

A1 Methods of Machine Learning

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Question 1: We then load the `penguins` dataset and Select only the columns containing the species, sex, body mass, flipper length and bill length. At the end we remove the rows with missing values in any of these columns.

```
## Warning: package 'palmerpenguins' was built under R version 4.1.3
```

```
##      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
```

```
## Warning: package 'tidyverse' was built under R version 4.1.3
```

```
## -- Attaching packages ----- tidyverse 1.3.2 --
## v ggplot2 3.4.0      v purrr  1.0.1
## v tibble  3.1.8      v dplyr  1.0.10
## v tidyr   1.3.0      v stringr 1.5.0
## v readr   2.1.3      v forcats 1.0.0
```

```
## Warning: package 'ggplot2' was built under R version 4.1.3
```

```
## Warning: package 'tibble' was built under R version 4.1.3
```

```
## Warning: package 'tidyr' was built under R version 4.1.3
```

```
## Warning: package 'readr' was built under R version 4.1.3
```

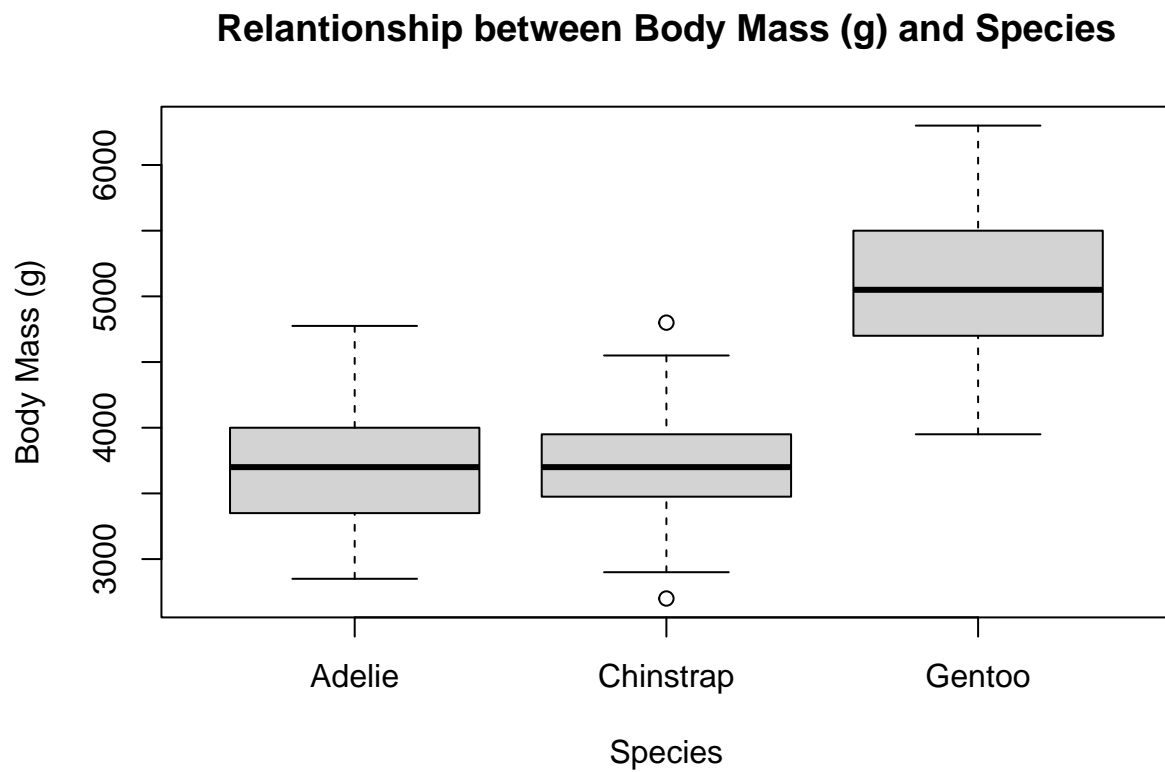
```
## Warning: package 'purrr' was built under R version 4.1.3
```

```
## Warning: package 'dplyr' was built under R version 4.1.3

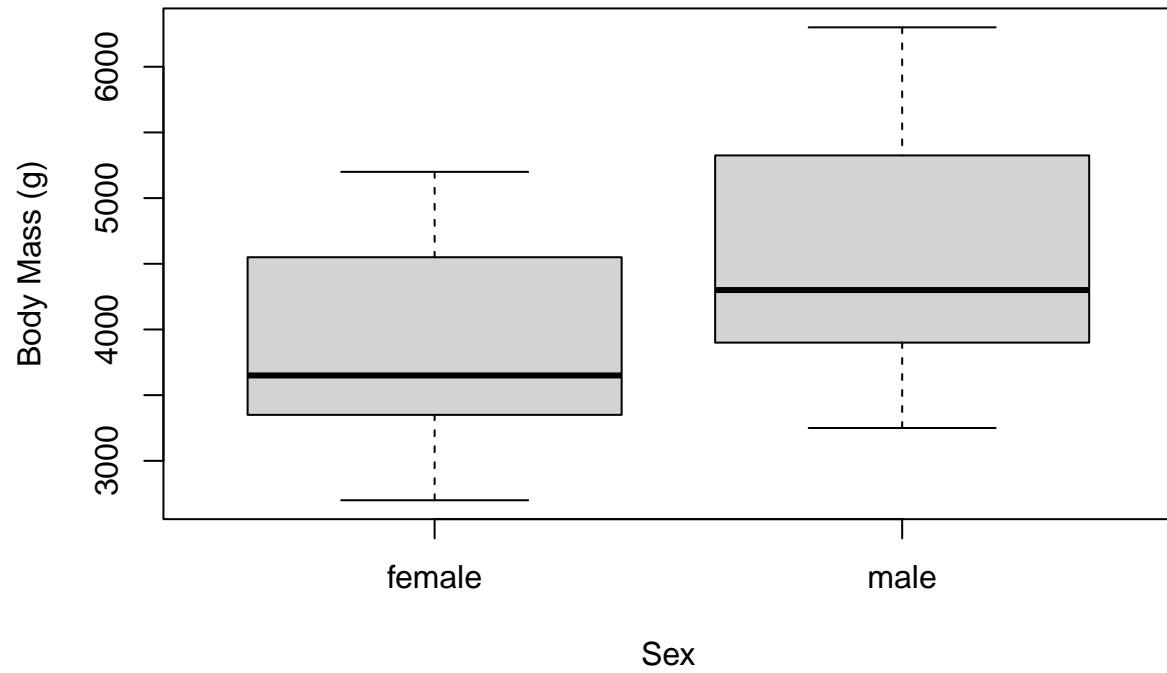
## Warning: package 'stringr' was built under R version 4.1.3

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
```

