Module 3: Reporting, Data Wrangling and Graphing (II)

Siyue Yang

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Outline

Last module we reviewed how to tidy and plot data.

In this module, we will continue our discussion on

- Graphing (ggplot2) with a real-world dataset
- Git + Github

ggplot

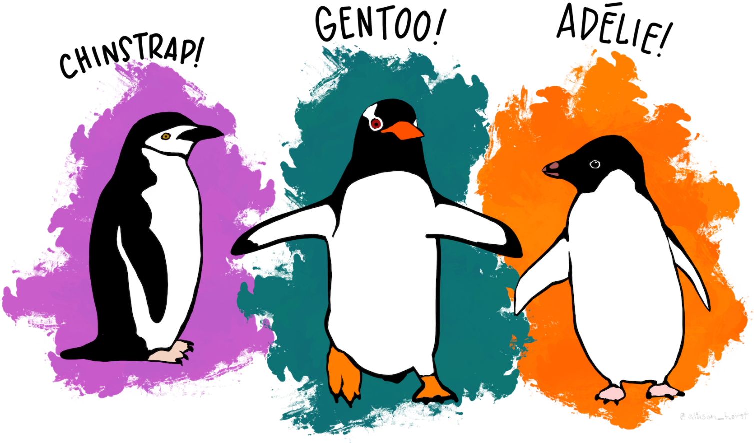
- `ggplot` is the graphing package that goes with the `tidyverse` in R
- Very powerful to make a wide range of graphics
- Same pattern as `tidyverse`"', but using"+" to connect.

How to write?

- Specify the data using
  `ggplot(data = diamonds)`
- Specify the x-/y-axis,
  `ggplot(data = diamonds, mapping = aes(x = cut))`
- Specify the types of plots with `geom`, e.g.
  `+ geom_bar()`

Data used - palmerpenguins

The palmerpenguins is a R package with data from the Long Term Ecological Research Network. It contains two dataset for 344 penguins and 3 species of penguins from 3 islands in the Palmer Archipelago, Antarctica.



Install and load package

From what we have learned so far, how to install package? What packages are we going to use?

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```
install.packages("palmerpenguins")
```

```
library(tidyverse)
library(palmerpenguins)
```

Skim the data

How many observations? How many variables? What type?

Skim the data

How many observations? How many variables? What type?

```
head(penguins)
```

Scatter plot

Consider a scatter plot of flipper length and body mass for `species = "Adelie"`

First let's prepare the data to plot (Hint: filter).

Scatter plot

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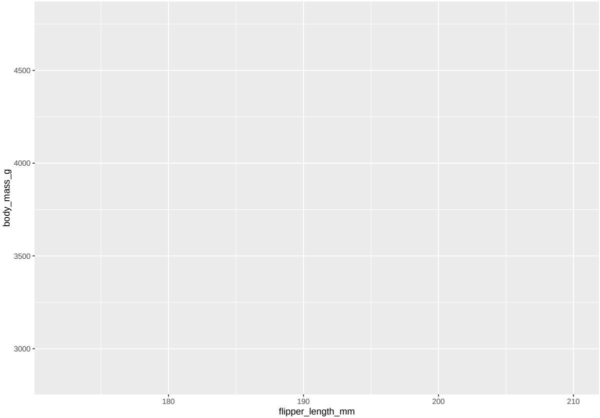
First let's prepare the data to plot (Hint: filter).

