Data analysis and visualization in R

UC Merced R curriculum

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today

- dplyr and the "tidyverse"
- the pipe operator
- tidy data, pivoting data, joining tables
- group and summarize
- data visualization with ggplot2

manipulating and analyzing data with dplyr

the tidyverse: an "umbrella" package

- **ggplot2**: a "grammar of graphics" by Hadley Wickham. Divide the data and the aesthetics. Create and modify the plots layer by layer
- **dplyr**: a way to deal with data frames, sql external data bases, written in `C++`
- **readr**: read data
- **tidyr**: format data frames
- **stringr**: deals with strings
- **forcats**: factors
- additional packages for other tasks: **tibble**, **lubridate** and many more

Most of R is still **base**-based and both philosophies communicate well with each other

reading data with readr

```
library(dplyr)
library(readr)
```

```
surveys <- readr::read_csv("data/raw/portal_data_joined.csv")
```

```
##
## ── Column specification ────────────────────────────────────────────────────────
## 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(),
```

the tibble

```
surveys
vignette("tibble")
```

- modified data frames
- do not change input type (characters into factors)
- do not change the name of the columns and allows for non-standard names, such as `1999` and `total count` (it will require back ticks)
- no rownames
- subsetting always returns a tibble

some principal functions in dplyr

- **select** (columns)
- **filter** (rows)
- **rename** (columns)
- **mutate** (create new columns or modify existing columns)
- **arrange** to sort according to a column
- **count** cases of one or many columns

select columns

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

1. there is no need to put quotes
2. there is no need to put variables between `c()`

base R still works in a tibble

```
surveys[, c("plot_id", "species_id", "weight")]
```

removing columns

```
select(surveys, -record_id, -species_id)
```

additional functions

```
select(surveys, -ends_with("id"))
```

`starts_with`, `contains`, `all_of`, `last_col`

filter rows

logical clauses!

```
surv_1995 <- filter(surveys, year == 1995)
```

No need to use $ or brackets

```
surveys$year == 1995
surveys[surveys$year == 1995 , ]
```

mutate creates or modifies columns

```
surveys <- mutate(surveys, weight_kg = weight / 1000)
```

```
mutate(surveys,
       weight_kg = weight / 1000,
       weight_lb = weight_kg * 2.2)
```

group_by() and summarise()

- if you have a column factor (e.g. sex) and want to apply a function to the levels of this factor

```
surveys_g <-group_by(surveys, sex) #does nothing?
summary_sex <- summarize(surveys_g,
                         mean_weight = mean(weight, na.rm = TRUE))
summary_sex
```

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

another example:

```
surveys_g2 <-group_by(surveys, sex, species_id)
mean_w <- summarize(surveys_g2,
                    mean_weight = mean(weight, na.rm = TRUE))
```

```
mean_w
```

```
## # A tibble: 92 x 3
## # Groups:   sex [3]
##    sex   species_id mean_weight
##    <chr> <chr>            <dbl>
##  1 F     BA                9.16
##  2 F     DM               41.6
##  3 F     DO               48.5
##  4 F     DS              118.
##  5 F     NL              154.
##  6 F     OL               31.1
##  7 F     OT               24.8
##  8 F     OX               21
##  9 F     PB               30.2
## 10 F     PE               22.8
## # … with 82 more rows
```

arrange sorts by a column

```
arrange(mean_w, mean_weight)


arrange(mean_w, desc(mean_weight))
```

the pipe operator %>%

Classic syntax goes like this

```
object1
object2 <- function1(object1)
object3 <- function2(object2)
```

...or you can nest functions and avoid create intermediary objects

```
object3 <- function2(function1(object1))
```

The pipe operator allows to apply functions sequentially:

```
object3 <- object1 %>% function1() %>% function2()
```

select and filter

```
surveys2 <- filter(surveys, weight < 5)
surveys_sml <- select(surveys2, species_id, sex, weight)

surveys %>%
  filter(weight < 5) %>%
  select(species_id, sex, weight)
```

group_by() and summarize()

```
surveys_g   <- group_by(surveys, sex) #does nothing?
summary_sex <- summarize(surveys_g,
                         mean_weight = mean(weight, na.rm = TRUE))


summary_sex <- surveys %>%
  group_by(sex) %>%
  summarize(mean_weight = mean(weight, na.rm = TRUE))
```

count

```
surveys %>%
    count(sex)

surveys %>%
  count(sex, species)

surveys %>%
  count(sex, species) %>%
  arrange(species, desc(n))
```

