STAT2430: Assignment 1

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Look at the data

Here is a condensed overview of the `penguins` data

```
str(penguins)
```

```
## tibble [344 x 8] (S3: tbl_df/tbl/data.frame)
##  $ species          : Factor w/ 3 levels "Adelie","Chinstrap",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ island           : Factor w/ 3 levels "Biscoe","Dream",..: 3 3 3 3 3 3 3 3 3 3 ...
##  $ bill_length_mm   : num [1:344] 39.1 39.5 40.3 NA 36.7 39.3 38.9 39.2 34.1 42 ...
##  $ bill_depth_mm    : num [1:344] 18.7 17.4 18 NA 19.3 20.6 17.8 19.6 18.1 20.2 ...
##  $ flipper_length_mm: int [1:344] 181 186 195 NA 193 190 181 195 193 190 ...
##  $ body_mass_g      : int [1:344] 3750 3800 3250 NA 3450 3650 3625 4675 3475 4250 ...
##  $ sex              : Factor w/ 2 levels "female","male": 2 1 1 NA 1 2 1 2 NA NA ...
##  $ year             : int [1:344] 2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 ...
```

and an overview of the `penguins_raw` supplementary data.

```
str(penguins_raw)
```

```
## tibble [344 x 17] (S3: tbl_df/tbl/data.frame)
##  $ studyName          : chr [1:344] "PAL0708" "PAL0708" "PAL0708" "PAL0708" ...
##  $ Sample Number      : num [1:344] 1 2 3 4 5 6 7 8 9 10 ...
##  $ Species            : chr [1:344] "Adelie Penguin (Pygoscelis adeliae)" "Adelie Penguin (Pygoscelis
##  $ Region             : chr [1:344] "Anvers" "Anvers" "Anvers" "Anvers" ...
##  $ Island             : chr [1:344] "Torgersen" "Torgersen" "Torgersen" "Torgersen" ...
##  $ Stage              : chr [1:344] "Adult, 1 Egg Stage" "Adult, 1 Egg Stage" "Adult, 1 Egg Stage" "A
##  $ Individual ID      : chr [1:344] "N1A1" "N1A2" "N2A1" "N2A2" ...
##  $ Clutch Completion  : chr [1:344] "Yes" "Yes" "Yes" "Yes" ...
##  $ Date Egg           : Date[1:344], format: "2007-11-11" "2007-11-11" ...
##  $ Culmen Length (mm) : num [1:344] 39.1 39.5 40.3 NA 36.7 39.3 38.9 39.2 34.1 42 ...
##  $ Culmen Depth (mm)  : num [1:344] 18.7 17.4 18 NA 19.3 20.6 17.8 19.6 18.1 20.2 ...
##  $ Flipper Length (mm): num [1:344] 181 186 195 NA 193 190 181 195 193 190 ...
##  $ Body Mass (g)      : num [1:344] 3750 3800 3250 NA 3450 ...
##  $ Sex                : chr [1:344] "MALE" "FEMALE" "FEMALE" NA ...
##  $ Delta 15 N (o/oo)  : num [1:344] NA 8.95 8.37 NA 8.77 ...
##  $ Delta 13 C (o/oo)  : num [1:344] NA -24.7 -25.3 NA -25.3 ...
##  $ Comments           : chr [1:344] "Not enough blood for isotopes." NA NA "Adult not sampled." ...
##  - attr(*, "spec")=
##   .. cols(
##   ..   studyName = col_character(),
##   ..   `Sample Number` = col_double(),
##   ..   Species = col_character(),
##   ..   Region = col_character(),
##   ..   Island = col_character(),
```

```
##   ..   Stage = col_character(),
##   ..   `Individual ID` = col_character(),
##   ..   `Clutch Completion` = col_character(),
##   ..   `Date Egg` = col_date(format = ""),
##   ..   `Culmen Length (mm)` = col_double(),
##   ..   `Culmen Depth (mm)` = col_double(),
##   ..   `Flipper Length (mm)` = col_double(),
##   ..   `Body Mass (g)` = col_double(),
##   ..   Sex = col_character(),
##   ..   `Delta 15 N (o/oo)` = col_double(),
##   ..   `Delta 13 C (o/oo)` = col_double(),
##   ..   Comments = col_character()
##   .. )
```

We will use the penguins dataset.