```
pdata <- penguins %>%
  filter(species == "Adelie")
```

A blank canvas

aes stands for aesthetic and tells ggplot the main characteristics of your plot (x, y, and if the color or fill vary by group)

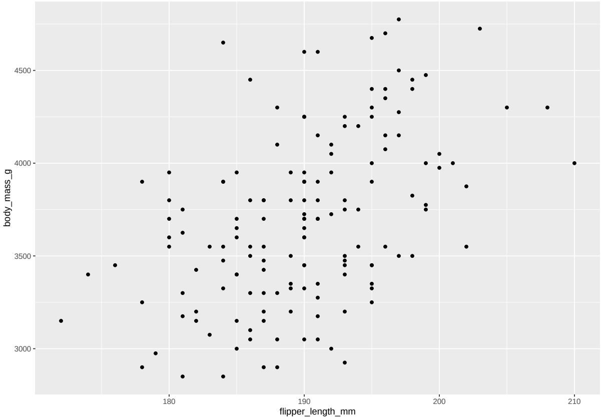
```
ggplot(data = pdata, aes(x = flipper_length_mm, y = body_mass_g))
```



Add the points

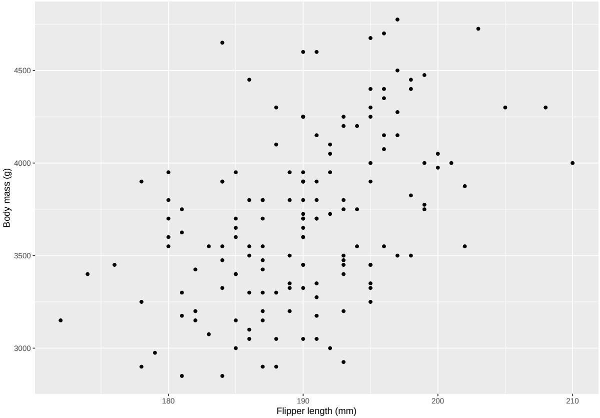
Add layers with ggplot using the +

```
ggplot(data = pdata, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point()
```



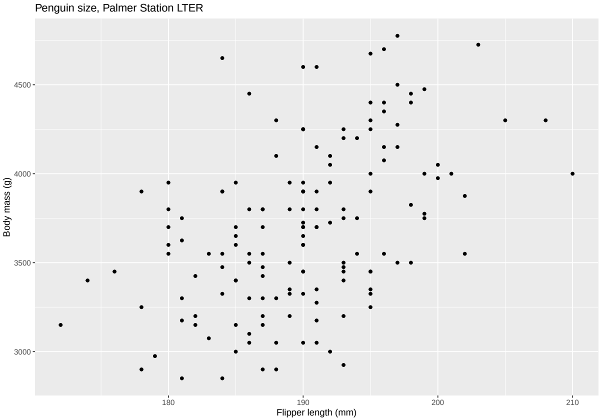
Tidy up labels

```
ggplot(data = pdata, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point() +
  xlab("Flipper length (mm)") +
  ylab("Body mass (g)")
```



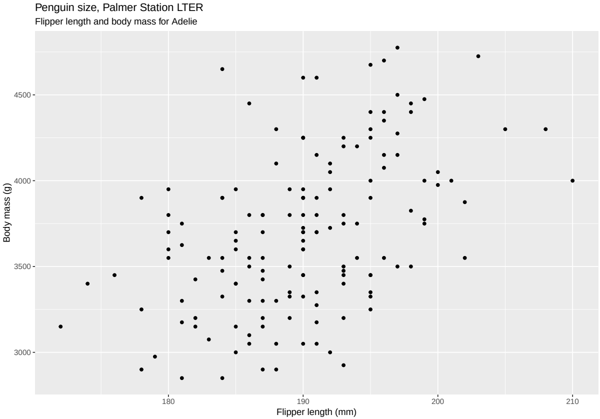
Add a title

