

EDA

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2023-09-13

Introduction

“Crab age prediction” is a kaggle dataset (<https://www.kaggle.com/datasets/sidhus/crab-age-prediction>) with the physical properties and age of crabs farmed around Boston area. Crab is a food eaten and imported in many countries. Crab farming has low labor costs, production cost is comparatively lower and crabs grow fast. By knowing the right time to harvest crabs, when they mostly stop growing, profits can be maximized. This exploratory data analysis is to find connections between the different physical properties and the age of crabs.

First look and preparation

The data set contains the data of 3893 crabs, with data in 9 categories. The 9 categories data was collected in are, this will later be added to a codebook:

- Sex (gender of the crab)
- Length (length of the crab in feet)
- Diameter (diameter of the crab in feet)
- Height (height of the crab in feet)
- Weight (weight of the crab in ounces)
- Shucked weight (weight of the crab without the shell in ounces)
- Viscera weight (weight that wraps around your abdominal organs deep inside body in ounces)
- Shell weight (weight of the shell in ounces)
- Age (age of the crab in months)

When importing the data set we can check if everything is as expected with a quick summary.

```
crab_data <- read.csv("CrabAgePrediction.csv")
summary(crab_data)
```

```
##      Sex          Length        Diameter       Height
##  Length:3893     Min.   :0.1875     Min.   :0.1375     Min.   :0.0000
##  Class :character 1st Qu.:1.1250    1st Qu.:0.8750    1st Qu.:0.2875
##  Mode  :character Median :1.3625    Median :1.0625    Median :0.3625
##                      Mean   :1.3113    Mean   :1.0209    Mean   :0.3494
##                      3rd Qu.:1.5375    3rd Qu.:1.2000    3rd Qu.:0.4125
##                      Max.  :2.0375    Max.  :1.6250    Max.  :2.8250
##      Weight        Shucked.Weight  Viscera.Weight  Shell.Weight
##  Min.   : 0.0567   Min.   : 0.02835   Min.   : 0.01418   Min.   : 0.04252
##  1st Qu.:12.6722  1st Qu.: 5.34388  1st Qu.: 2.66485  1st Qu.: 3.71378
##  Median :22.7930  Median : 9.53961  Median : 4.86194  Median : 6.66213
```

```

##   Mean    :23.5673  Mean    :10.20734  Mean    : 5.13655  Mean    : 6.79584
## 3rd Qu.:32.7862  3rd Qu.:14.27397  3rd Qu.: 7.20077  3rd Qu.: 9.35534
## Max.   :80.1015  Max.   :42.18406  Max.   :21.54562  Max.   :28.49125
##          Age
##  Min.   : 1.000
##  1st Qu.: 8.000
##  Median :10.000
##  Mean   : 9.955
##  3rd Qu.:11.000
##  Max.   :29.000

```

A quick summary shows that there are indeed 9 categories collected for 3893 entries. It also gives a first insight into the distribution of the data. The age of the crabs goes from 1 month to 29 months with a mean of 9.955 which suggest that most crabs are young compared to the oldest entry. A deeper exploration of the distribution will be done later. First there will be a check for missing data also in the form of zeros and a conversion to centimeters and grams.

```
colSums(is.na(crab_data))
```

	Sex	Length	Diameter	Height	Weight
##	0	0	0	0	0
##	Shucked.Weight	Viscera.Weight	Shell.Weight	Age	
##	0	0	0	0	

```
colSums(crab_data == 0)
```

	Sex	Length	Diameter	Height	Weight
##	0	0	0	2	0
##	Shucked.Weight	Viscera.Weight	Shell.Weight	Age	
##	0	0	0	0	

A sum of the NA values shows that there are no missing value which means the data set is complete for all categories. The zero value sum shows that there are 2 crabs with the height of 0 which is impossible, especially considering that they do have a length and weight. Since this are only 2 entries in a dataset with 3893 datapoints and they can't be accurate we will remove them.

```
crab_data = subset(crab_data, crab_data$Height != 0)
nrow(crab_data)
```

```
## [1] 3891
```

A quick nrow count shows that the two zero height value rows have been successfully removed.

The next step is conversion to centimeters and grams since that are the conventional metrics in the Netherlands where this EDA is conducted.

1 foot equals 30.48 centimeters and 1 ounces equals 28.3495231 grams, this can then be applied to the correct categories with simple indexing and concatenation.

```
crab_data[,c("Length", "Diameter", "Height")] <- crab_data[,c("Length", "Diameter", "Height")] * 30.48
crab_data[,c("Weight", "Shucked.Weight", "Viscera.Weight", "Shell.Weight")] <- crab_data[,c("Weight", "Shucked.Weight", "Viscera.Weight", "Shell.Weight")] * 28.3495231
```

To check if the conversion worked the head is looked at.

```

head(crab_data)

##   Sex Length Diameter Height    Weight Shucked.Weight Viscera.Weight
## 1   F  43.815    35.814 12.573 698.4108      349.60724     158.32788
## 2   M  27.051    19.812   6.477 153.1039       65.09928      38.97920
## 3   I  31.623    23.622   7.620 225.4364      91.62121      45.40876
## 4   F  35.814    27.051   7.620 382.1569     134.61888      64.69743
## 5   I  27.051    20.193   6.477 195.6997      98.05077      42.19398
## 6   F  47.244    35.433  10.668 812.5354     384.96981     191.68121
##   Shell.Weight Age
## 1     191.27936  9
## 2      44.20321  6
## 3     78.36024  6
## 4    148.68354 10
## 5     48.22169  6
## 6    204.94218  8

```

The values in the desired columns have changed so the conversions seem to have worked.

