

Core ggplot concepts

- *Aesthetics* map data to visual properties of the plot
- Geometries ("geoms") actually put "ink on the page"
 - Each type of graph (scatterplot, etc.) has a corresponding geom
 - Different geoms attend to different aesthetics
 - e.g., geom_point cares about x and y
 - Multiple geoms can be combined on the same plot
- *Scales* control axes, fills, etc.
- *Themes* control visual properties (fonts, background colors, etc.)

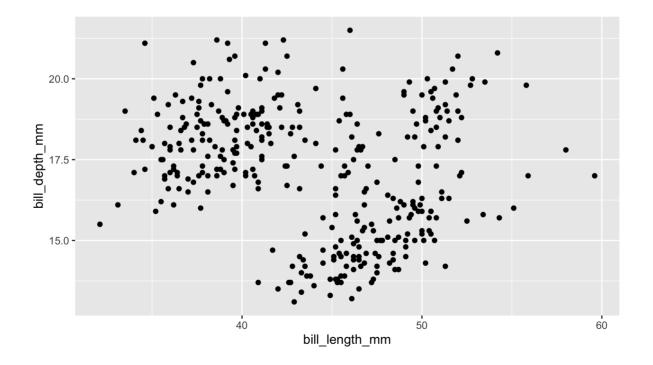
ggplot is an opinionated tool!

Data considerations

- By default, ggplot assumes "tidy" data
- Think: one "row" per mark on the graph...
- ... and then the various properties for each mark in columns.

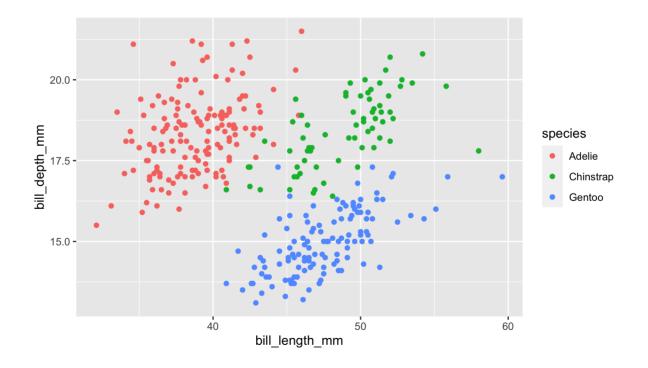
Our first plot

```
penguins %>% ggplot(
  mapping=aes(x=bill_length_mm, y=bill_depth_mm)
) + geom_point()
```



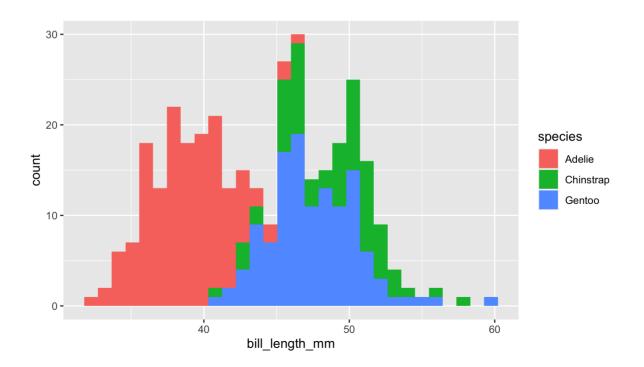
What about color?

```
penguins %>% ggplot(
  mapping=aes(x=bill_length_mm, y=bill_depth_mm, color=species)
) + geom_point()
```



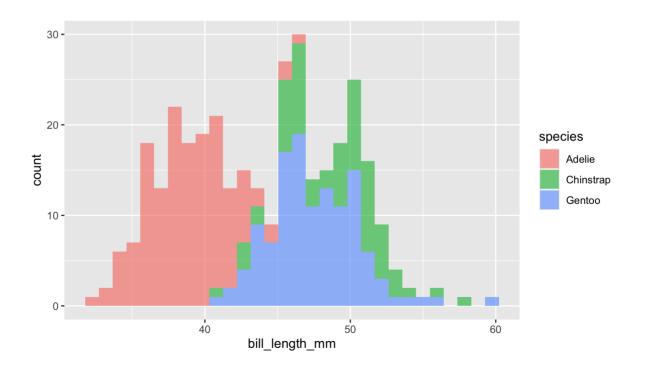
Want a different plot? Try a different geom

```
penguins %>% ggplot(
  mapping=aes(x=bill_length_mm, fill=species)
) + geom_histogram()
```



We can specify aesthetic values by hand:

```
penguins %>% ggplot(
  mapping=aes(x=bill_length_mm, fill=species)
  ) + geom_histogram(alpha=0.6)
```



Customizing other aspects of the plot

```
penguins %>% ggplot(
  mapping=aes(x=bill_length_mm, fill=species)
  ) + geom_histogram(alpha=0.6) +
  labs(x="Bill Length (mm)", y="Frequency") +
  ggtitle("Bill Length, by species")
```