challenge

- How many animals were caught in each `plot_type` surveyed?
- Use `group_by()` and `summarize()` to find the mean, min, and max hindfoot length for each species (using `species_id`). Also add the number of observations (hint: see `?n`).

```
## `summarise()` ungrouping output (override with `.groups` argument)

## # A tibble: 5 x 2
##   plot_type                    n
##   <chr>                    <int>
## 1 Control                  15611
## 2 Long-term Krat Exclosure   5118
## 3 Rodent Exclosure           4233
## 4 Short-term Krat Exclosure  5906
## 5 Spectab exclosure          3918

## `summarise()` regrouping output by 'plot_type' (override with `.groups` argument)

## # A tibble: 181 x 3
## # Groups:   plot_type [5]
##    plot_type                  species_id     n
##    <chr>                      <chr>      <int>
```

save data!

```
surveys <- readr::read_csv("data/raw/portal_data_joined.csv")
```

```
##
## ── Column specification ────────────────────────────────────────────────────────
## 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()
## )
```

tidy data as a philosohpy

- most datasets are organized as observations in rows and variables in columns
- tidy data refer to reorganizing such data in pairs of observation-key-values
- do you have variables in the title of your dataframe? ex. if you have two columns: `1999` and `2000`, they should be inside a variable called year.

```
library(tidyr)
table4a
```

```
## # A tibble: 3 x 3
##   country     `1999` `2000`
## * <chr>        <int>  <int>
## 1 Afghanistan    745   2666
## 2 Brazil       37737  80488
## 3 China       212258 213766
```

```
table4a %>%
  pivot_longer(cols = c(`1999`, `2000`), names_to = "year", values_to = "cases")
```

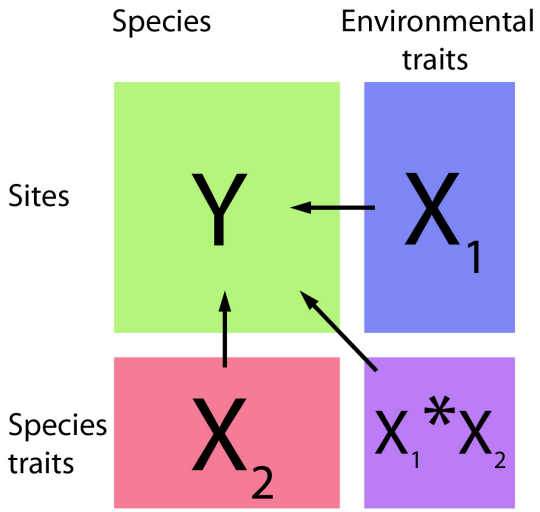
pivoting to format tables

- `pivot_long()`, `pivot_large()`

working with several tables: merges and joins

- in real analysis settings you will have many tables that are related

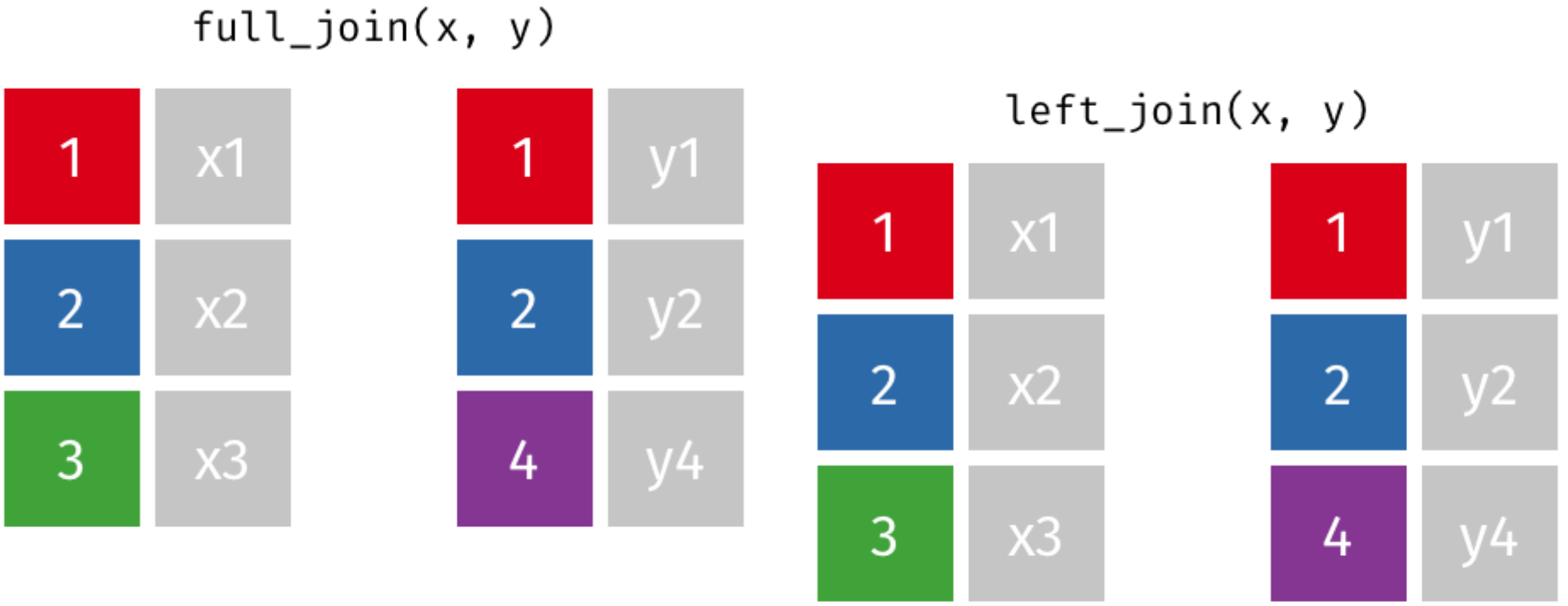
- in ecology for example:
  - sites x species
  - sites x environmental conditions
  - species x characteristics
  - individuals x individual measurement