The next step is to make a codebook for readability and easy labeling. The codebook is made by using the colnames of the crab_data dataframe as the attributes and manually adding the units and descriptions to it.

```

codebook <- list("Attribute" = c(colnames(crab_data)),
                 "Units" = c("-", "cm", "cm", "cm", "gram",
                            "gram", "gram", "gram", "months"),
                 "Description" =
                   c("Gender of the crab,
                     female(F) male(M) or interderminate(I)",
                     "Length of the crab in centimeters",
                     "Diameter of the crab in centimeters",
                     "Height of the crab in centimeters",
                     "Weight of the crab in grams",
                     "Weight without the shell in grams",
                     "Weight that wraps around your abdominal
                     organs deep inside body in grams",
                     "Weight of the shell in grams",
                     "Age of the crab in months"))

codebook_df <- as.data.frame(codebook)

knitr::kable(codebook_df, format = "latex")

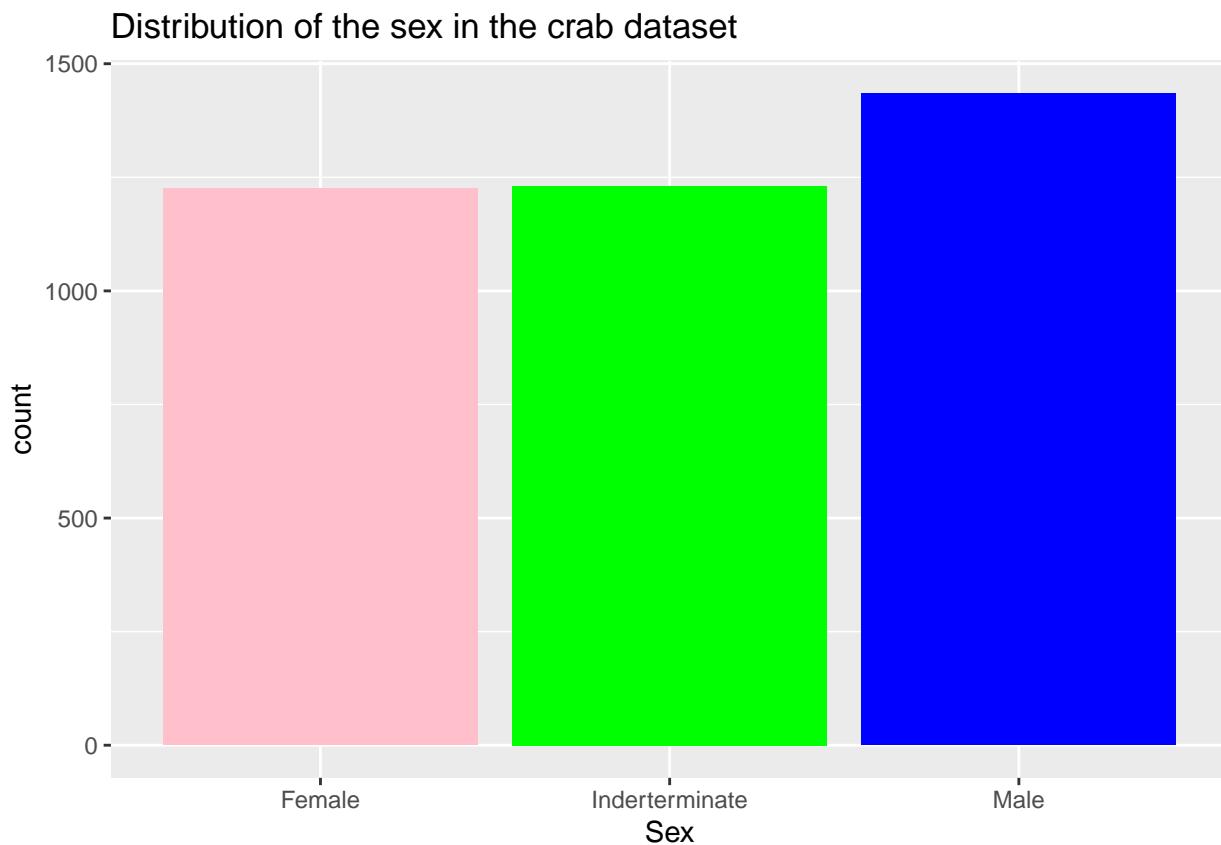
```

Attribute	Units	Description
Sex	-	Gender of the crab, female(F) male(M) or interderminate(I)
Length	cm	Length of the crab in centimeters
Diameter	cm	Diameter of the crab in centimeters
Height	cm	Height of the crab in centimeters
Weight	gram	Weight of the crab in grams
Shucked.Weight	gram	Weight without the shell in grams
Viscera.Weight	gram	Weight that wraps around your abdominal organs deep inside body in grams
Shell.Weight	gram	Weight of the shell in grams
Age	months	Age of the crab in months

Data exploration

The first thing to do is to look at the distribution of the categories. The gender is the only nominal category for now, we will change the age category later.

```
gender_count <- ggplot(data = crab_data,
  aes(x=Sex, fill=Sex)) +
  geom_bar(fill = c('pink', 'green', 'blue'))
gender_count +
  ggtitle("Distribution of the sex in the crab dataset") +
  scale_x_discrete(labels = c("Female", "Indeterminate", "Male"))
```



The barplot shows a fairly even distribution between the sexes and indeterminate sex, there seem to be a bit more males.

A boxplot with the categories in centimeters is made. First the data is reshaped to be able to plot them together.