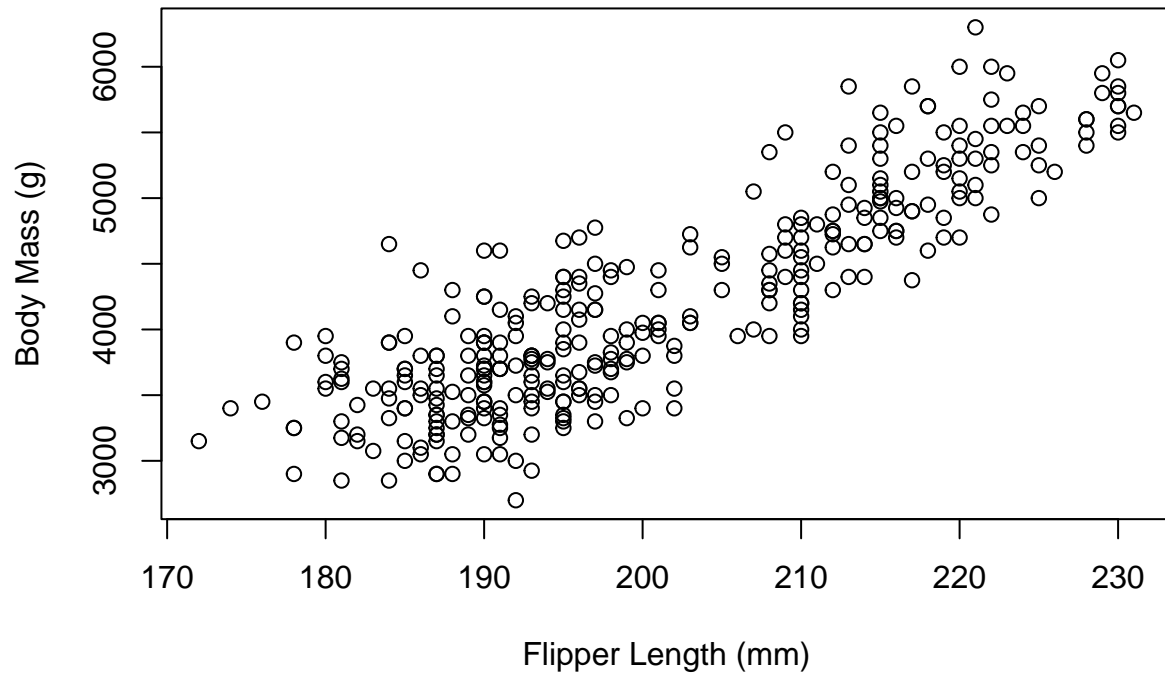
Now we create plots to visualize the relationship between body mass and the other 4 variables:



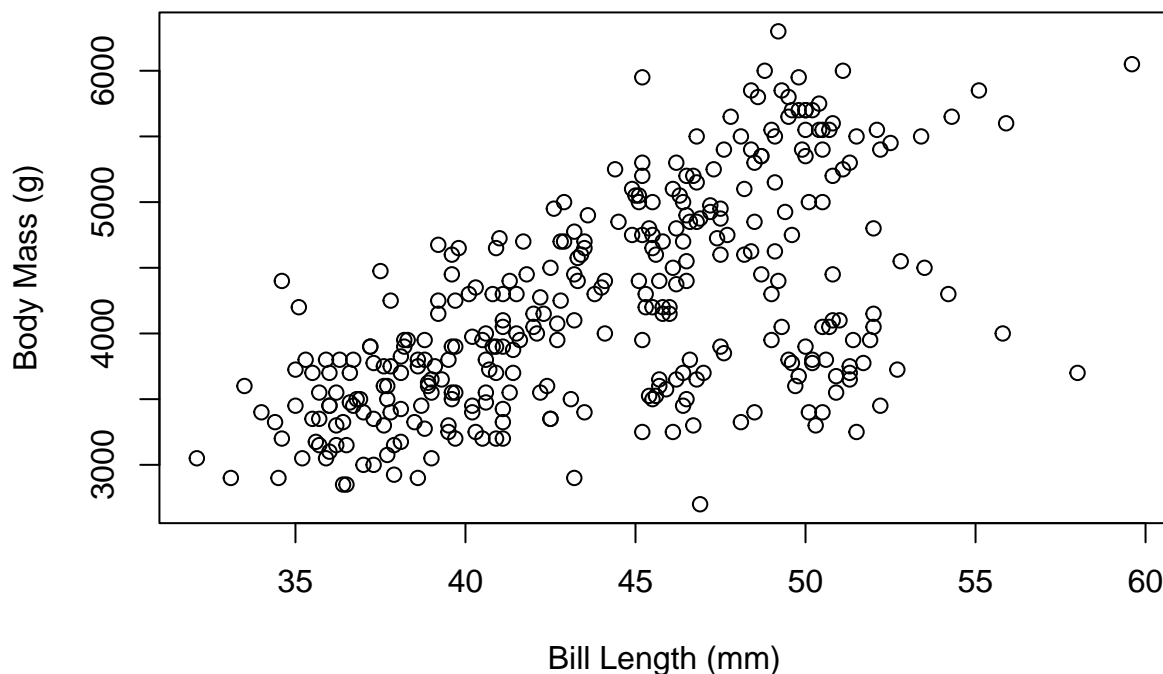
Relationship between Body Mass (g) and Sex



Relationship between Body Mass (g) and Flipper Length (mm)



Relationship between Body Mass (g) and Bill Length (mm)