working with several tables

- keep the data as simple as possible, even if that means having different tables
- for each data table have in mind which is your sampling unit. is it the species, is it the plot?
- have a **unique identifier for each observation** so you can merge the data

working with several tables: joins



gadenbuie/tidyexplain

data visualization with ggplot2

ggplot2

- **ggplot2** separates the data from the aesthetics part and allows layers of information to be added sequentially with `+`

```
ggplot(data = <data>,
       mapping = aes(<mappings>)) +
  geom_xxx()
```

- **data**
- **mappings**: the specific variables (x, y, z, group...)
- **geom_xxx()**: functions for plotting options `geom_point()`, `geom_line()`

cheat sheet link

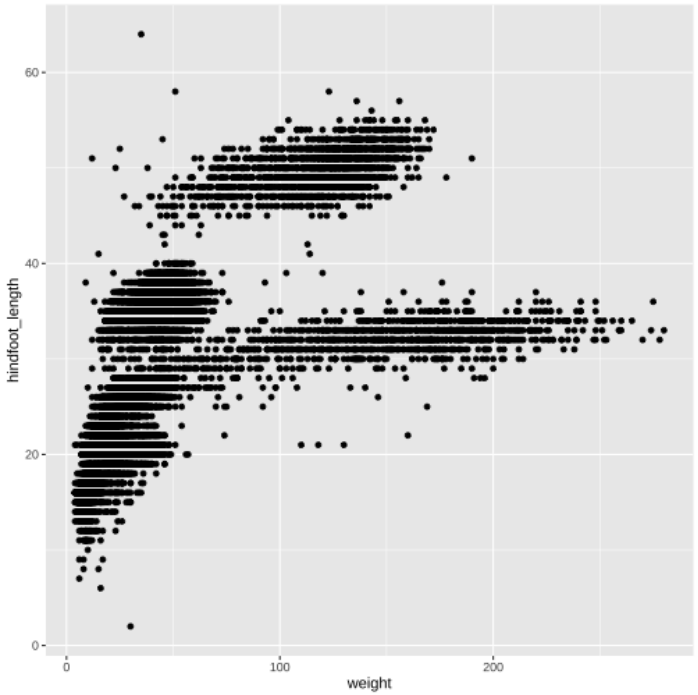
ggplot2 plots are built sequentially in layers

```
library(ggplot2)
library(readr)

surveys_complete <- read_csv("data/processed/surveys_mod_dplyr.csv")
```

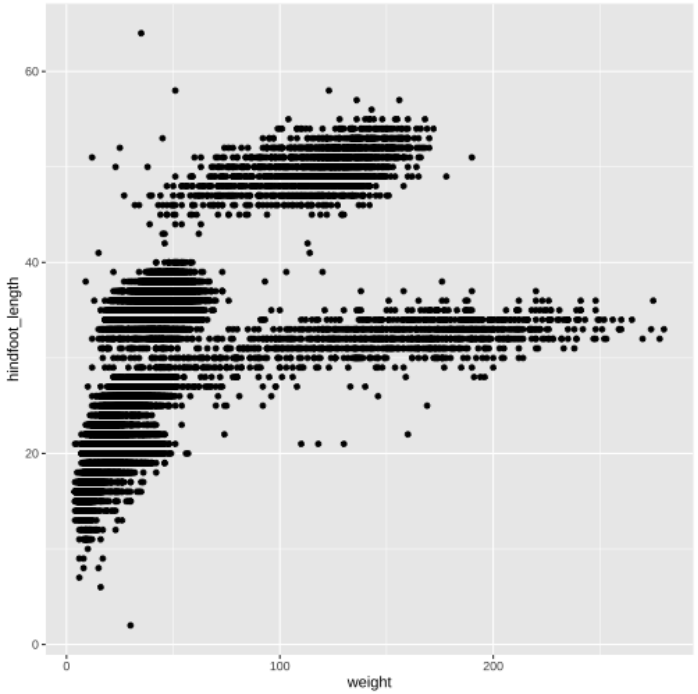
ggplot2 plots are built sequentially in layers

```
ggplot(data = surveys_complete,                                  # data
       mapping = aes(x = weight, y = hindfoot_length)) + # aesthetics
  geom_point()                                                  # plot function
```