New visualization

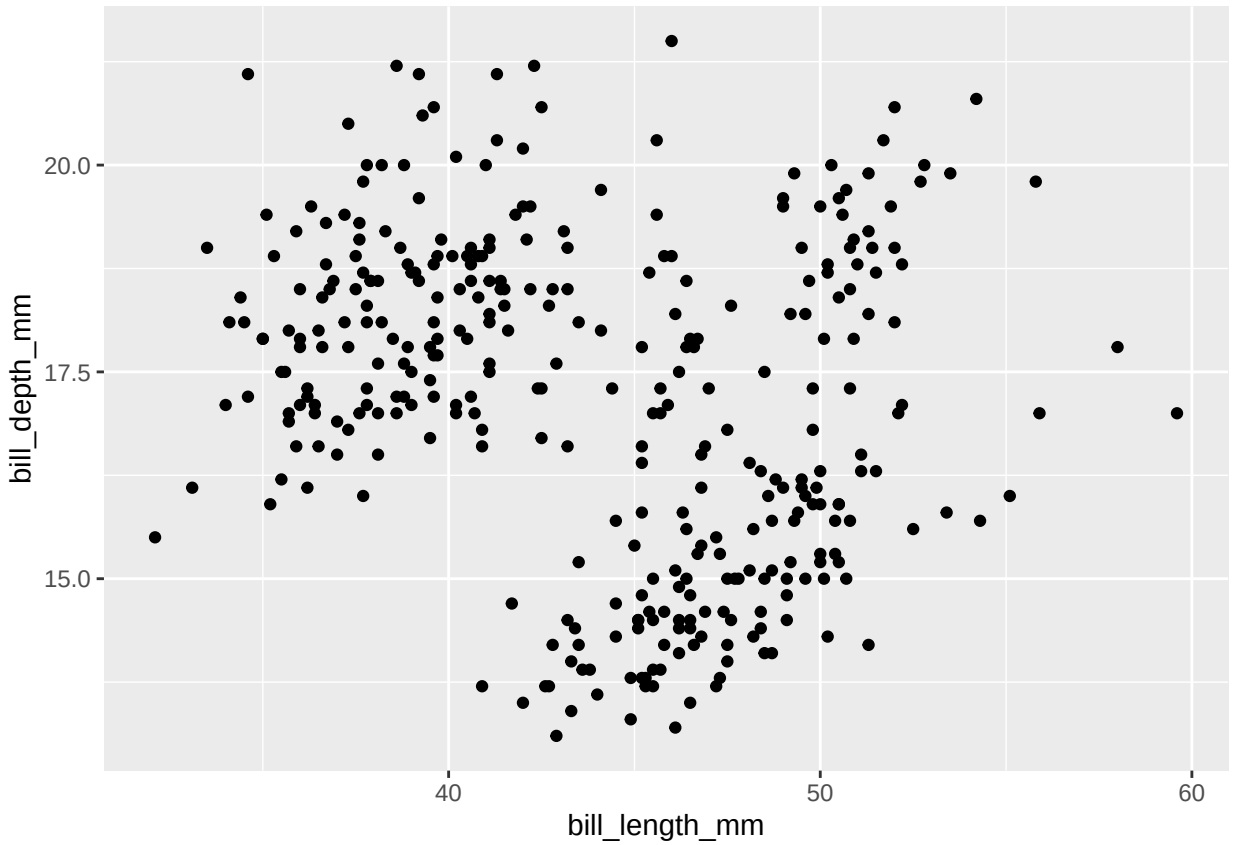
Step 1 (3 pts)

```
colnames(penguins)
```

```
## [1] "species"           "island"            "bill_length_mm"
## [4] "bill_depth_mm"     "flipper_length_mm" "body_mass_g"
## [7] "sex"               "year"
```

```
ggplot(data = penguins, aes(x = bill_length_mm, y = bill_depth_mm)) +
  geom_point()
```