```
ggplot(data = pdata, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point() +
  xlab("Flipper length (mm)") +
  ylab("Body mass (g)") +
  labs(title = "Penguin size, Palmer Station LTER")
```



Subtitle

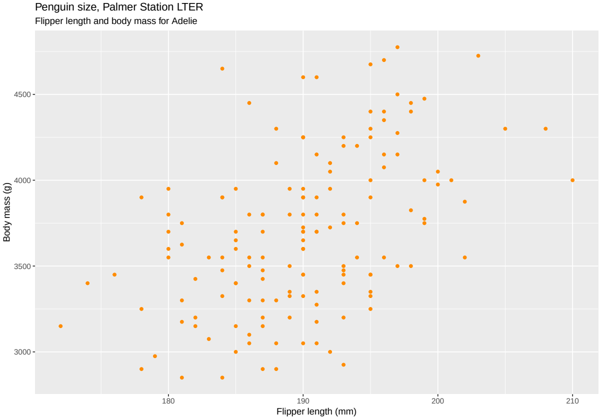
```
ggplot(data = pdata, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point() +
  xlab("Flipper length (mm)") +
  ylab("Body mass (g)") +
  labs(title = "Penguin size, Palmer Station LTER",
       subtitle = "Flipper length and body mass for Adelie")
```



Change color of points

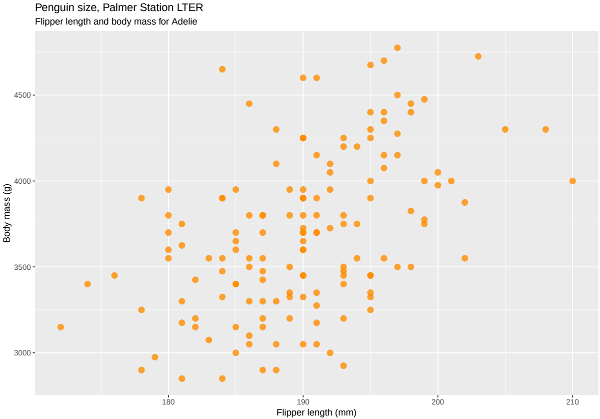
To see all colors, type `colors()`

```
ggplot(data = pdata, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(color = "darkorange") +
  xlab("Flipper length (mm)") +
  ylab("Body mass (g)") +
  labs(title = "Penguin size, Palmer Station LTER",
       subtitle = "Flipper length and body mass for Adelie")
```



Size of points

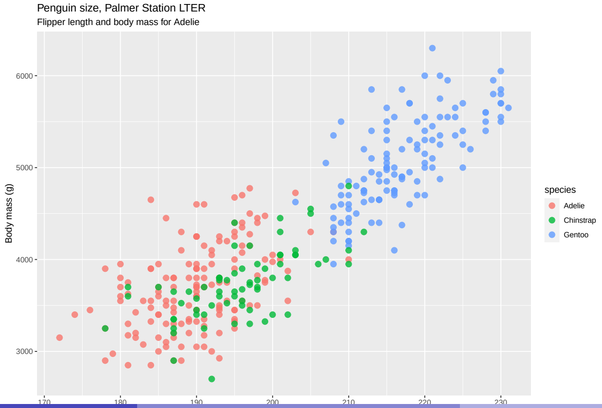
```
ggplot(data = pdata, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(color = "darkorange",
             size = 3,
             alpha = 0.8) +
  xlab("Flipper length (mm)") +
  ylab("Body mass (g)") +
  labs(title = "Penguin size, Palmer Station LTER",
       subtitle = "Flipper length and body mass for Adelie")
```



Coloring by group

Now use the whole data `penguins`. Specifying the color in `aes()` because it **depends on the data**.

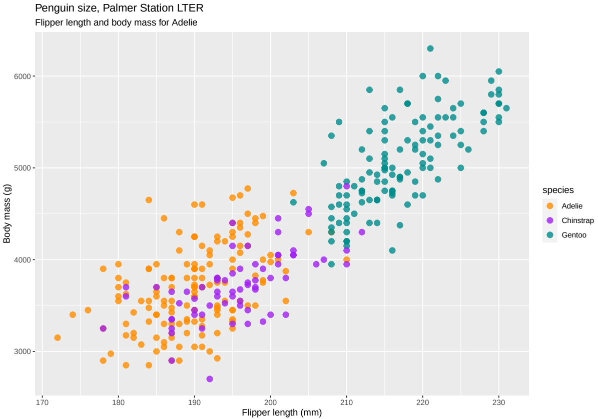
```
ggplot(data = penguins, aes(x = flipper_length_mm, y = body_mass_g, color = species)) +
  geom_point(size = 3, alpha = 0.8) +
  xlab("Flipper length (mm)") +
  ylab("Body mass (g)") +
  labs(title = "Penguin size, Palmer Station LTER",
       subtitle = "Flipper length and body mass for Adelie")
```



Change the color manually by group

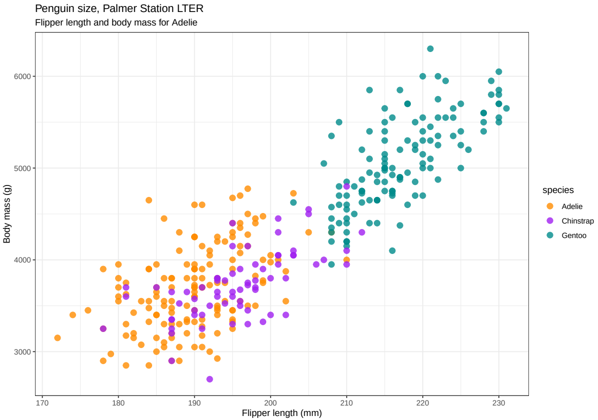
Specifying the color in `aes()` because it **depends on the data**.