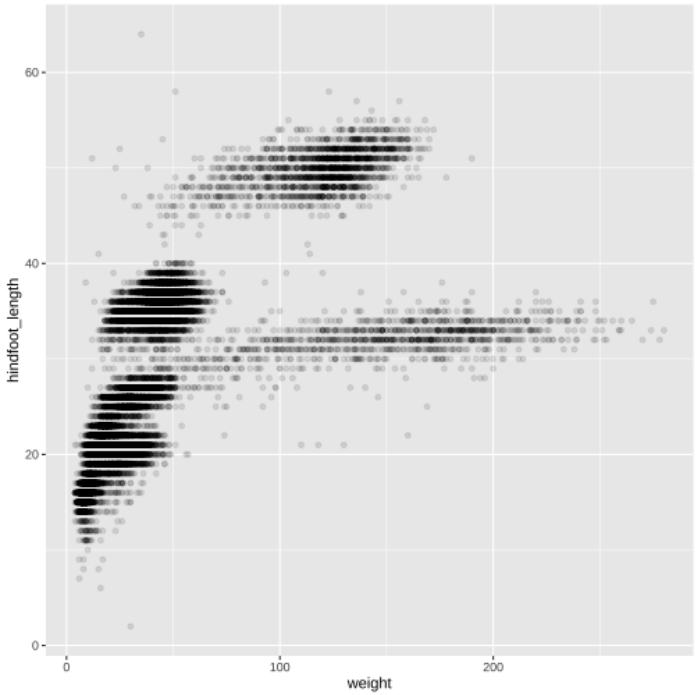
you can assign a plot to an object and build on it

```
weight_hind <- ggplot(data = surveys_complete,
                      mapping = aes(x = weight,
                                    y = hindfoot_length))
weight_hind +
    geom_point()
```



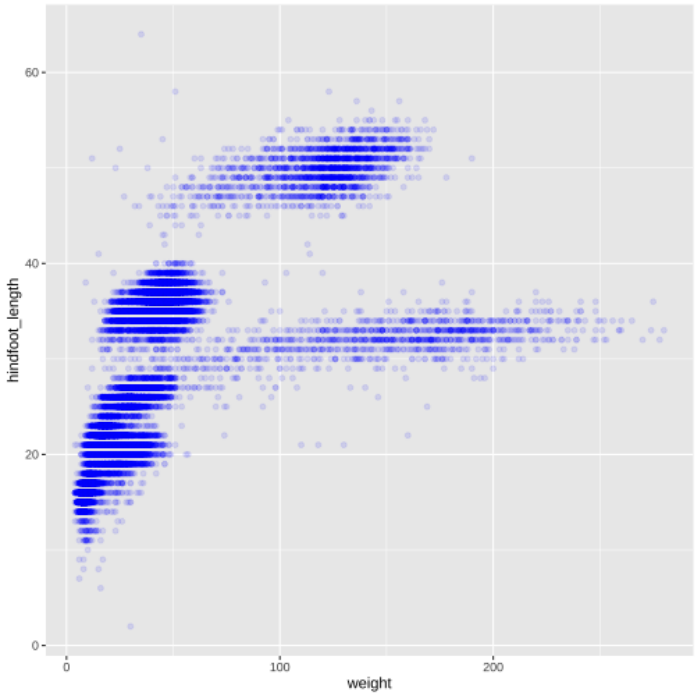
ggplot2 plots are built sequentially in layers

```
weight_hind +
    geom_point(alpha = 0.1) #transparency
```



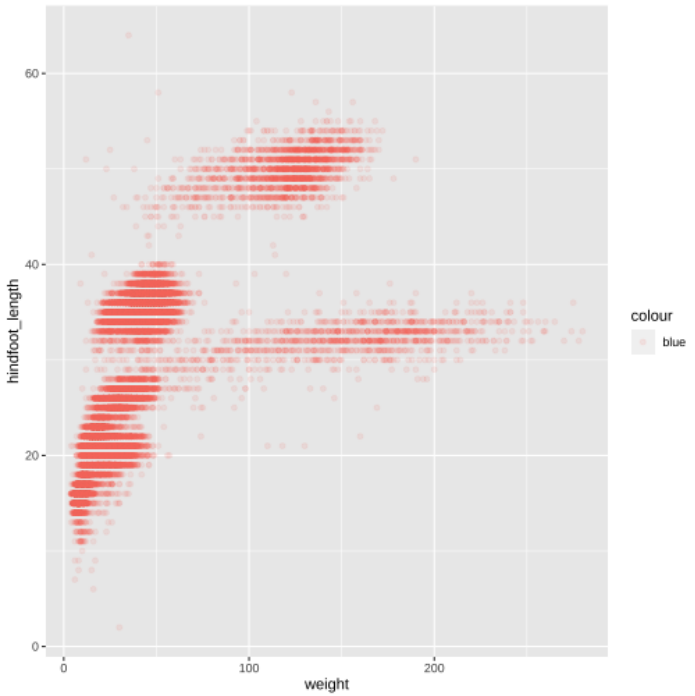
ggplot2 plots are built sequentially in layers

```
weight_hind +
    geom_point(alpha = 0.1, color = "blue") #color
```