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

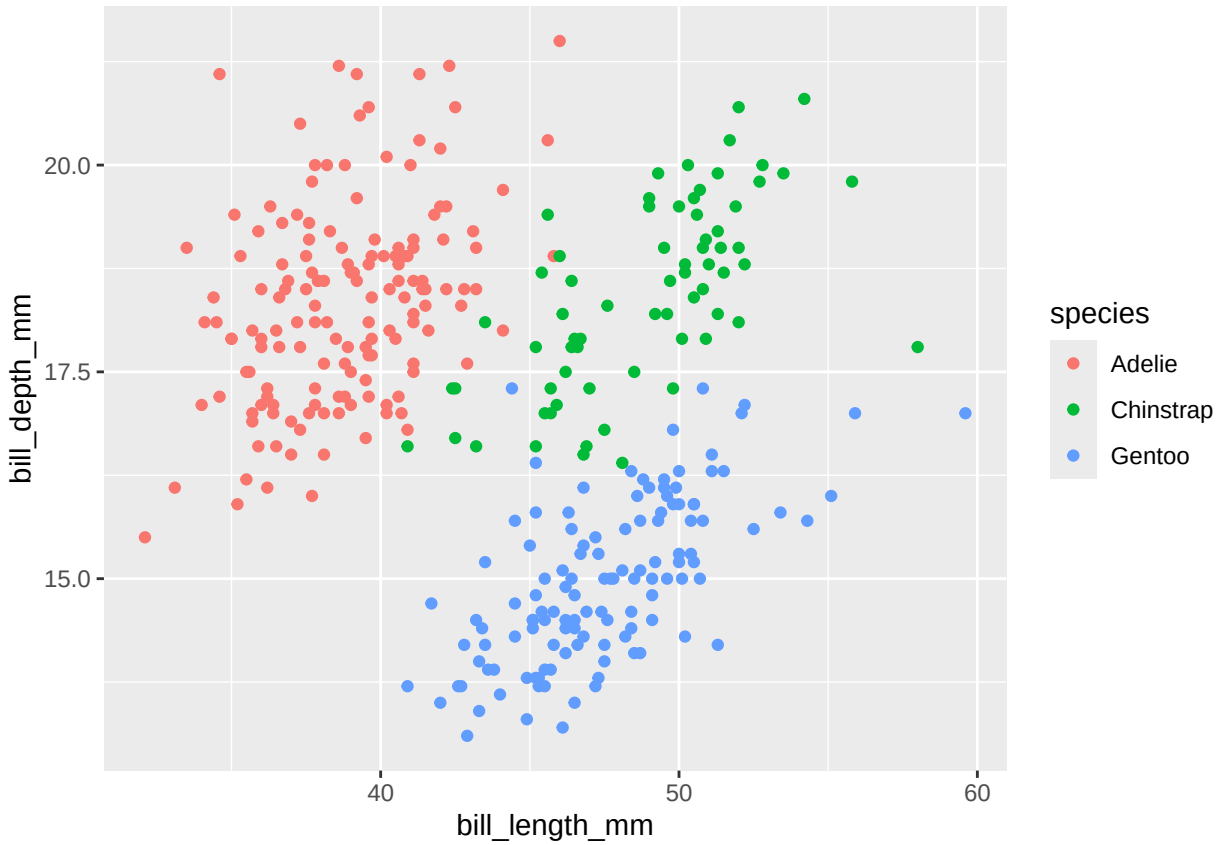


The scatter plot shows the distribution among different beak lengths and beak depths, but there is no direct grouping information.

