Hello, Penguins

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Introduction

I have been learning data science as a fellow of the Arewa Data Science Academy since January, 2023 and I have picked many skills. This is an attempt to practice quarto using the R programming language, in the RStudio IDE. I will work on the palmerpenguins dataset. Work in progress!

Data

For this analysis, we ’ll use the penguins dataset from the palmerpenguins package. (Gorman, Williams, and Fraser 2014)

Converting the dataset to a tibble for a more aesthetic display

```r
penguins <- as_tibble(penguins)
```

```r
glimpse(penguins)
```

```
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~
```

Getting summary statistics of the dataset using the summary function in base R

```
penguins %>% summary()
```

```
      species          island    bill_length_mm  bill_depth_mm  
 Adelie   :152   Biscoe   :168   Min.   :32.10   Min.   :13.10  
 Chinstrap: 68   Dream    :124   1st Qu.:39.23   1st Qu.:15.60  
 Gentoo   :124   Torgersen: 52   Median :44.45   Median :17.30  
                                 Mean   :43.92   Mean   :17.15  
                                 3rd Qu.:48.50   3rd Qu.:18.70  
                                 Max.   :59.60   Max.   :21.50  
                                 NA's   :2       NA's   :2      
 flipper_length_mm  body_mass_g       sex           year     
 Min.   :172.0     Min.   :2700   female:165   Min.   :2007  
 1st Qu.:190.0     1st Qu.:3550   male  :168   1st Qu.:2007  
 Median :197.0     Median :4050   NA's  : 11   Median :2008  
 Mean   :200.9     Mean   :4202                Mean   :2008  
 3rd Qu.:213.0     3rd Qu.:4750                3rd Qu.:2009  
 Max.   :231.0     Max.   :6300                Max.   :2009  
 NA's   :2         NA's   :2                                 
```

Exploring a bit more to see the initial few rows

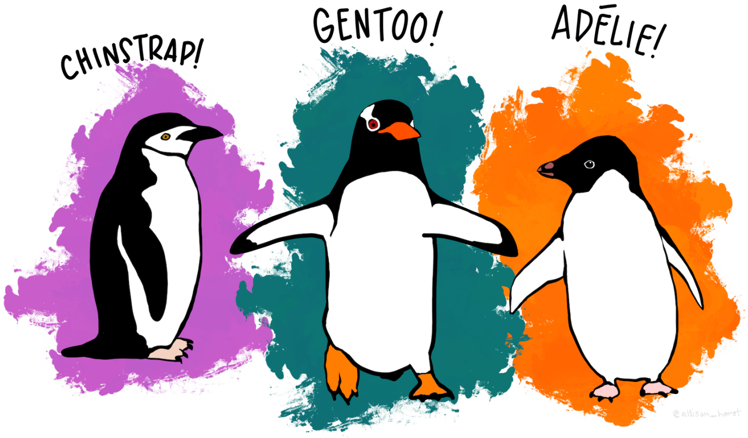
```
penguins %>%

  head()
```

```
# A tibble: 6 x 8
  species island    bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
  <fct>   <fct>              <dbl>         <dbl>             <int>       <int>
1 Adelie  Torgersen           39.1          18.7               181        3750
2 Adelie  Torgersen           39.5          17.4               186        3800
3 Adelie  Torgersen           40.3          18                 195        3250
4 Adelie  Torgersen           NA            NA                  NA          NA
5 Adelie  Torgersen           36.7          19.3               193        3450
6 Adelie  Torgersen           39.3          20.6               190        3650
# i 2 more variables: sex <fct>, year <int>
```