ggplot2 plots are built sequentially in layers

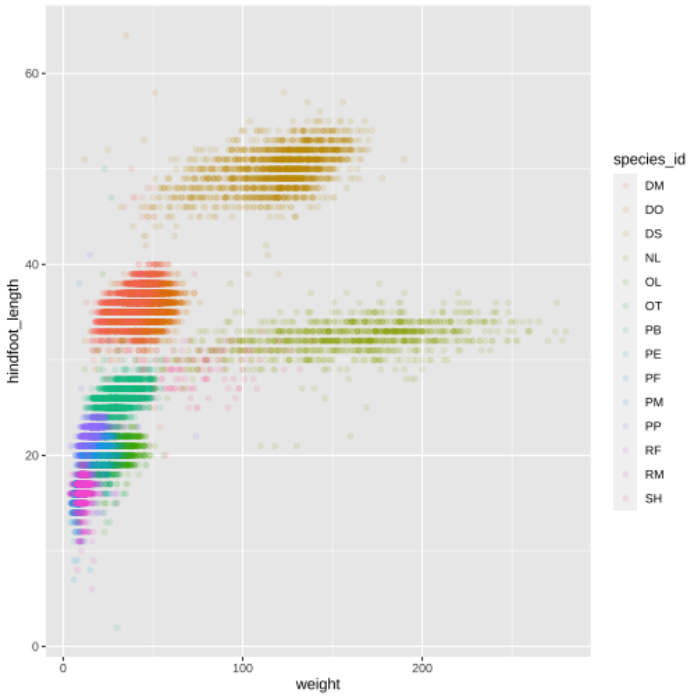
```
weight_hind +
    geom_point(alpha = 0.1, aes(color = "blue")) #this is a mistake!
```




```
#blue is not a variable so it should not go inside aes()
```

ggplot2 plots are built sequentially in layers

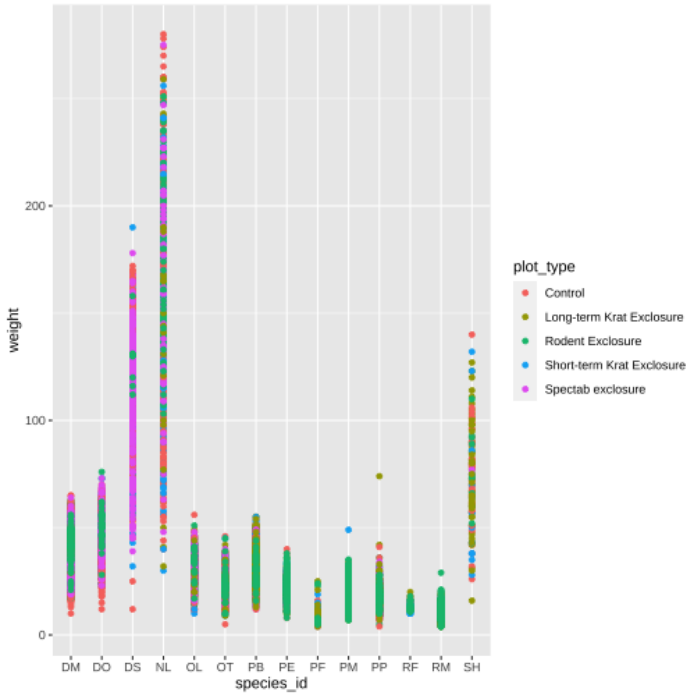
```
weight_hind +
    geom_point(alpha = 0.1, aes(color = species_id))
```




```
# but variables do go inside aes()
```

