Workspace

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Welcome

This Quarto Book[1] is a workspace for the notes and projects of the programming/scripting languages that I am learning.

[1] Quarto Books Documentation

Part I

Notebooks

This section contains notes for the programming/scripting languages that I am learning.

1 R

1.1 General Notes

- When writing R code, create a project instead of a file which will enable saving the workspace settings
- An R package usually includes:
    a. reusable functions
    b. documentation describing how to use the function
    c. sample data
- Before running a project, clear the objects in its workspace environment to avoid mixing up objects created in other files. This can be done either:
    a. pragmatically as shown below OR
    b. Environment window -> Broom icon

Clear the objects in its workspace environment to avoid mixing up objects created in other files

```
rm(list = ls())
```

List all the packages that will be used in this script.

```
packages = c("here")
```

Any missing package will be installed automatically

```
# Do NOT modify
install.packages(setdiff(packages, rownames(installed.packages())))
```

Load all packages

```
# Do NOT modify
lapply(packages, require, character.only = TRUE)
```

```
[[1]]
[1] TRUE
```

1.2 Data Types

- character
- numeric
- logical
- raw
- imaginary numbers

To know the datatype of an object, run the command:

```
class(x)    # give the data type of x
```

1.2.1 Mixing Data Types

- character + numeric –> character
- numeric + logical –> numeric
- numeric + character + logical –> character

1.3 Data Structures

- **vector**: hold single type of data
- **matrix**: 2D vector
- **array**: nD vector
- **list**: generic vector, can hold mixed type of data, eg, one element can a character, another a list of integers, and the third could be a logical
- **data frame**: table where columns represent vectors
- **tibbles**: data frames, but slightly tweaked to work better with `tidyverse` package
- **factor**

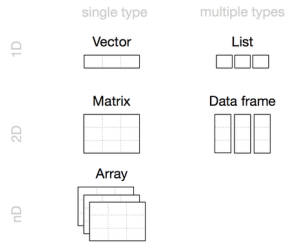


Figure 1.1: Common data structures in R (Source: Grolemund, 2014)

To know the data structure and length of the object, run the command:

```r
str(x)      # give the structure type of x
length(x)   # length of structure
```

1.4 Basics Operations

Assignment

```r
x <- 3      # assign 3 to x
(x <- 3)    # assign 3 to x & print the result to console
```

```
[1] 3
```

Getting Help

```r
args(round) # print the argument list of function
?round        # show documentation of function in Help window
```

Dealing with Structure

```r
# concatenate set of values to create vector
weight_g <- c(50, 60, 3, 9)
animals <- c("dog", "bat", "cat")

# utilizing logical values to pull specific values
weight_g[weight_g < 10 & weight_g > 60 | weight_g == 50]
```

```
[1] 50
```

```r
# pull dog & cat records
animals[animals %in% c("dog", "cat")]
```

```
[1] "dog" "cat"
```

```r
animals[animals == "dog" | animals == "cat"]
```

```
[1] "dog" "cat"
```

Statistics

```
# signaling missing data using NA
heights <- c(2, 3, NA, 4)

# get mean while ignoring missing data
mean(heights, na.rm = TRUE)
```

```
[1] 3
```

```
# how to use mean
# ?mean
```

1.5 Exploratory Operations

The **here** package makes it easy to point to files starting from the project main directory.

```
library(here)
```

Loading file from repository and saving it locally on disk. It is always a good idea to structure the workspace–for more information, see Best Practices for Scientific Computing paper.

```
download.file(url = "https://ndownloader.figshare.com/files/2292169",
    destfile = here("data", "portal_data_joined.csv"))
```

Load file to R as data frame

```
surveys <- read.csv(here("data", "portal_data_joined.csv"))
```

Inspecting data frame

```
class(surveys)  # data type
```

```
[1] "data.frame"
```

```
str(surveys)      # structure
```

```
'data.frame':   34786 obs. of  13 variables:
 $ record_id      : int  1 72 224 266 349 363 435 506 588 661 ...
 $ month          : int  7 8 9 10 11 11 12 1 2 3 ...
 $ day            : int  16 19 13 16 12 12 10 8 18 11 ...
 $ year           : int  1977 1977 1977 1977 1977 1977 1977 1978 1978 1978 ...
 $ plot_id        : int  2 2 2 2 2 2 2 2 2 2 ...
 $ species_id     : chr  "NL" "NL" "NL" "NL" ...
 $ sex            : chr  "M" "M" "" "" ...
 $ hindfoot_length: int  32 31 NA NA NA NA NA NA NA NA ...
 $ weight         : int  NA NA NA NA NA NA NA NA 218 NA ...
 $ genus          : chr  "Neotoma" "Neotoma" "Neotoma" "Neotoma" ...
 $ species        : chr  "albigula" "albigula" "albigula" "albigula" ...
 $ taxa           : chr  "Rodent" "Rodent" "Rodent" "Rodent" ...
 $ plot_type      : chr  "Control" "Control" "Control" "Control" ...
```

```
dim(surveys)      # dimensions
```

```
[1] 34786    13
```

```
nrow(surveys)
```

```
[1] 34786
```

```
ncol(surveys)
```

```
[1] 13
```

```
summary(surveys)
```

```
   record_id         month              day             year         plot_id
 Min.   :    1   Min.   : 1.000   Min.   : 1.0   Min.   :1977   Min.   : 1.00
 1st Qu.: 8964   1st Qu.: 4.000   1st Qu.: 9.0   1st Qu.:1984   1st Qu.: 5.00
 Median :17762   Median : 6.000   Median :16.0   Median :1990   Median :11.00
 Mean   :17804   Mean   : 6.474   Mean   :16.1   Mean   :1990   Mean   :11.34
 3rd Qu.:26655   3rd Qu.:10.000   3rd Qu.:23.0   3rd Qu.:1997   3rd Qu.:17.00
 Max.   :35548   Max.   :12.000   Max.   :31.0   Max.   :2002   Max.   :24.00

  species_id            sex            hindfoot_length     weight
 Length:34786       Length:34786       Min.   : 2.00   Min.   :  4.00
```

```
 Class :character   Class :character   1st Qu.:21.00   1st Qu.: 20.00
 Mode  :character   Mode  :character   Median :32.00   Median : 37.00
                                       Mean   :29.29   Mean   : 42.67
                                       3rd Qu.:36.00   3rd Qu.: 48.00
                                       Max.   :70.00   Max.   :280.00
                                       NA's   :3348    NA's   :2503
   genus              species              taxa            plot_type
 Length:34786       Length:34786       Length:34786       Length:34786
 Class :character   Class :character   Class :character   Class :character
 Mode  :character   Mode  :character   Mode  :character   Mode  :character
```

Show first/last few objects/records/rows

```
head(surveys)
```

```
  record_id month day year plot_id species_id sex hindfoot_length weight
1         1     7  16 1977       2         NL   M              32     NA
2        72     8  19 1977       2         NL   M              31     NA
3       224     9  13 1977       2         NL                  NA     NA
4       266    10  16 1977       2         NL                  NA     NA
5       349    11  12 1977       2         NL                  NA     NA
6       363    11  12 1977       2         NL                  NA     NA
    genus  species   taxa plot_type
1 Neotoma albigula Rodent   Control
2 Neotoma albigula Rodent   Control
3 Neotoma albigula Rodent   Control
4 Neotoma albigula Rodent   Control
5 Neotoma albigula Rodent   Control
6 Neotoma albigula Rodent   Control
```

```
tail(surveys)
```

```
      record_id month day year plot_id species_id sex hindfoot_length weight
34781     26787     9  27 1997       7         PL   F              21     16
34782     26966    10  25 1997       7         PL   M              20     16
34783     27185    11  22 1997       7         PL   F              21     22
34784     27792     5   2 1998       7         PL   F              20      8
```

```
34785     28806    11  21 1998       7         PX                  NA      NA
34786     30986     7   1 2000       7         PX                  NA      NA
           genus  species   taxa        plot_type
34781  Peromyscus leucopus Rodent Rodent Exclosure
34782  Peromyscus leucopus Rodent Rodent Exclosure
34783  Peromyscus leucopus Rodent Rodent Exclosure
34784  Peromyscus leucopus Rodent Rodent Exclosure
34785 Chaetodipus      sp. Rodent Rodent Exclosure
34786 Chaetodipus      sp. Rodent Rodent Exclosure
```

1.5.1 Retrieve specific element/row/column

```
surveys[1,1]    # element[1,1]
```

```
[1] 1
```

```
surveys[1, ]    # row 1
```

```
  record_id month day year plot_id species_id sex hindfoot_length weight
1         1     7  16 1977       2         NL   M              32     NA
    genus  species   taxa plot_type
1 Neotoma albigula Rodent   Control
```

```
head(surveys[ ,1])  # column 1
```

```
[1]   1  72 224 266 349 363
```

```
head(surveys$sex)     # column by name
```

```
[1] "M" "M" ""  ""  ""  ""
```

1.5.2 Dealing with factor (categorical) columns

R convert columns that contain characters to factors by default. Factors are treated as integer vectors. By default, R sorts levels in alphabetical order.

```
levels(surveys$sex)
```

```
NULL
```

```
nlevels(surveys$sex)
```

```
[1] 0
```

Reorder factors (to get better plots)

```
surveys$sex_ordered <- factor(surveys$sex, level=c("F", "M", ""))
str(surveys$sex_ordered)
```

```
 Factor w/ 3 levels "F","M","": 2 2 3 3 3 3 3 3 2 3 ...
```

```
levels(surveys$sex_ordered)
```

```
[1] "F" "M" ""
```

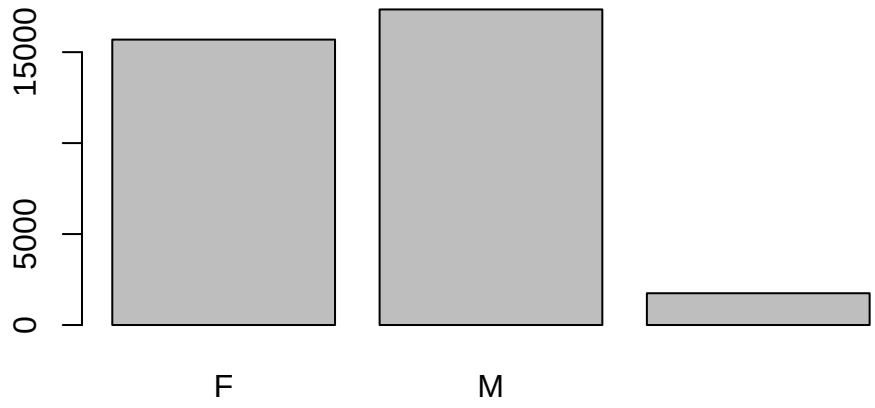
```
nlevels(surveys$sex_ordered)
```

```
[1] 3
```

1.5.3 Basic Plotting

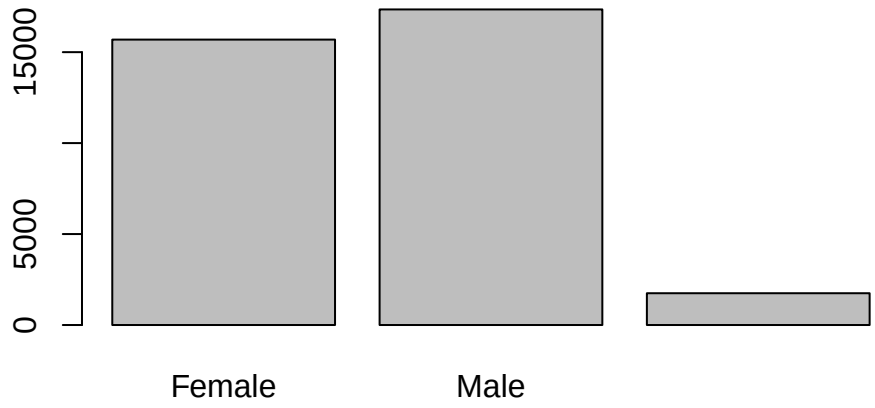
Histogram

```
# plot(surveys$sex)  # not possible
plot(surveys$sex_ordered)
```



Enhance the plot

```
levels(surveys$sex_ordered)[1] <- "Female"
levels(surveys$sex_ordered)[2] <- "Male"
plot(surveys$sex_ordered)
```



1.6 Data Manipulation

- `tdlyr`
  - makes manipulation of data easier
  - built to work with data frames directly
  - can directly work with data stored in an external database which give the advantage of only bringing what we need to the memory to work on without having to bring the whole database
- `tidyr`
  - allows to swiftly convert b/w different data formats for plotting & analysis in order to accommodate the different requirements by different functions
    - sometime we want one row per measurement
    - other times we want the data aggregated like when plotting

Before using `tdlyr` and `tidyr`:

- Install `tidyverse` package: umbrella-package that install several packages (tidyr, dplyr, ggplot2 tibble, magrittr, etc.)
- Load the package each session

Load packages

```
library("tidyverse")
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.5.1     v tibble    3.2.1
v lubridate 1.9.3     v tidyr     1.3.1
v purrr     1.0.2
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becor
```