Meet Quarto

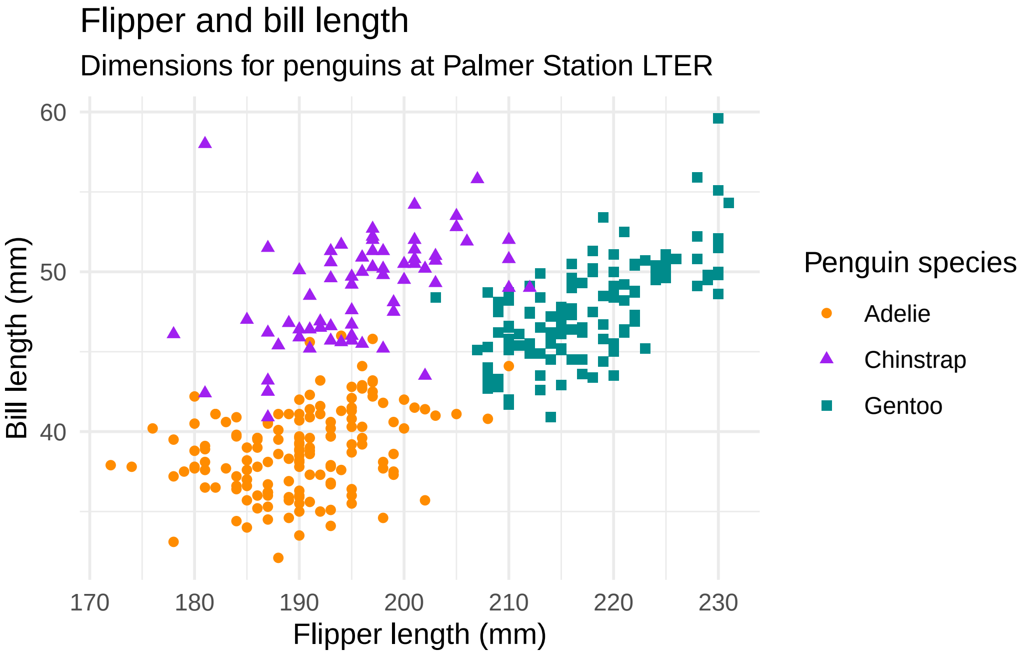
Quarto enables you to weave together content and executable code into a finished document. To learn more about Quarto see https://quarto.org.

Meet the penguins



The `penguins` data from the **palmerpenguins** package contains size measurements for 344 penguins from three species observed on three islands in the Palmer Archipelago, Antarctica.

The plot below shows the relationship between flipper and bill lengths of these penguins.



Species

Figure 1 is a scatter plot of species of penguins

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

```
Warning: Removed 2 rows containing missing values (`geom_point()`).
```

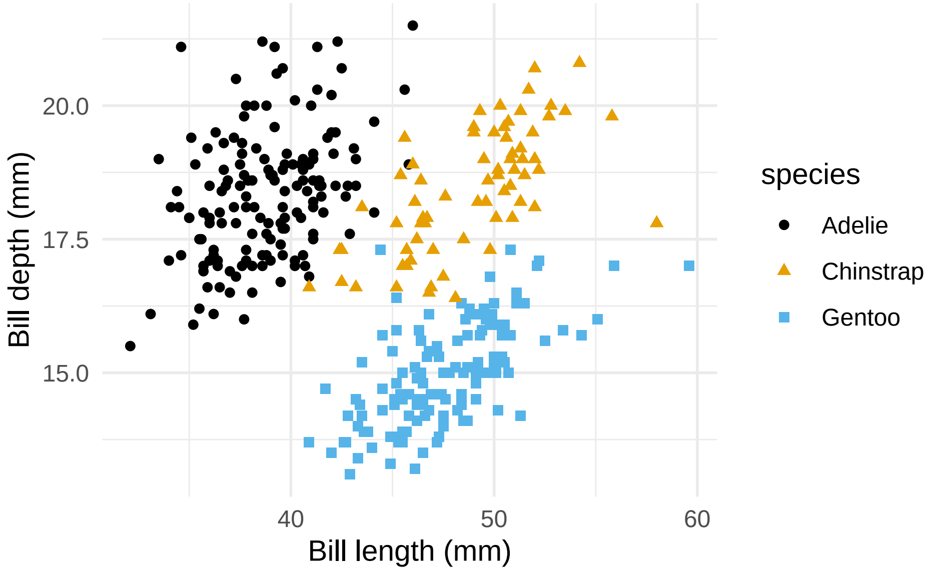


Figure 1: A scatterplot of penguin's bill depth and length, colored by species of penguins. output-location: slide

Penguins

Table 1 shows the first ten 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