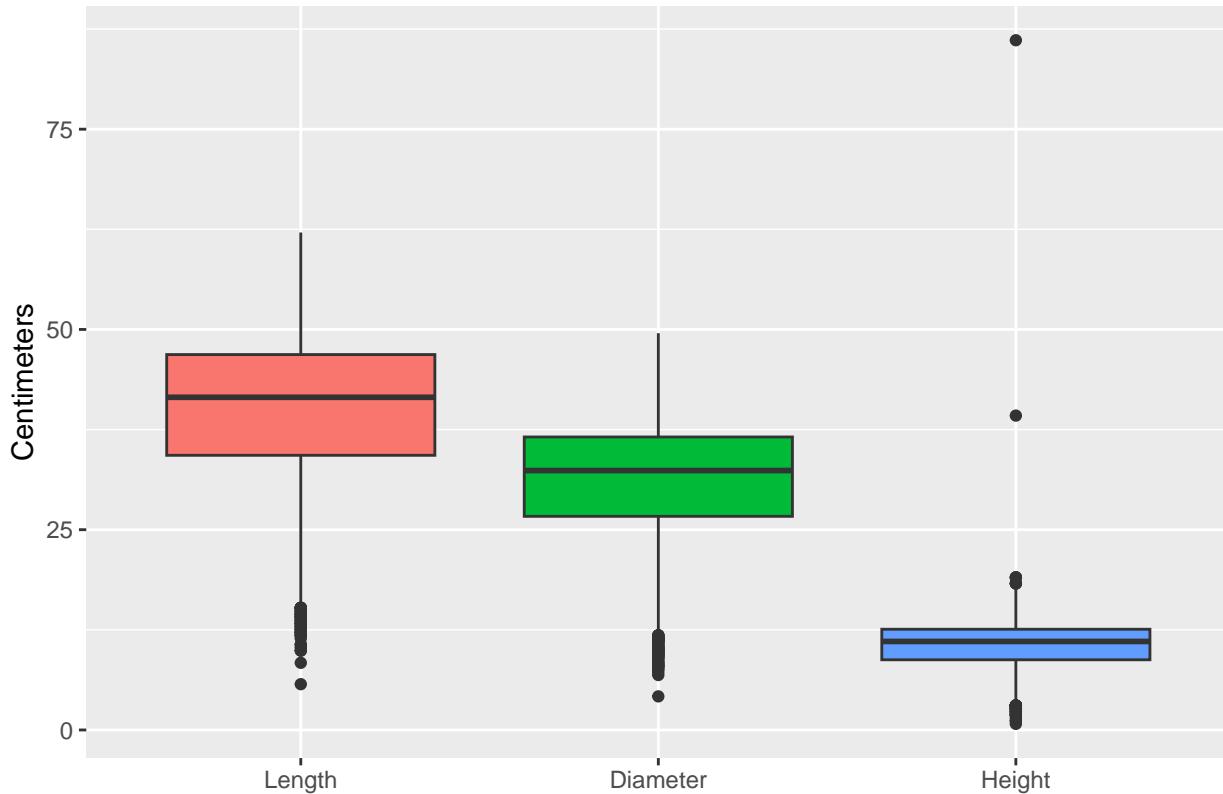
```
cm_data <- melt(crab_data[2:4])

## Using as id variables

ggplot(cm_data, aes(x=variable, y=value, fill = variable)) +
  geom_boxplot() +
  ggtitle("Distribution plots of the size categories") +
  ylab("Centimeters") +
```

```
#Removed the x axis title and legend since the variables speak for themselves
theme(axis.title.x = element_blank(), legend.position = "none")
```

Distribution plots of the size categories



The boxplots show that each categorie has some outliers but the height category has 2 extreme outliers with no corresponding outliers in the other categories. Since it are only 2 rows and it seems unlikely that these crabs with these porportions exist they will be removed.

```
crab_data = subset(crab_data, crab_data$Height < 30)
nrow(crab_data)
```

```
## [1] 3889
```

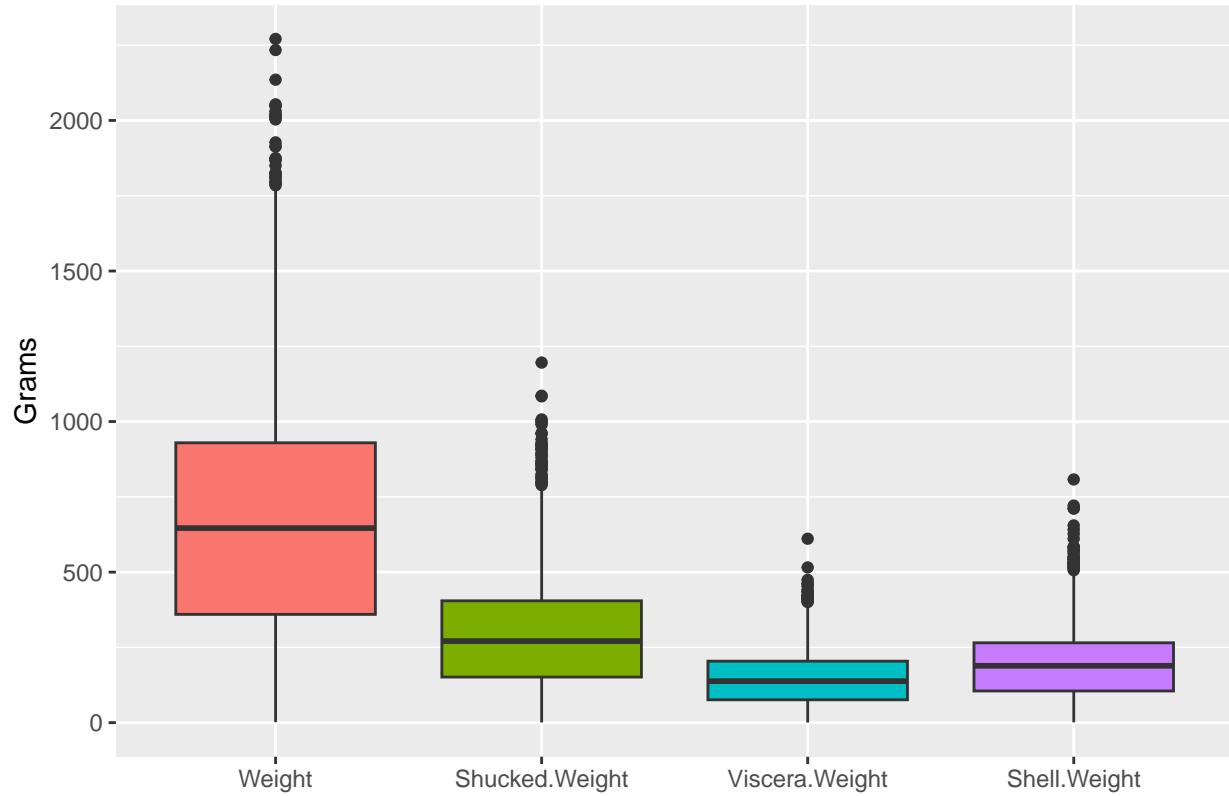
A quick nrow shows us that we indeed have removed 2 rows again. The same boxplots as with the length categories are made with the weight categories.

```
gram_data <- melt(crab_data[5:8])

## Using   as id variables

ggplot(gram_data, aes(x=variable, y=value, fill=variable)) +
  geom_boxplot() +
  ggtitle("Distribution of the weight categories") +
  ylab("Grams") +
  #Again x axis title and legend removed due to the values speaking for themselves
  theme(axis.title.x = element_blank(), legend.position = "none")
```