Load & inspect data

```
# notice the '_' instead of '.' of basic R
surveys <- read_csv(here("data", "portal_data_joined.csv"))
```

```
Rows: 34786 Columns: 13
-- Column specification --------------------------------------------------------
Delimiter: ","
chr (6): species_id, sex, genus, species, taxa, plot_type
dbl (7): record_id, month, day, year, plot_id, hindfoot_length, weight

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
str(surveys)    # structure: tbl_df (tibble)
```

```
spc_tbl_ [34,786 x 13] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
 $ record_id      : num [1:34786] 1 72 224 266 349 363 435 506 588 661 ...
 $ month          : num [1:34786] 7 8 9 10 11 11 12 1 2 3 ...
 $ day            : num [1:34786] 16 19 13 16 12 12 10 8 18 11 ...
 $ year           : num [1:34786] 1977 1977 1977 1977 1977 ...
 $ plot_id        : num [1:34786] 2 2 2 2 2 2 2 2 2 2 ...
 $ species_id     : chr [1:34786] "NL" "NL" "NL" "NL" ...
 $ sex            : chr [1:34786] "M" "M" NA NA ...
 $ hindfoot_length: num [1:34786] 32 31 NA NA NA NA NA NA NA NA ...
```

```
 $ weight         : num [1:34786] NA NA NA NA NA NA NA NA 218 NA ...
 $ genus          : chr [1:34786] "Neotoma" "Neotoma" "Neotoma" "Neotoma" ...
 $ species        : chr [1:34786] "albigula" "albigula" "albigula" "albigula" ...
 $ taxa           : chr [1:34786] "Rodent" "Rodent" "Rodent" "Rodent" ...
 $ plot_type      : chr [1:34786] "Control" "Control" "Control" "Control" ...
 - attr(*, "spec")=
  .. cols(
  ..   record_id = col_double(),
  ..   month = col_double(),
  ..   day = col_double(),
  ..   year = col_double(),
  ..   plot_id = col_double(),
  ..   species_id = col_character(),
  ..   sex = col_character(),
  ..   hindfoot_length = col_double(),
  ..   weight = col_double(),
  ..   genus = col_character(),
  ..   species = col_character(),
  ..   taxa = col_character(),
  ..   plot_type = col_character()
  .. )
 - attr(*, "problems")=<externalptr>
```

```
# view(surveys) # preview in the viewer window, avoid when rendering
```

1.6.1 Selection

Select certain columns

```
select(surveys, plot_id, species_id, weight)
```

```
# A tibble: 34,786 x 3
   plot_id species_id weight
     <dbl> <chr>       <dbl>
 1       2 NL             NA
 2       2 NL             NA
 3       2 NL             NA
 4       2 NL             NA
 5       2 NL             NA
 6       2 NL             NA
 7       2 NL             NA
```

```
 8       2 NL             NA
 9       2 NL            218
10       2 NL             NA
# i 34,776 more rows
```

Select all columns except …

```
select(surveys, -sex)
```

```
# A tibble: 34,786 x 12
   record_id month   day  year plot_id species_id hindfoot_length weight genus
       <dbl> <dbl> <dbl> <dbl>   <dbl> <chr>                <dbl>  <dbl> <chr>
 1         1     7    16  1977       2 NL                      32     NA Neotoma
 2        72     8    19  1977       2 NL                      31     NA Neotoma
 3       224     9    13  1977       2 NL                      NA     NA Neotoma
 4       266    10    16  1977       2 NL                      NA     NA Neotoma
 5       349    11    12  1977       2 NL                      NA     NA Neotoma
 6       363    11    12  1977       2 NL                      NA     NA Neotoma
 7       435    12    10  1977       2 NL                      NA     NA Neotoma
 8       506     1     8  1978       2 NL                      NA     NA Neotoma
 9       588     2    18  1978       2 NL                      NA    218 Neotoma
10       661     3    11  1978       2 NL                      NA     NA Neotoma
# i 34,776 more rows
# i 3 more variables: species <chr>, taxa <chr>, plot_type <chr>
```

Select rows based on criteria

```
filter(surveys, year == 1995)
```

```
# A tibble: 1,180 x 13
   record_id month   day  year plot_id species_id sex   hindfoot_length weight
       <dbl> <dbl> <dbl> <dbl>   <dbl> <chr>      <chr>           <dbl>  <dbl>
 1     22314     6     7  1995       2 NL         M                  34     NA
 2     22728     9    23  1995       2 NL         F                  32    165
 3     22899    10    28  1995       2 NL         F                  32    171
 4     23032    12     2  1995       2 NL         F                  33     NA
 5     22003     1    11  1995       2 DM         M                  37     41
 6     22042     2     4  1995       2 DM         F                  36     45
 7     22044     2     4  1995       2 DM         M                  37     46
 8     22105     3     4  1995       2 DM         F                  37     49
 9     22109     3     4  1995       2 DM         M                  37     46
```

```
10     22168     4     1  1995       2 DM         M                    36     48
# i 1,170 more rows
# i 4 more variables: genus <chr>, species <chr>, taxa <chr>, plot_type <chr>
```

1.6.2 Piping

Sending the results of one function to another

```
# in multiple steps
survey_less5 <- filter(surveys, weight < 5)
survey_sml <- select(survey_less5, species_id, sex, weight)

# in one long step
survey_sml <- select(filter(surveys, weight < 5), species_id, sex, weight)

# using pipe %>% of magritter package.  Use Ctrl + Shift + M to add
survey_sml <- surveys %>%
    filter(weight < 5) %>%
    select(species_id, sex, weight)
```

1.6.3 Summary

Summary of groups (1+ columns)

one factor

```
surveys %>%
    group_by(sex) %>%
    summarise(mean_weight = mean(weight, na.rm = TRUE))
```

```
# A tibble: 3 x 2
  sex   mean_weight
  <chr>       <dbl>
1 F            42.2
2 M            43.0
3 <NA>         64.7
```

two factors

```r
surveys %>%
    group_by(sex, species) %>%
    summarise(mean_weight = mean(weight, na.rm = TRUE))
```

```
`summarise()` has grouped output by 'sex'. You can override using the `.groups`
argument.
```

```
# A tibble: 81 x 3
# Groups:   sex [3]
   sex   species     mean_weight
   <chr> <chr>             <dbl>
 1 F     albigula         154.
 2 F     baileyi           30.2
 3 F     eremicus          22.8
 4 F     flavus             7.97
 5 F     fulvescens        13.7
 6 F     fulviventer       69
 7 F     hispidus          69.0
 8 F     leucogaster       31.1
 9 F     leucopus          19.3
10 F     maniculatus       22.1
# i 71 more rows
```

```r
surveys %>%
    group_by(species, sex) %>%
    summarise(mean_weight = mean(weight, na.rm = TRUE))
```

```
`summarise()` has grouped output by 'species'. You can override using the
`.groups` argument.
```

```
# A tibble: 81 x 3
# Groups:   species [40]
   species         sex   mean_weight
   <chr>           <chr>       <dbl>
 1 albigula        F           154.
 2 albigula        M           166.
 3 albigula        <NA>        168.
 4 audubonii       <NA>        NaN
 5 baileyi         F            30.2
 6 baileyi         M            33.8
```

```
 7 baileyi          <NA>          30.6
 8 bilineata        <NA>         NaN
 9 brunneicapillus <NA>         NaN
10 chlorurus        <NA>         NaN
# i 71 more rows
```

to avoid using `na.rm = FALSE` each statistics

```
surveys %>%
    filter(!is.na(weight)) %>%
    group_by(species, sex) %>%
    summarise(mean_weight = mean(weight), sd_weight = sd(weight), sd_count = n())
```

```
`summarise()` has grouped output by 'species'. You can override using the
`.groups` argument.
```

```
# A tibble: 59 x 5
# Groups:   species [22]
   species  sex   mean_weight sd_weight sd_count
   <chr>    <chr>       <dbl>     <dbl>    <int>
 1 albigula F           154.      39.2        652
 2 albigula M           166.      49.0        484
 3 albigula <NA>        168.      44.2         16
 4 baileyi  F            30.2      5.27      1617
 5 baileyi  M            33.8      8.27      1188
 6 baileyi  <NA>         30.6      9.96         5
 7 eremicus F            22.8      4.57       568
 8 eremicus M            20.6      3.49       689
 9 eremicus <NA>         17.7      0.577        3
10 flavus   F             7.97     1.69       742
# i 49 more rows
```

arrange by mean weight

```
surveys %>%
    filter(!is.na(weight)) %>%
    group_by(species, sex) %>%
    summarise(mean_weight = mean(weight), sd_weight = sd(weight), sd_count = n()) %>%
    arrange(mean_weight)
```

```
`summarise()` has grouped output by 'species'. You can override using the
`.groups` argument.
```

```
# A tibble: 59 x 5
# Groups:   species [22]
   species   sex   mean_weight sd_weight sd_count
   <chr>     <chr>       <dbl>     <dbl>    <int>
 1 flavus    <NA>         6        1.63         4
 2 taylori   M            7.36     0.842       14
 3 flavus    M            7.89     1.59       802
 4 flavus    F            7.97     1.69       742
 5 taylori   F            9.16     2.24        31
 6 montanus  M            9.5      1.29         4
 7 megalotis M           10.1      1.73      1339
 8 montanus  F           11        2.16         4
 9 megalotis <NA>        11.1      2.57        12
10 megalotis F           11.1      2.56      1184
# i 49 more rows
```

in descending order

```
surveys %>%
    filter(!is.na(weight)) %>%
    group_by(species, sex) %>%
    summarise(mean_weight = mean(weight), sd_weight = sd(weight), sd_count = n()) %>%
    arrange(desc(mean_weight))
```

```
`summarise()` has grouped output by 'species'. You can override using the
`.groups` argument.
```

```
# A tibble: 59 x 5
# Groups:   species [22]
   species     sex   mean_weight sd_weight sd_count
   <chr>       <chr>       <dbl>     <dbl>    <int>
 1 albigula    <NA>        168.       44.2       16
 2 albigula    M           166.       49.0      484
 3 albigula    F           154.       39.2      652
 4 hispidus    <NA>        130        NA          1
 5 spilosoma   M           130        NA          1
 6 spectabilis M           122.       24.0     1220
 7 spectabilis <NA>        120        18.5       18
```

```
 8 spectabilis F           118.       21.5     1106
 9 fulviventer F            69        37.8       16
10 hispidus    F            69.0      29.7       98
# i 49 more rows
```

by count

```
surveys %>%
    filter(!is.na(weight)) %>%
    group_by(species, sex) %>%
    summarise(mean_weight = mean(weight), sd_weight = sd(weight), sd_count = n()) %>%
    arrange(sd_count)
```

```
`summarise()` has grouped output by 'species'. You can override using the
`.groups` argument.
```

```
# A tibble: 59 x 5
# Groups:   species [22]
   species     sex   mean_weight sd_weight sd_count
   <chr>       <chr>       <dbl>     <dbl>    <int>
 1 hispidus    <NA>        130      NA            1
 2 intermedius <NA>         18      NA            1
 3 leucopus    <NA>         25      NA            1
 4 spilosoma   F            57      NA            1
 5 spilosoma   M           130      NA            1
 6 fulviventer <NA>         40.5     6.36         2
 7 leucogaster <NA>         29      11.3          2
 8 eremicus    <NA>         17.7     0.577        3
 9 ordii       <NA>         50.7     6.51         3
10 sp.         F            20.7     1.15         3
# i 49 more rows
```

1.6.4 Count

Count of a categorical column

```
surveys %>%
    count(sex)
```

```
# A tibble: 3 x 2
  sex       n
  <chr> <int>
1 F     15690
2 M     17348
3 <NA>   1748
```

1.6.5 Reshaping

Using gather & spreed

prepare the needed data first

```
surveys_gw <- surveys %>%
    filter(!is.na(weight)) %>%
    group_by(genus, plot_id) %>%
    summarize(mean_weight = mean(weight))
```

```
`summarise()` has grouped output by 'genus'. You can override using the
`.groups` argument.
```

creating a 2D table where each dimension represent a category the cell will represent a statistics

```
surveys_spread <- surveys_gw %>%
    spread(key = genus, value = mean_weight)
str(surveys_spread)
```

```
tibble [24 x 11] (S3: tbl_df/tbl/data.frame)
 $ plot_id        : num [1:24] 1 2 3 4 5 6 7 8 9 10 ...
 $ Baiomys        : num [1:24] 7 6 8.61 NA 7.75 ...
 $ Chaetodipus    : num [1:24] 22.2 25.1 24.6 23 18 ...
 $ Dipodomys      : num [1:24] 60.2 55.7 52 57.5 51.1 ...
 $ Neotoma        : num [1:24] 156 169 158 164 190 ...
 $ Onychomys      : num [1:24] 27.7 26.9 26 28.1 27 ...
 $ Perognathus    : num [1:24] 9.62 6.95 7.51 7.82 8.66 ...
 $ Peromyscus     : num [1:24] 22.2 22.3 21.4 22.6 21.2 ...
 $ Reithrodontomys: num [1:24] 11.4 10.7 10.5 10.3 11.2 ...
 $ Sigmodon       : num [1:24] NA 70.9 65.6 82 82.7 ...
 $ Spermophilus   : num [1:24] NA NA NA NA NA NA NA NA NA NA ...
```

```
head(surveys_spread)
```

```
# A tibble: 6 x 11
  plot_id Baiomys Chaetodipus Dipodomys Neotoma Onychomys Perognathus Peromyscus
    <dbl>   <dbl>       <dbl>     <dbl>   <dbl>     <dbl>       <dbl>      <dbl>
1       1    7           22.2      60.2    156.      27.7        9.62       22.2
2       2    6           25.1      55.7    169.      26.9        6.95       22.3
3       3    8.61        24.6      52.0    158.      26.0        7.51       21.4
4       4   NA           23.0      57.5    164.      28.1        7.82       22.6
5       5    7.75        18.0      51.1    190.      27.0        8.66       21.2
6       6   NA           24.9      58.6    180.      25.9        7.81       21.8
# i 3 more variables: Reithrodontomys <dbl>, Sigmodon <dbl>, Spermophilus <dbl>
```

bring spread back

```
surveys_gw <- surveys_spread %>%
    gather(key = genus, value = mean_weight, -plot_id)
str(surveys_gw)
```

```
tibble [240 x 3] (S3: tbl_df/tbl/data.frame)
 $ plot_id    : num [1:240] 1 2 3 4 5 6 7 8 9 10 ...
 $ genus      : chr [1:240] "Baiomys" "Baiomys" "Baiomys" "Baiomys" ...
 $ mean_weight: num [1:240] 7 6 8.61 NA 7.75 ...
```

```
head(surveys_gw)
```

```
# A tibble: 6 x 3
  plot_id genus   mean_weight
    <dbl> <chr>         <dbl>
1       1 Baiomys        7
2       2 Baiomys        6
3       3 Baiomys        8.61
4       4 Baiomys       NA
5       5 Baiomys        7.75
6       6 Baiomys       NA
```

1.6.6 Filtering

Remove missing data

```
survey_complete <- surveys %>%
  filter(!is.na(weight), !is.na(hindfoot_length), !is.na(sex))
```

