Regression Modelling of infectious diseases

Subproject 2 goes here

Introduction

Data

I start it with the penguins dataset from @palmerpenguins package [@corsi2021]

```
Rows: 344
Columns: 8
$ species           <fct> Adelie, Adelie, Adelie, Adelie, Adelie, Adelie, Adel~
$ island            <fct> Torgersen, Torgersen, Torgersen, Torgersen, Torgerse~
$ bill_length_mm    <dbl> 39.1, 39.5, 40.3, NA, 36.7, 39.3, 38.9, 39.2, 34.1, ~
$ bill_depth_mm     <dbl> 18.7, 17.4, 18.0, NA, 19.3, 20.6, 17.8, 19.6, 18.1, ~
$ flipper_length_mm <int> 181, 186, 195, NA, 193, 190, 181, 195, 193, 190, 186~
$ body_mass_g       <int> 3750, 3800, 3250, NA, 3450, 3650, 3625, 4675, 3475, ~
$ sex               <fct> male, female, female, NA, female, male, female, male~
$ year              <int> 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007~
```

Species

Figure 1 is a scatter plot of species of penguins

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

```
  #scale_color_continuous()+
  labs(x= "Bill length (mm)", y="Bill depth (mm)")
```

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

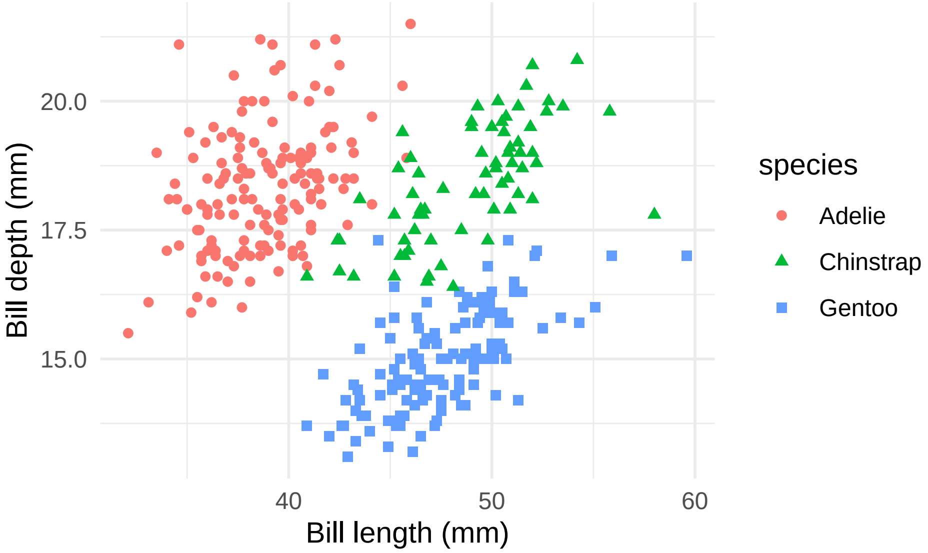

Figure 1: A scatter plot

Penguins

Table 1 below shows first 10 penguins from the dataset.

```
penguins |>
  slice_head(n=10) |>
  select(species, island, bill_length_mm, bill_depth_mm) |>
  gt()
```

Table 1: First 10 penguins

species	island	bill_length_mm	bill_depth_mm
Adelie	Torgersen	39.1	18.7
Adelie	Torgersen	39.5	17.4

Adelie	Torgersen	40.3	18.0
Adelie	Torgersen	NA	NA
Adelie	Torgersen	36.7	19.3
Adelie	Torgersen	39.3	20.6
Adelie	Torgersen	38.9	17.8
Adelie	Torgersen	39.2	19.6
Adelie	Torgersen	34.1	18.1
Adelie	Torgersen	42.0	20.2

Analysis

modelling

References