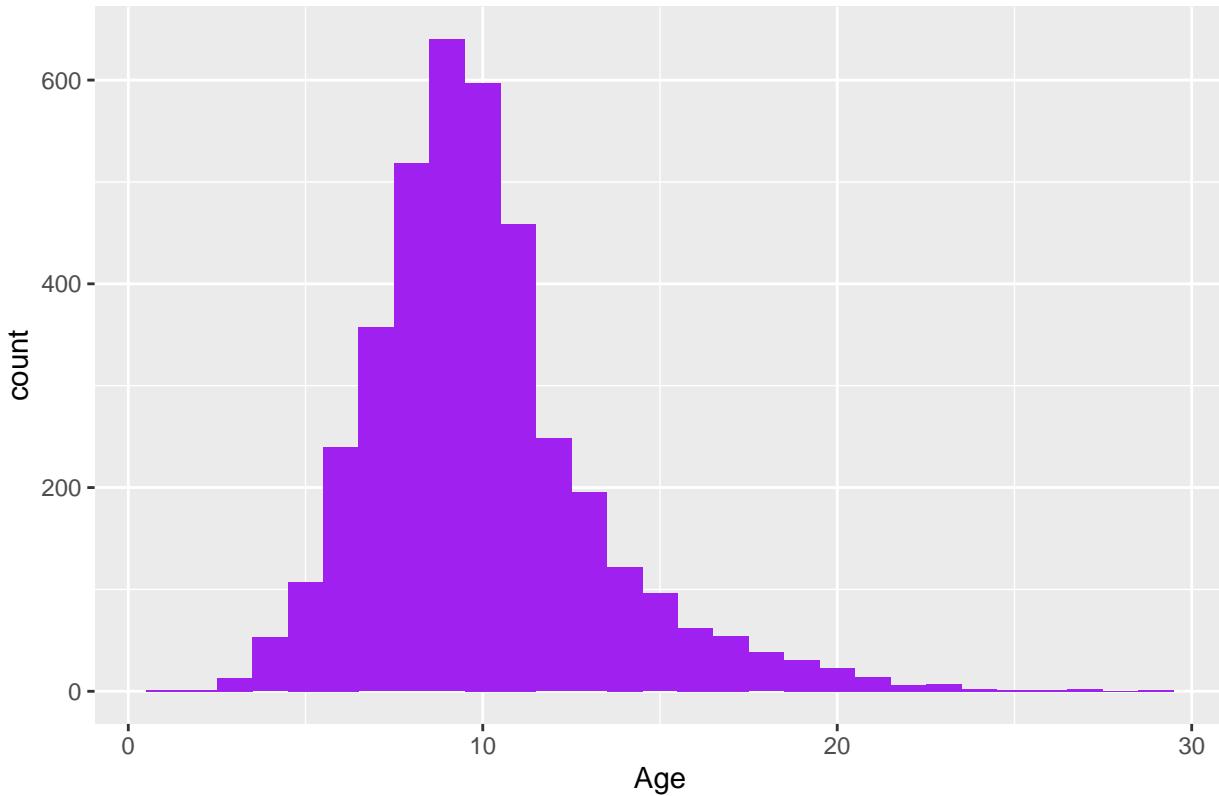
Distribution of the weight categories



The weight categories also have outliers but they do not seem extreme. Next let's look at the distribution of the age through a histogram.

```
ggplot(crab_data, aes(Age)) +  
  geom_histogram(binwidth = 1, fill = "purple") +  
  ggtitle("Distribution of the age of the crabs")
```

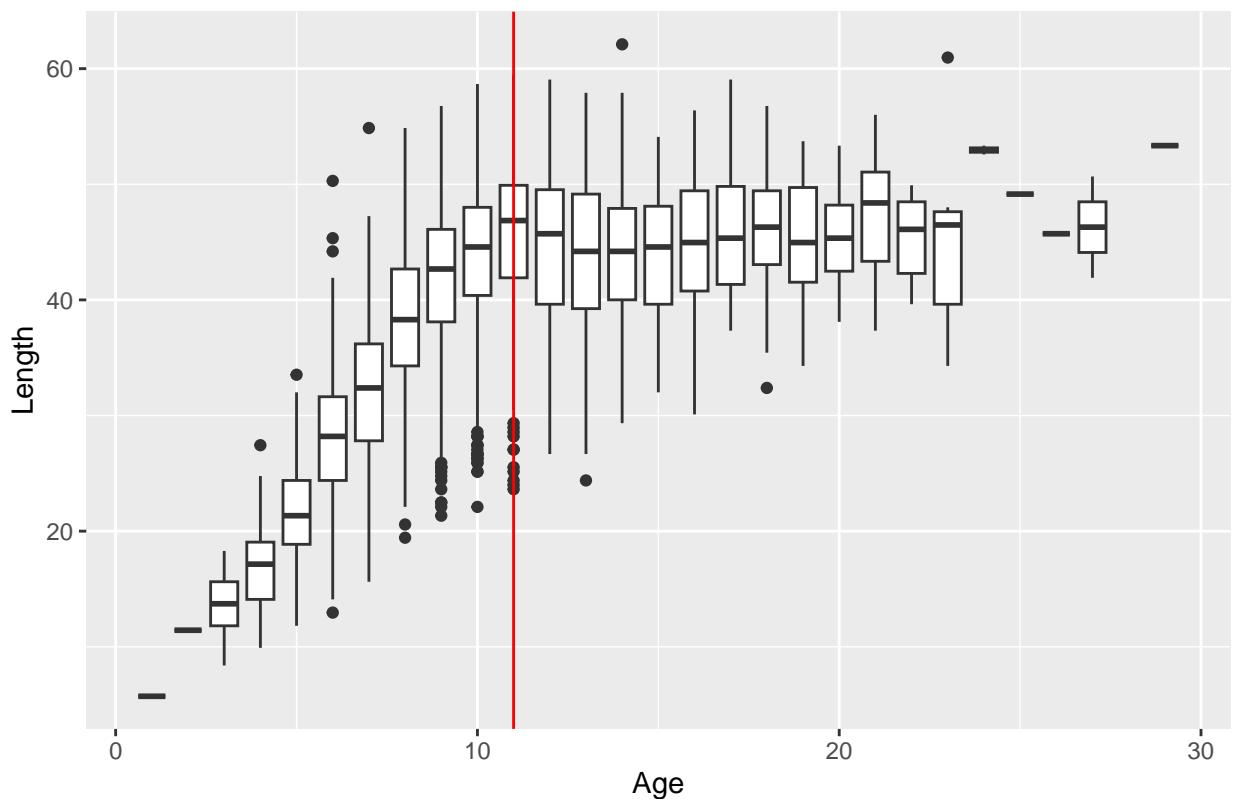
Distribution of the age of the crabs



Most of the crabs appear to be younger than 10 years and there are very little crabs older than 20 months. Since a regression model is out of scope for this research and we want to predict the age, the age group needs to be split in groups. A boxplot with the age as a group is made vs some of the physical properties. Then a point of interest is added with a line.