Step 2 (2 pts)

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

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

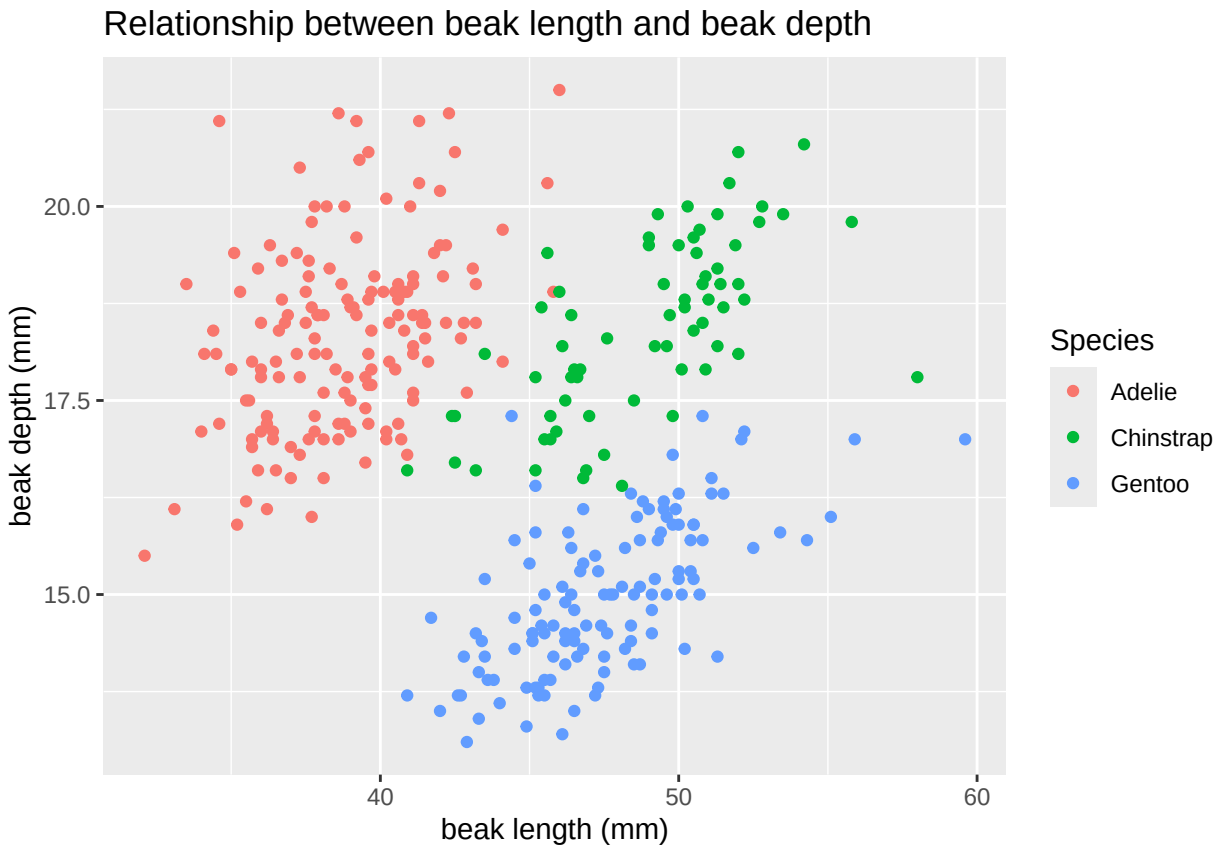


*After using color to distinguish species, differences in the distribution of beak length and beak depth between species can be observed.