Question 2

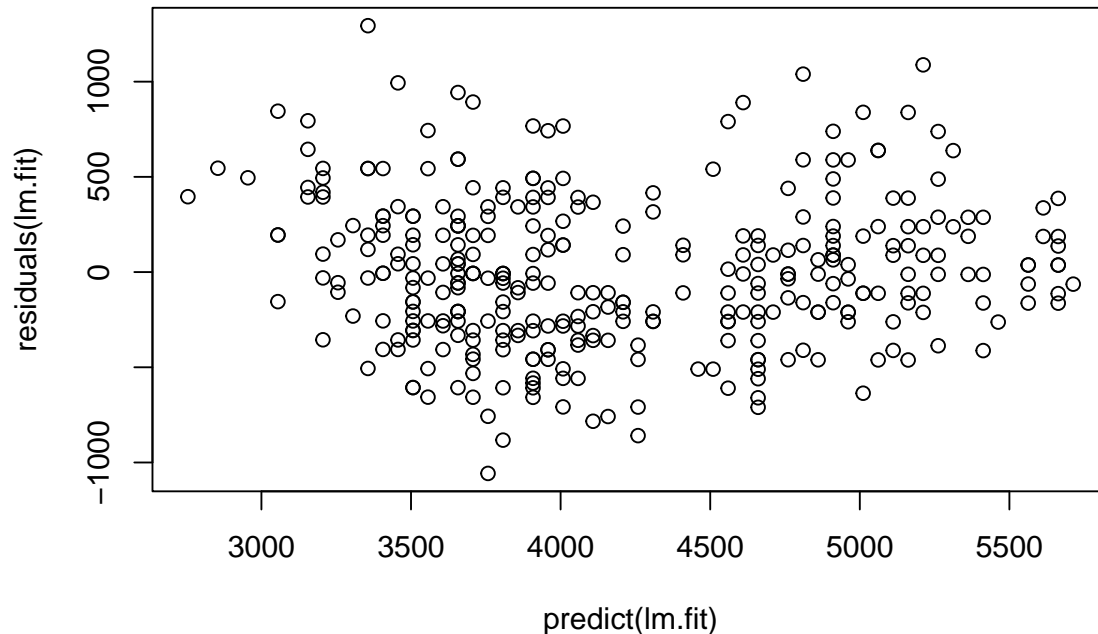
Performing a simple OLS linear regression of body mass (the response variable) on flipper length (the predictor), using all rows from the data.

```
##
## Call:
## lm(formula = body_mass_g ~ flipper_length_mm, data = df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1057.33  -259.79   -12.24    242.97   1293.89
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -5872.09     310.29  -18.93  <2e-16 ***
## flipper_length_mm    50.15       1.54   32.56  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 393.3 on 331 degrees of freedom
## Multiple R-squared:  0.7621, Adjusted R-squared:  0.7614
## F-statistic: 1060 on 1 and 331 DF, p-value: < 2.2e-16

## [1] -5872.093
```

A) Linear model obtained from OLS: $\text{body mass} = -5872.0927 + 50.1533 * (\text{flipper length})$.

The value for R^2 is $R^2 = 0.7620922$.



B)

This is a good model, residuals seem normally distributed around zero, with a mean and variance that is independent of the predicted value. Looking at the R^2 value it is a pretty high value.

Question 3

A) Do an OLS multiple linear regression of body mass on the four predictors: species, sex, flipper length and bill length. You may use any sensible encoding of your qualitative predictors. State the resulting linear model in the same form as in Question 2(A). Report R^2 and also the residual sum of squares (RSS), which is the same thing as the sum of squared errors (SSE).

```
##
## Call:
## lm(formula = body_mass_g ~ species + sex + flipper_length_mm +
##     bill_length_mm, data = df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -718.50 -201.60  -12.75   198.45   878.24
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -759.064    541.377  -1.402  0.161834
## speciesChinstrap -291.711     81.502  -3.579  0.000397 ***
## speciesGentoo    707.028     94.359   7.493  6.35e-13 ***
## sexmale         465.395     43.081  10.803 < 2e-16 ***
## flipper_length_mm  17.847       2.902   6.150  2.25e-09 ***
```

```
## bill_length_mm      21.633      7.148   3.027 0.002670 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 292 on 327 degrees of freedom
## Multiple R-squared:  0.8705, Adjusted R-squared:  0.8685
## F-statistic: 439.7 on 5 and 327 DF,  p-value: < 2.2e-16
```

```
## Warning: package 'fastDummies' was built under R version 4.1.3
```

```
## # A tibble: 333 x 8
##   bill_length_mm flipper_leng~1 body_~2 speci~3 speci~4 speci~5 sex_f~6 sex_m~7
##         <dbl>         <int>   <int>   <int>   <int>   <int>   <int>   <int>
## 1          39.1           181   3750       1       0       0       0       1
## 2          39.5           186   3800       1       0       0       1       0
## 3          40.3           195   3250       1       0       0       1       0
## 4          36.7           193   3450       1       0       0       1       0
## 5          39.3           190   3650       1       0       0       0       1
## 6          38.9           181   3625       1       0       0       1       0
## 7          39.2           195   4675       1       0       0       0       1
## 8          41.1           182   3200       1       0       0       1       0
## 9          38.6           191   3800       1       0       0       0       1
## 10         34.6           198   4400       1       0       0       0       1
## # ... with 323 more rows, and abbreviated variable names 1: flipper_length_mm,
## # 2: body_mass_g, 3: species_Adelie, 4: species_Chinstrap, 5: species_Gentoo,
## # 6: sex_female, 7: sex_male
```