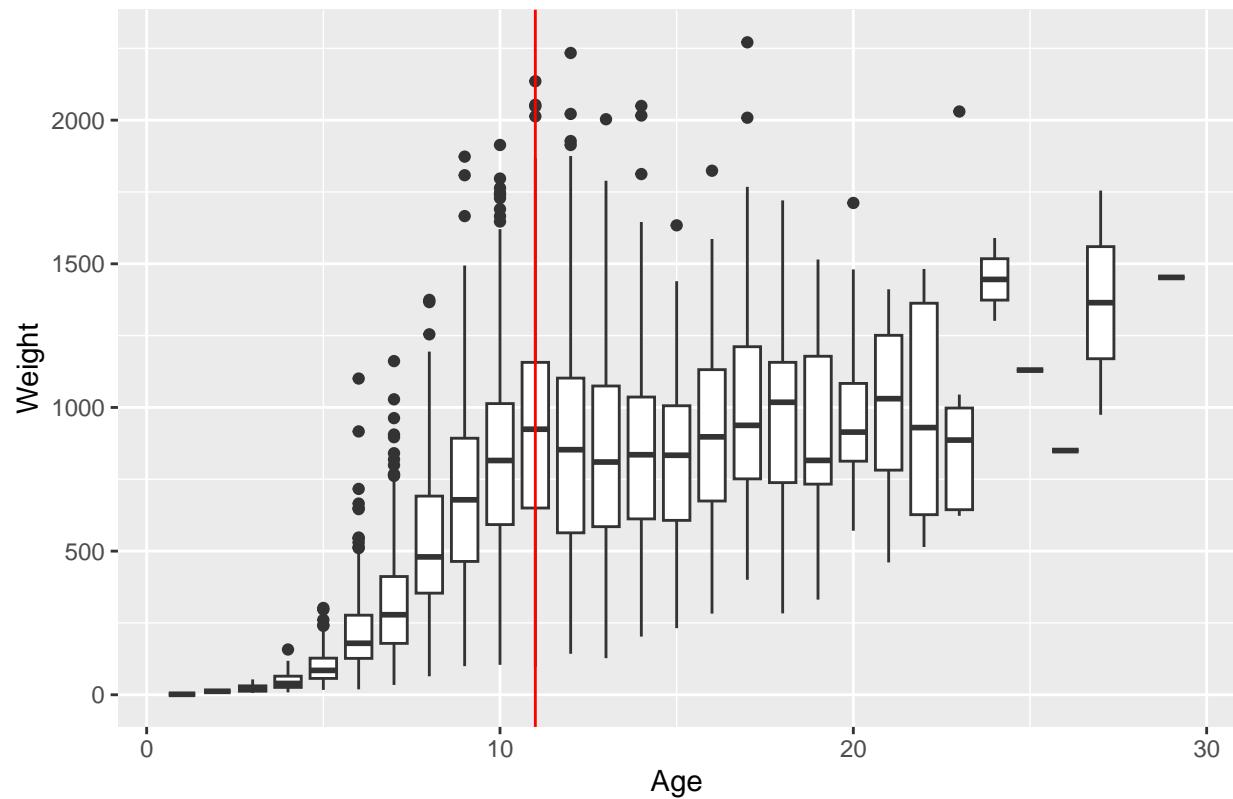
```
ggplot(crab_data, aes(x=Age, y=Length, group=Age)) +  
  geom_boxplot() +  
  geom_vline(xintercept = 11, color = "red") +  
  ggtitle("Length of crabs compared to the age")
```

Length of crabs compared to the age



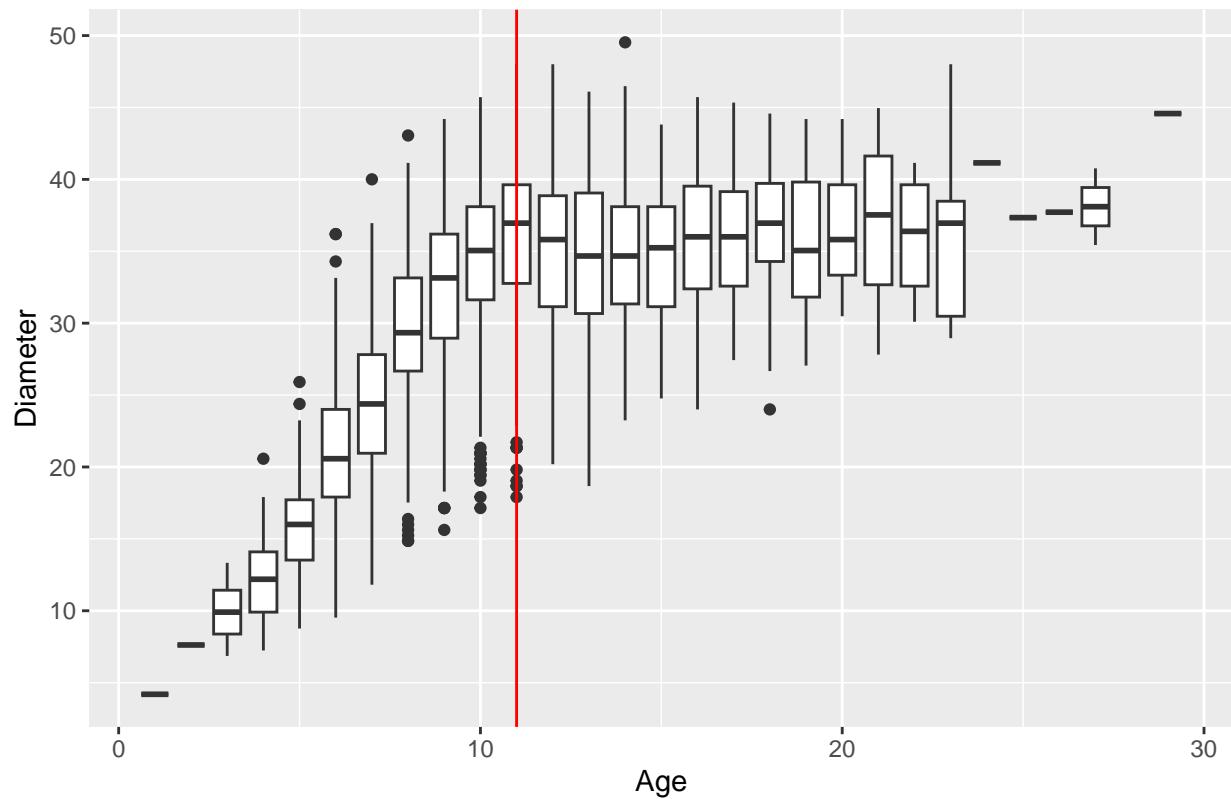
```
ggplot(crab_data, aes(x=Age, y=Length, group=Age)) +  
  geom_boxplot() +  
  geom_vline(xintercept = 11, color = "red") +  
  ggtitle("Length of crabs compared to the age")
```