Filter those that has sample greater than 50

```
species_counts <- survey_complete %>%
  count(species_id) %>%
  filter(n >= 50)
```

filter only those in the indicated category

```
surveys_com <- surveys %>%
    filter(species_id %in% c("albigula", "eremicus"))
```

1.6.7 Saving to disk

```
write_cvs()
```

1.7 Visualization

- Help in making complex plots from data frames in simple steps
- ggplot graphics are built step by step by adding new elements; this makes it flexible as well as customization

Step 1: Bind the plot to specific data frame

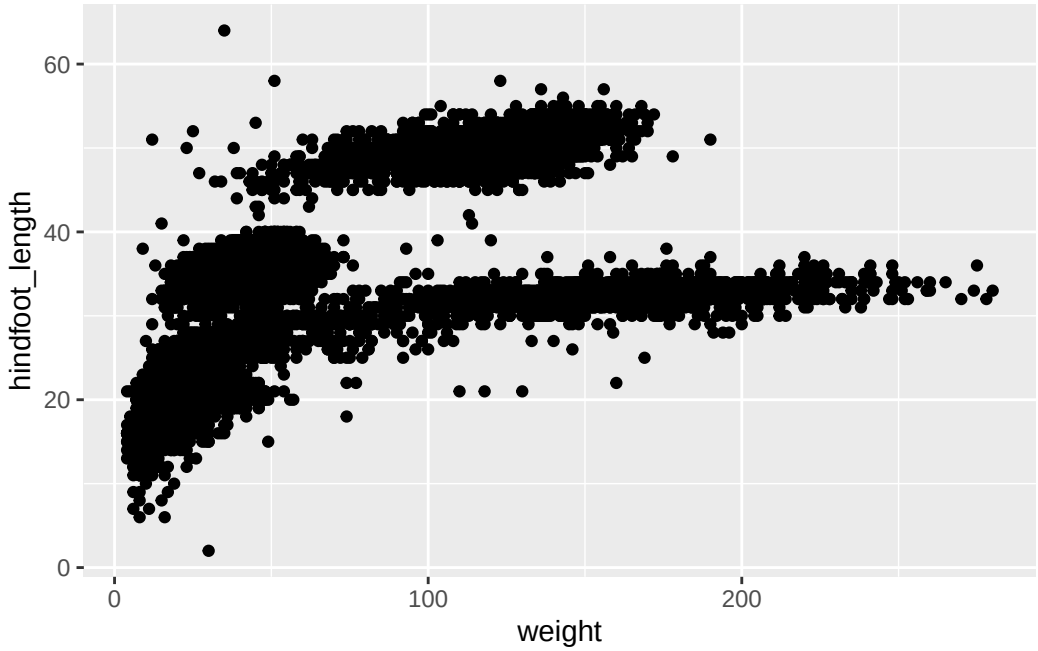
```
surveys_plot <- ggplot(data = survey_complete,
    mapping = aes(x = weight, y = hindfoot_length))

# Color for each group
surveys_plot <- ggplot(data = survey_complete,
    mapping = aes(x = weight, y = hindfoot_length),
    color=species_id)
```

Step 2: Select the type of the plot

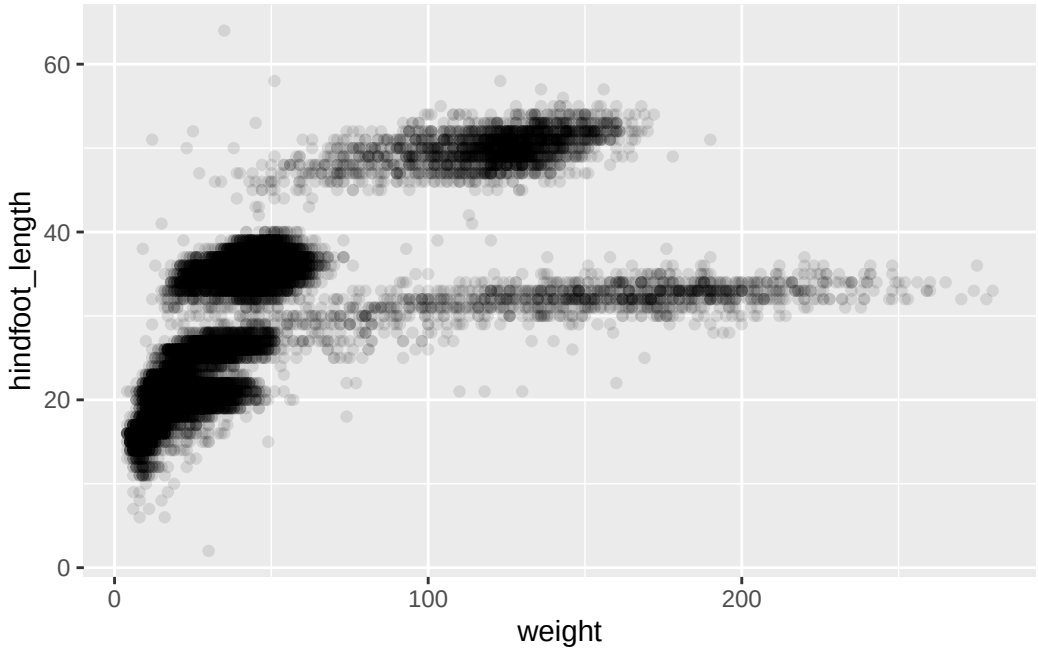
- scatter plot, dot plots, etc. > geom_point()
- boxplots > geom_boxplot()
- trend lines, time series, etc. > geom_line()

1.7.1 Scatter plot

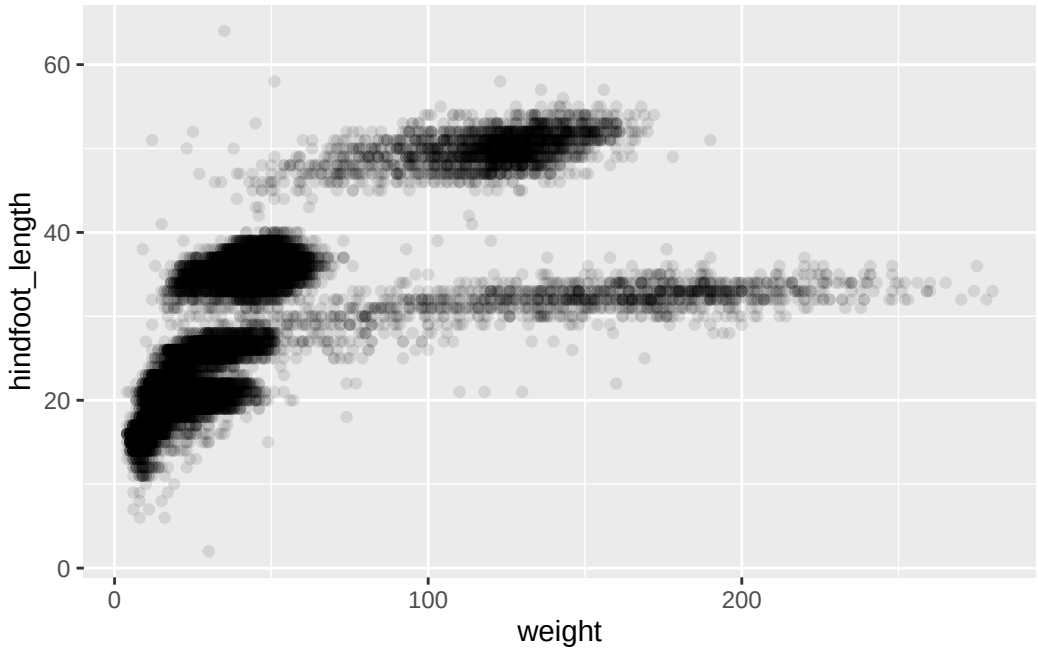
```
surveys_plot + geom_point()
```



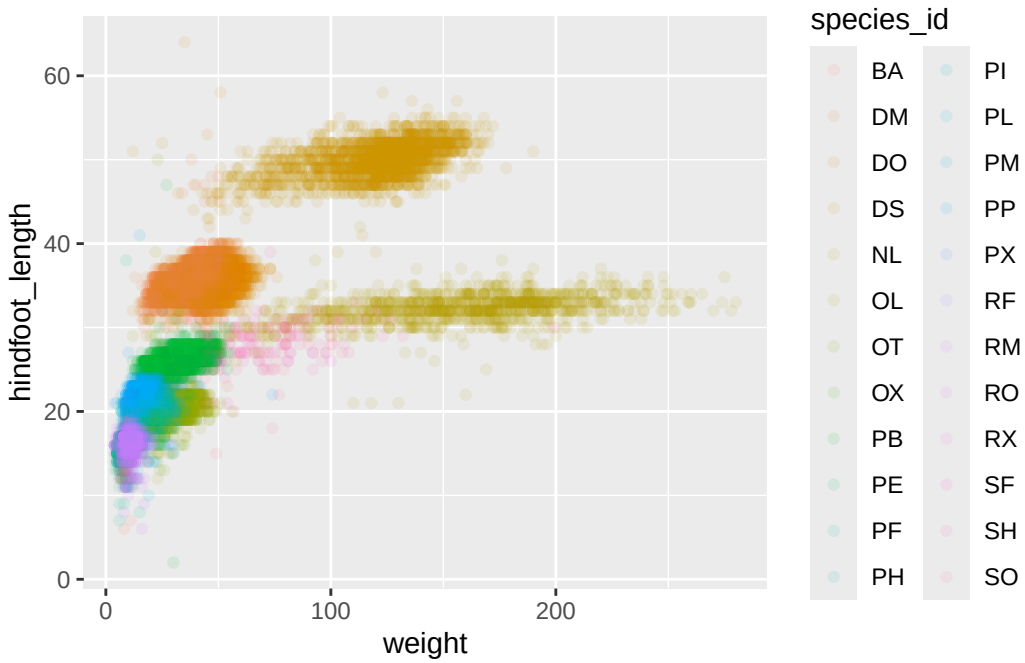

```
# add transparency
surveys_plot + geom_point(alpha = 0.1)
```



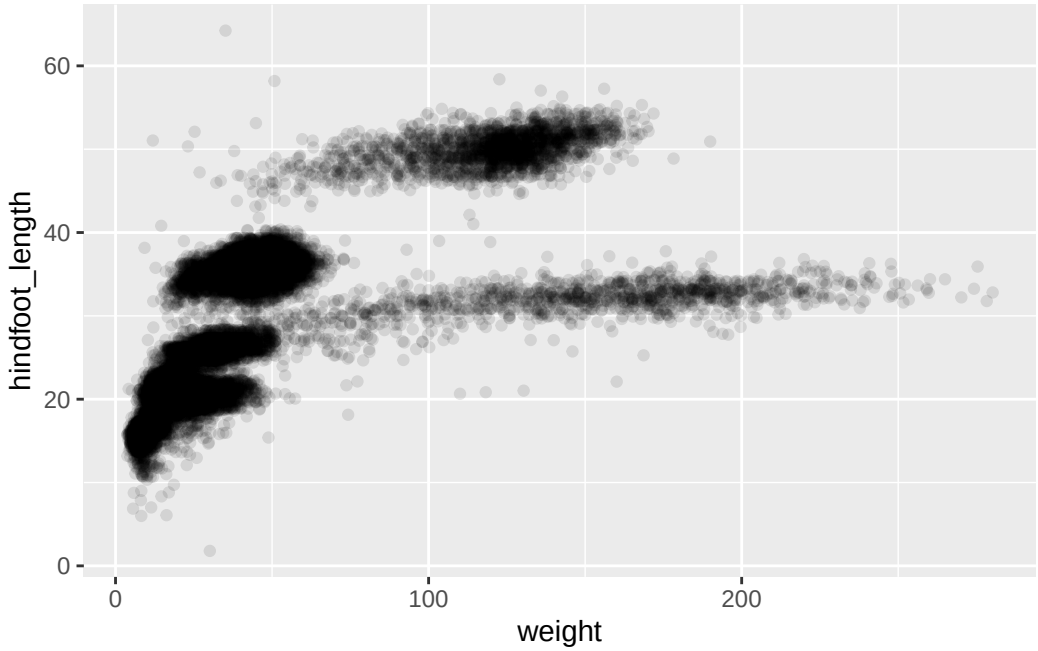

```
# color if not used in binding
surveys_plot + geom_point(alpha = 0.1, color = "black")
```



```
# add color if not used in binding
surveys_plot + geom_point(alpha = 0.1, aes(color = species_id))
```

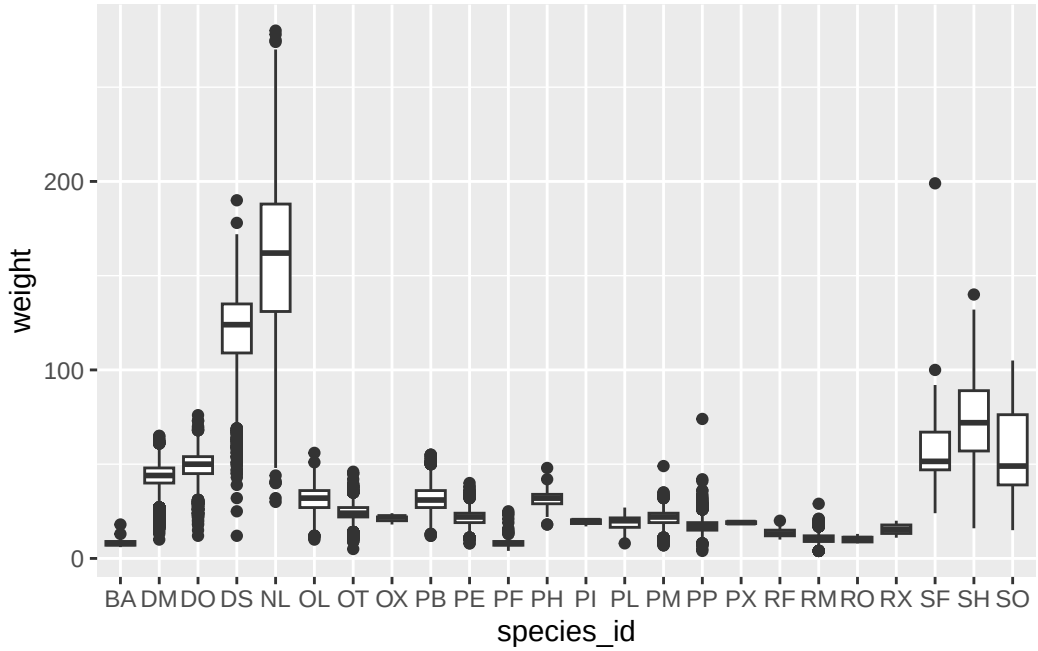



```
# make the color blend by introducing small random variation in points locations
# used when having small data sets
surveys_plot + geom_jitter(alpha = 0.1)
```