Check for missing values

```
missing_values <- penguins %>%

  summarise(across(everything(), ~sum(is.na(.))))  # Calculate missing values for each var
cat("Missing values:\n")
```

```
Missing values:
```

```
print(missing_values)
```

```
# A tibble: 1 x 8
  species island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
    <int>  <int>          <int>         <int>             <int>       <int>
1       0      0              2             2                 2           2
# i 2 more variables: sex <int>, year <int>
```

Data Pre-processing

First we need to remove rows with missing values to enable easy and accurate modelling

```r
# Remove rows with missing values
penguins <- penguins %>%
  drop_na()
```

Modelling

We begin by splitting the data into training and testing sets

```r
# Split the data into training and testing sets

set.seed(123)  # For reproducibility

split <- initial_split(penguins, prop = 0.7)

train_data <- training(split)

test_data <- testing(split)
```

Then we build a simple linear regression model using tidymodels package

```r
# Build a simple model using tidymodels

model <- linear_reg() %>%

  set_engine("lm") %>%

  set_mode("regression")

model_fit <- model %>%

  fit(body_mass_g ~ bill_length_mm + bill_depth_mm, data = train_data)
```

Then, we evaluate the model, testing it on the test data

```r
# Model evaluation

train_predictions <- predict(model_fit, train_data) %>%

  bind_cols(train_data)
```

```
test_predictions <- predict(model_fit, test_data) %>%

  bind_cols(test_data)
```

We then calculate the evaluation for and testing data

```
# Calculate evaluation metrics for training data
train_metrics <- train_predictions %>%
  summarize(
    rmse = sqrt(mean((body_mass_g - .pred)^2)),
    r_squared = cor(body_mass_g, .pred)^2
  )

cat("Training metrics:\n")
```

```
Training metrics:
```

```
print(train_metrics)
```

```
# A tibble: 1 x 2
   rmse r_squared
  <dbl>     <dbl>
1  578.     0.488
```

```
# Calculate evaluation metrics for testing data
test_metrics <- test_predictions %>%
  summarize(
    rmse = sqrt(mean((body_mass_g - .pred)^2)),
    r_squared = cor(body_mass_g, .pred)^2
  )

cat("Testing metrics:\n")
```

```
Testing metrics:
```

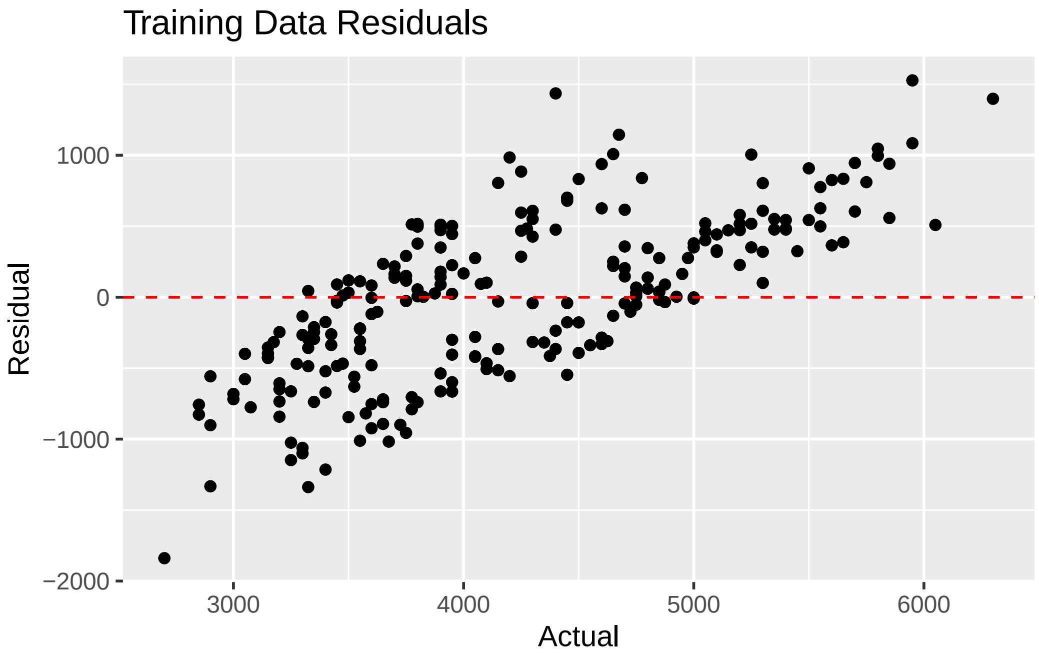
```
print(test_metrics)
```

```
# A tibble: 1 x 2
   rmse r_squared
  <dbl>     <dbl>
1  616.     0.411
```