Weight of crabs compared to the age



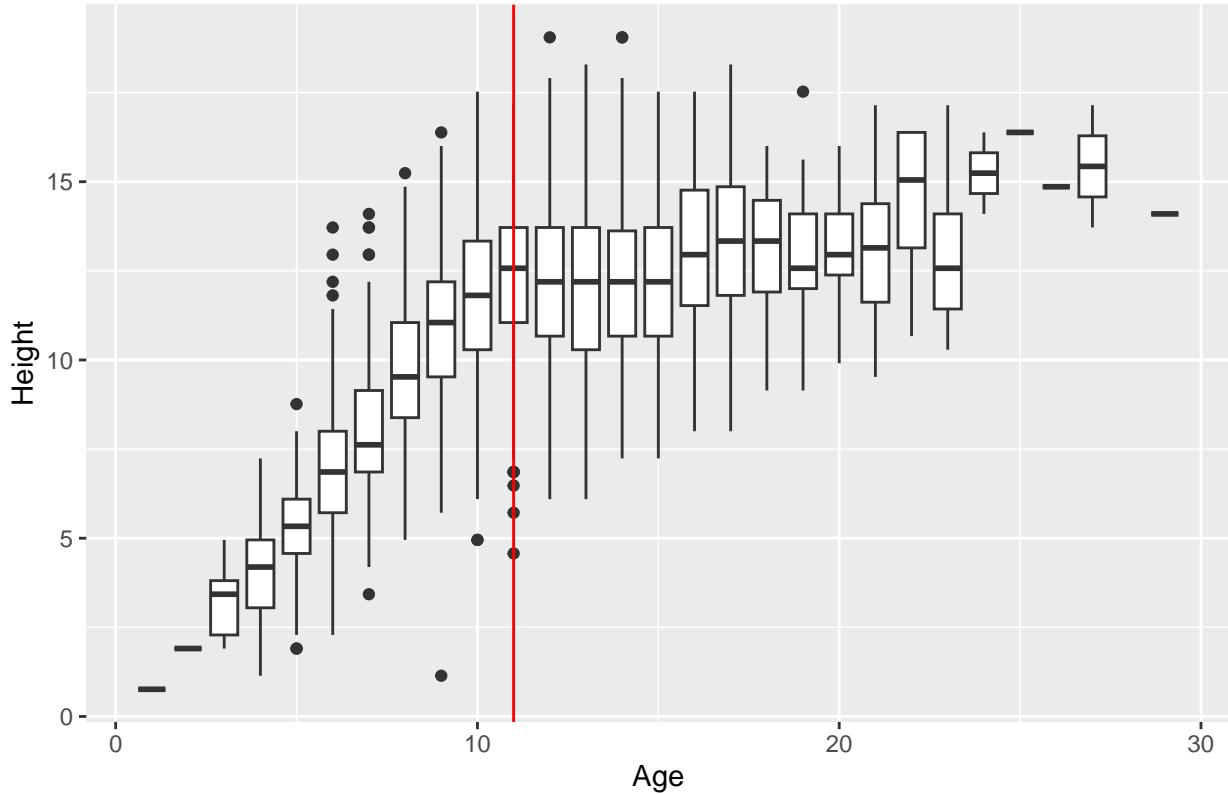
```
ggplot(crab_data, aes(x=Age, y=Diameter, group=Age)) +  
  geom_boxplot() +  
  geom_vline(xintercept = 11, color = "red") +  
  ggtitle("Diameter of crabs compared to the age")
```

Diameter of crabs compared to the age



```
ggplot(crab_data, aes(x=Age, y=Height, group=Age)) +  
  geom_boxplot() +  
  geom_vline(xintercept = 11, color = "red") +  
  ggtitle("Height of crabs compared to the age")
```