Linear model obtained from OLS multiple linear regression: body mass = $-759.0644 + -291.7106 * (\text{species}) + 707.028 * (\text{sex}) + 465.395 * (\text{flipper length}) + 17.8465 * (\text{bill length})$.

The value for R^2 is $R^2 = 0.8705155$.

The value for the Residual Sum of Squares(RSS) is $\text{RSS} = 2.7872792 \times 10^7$.

B)

```
##
## Call:
## lm(formula = body_mass_g ~ species_Chinstrap + species_Gentoo +
##     sex_male + flipper_length_mm + bill_length_mm, data = penguins_dummy)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -718.50 -201.60  -12.75   198.45   878.24
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -759.064    541.377  -1.402  0.161834
## species_Chinstrap -291.711    81.502  -3.579  0.000397 ***
## species_Gentoo    707.028    94.359   7.493 6.35e-13 ***
## sex_male        465.395    43.081  10.803 < 2e-16 ***
## flipper_length_mm  17.847     2.902   6.150 2.25e-09 ***
## bill_length_mm   21.633     7.148   3.027 0.002670 **
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 292 on 327 degrees of freedom
## Multiple R-squared:  0.8705, Adjusted R-squared:  0.8685
## F-statistic: 439.7 on 5 and 327 DF,  p-value: < 2.2e-16
```

```
dfz = as.data.frame(scale(penguins_dummy))
lm4.fit = lm(body_mass_g ~ species_Chinstrap + species_Gentoo + sex_male + flipper_length_mm + bill_length_mm, data = dfz)
summary(lm4.fit)
```

```
##
## Call:
## lm(formula = body_mass_g ~ species_Chinstrap + species_Gentoo +
##     sex_male + flipper_length_mm + bill_length_mm, data = dfz)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.89231 -0.25037 -0.01584  0.24646  1.09069
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -4.946e-16  1.987e-02   0.000 1.000000
## species_Chinstrap -1.463e-01  4.086e-02  -3.579 0.000397 ***
## species_Gentoo    4.214e-01  5.624e-02   7.493 6.35e-13 ***
## sex_male         2.894e-01  2.679e-02  10.803 < 2e-16 ***
## flipper_length_mm 3.106e-01  5.051e-02   6.150 2.25e-09 ***
## bill_length_mm    1.469e-01  4.854e-02   3.027 0.002670 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3626 on 327 degrees of freedom
## Multiple R-squared:  0.8705, Adjusted R-squared:  0.8685
## F-statistic: 439.7 on 5 and 327 DF,  p-value: < 2.2e-16
```

After standardizing the variables, we can see the coefficients of speciesGentoo has the largest absolute value(4.214e_01) so it has the strongest value on the prediction of the variable of body mass.

Question 4

A)

```
SSE <- function(ypred,ytrue)
{
  sum=0
  for(x in 1:length(ypred)){
    ss = (ypred[x] - ytrue[x])**2
    sum = sum + ss
  }
  return(sum)
}
```

B)


```
##
## Call:
## lm(formula = body_mass_g ~ flipper_length_mm, data = train)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -885.93 -247.61  -32.89   265.04 1056.83
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -5667.743     458.518  -12.36  <2e-16 ***
## flipper_length_mm    49.112       2.295   21.40  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 385.7 on 164 degrees of freedom
## Multiple R-squared:  0.7363, Adjusted R-squared:  0.7347
## F-statistic:  458 on 1 and 164 DF,  p-value: < 2.2e-16
```

The values for SSE_Training and SSE_Test are : SEE_Training = 2.4398752×10^7 and SEE_Test = 2.6891724×10^7

C)

The values for SSE_Training and SSE_Test are : SEE_Training = 1.2169172×10^7 and SEE_Test = 1.5841883×10^7

D)

Method	Training SSE	Test SSE
Simple Linear (flipper only)	2.4398752×10^7	2.6891724×10^7
Multiple Linear	1.2169172×10^7	1.5841883×10^7