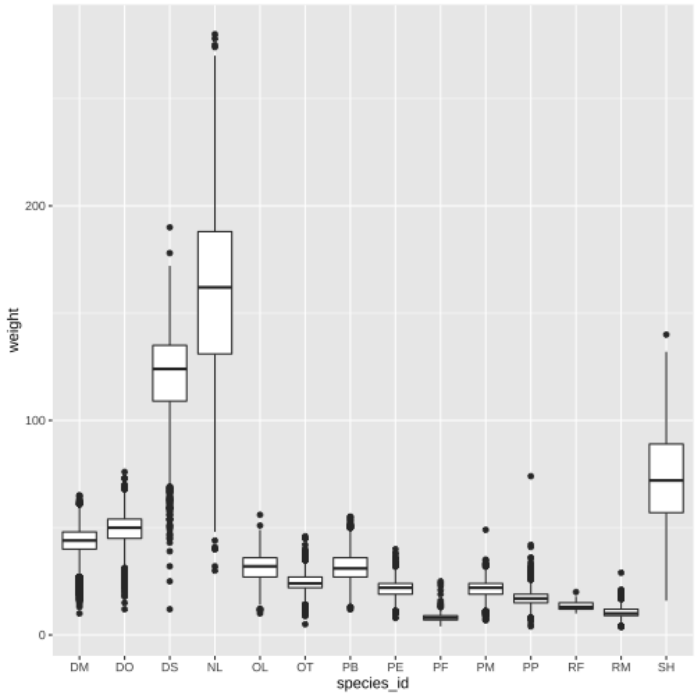
challenge: change x to categorial variable

```
ggplot(data = surveys_complete,
       mapping = aes(x = species_id, y = weight)) +
   geom_point(aes(color = plot_type))
```



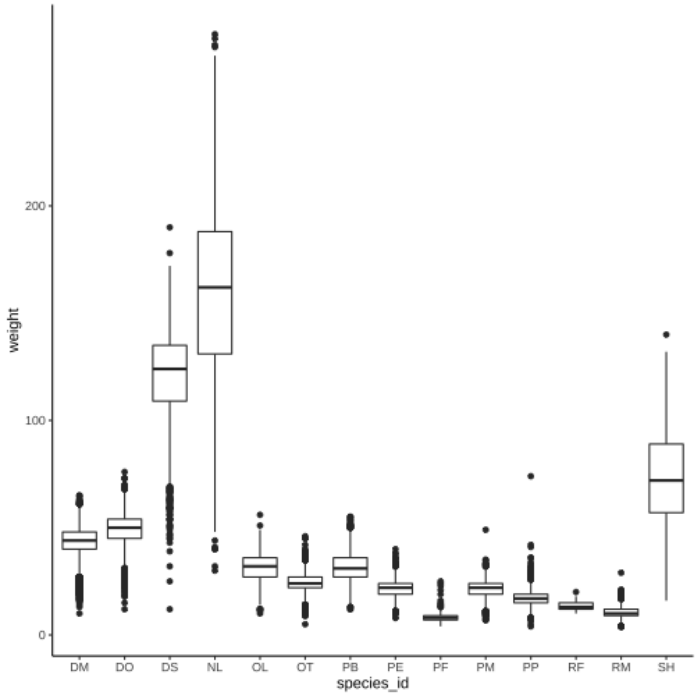
boxplots!

```
# boxplots
ggplot(data = surveys_complete,
       mapping = aes(x = species_id, y = weight)) +
   geom_boxplot()
```



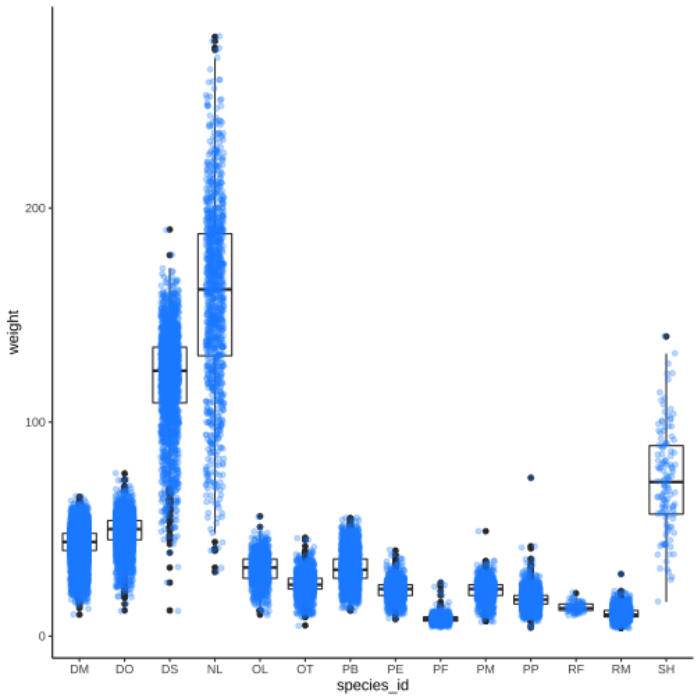
theme options theme_

```
ggplot(data = surveys_complete,
       mapping = aes(x = species_id, y = weight)) +
   geom_boxplot() +
  theme_classic()
```