```
ggplot(data = penguins, aes(x = flipper_length_mm, y = body_mass_g, color = species)) +
  geom_point(size = 3, alpha = 0.8) +
  scale_color_manual(values = c("darkorange","purple","cyan4")) +
  xlab("Flipper length (mm)") +
  ylab("Body mass (g)") +
  labs(title = "Penguin size, Palmer Station LTER",
       subtitle = "Flipper length and body mass for Adelie")
```



Change the theme

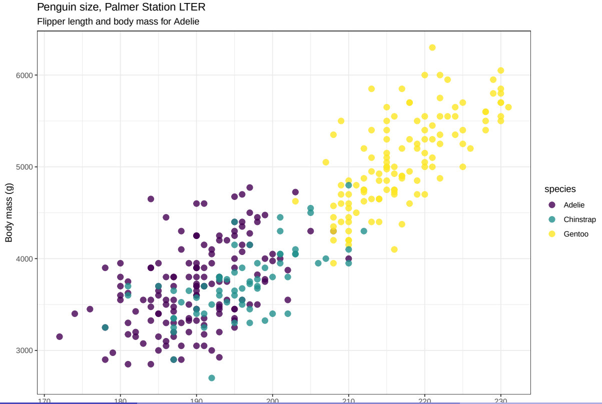
```
ggplot(data = penguins, aes(x = flipper_length_mm, y = body_mass_g, color = species)) +
  geom_point(size = 3, alpha = 0.8) +
  scale_color_manual(values = c("darkorange","purple","cyan4")) +
  xlab("Flipper length (mm)") +
  ylab("Body mass (g)") +
  labs(title = "Penguin size, Palmer Station LTER",
       subtitle = "Flipper length and body mass for Adelie") +
  theme_bw()
```



Change the color scheme

Optional: try `ggsci` functions.

```
ggplot(data = penguins, aes(x = flipper_length_mm, y = body_mass_g, color = species)) +
  geom_point(size = 3, alpha = 0.8) +
  xlab("Flipper length (mm)") +
  ylab("Body mass (g)") +
  labs(title = "Penguin size, Palmer Station LTER",
       subtitle = "Flipper length and body mass for Adelie") +
  theme_bw() +
  scale_color_viridis_d()
```

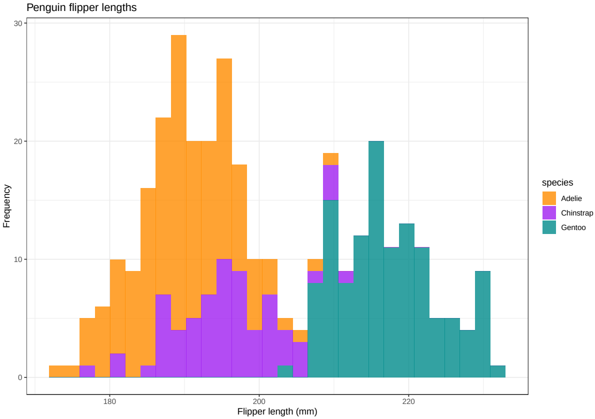


Other plot types?

Other types are also available, e.g. histograms, bar charts, box plots, line graphs and scatter plots.

Histograms

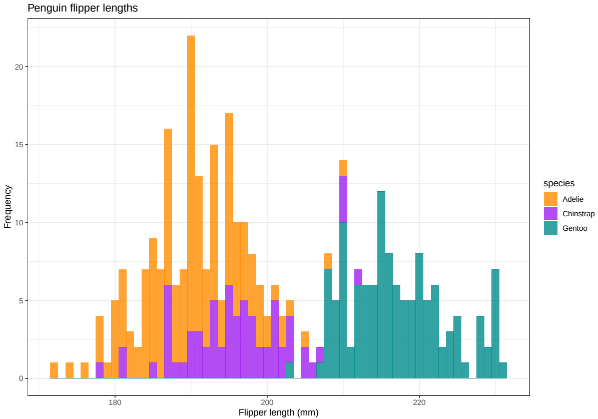
```
ggplot(data = penguins, aes(x = flipper_length_mm, fill = species)) +
  geom_histogram(alpha = 0.8) +
  scale_fill_manual(values = c("darkorange","purple","cyan4")) +
  xlab("Flipper length (mm)") +
  ylab("Frequency") +
  labs(title = "Penguin flipper lengths") +
  theme_bw()
```



Histogram

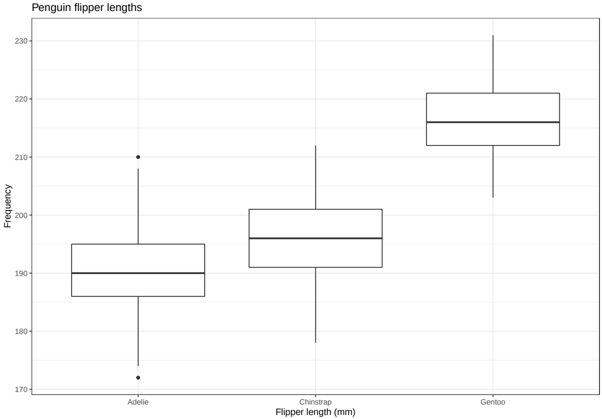
Try `binwidth =` and `bins ==`