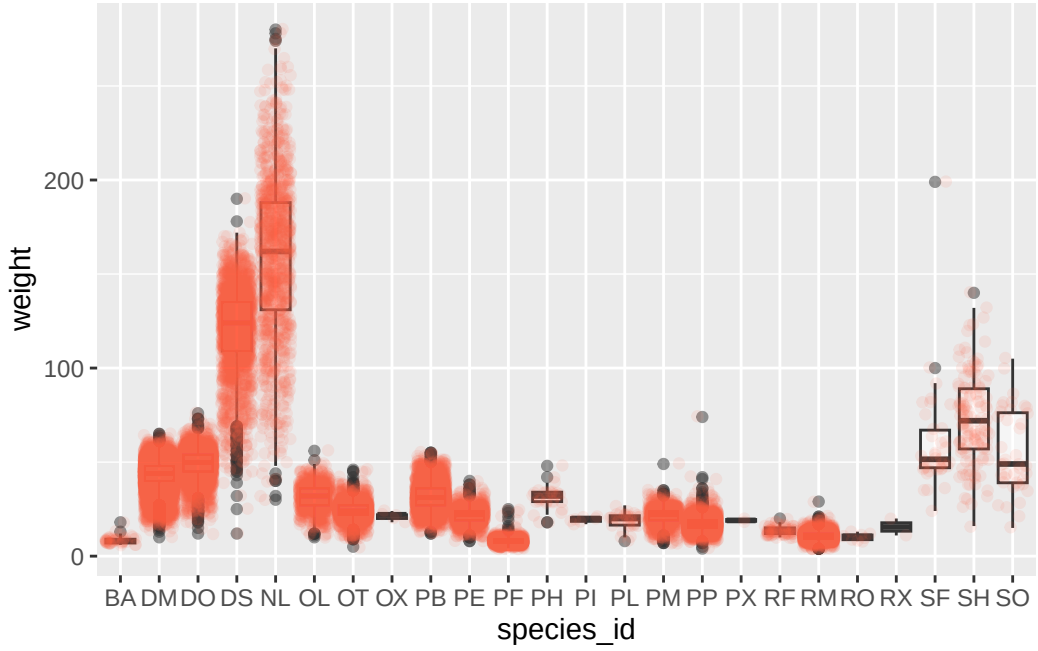


1.7.2 Boxplot

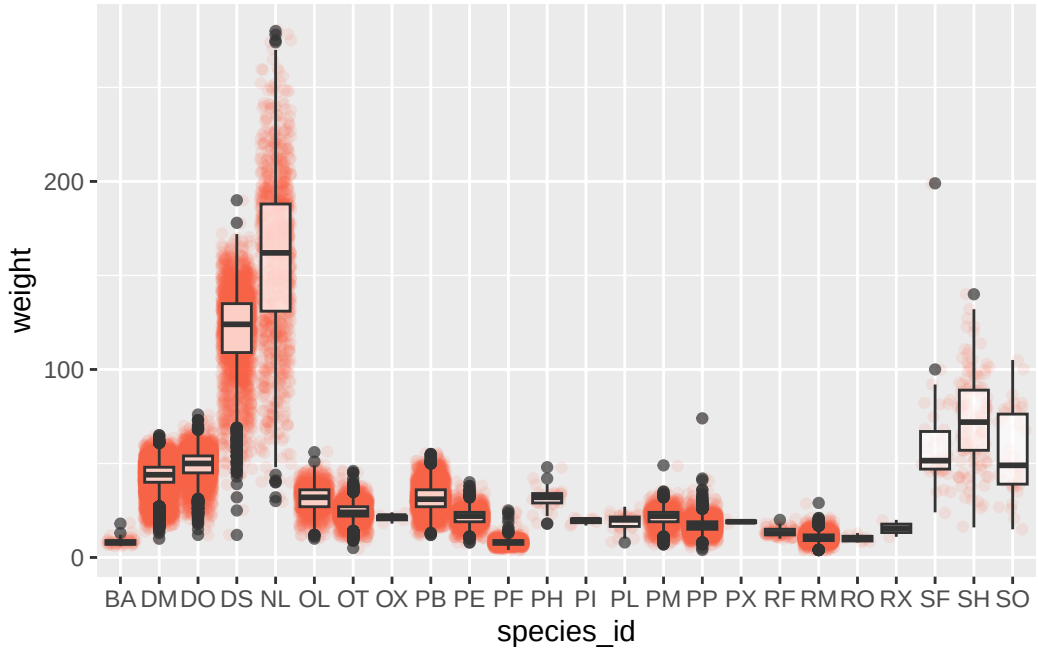
```
surveys_plot <- ggplot(data = survey_complete,
    mapping = aes(x = species_id, y = weight))

surveys_plot + geom_boxplot()
```




```
# show data
surveys_plot + geom_boxplot(alpha = 0.5) +
    geom_jitter(alpha = 0.1, color = "tomato")
```

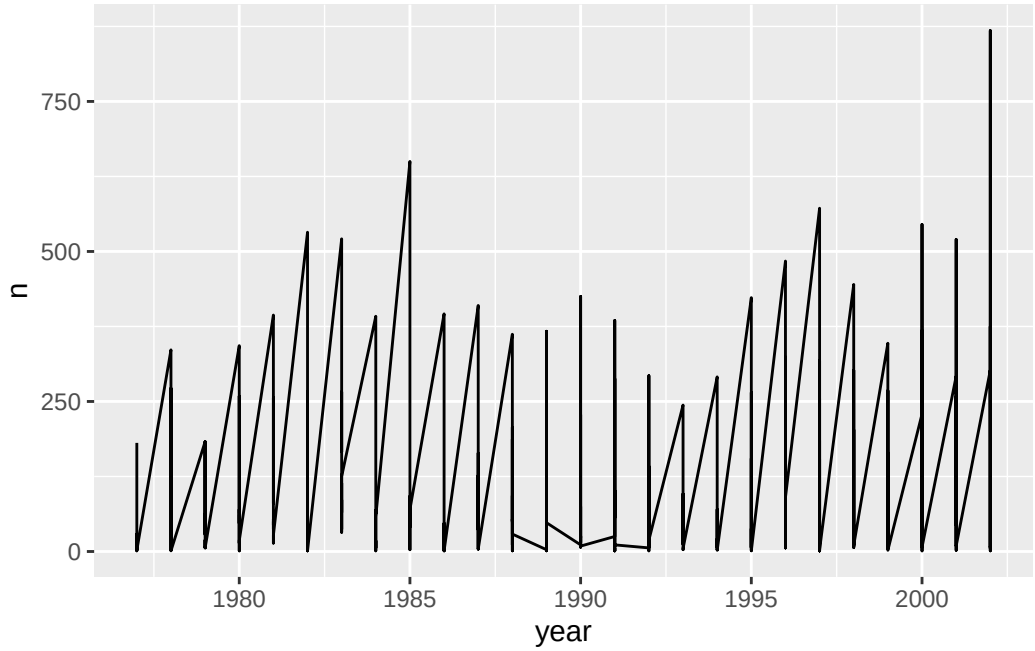


```
# bring boxplot layer in front
surveys_plot + geom_jitter(alpha = 0.1, color = "tomato") +
    geom_boxplot(alpha = 0.7)
```

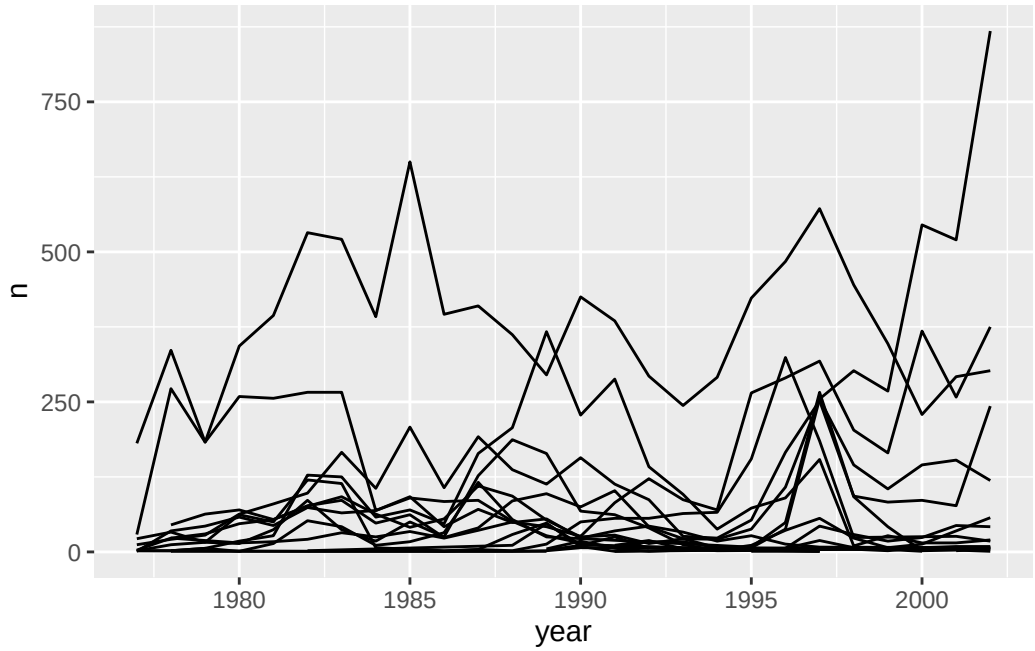


1.7.3 Time series data

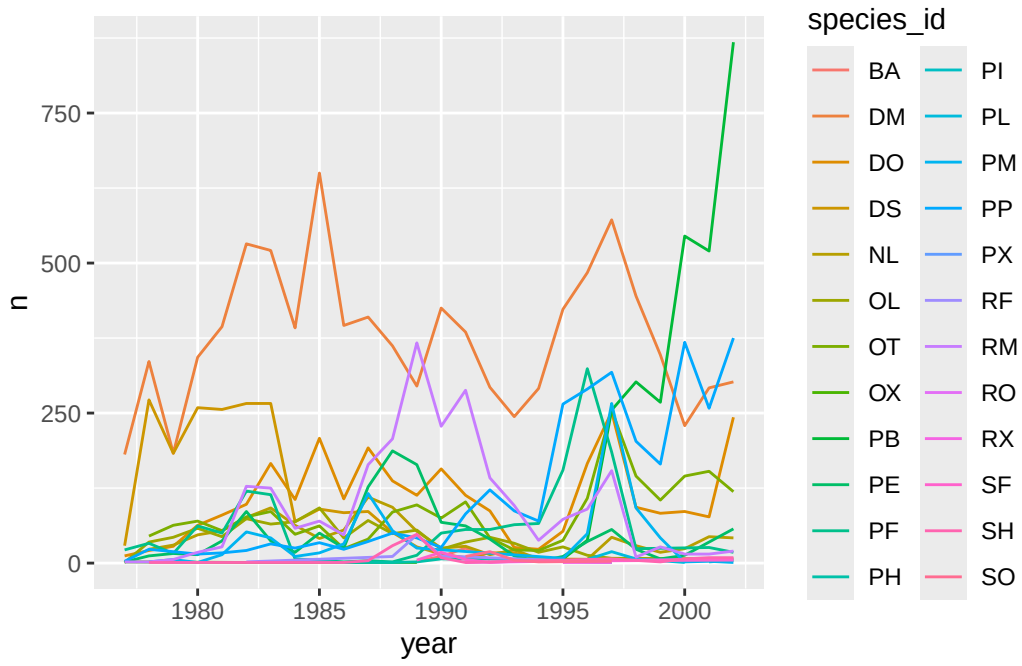
```
# create appropriate dataset
yearly_count <- survey_complete %>%
    count(year, species_id)

surveys_plot <- ggplot(data = yearly_count,
    mapping = aes(x = year, y = n))

surveys_plot + geom_line()
```




```
# make it more meaningful by breaking it by category
surveys_plot + geom_line(aes(group = species_id))
```

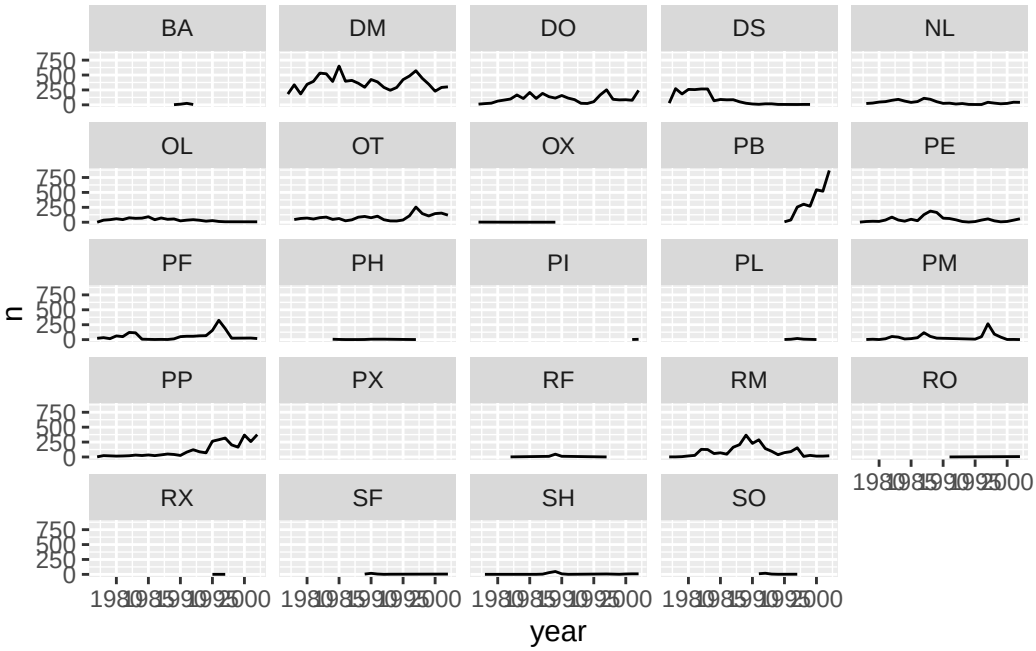


```
# make it more colorful
surveys_plot + geom_line(aes(color = species_id))
```