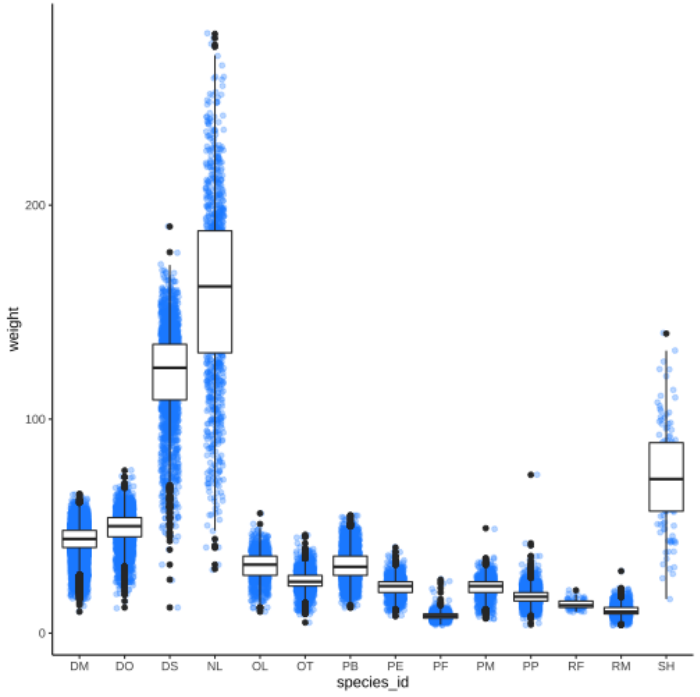
add jitter layer

```
ggplot(data = surveys_complete,
       mapping = aes(x = species_id, y = weight)) +
   geom_boxplot() +
  geom_jitter(alpha = 0.3, color = "dodgerblue", width = 0.2) +
  theme_classic()
```



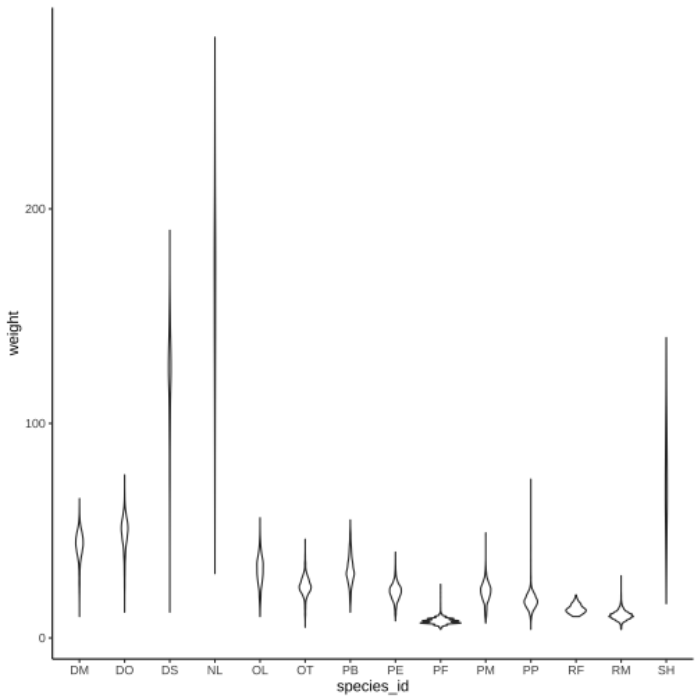
change plot order

```
ggplot(data = surveys_complete,
       mapping = aes(x = species_id, y = weight)) +
  geom_jitter(alpha = 0.3, color = "dodgerblue", width = 0.2) +
  geom_boxplot() +
  theme_classic()
```



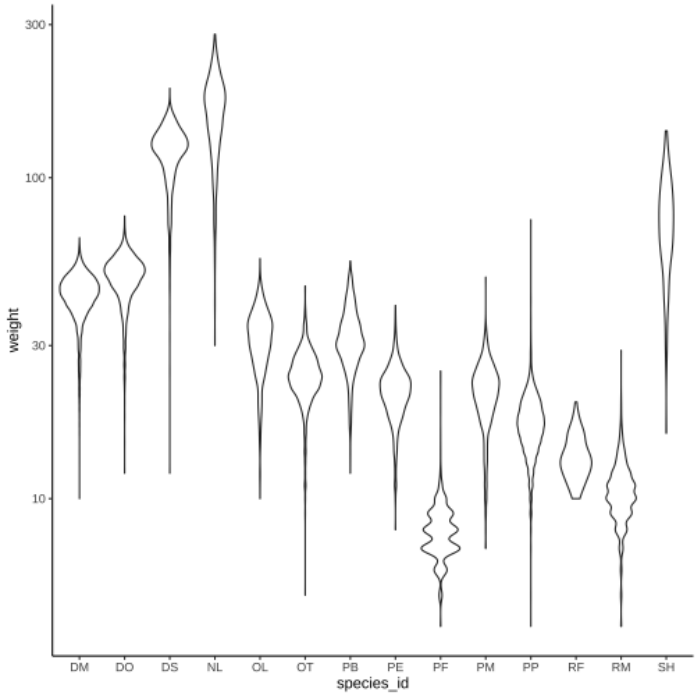
violin plots

```
ggplot(data = surveys_complete,
       mapping = aes(x = species_id, y = weight)) +
   geom_violin() + theme_classic()
```