Step 3 (2 pts)

```
ggplot(data = penguins, aes(x = bill_length_mm, y = bill_depth_mm, color = species)) +
  geom_point() +
  labs(
    title = "Relationship between beak length and beak depth",
    x = "beak length (mm)",
    y = "beak depth (mm)",
    color = "Species"
  )
```

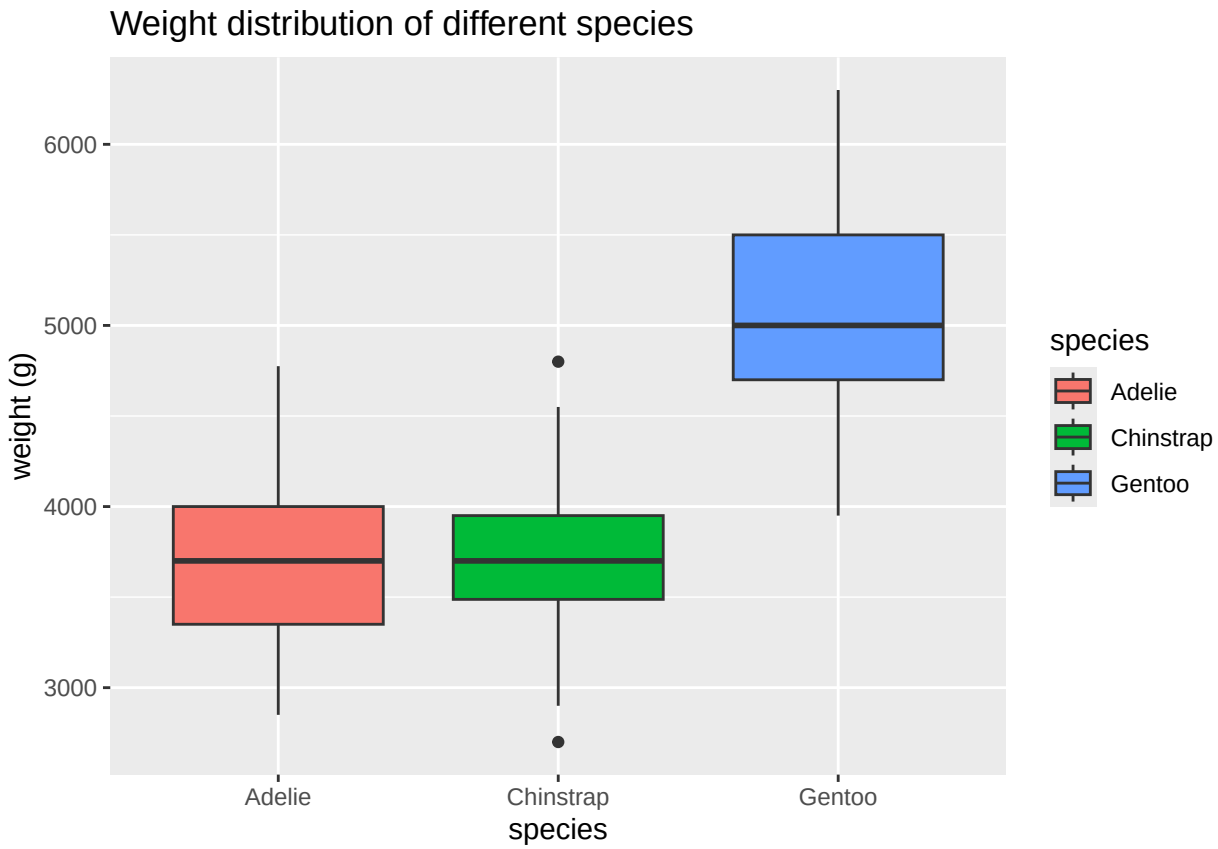
```
## Warning: Removed 2 rows containing missing values or values outside the scale range
## (`geom_point()`).
```



Another comparison

```
ggplot(data = penguins, aes(x = species, y = body_mass_g, fill = species)) +
  geom_boxplot() +
  labs(
    title = "Weight distribution of different species",
    x = "species",
    y = "weight (g)",
    fill = "species"
  )
```

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


Weight distribution of different species
6000
5000
4000
3000
weight (g)
Adelie
Chinstrap
Gentoo
species
species
Adelie
Chinstrap
Gentoo