```r
ggplot(data = penguins, aes(x = flipper_length_mm, fill = species)) +
  geom_histogram(binwidth = 1, alpha = 0.8) +
  scale_fill_manual(values = c("darkorange","purple","cyan4")) +
  xlab("Flipper length (mm)") +
  ylab("Frequency") +
  labs(title = "Penguin flipper lengths") +
  theme_bw()
```



Boxplots

```
ggplot(data = penguins, aes(x = species, y = flipper_length_mm)) +
  geom_boxplot(show.legend = FALSE) +
  xlab("Flipper length (mm)") +
  ylab("Frequency") +
  labs(title = "Penguin flipper lengths") +
  theme_bw()
```



Barcharts

First, try to summarize the penguin data by species and returns the proportion of each penguin types.

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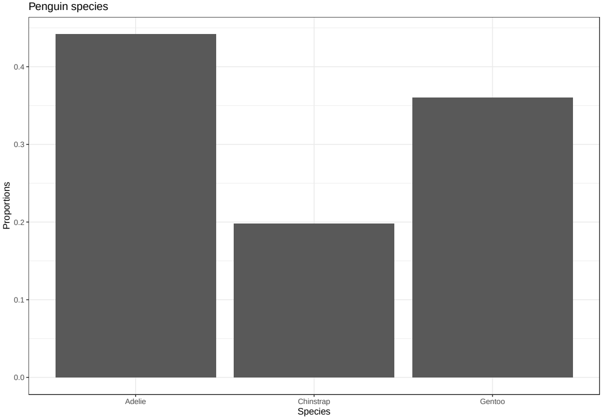
```
gplot <- penguins %>%
  group_by(species) %>%
  tally() %>%
  mutate(prop = n / sum(n))
gplot
```

```
## # A tibble: 3 x 3
##   species       n  prop
##   <fct>     <int> <dbl>
## 1 Adelie      152 0.442
## 2 Chinstrap    68 0.198
## 3 Gentoo      124 0.360
```

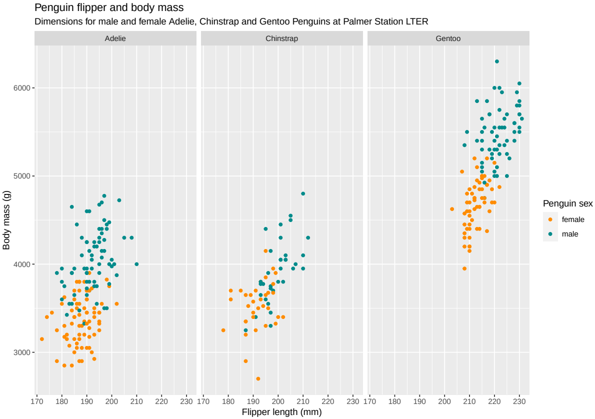
Barcharts