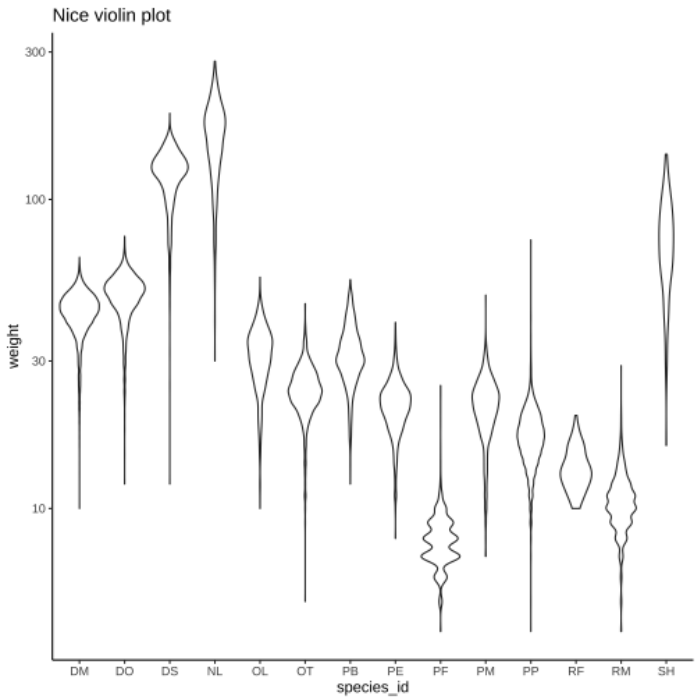
change scale (scale_xx options)

```
p <- ggplot(data = surveys_complete,
       mapping = aes(x = species_id, y = weight)) +
   geom_violin() + scale_y_log10() + theme_classic() #nice!
p
```



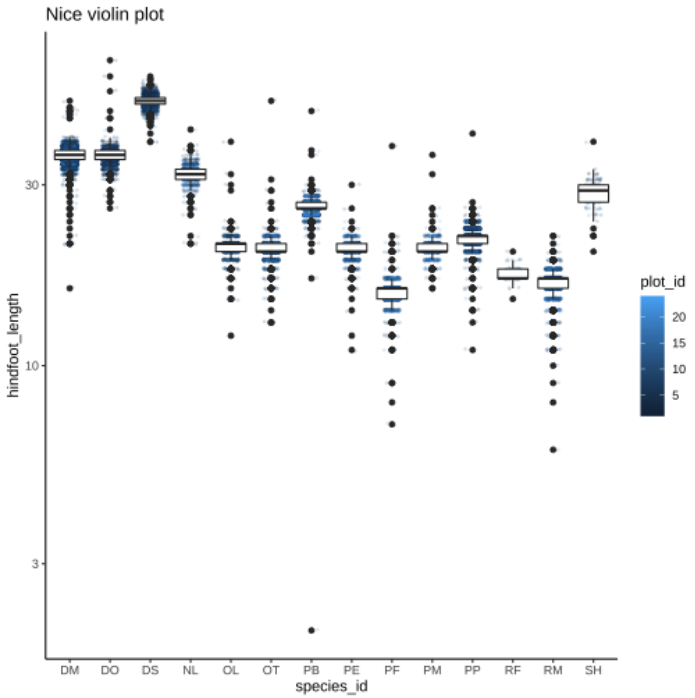
add title ggtitle()

```
p +  #remember the plot can be an object
  ggtitle("Nice violin plot")
```



ggplot2 plots are built sequentially in layers

```
ggplot(data = surveys_complete,
       mapping = aes(x = species_id, y = hindfoot_length)) +
   geom_jitter(size = 0.5, alpha = 0.1, width = 0.2, aes(col = plot_id)) +
   geom_boxplot() + scale_y_log10() + theme_classic() + ggtitle("Nice violin plot")
```



what would be next?

- learn to write **functions** for your own workflow and other programming tools to **iterate** these functions accross many inputs (loops and the **purrr** package)
- study R-specific literature such as R4DS and Advanced R
- study specific packages in your area, read their vignettes and documentation, get acquainted with the workflows
- learn tools for **communicating** your results (text, presentations, dashboards): markdown & R markdown, **xaringan** (presentations)
- learn about version control (**git**) to backup and control changes for your projects

references

- R for data science
- Reproducible workflows
- https://github.com/gadenbuie/tidyexplain