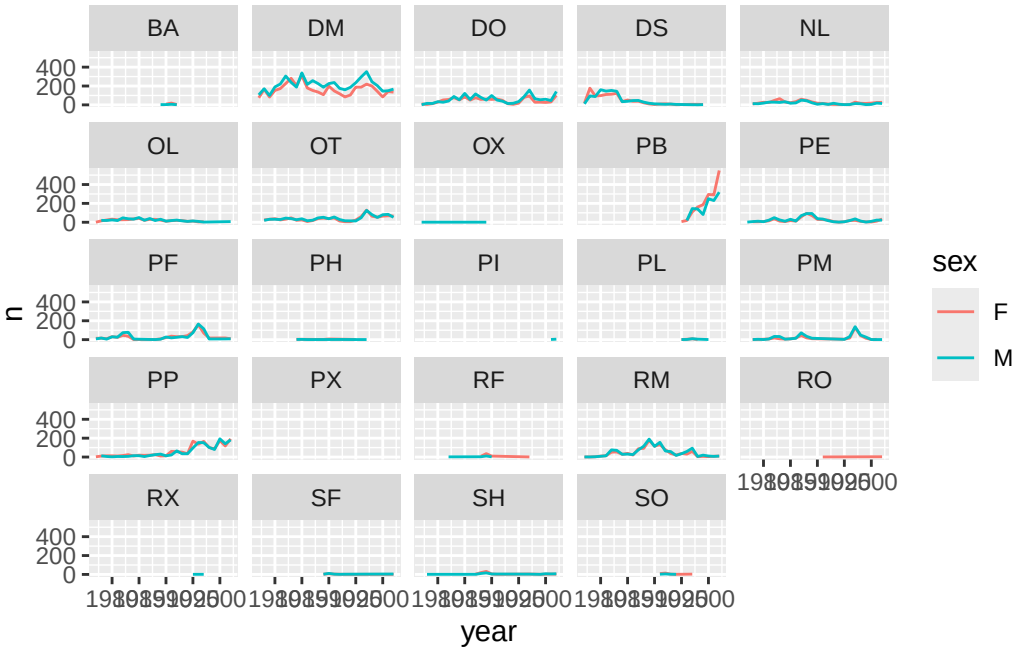

```
# split into multiple plots
surveys_plot + geom_line() + facet_wrap(~ species_id)
```

```
`geom_line()`: Each group consists of only one observation.
i Do you need to adjust the group aesthetic?
```



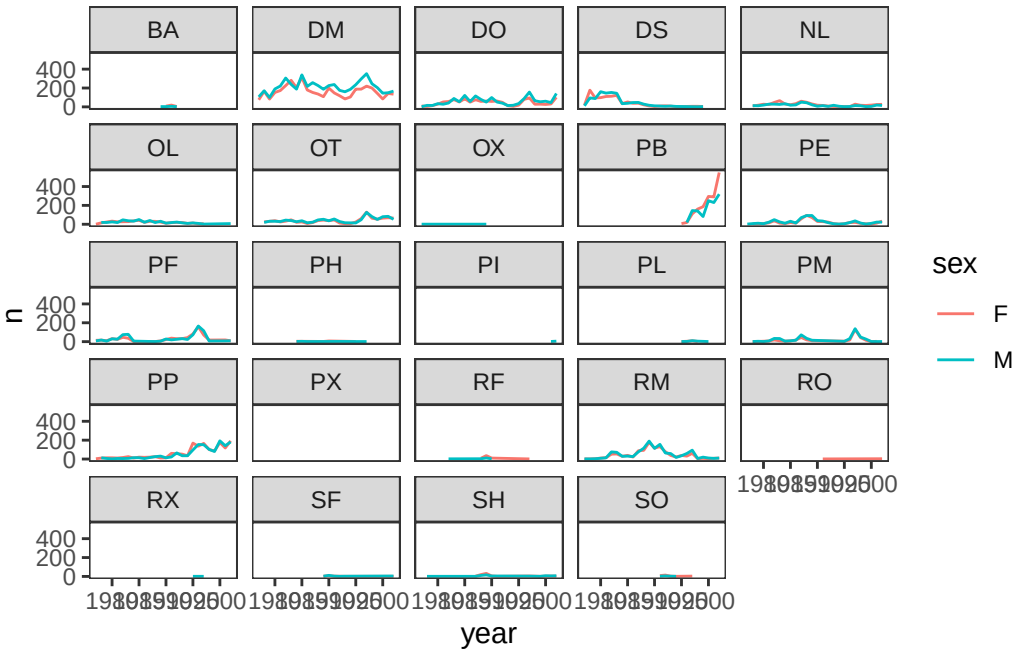

```
# split the line in each plot by sex
yearly_sex_counts <- survey_complete %>%
    count(year, species_id, sex)

surveys_plot <- ggplot(data = yearly_sex_counts,
    mapping = aes(x = year, y = n))

surveys_plot + geom_line(aes(color = sex)) +
    facet_wrap(~ species_id)
```

```
`geom_line()`: Each group consists of only one observation.
i Do you need to adjust the group aesthetic?
```




```
# remove background
surveys_plot + geom_line(aes(color = sex)) +
    facet_wrap(~ species_id) +
    theme_bw() +
    theme(panel.grid = element_blank())
```

```
`geom_line()`: Each group consists of only one observation.
i Do you need to adjust the group aesthetic?
```



1.8 References

- OU Software Carpentry Workshop (check other workshops here)
  - Main Tutorial
  - Data Carpentry with R
  - Software Carpentry with R
  - Etherpad
  - Google Doc
- Intro to ggplot by Allison Horst
- R for Data Science book by Garrett Grolemund and Hadley Wickham
- Best Practices for Scientific Computing paper

2 Quarto

2.1 Render & Review

1. VSCode/RStudio -> *Render* button
2. Terminal -> `quarto preview`
3. Terminal -> `quarto preview help`

2.2 Render w/o Review

1. Terminal -> `quarto render`
2. Terminal -> `quarto render help`

2.3 References

- Quarto Reference

3 RStudio

3.1 Keyboard Shortcuts

- `Ctrl+Enter`: run line on which cursor is standing
- `Ctrl+Alt+I`: insert new code chunk
- `Ctrl+Shift+C`: comment/un-comment
- `Alt-` : move line up
- `Alt-` : move line down
- `Ctrl+D`: delete line
- `Ctrl+Shift+A`: format code
- `Ctrl+M`: add pipe `|>` operator

Part II

R for Data Science (2e)

This section contains replications for the examples used in the R for Data Science (2e) book, one Quarto file per chapter of the book.

4 Data visualization

Clear the workspace to avoid any problems

List all the packages that will be used in this script.

```
packages = c("palmerpenguins", 'ggthemes', 'ggplot2')
```

Any missing package will be installed automatically

```
# Do NOT modify
install.packages(setdiff(packages, rownames(installed.packages())))
```

Load all packages

```
# Do NOT modify
lapply(packages, require, character.only = TRUE)
```

```
[[1]]
[1] TRUE

[[2]]
[1] TRUE

[[3]]
[1] TRUE
```

4.1 Steps of plot creation

We will work on the `penguins` dataset from the `palmerpenguins` package. Although the package can be loaded using the command below, it listed and automatically loaded using the above chunks.

```
library(palmerpenguins)
```

4.1.1 Load `ggplot2` Package

Load the `ggplot2` package using the `library` function–it was listed and automatically loaded using the above chunks.

```
library(ggplot2)
```

4.1.2 Create `ggplot` object

Create an empty canvas by instantiating a `ggplot` object using the `ggplot()` function.

```
ggplot()
```


4.1.3 Link Dataset

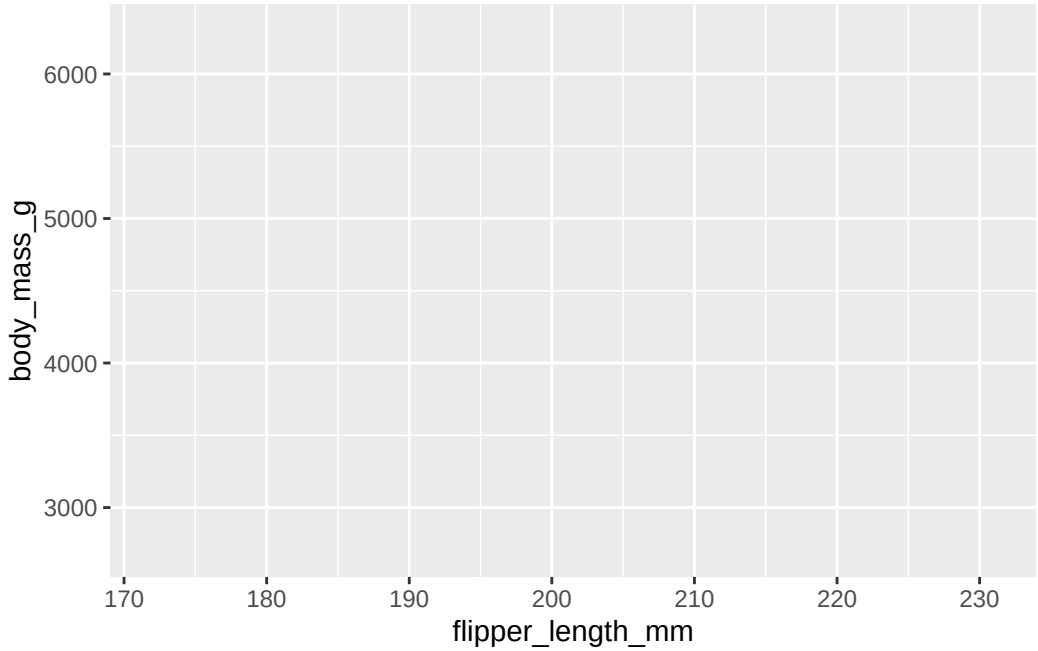
Link the dataset with the instantiated `ggplot` object using the `data` parameter.

```
ggplot(data = penguins)
```


4.1.4 Map 2 Variables

Specify which of the variables in the dataset will be used as the plot aesthetics (visual properties) using the `mapping` argument done via the `aes()` function.

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

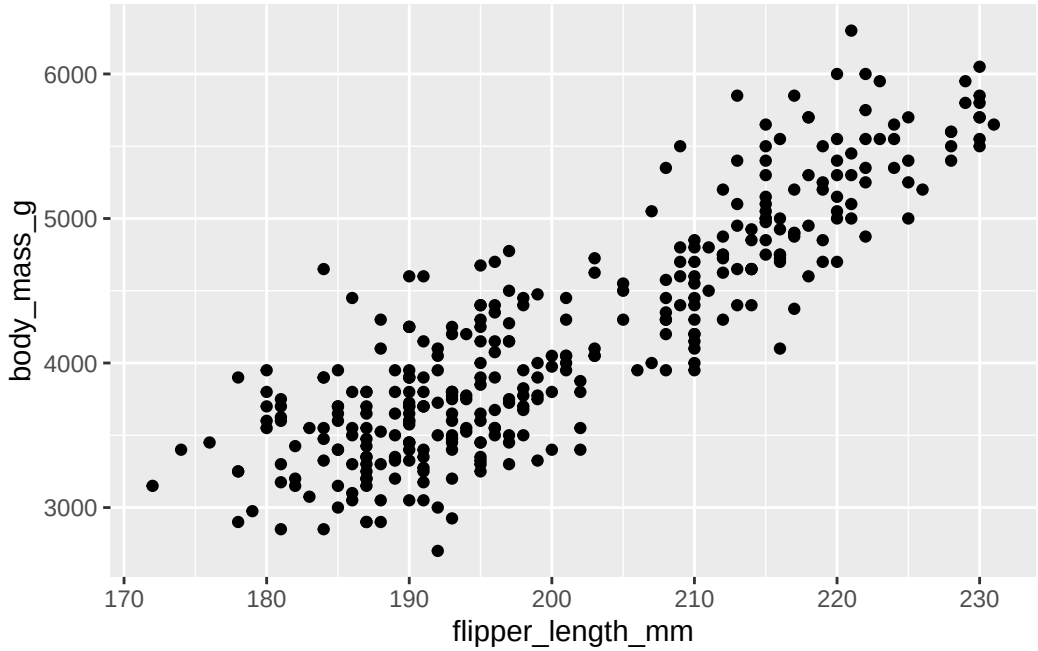


4.1.5 Show Data

Specify how the data (observations) will be represented geometrically on the plot, eg, bars, points, or line. The functions starting with `geom_` is used for this purpose. These functions add layer of the selected geometric object to the plot.