Height of crabs compared to the age



The red line represents the age of 11 from where the growth seems to stagnate in all of the 4 categories. With this in mind 2 groups of crabs are created, aged 1 through 10 months and 11 and above months.

```
crab_data$Age[crab_data$Age < 11] <- 1
crab_data$Age[crab_data$Age > 10] <- 2

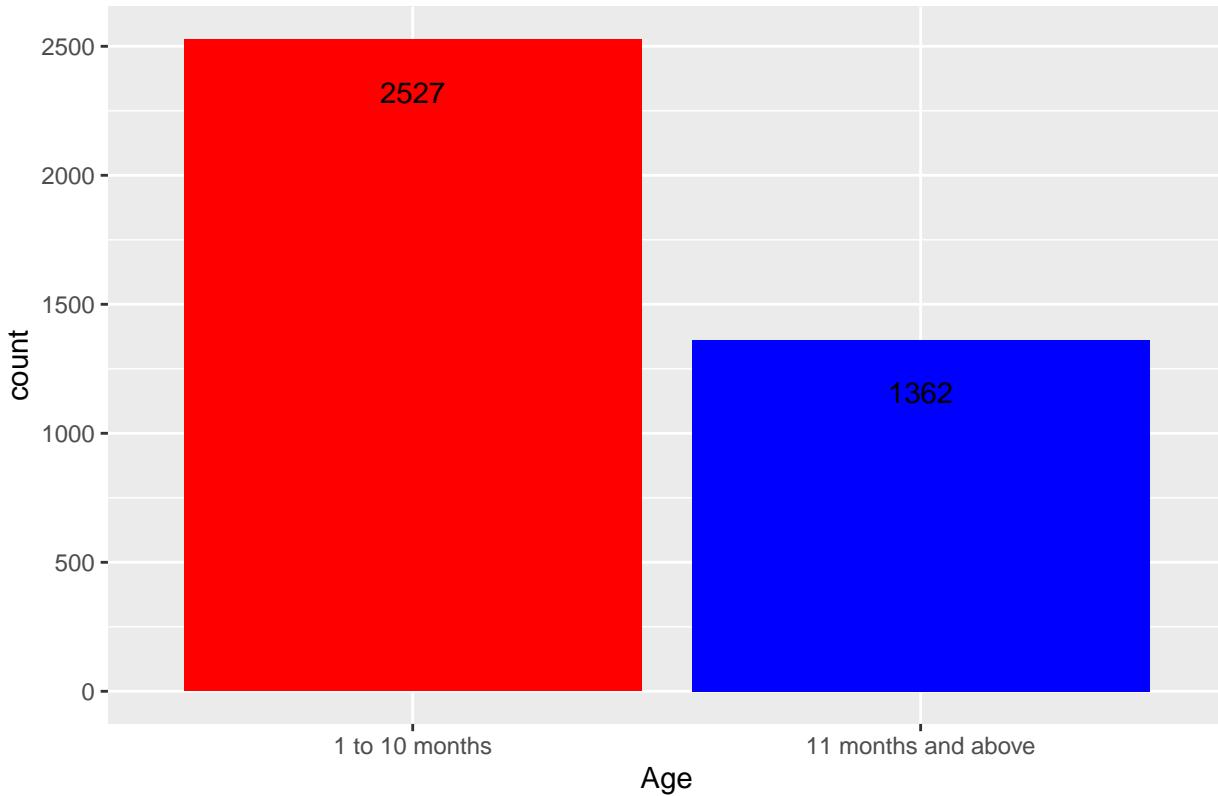
crab_data$Age <- as.factor(crab_data$Age)
```

The crab data age column has been changed to a 1 for 1 to 10 months and a 2 for 11 and above months. The age is then converted to a factor since it can only be 1 or 2. The age category has been overwritten since the actual age can not be used in machine learning purposes due to the fact that it is easily clear in what group the crab belongs.

A look at the new age distribution in a count barplot shows the following new distribution.

```
ggplot(crab_data, aes(Age)) +
  geom_bar(fill= c('red', 'blue')) +
  geom_text(stat='count', aes(label=after_stat(count)), vjust = 3) +
  ggtitle("Amount of crabs per age group") +
  scale_x_discrete(labels = c("1 to 10 months", "11 months and above"))
```

Amount of crabs per age group



The barplot shows that there are 2527 crabs under the age of 11 months and 1362 crabs 11 months or older. Most crabs are young (under 11 months) but the second group should be large enough for machine learning.

The codebook needs to be updated now

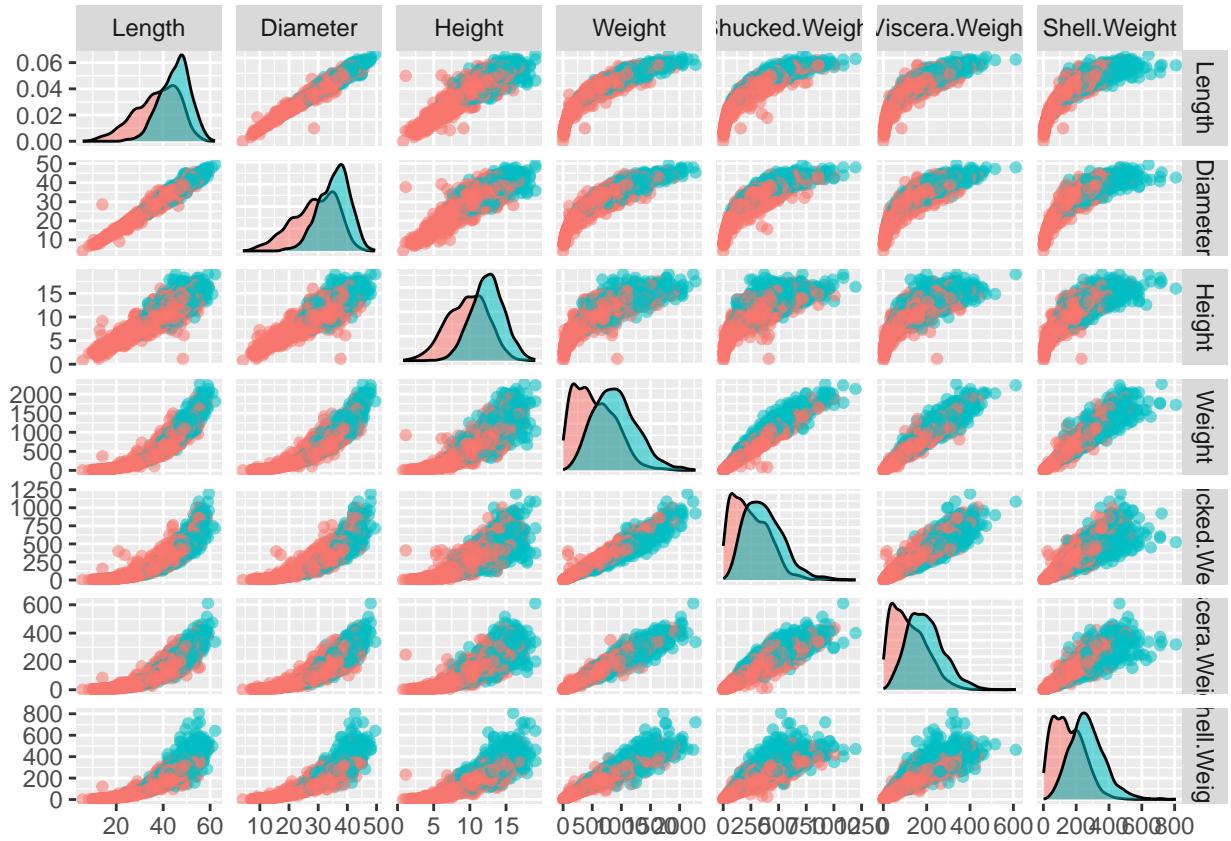
```
codebook_df$Units[codebook_df$Attribute == "Age"] <- "--"
codebook_df$Description[codebook_df$Attribute == "Age"] <- "Age group, 1 for 1 to 10 months and 2 for 11+ months"

knitr::kable(codebook_df, format = "latex")
```