```
ggplot(data = gplot, aes(x = species, y = prop))  +
  geom_bar(stat = "identity") +
  xlab("Species") +
  ylab("Proportions") +
  labs(title = "Penguin species") +
  theme_bw()
```



Faceting

```
ggplot(penguins, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(aes(color = sex)) +
  scale_color_manual(values = c("darkorange","cyan4"), na.translate = FALSE) +
  labs(title = "Penguin flipper and body mass",
       subtitle = "Dimensions for male and female Adelie, Chinstrap and Gentoo Penguins at Palmer Station LTER"
       x = "Flipper length (mm)",
       y = "Body mass (g)",
       color = "Penguin sex") +
  facet_wrap(~species)
```



Git + Github

What is Git?

- A control system to manage projects
- Good for tracking history

Git + Github

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- A control system to manage projects
- Good for tracking history

What about Github?

- Cloud-based service for managing Git repositories
- Useful for teamwork
- Just like "Dropbox"

Why Git + Github?

- You can undo anything
- You won't need to keep undo-ing things (merge/load difference)
- You can identify exactly when and where changes were made
- Teamwork

Some github terminology

- User: A Github account for you (e.g., jules32).
- Organization: The Github account for one or more user (e.g., datacarpentry).
- Repository: A folder within the organization that includes files dedicated to a project.
- Local Github: Copies of Github files located your computer.
- Remote Github: Github files located on the https://github.com website.

Basic Git commands and workflow

When you are working on a your local machine you typically get started by:

- `git clone`: Cloning a remote repository to work on locally. This is a way to work with an ongoing project or edit someone else's project that is available remotely (aka on GitHub).

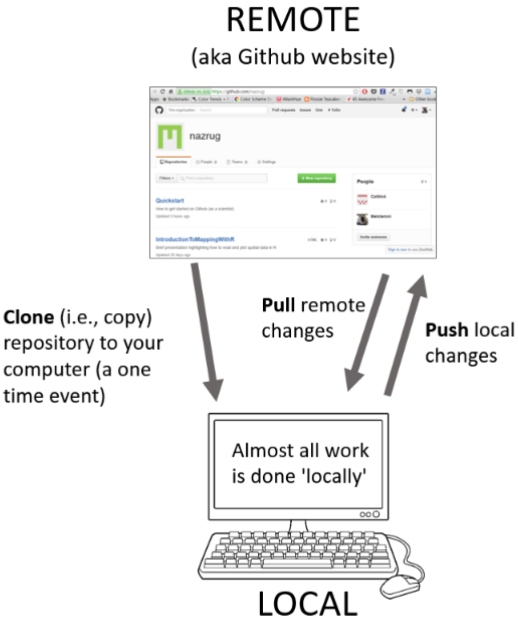
From there, the typical workflow involves:

- `git add`: Adding files to your repo
- `git commit`: Commiting changes you have made
- `git push`: Pushing changes to a remote repository (aka GitHub)

For a collaborative project, or work between desktop and personal laptop, you would use the following first before `git add`

- `git pull`: Pulling changes from a remote repository

Illustration diagram



nazrug
Quickstart
How to get started on Github (as a scientist)
IntroductionToMappingWithR
Brief presentation highlighting how to read and plot spatial data in R
People
New repository

REMOTE

(aka Github website)

Clone (i.e., copy) repository to your computer (a one time event)

Pull remote changes

Push local changes

Almost all work is done 'locally'

LOCAL

Let's Git

Download Github and set up your github profile.

- Github Desktop, a GUI for using Github [link]
- (Optional) Learn how to use command line for Github management
    - Command line tutorial [link]

Resources

This tutorial is based on

- Monica Alexander's ggplot tutorial [link]
- Jesse Gronsbell's Github tutorial [link]

Other resources:
https://kbroman.org/github_tutorial/pages/resources.html