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

```
Warning: Removed 2 rows containing missing values or values outside the scale range
(`geom_point()`).
```

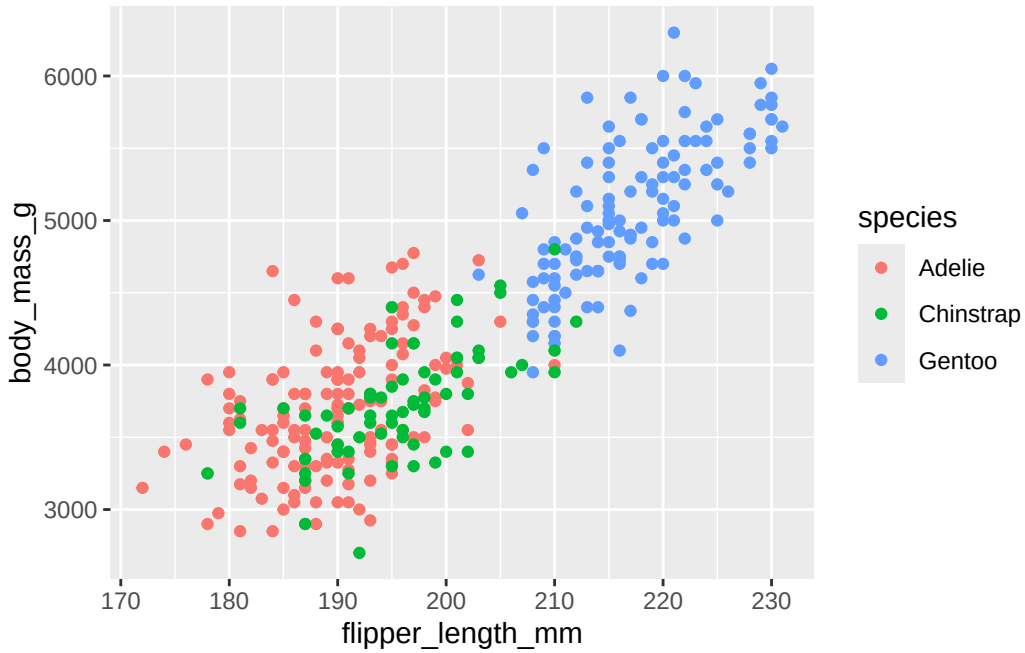


4.1.6 Map 1 More Variables

Other variables in the dataset can be linked to plot aesthetics (visual properties) using the `mapping` argument done via the `aes()` function.

```
ggplot(
  data = penguins,
  mapping = aes(x = flipper_length_mm, y = body_mass_g, color = species)
) +
  geom_point()
```

```
Warning: Removed 2 rows containing missing values or values outside the scale range
(`geom_point()`).
```



4.1.7 Show Data Again Differently

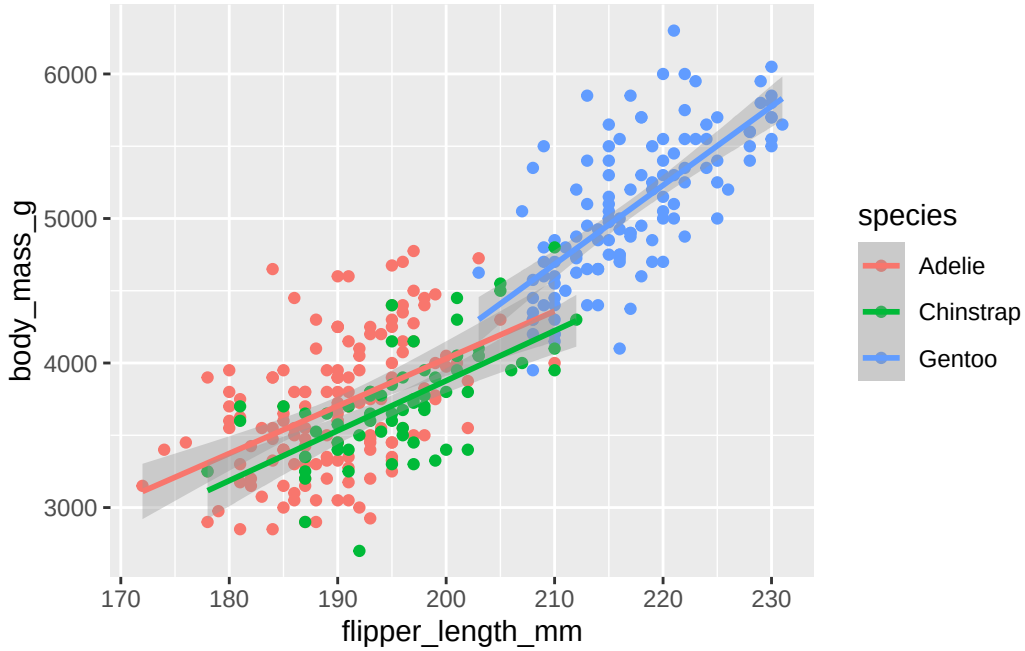
More geometric representations for the data can be specified using the functions starting with `geom_` which will add layer of the selected geometric object to the plot.

```
ggplot(
  data = penguins,
  mapping = aes(x = flipper_length_mm, y = body_mass_g, color = species)
) +
  geom_point() +
  geom_smooth(method = "lm")
```

```
`geom_smooth()` using formula = 'y ~ x'
```

```
Warning: Removed 2 rows containing non-finite outside the scale range
(`stat_smooth()`).
```

```
Warning: Removed 2 rows containing missing values or values outside the scale range
(`geom_point()`).
```



4.1.8 Globally & Locally Mapped Variables

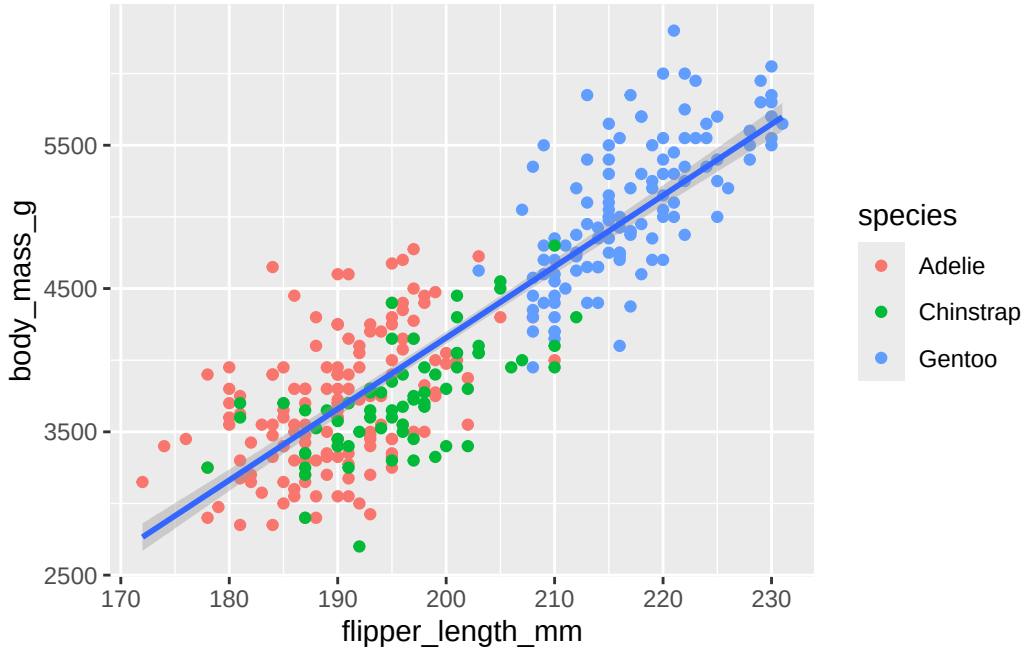
The aesthetic mapping defined in the `ggplot()` function is *global* meaning that all the `geom_()` functions inherit it. However, the aesthetic mapping defined in the `geom_()` functions are local, ie, not shared with other `gemo_()` functions.

```
ggplot(data = penguins,
       mapping = aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(mapping = aes(color = species)) +
  geom_smooth(method = "lm")
```

```
`geom_smooth()` using formula = 'y ~ x'
```

```
Warning: Removed 2 rows containing non-finite outside the scale range
(`stat_smooth()`).
```

```
Warning: Removed 2 rows containing missing values or values outside the scale range
(`geom_point()`).
```



4.1.9 Map Same Variable Multiple Ways

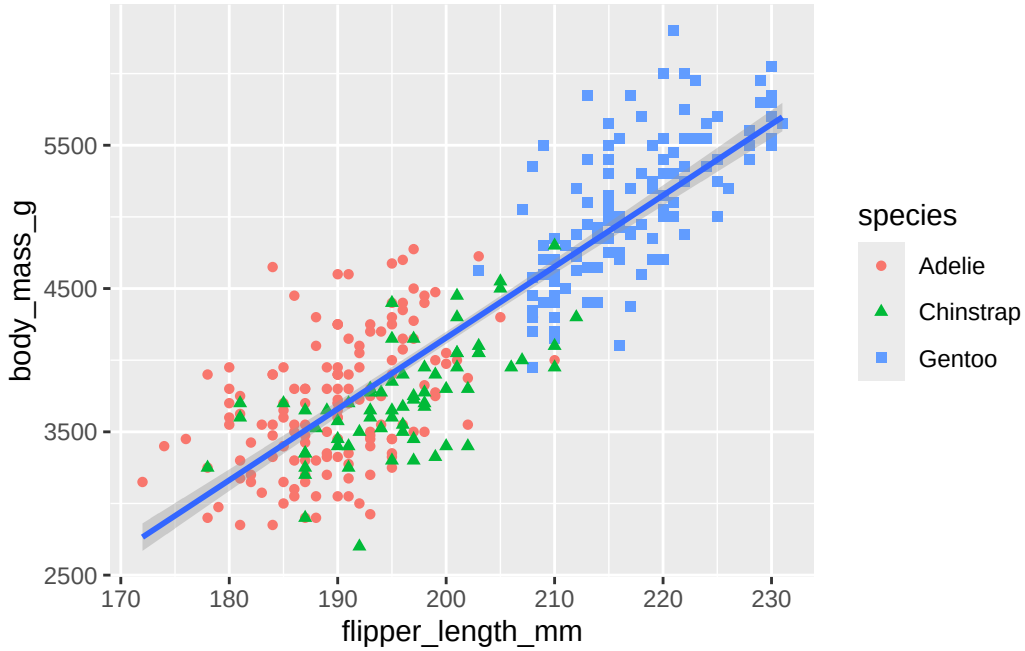
We can link the same variable to multiple plot aesthetics (visual properties) using the `mapping` parameter done via the `aes()` function.

```
ggplot(data = penguins,
       mapping = aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(mapping = aes(color = species, shape = species)) +
  geom_smooth(method = "lm")
```

```
`geom_smooth()` using formula = 'y ~ x'
```

```
Warning: Removed 2 rows containing non-finite outside the scale range
(`stat_smooth()`).
```

```
Warning: Removed 2 rows containing missing values or values outside the scale range
(`geom_point()`).
```



4.1.10 More Accessible

The `labs()` function can be used to make the plot more accessible. The function will add new layer to the plot and the following items can be added to the layer using the corresponding parameters

- a title using the `title` parameter
- a sub-title, if necessary, using the `subtitle` parameter
- x-axis title using the `x` parameter
- y-axis title using the `y` parameter
- data-series label or legend using the `color` and/or `shape` parameters

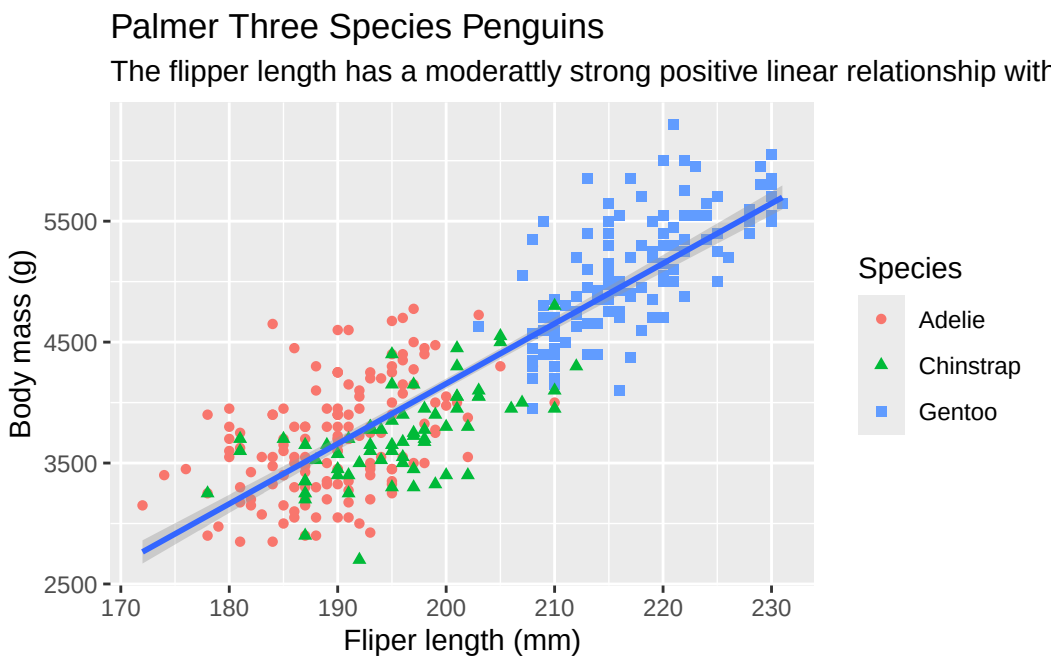
```
ggplot(data = penguins,
       mapping = aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(mapping = aes(color = species, shape = species)) +
  geom_smooth(method = "lm") +
  labs(
    title = 'Palmer Three Species Penguins',
    subtitle = 'The flipper length has a moderattly strong positive linear relationship with
    x = 'Fliper length (mm)',
    y = 'Body mass (g)',
    shape = 'Species',
```

```
    color = 'Species'
  )
```

```
`geom_smooth()` using formula = 'y ~ x'
```

```
Warning: Removed 2 rows containing non-finite outside the scale range
(`stat_smooth()`).
```

```
Warning: Removed 2 rows containing missing values or values outside the scale range
(`geom_point()`).
```



Other types of texts can be added using other functions. The other types of texts are:

- x-axis label
- y-axis label
- data labels, if necessary
- annotation for interesting or important data, if exist