Attribute	Units	Description
Sex	-	Gender of the crab, female(F) male(M) or interderminate(I)
Length	cm	Lenght of the crab in centimeters
Diameter	cm	Diameter of the crab in centimeters
Height	cm	Height of the crab in centimeters
Weight	gram	Weight of the crab in grams
Shucked.Weight	gram	Weight without the shell in grams
Viscera.Weight	gram	Weight that wraps around your abdominal organs deep inside body in grams
Shell.Weight	gram	Weight of the shell in grams
Age	-	Age group, 1 for 1 to 10 months and 2 for 11+ months

Next a pair plot is made with the continuous categories and the points are colored in with the age groups.

```
ggpairs(crab_data, columns = 2:8, aes(color=Age, alpha=0.3), upper = list(continuous = "points"))
```



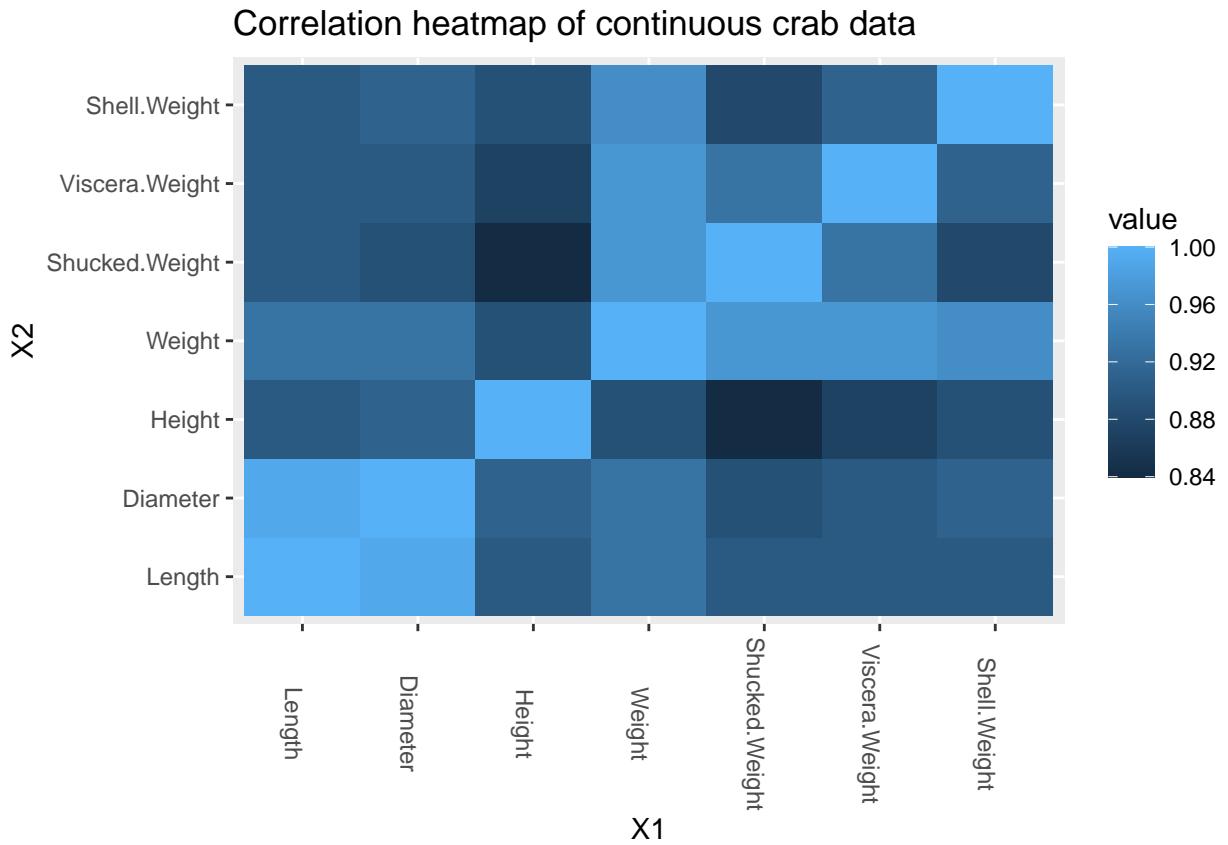
The pair plot shows that the young crabs under 11 months colored in red are mostly at the left side of the graph and the crabs which are 11+ months colored in blue are mostly on the right side in the graphs. The middle part does not show a clear line between red and blue which means that it can be harder to predict with machine learning. There seem to be some correlation between the different categories, especially the length compared to the diameter. Let's look deeper into the correlations with a correlation heatmap.

```
cormat <- round(cor(crab_data[2:8]), 2)
melted_cormat <- melt(cormat)

## Warning in type.convert.default(X[[i]], ...): 'as.is' should be specified by
## the caller; using TRUE

## Warning in type.convert.default(X[[i]], ...): 'as.is' should be specified by
## the caller; using TRUE

ggplot(melted_cormat, aes(x=X1, y=X2, fill=value)) +
  geom_tile() +
  ggtitle("Correlation heatmap of continuous crab data") +
  theme(axis.text.x = element_text(angle = -90))
```



The lowest correlation seems to be between the shucked weight and the height, but this is still around 0.84 which suggest they are correlated. The category that seems to be correlating the most is the weight category, not only does it get high correlation scores in the weight categories but also the lenght and diameter seem te be of importance.

Conclusion

The data was already very clean but was cleaned further bij removing 2 extreme outliers and 2 zero values. There seems to be some correlation based on pair plots and heatplots. The pair plot seems to show the separation of the 2 age categories up to some degree with a bit of a less defined seperation in the middle. All by all does it seem to be a good dataset to answer the question: "How accurately can you predict the age group of crabs based on physical properties and gender?".