Modelling Results

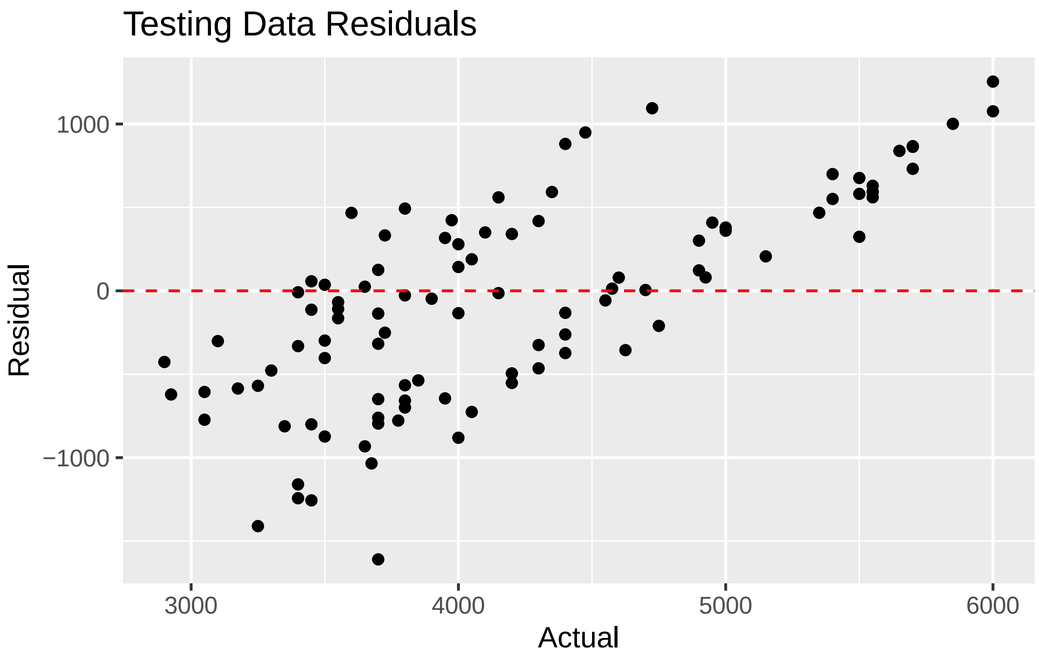
Here, I will show the plots for both the training and testing data

```
# Calculate residuals for training data
train_residuals <- train_predictions %>%
  mutate(residual = body_mass_g - .pred)

# Create a scatter plot for training data residuals
ggplot(train_residuals, aes(x = body_mass_g, y = residual)) +
  geom_point() +
  geom_hline(yintercept = 0, linetype = "dashed", color = "red") +
  labs(x = "Actual", y = "Residual", title = "Training Data Residuals")
```



For the testing data

```
# Calculate residuals for testing data
test_residuals <- test_predictions %>%
  mutate(residual = body_mass_g - .pred)

# Create a scatter plot for testing data residuals
ggplot(test_residuals, aes(x = body_mass_g, y = residual)) +
  geom_point() + geom_hline(yintercept = 0, linetype = "dashed", color = "red") + labs(x =
```



Work in progress.

References

Gorman, Kristen B., Tony D. Williams, and William R. Fraser. 2014. "Ecological Sexual Dimorphism and Environmental Variability Within a Community of Antarctic Penguins (Genus Pygoscelis)." Edited by André Chiaradia. *PLoS ONE* 9 (3): e90081. https://doi.org/10.1371/journal.pone.0090081.