4.1.11 Color-blind Safe

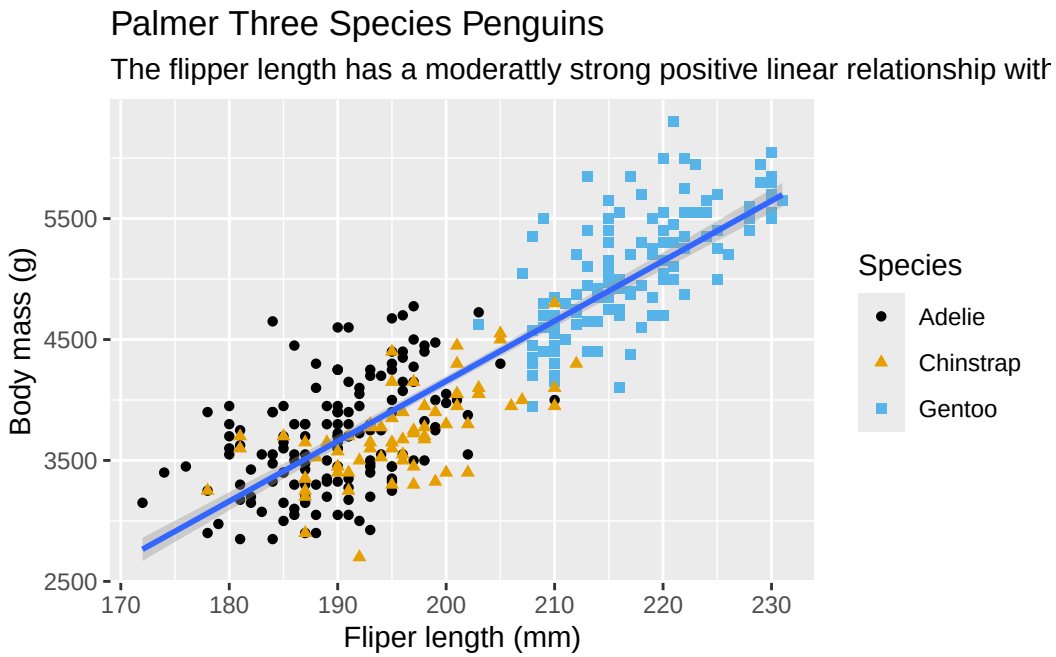
Make the plot more color-blind safe by using the `scale_color_colorblind()` function from the `ggthemes` package which will add new layer to the plot.

```
ggplot(data = penguins,
       mapping = aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(mapping = aes(color = species, shape = species)) +
  geom_smooth(method = "lm") +
  labs(
    title = 'Palmer Three Species Penguins',
    subtitle = 'The flipper length has a moderattly strong positive linear relationship with
    x = 'Fliper length (mm)',
    y = 'Body mass (g)',
    shape = 'Species',
    color = 'Species'
  ) +
  scale_color_colorblind()
```

```
`geom_smooth()` using formula = 'y ~ x'
```

```
Warning: Removed 2 rows containing non-finite outside the scale range
(`stat_smooth()`).
```

```
Warning: Removed 2 rows containing missing values or values outside the scale range
(`geom_point()`).
```



4.1.12 Implicit Call

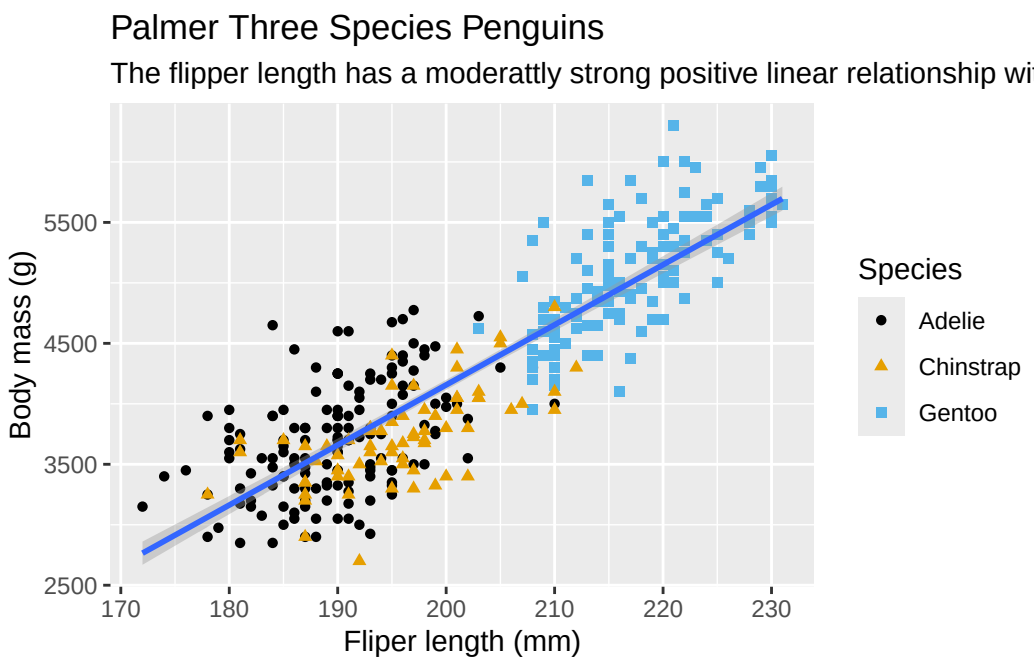
The first one or two arguments of functions are so important that scientists should know them by heart. Hence, to save some typing, the name of these arguments are usually omitted and only the values assigned to them are kept, ie, the names becomes implicit and no more explicit. Hence, the above call can be written as follows–the arguments `data` and `mapping` were omitted.

```
ggplot(penguins, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(aes(color = species, shape = species)) +
  geom_smooth(method = "lm") +
  labs(
    title = 'Palmer Three Species Penguins',
    subtitle = 'The flipper length has a moderattly strong positive linear relationship with
    x = 'Fliper length (mm)',
    y = 'Body mass (g)',
    shape = 'Species',
    color = 'Species'
  ) +
  scale_color_colorblind()
```

```
`geom_smooth()` using formula = 'y ~ x'
```

```
Warning: Removed 2 rows containing non-finite outside the scale range
(`stat_smooth()`).
```

```
Warning: Removed 2 rows containing missing values or values outside the scale range
(`geom_point()`).
```



4.1.13 Pipe Operator

The pipe operator `\>` (shortcut: `Ctrl+M`) can be used to make the code tidy. The above code can be re-written as follow–notice the dataset was pulled before the call to the `ggplot` function.

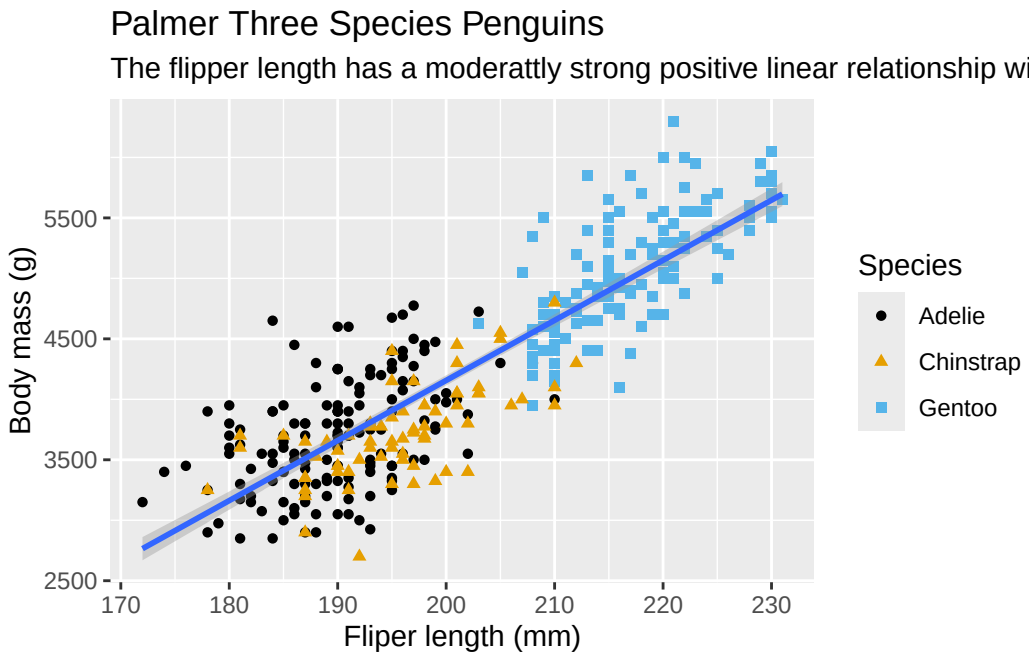
```
penguins |>
  ggplot(aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(aes(color = species, shape = species)) +
  geom_smooth(method = "lm") +
  labs(
    title = 'Palmer Three Species Penguins',
    subtitle = 'The flipper length has a moderattly strong positive linear relationship with
    x = 'Fliper length (mm)',
    y = 'Body mass (g)',
```

```
    shape = 'Species',
    color = 'Species'
  ) +
  scale_color_colorblind()
```

```
`geom_smooth()` using formula = 'y ~ x'
```

```
Warning: Removed 2 rows containing non-finite outside the scale range
(`stat_smooth()`).
```

```
Warning: Removed 2 rows containing missing values or values outside the scale range
(`geom_point()`).
```



Part III

Practice

This section contains practices for the programming/scripting languages that I am learning.

5 Topic Modeling in R

5.1 Introduction

An attempt to understand Sherlock Holmes short stories found in Adventures of Sherlock Holmes book by Arthur Conan Doyle. After inspecting the table of content, the book seems to have 12 stories, one story per chapter. The analysis is inspired by Julia Silge's YouTube video Topic modeling with R and tidy data principles

5.2 Download Book

```
library(gutenbergr)  # download books from Project Gutenberg using book ID
library(tidyverse)
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.5.1     v tibble    3.2.1
v lubridate 1.9.3     v tidyr     1.3.1
v purrr     1.0.2
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becor
```

```
library(tidytext)

# Download the book, each line of the book is read into a seperate row
sherlock_raw <- gutenberg_download(48320)
```

```
Determining mirror for Project Gutenberg from https://www.gutenberg.org/robot/harvest
Using mirror http://aleph.gutenberg.org
```

```
dim(sherlock_raw)
```

```
[1] 12350     2
```

```
head(sherlock_raw)
```

```
# A tibble: 6 x 2
  gutenberg_id text
         <int> <chr>
1        48320 "ADVENTURES OF SHERLOCK HOLMES"
2        48320 ""
3        48320 ""
4        48320 ""
5        48320 ""
6        48320 "[Illustration:"
```

```
tail(sherlock_raw)
```

```
# A tibble: 6 x 2
  gutenberg_id text
         <int> <chr>
1        48320 "  boisterious fashion, and on the whole _changed to_"
2        48320 "  boisterous fashion, and on the whole"
3        48320 ""
4        48320 "  Page 297"
5        48320 "  wrapt in the peaceful beauty _changed to_"
6        48320 "  rapt in the peaceful beauty"
```

5.3 Wrangle: Label Stories

```
sherlock <- sherlock_raw %>%

  # determine start of each story/chapter
  mutate(story = ifelse(str_detect(text, "^(A SCANDAL IN BOHEMIA|THE RED-HEADED LEAGUE|A CASE

  # determine lines belonging to each story/chapter by
  # filling down the N/A rows of story column
```

```
  fill(story) %>%

  # remove the part that does not belong to any story/chapter,
  # i.e, the introduction
  filter(!is.na(story)) %>%

  # convert story column to factor
  mutate(story = factor(story))
```

5.4 Wrangle: Put in Tidy Format

The row of `text` column contains multiple words/tokens. We want to put each word/token of each `text` row into a separate row. This makes the dataframe follows the tidy format and hence makes it easy to process.

```
tidy_sherlock <- sherlock %>%

  # number the rows
  mutate(line = row_number()) %>%

  # break the text column into multiple row where each row contain one token
  unnest_tokens(word, text) %>%

  # remove the stopwords--the rows where the word column is a stopword
  anti_join(stop_words) %>%

  # remove holmes rows which might affect our topic models
  filter(word != "holmes")
```

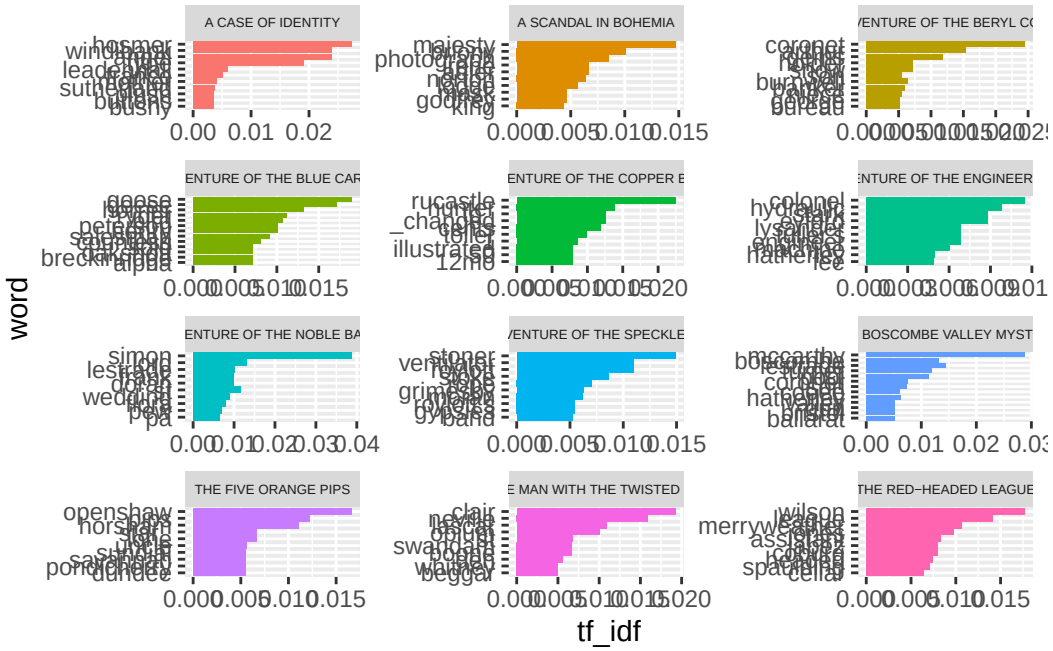
```
Joining with `by = join_by(word)`
```

5.5 Explore tf-idf

- To see which words are important in each story/chapter, i.e.,the words that appears many times in that story but few or none in the other stories.
- tf-idf (term frequency-inverse document frequency) is a great exploratory tool before starting with topic modeling

```r
library(ggplot2)

tidy_sherlock %>%

  # count number of occurrence of words in stories
  count(story, word, sort = TRUE) %>%

  # compute and add tf, idf, and tf_idf values for words
  bind_tf_idf(word, story, n) %>%

  # group by story
  group_by(story) %>%

  # take top 10 words of each story with highest tf_idf (last column)
  top_n(10) %>%

  # unpack
  ungroup() %>%

  # turn words into factors and order them based on their tf_idf values
  # NOTE: This will not affect order the dataframe rows which is can be
  #   done via the arrange function
  # NOTE: Recording the word column this way is for ggplot to visualize them
  #   as desired from top tf_idf to lowest
  mutate(word = reorder(word, tf_idf)) %>%

  # plot
  ggplot(aes(word, tf_idf, fill = story)) +
  geom_col(show.legend = FALSE) +
  facet_wrap(~story, scales = "free", ncol = 3) +
  theme(strip.text.x = element_text(size = 5)) +
  coord_flip()
```

```
Selecting by tf_idf
```



5.6 Implement Topic Modeling

Training the model for the topics

```
library(stm)        # for do topic modeling
```

```
stm v1.3.7 successfully loaded. See ?stm for help.
 Papers, resources, and other materials at structuraltopicmodel.com
```

```
library(quanteda)   # great text mining, will be used to structure the input
```

```
Package version: 4.0.2
Unicode version: 15.1
ICU version: 74.1
```

```
Parallel computing: 8 of 8 threads used.
```

```
See https://quanteda.io for tutorials and examples.
```

```
                    #   to stm

# Convert from tidy form to quanteda form (document x term matrix)
sherlock_stm <- tidy_sherlock %>%
  count(story, word, sort = TRUE) %>%
  cast_dfm(story, word, n)

# Train the model
topic_model <- stm(sherlock_stm, K=6, init.type = "Spectral")
```

```
Beginning Spectral Initialization
     Calculating the gram matrix...
     Finding anchor words...
    ......
     Recovering initialization...
    ..........................................................................
Initialization complete.
............
Completed E-Step (0 seconds).
Completed M-Step.
Completing Iteration 1 (approx. per word bound = -7.785)
............
Completed E-Step (0 seconds).
Completed M-Step.
Completing Iteration 2 (approx. per word bound = -7.593, relative change = 2.458e-02)
............
Completed E-Step (0 seconds).
Completed M-Step.
Completing Iteration 3 (approx. per word bound = -7.481, relative change = 1.473e-02)
............
Completed E-Step (0 seconds).
Completed M-Step.
Completing Iteration 4 (approx. per word bound = -7.455, relative change = 3.469e-03)
............
Completed E-Step (0 seconds).
Completed M-Step.
Completing Iteration 5 (approx. per word bound = -7.450, relative change = 7.612e-04)
Topic 1: st, simon, lord, day, lady
 Topic 2: door, miss, house, rucastle, matter
 Topic 3: hat, goose, stone, bird, geese
 Topic 4: father, time, mccarthy, son, hand
 Topic 5: house, time, night, door, heard
```

```
 Topic 6: red, time, wilson, business, headed
.............
Completed E-Step (0 seconds).
Completed M-Step.
Completing Iteration 6 (approx. per word bound = -7.449, relative change = 1.233e-04)
.............
Completed E-Step (0 seconds).
Completed M-Step.
Completing Iteration 7 (approx. per word bound = -7.449, relative change = 1.168e-05)
.............
Completed E-Step (0 seconds).
Completed M-Step.
Model Converged
```

```
summary(topic_model)
```

```
A topic model with 6 topics, 12 documents and a 7709 word dictionary.

Topic 1 Top Words:
     Highest Prob: st, simon, lord, day, lady, found, matter
     FREX: simon, clair, neville, lascar, opium, doran, flora
     Lift: aloysius, ceremony, doran, millar, 2_s, aberdeen, absurdly
     Score: simon, st, clair, neville, _danseuse_, lestrade, doran
Topic 2 Top Words:
     Highest Prob: door, miss, house, rucastle, matter, street, lady
     FREX: rucastle, hosmer, hunter, angel, windibank, _changed, 1
     Lift: advertised, angel, annoyance, brothers, employed, factor, fowler
     Score: rucastle, hosmer, angel, windibank, hunter, type, 1
Topic 3 Top Words:
     Highest Prob: hat, goose, stone, bird, geese, baker, sir
     FREX: geese, horner, ryder, henry, peterson, salesman, countess
     Lift: battered, bet, bred, brixton, cosmopolitan, covent, cream
     Score: goose, geese, horner, _alias_, ryder, henry, peterson
Topic 4 Top Words:
     Highest Prob: father, time, mccarthy, son, hand, lestrade, left
     FREX: mccarthy, pool, boscombe, openshaw, pips, horsham, turner
     Lift: bone, dundee, horsham, pondicherry, presumption, savannah, sundial
     Score: mccarthy, pool, lestrade, boscombe, openshaw, _détour_, turner
Topic 5 Top Words:
     Highest Prob: house, time, night, door, heard, hand, round
     FREX: coronet, stoner, arthur, roylott, ventilator, gems, stoke
     Lift: _absolute_, _all_, _en, 1100, 16a, 3d, 4000
```

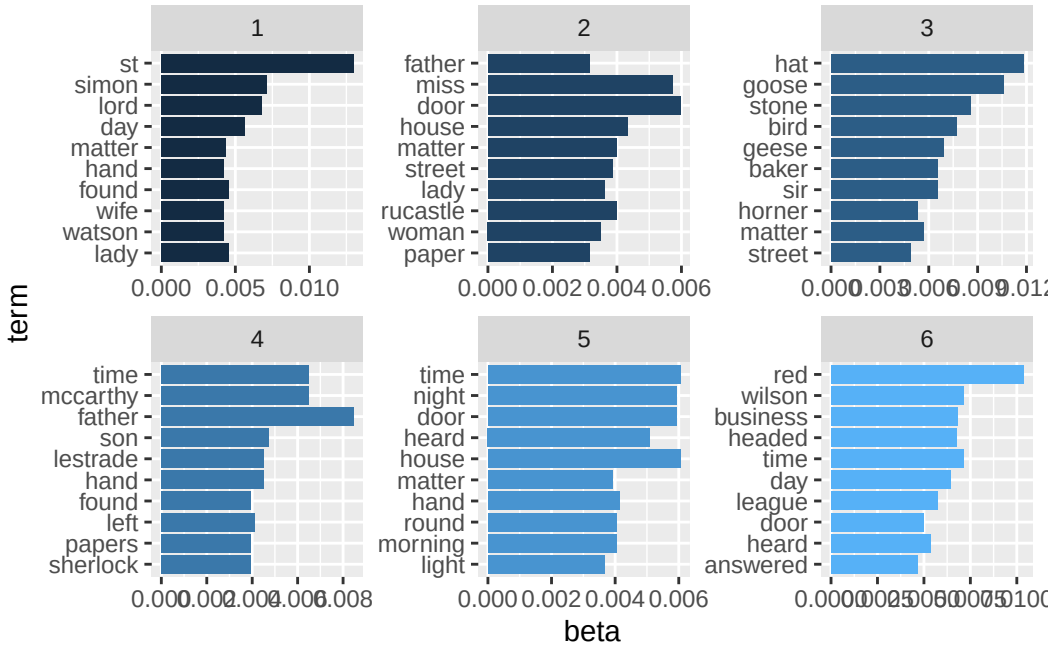
```
     Score: coronet, arthur, stoner, gems, 4000, roylott, ventilator
Topic 6 Top Words:
     Highest Prob: red, time, wilson, business, headed, day, league
     FREX: wilson, league, merryweather, jones, coburg, jabez, headed
     Lift: daring, saturday, vincent, _employé_, _october, _partie, 17
     Score: wilson, league, merryweather, _employé_, jones, headed, coburg
```

5.7 Contribution of Words in Topics

Looking at which words contribute the most in each topic.

```
# Extracting betas and putting them in a tidy format
tm_beta <- tidy(topic_model)

# Visualizing the top words contributing to each topic
tm_beta %>%
  group_by(topic) %>%
  # top 10 word in each topic with higest beta (last column)
  top_n(10) %>%
  ungroup() %>%
  # turn words into factors and order them based on their tf_idf values
  # NOTE: This will not affect order the dataframe rows which is can be
  #   done via the arrange function
  # NOTE: Recording the word column this way is for ggplot to visualize them
  #   as desired from top tf_idf to lowest
  mutate(term = reorder(term, beta)) %>%
  ggplot(aes(term, beta, fill = topic)) +
  geom_col(show.legend = FALSE) +
  facet_wrap(~topic, scales = "free", ncol = 3) +
  coord_flip()
```

```
Selecting by beta
```

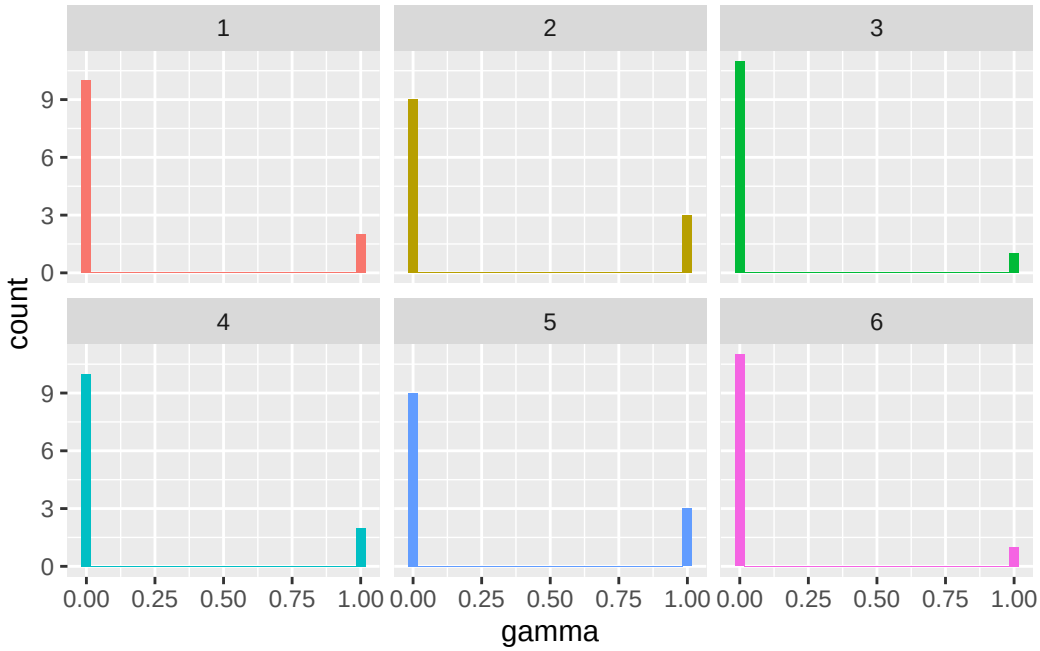


5.8 Distribution of Topics in Stories

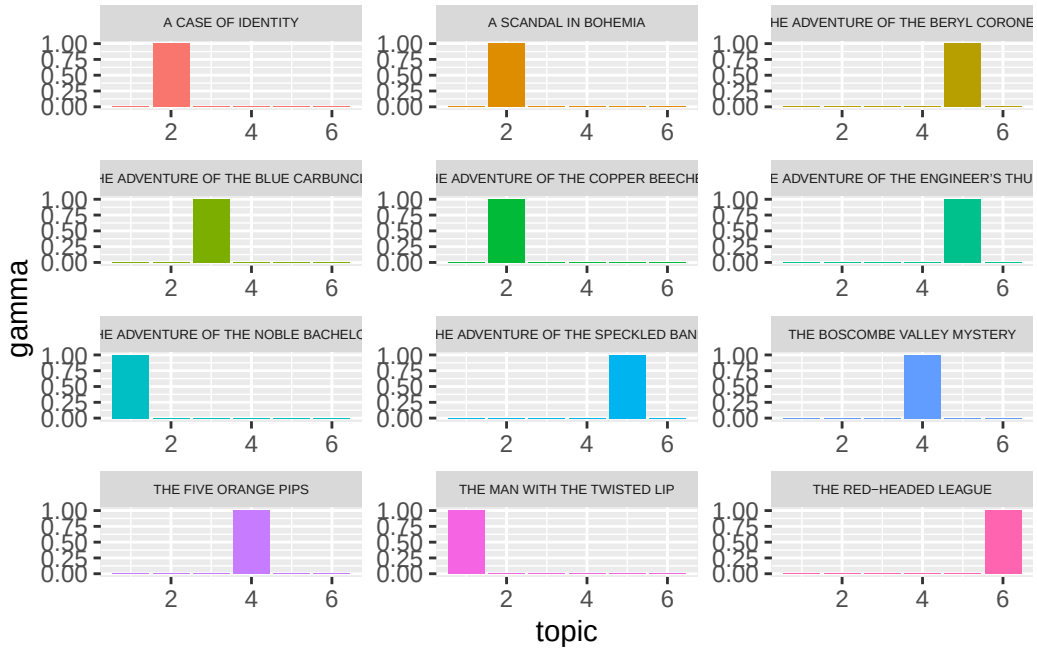
Looking at how the stories are associated with each topic and how strong each association is.

```
# Extracting gammas and putting them in a tidy format
tm_gamma <- tidy(topic_model, matrix = "gamma",
                 # use the names of the stories instead of the default numbers
                 document_names = rownames(sherlock_stm))


# Visualizing the number of stories belonging to each topics and the confidence
#   of the belonging
tm_gamma %>%
  ggplot(aes(gamma, fill = as.factor(topic))) +
  geom_histogram(show.legend = FALSE) +
  facet_wrap(~topic, ncol = 3)
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
# Visualizing how much each topic appear in each story
tm_gamma %>%
  ggplot(aes(topic, gamma, fill = document)) +
  geom_col(show.legend = FALSE) +
  facet_wrap(~document, scales = "free", ncol = 3) +
  theme(strip.text.x = element_text(size = 5))
```



The model did an excellent job strongly associating the stories into one or more topics. This perfect association is rare in the world of topic modeling. The reason behind this perfect association here could be due to the small number of documents that we have.

5.9 References

- Adventures of Sherlock Holmes book by Arthur Conan Doyle on Project Gutenberg
- Regular Expressions 101