

```
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```

```
BirdBones <- read.csv("../data/bird.csv",header = T, sep = ",")  
#respective collums for the lenght and diameter  
length <- c(2,4,6,8,10)  
diameter <- c(3,5,7,9,11)
```

Introduction

In this research project we will be going through data of varying ecological bird groups. In this data the bone lengths and diameters are provided of a bird with a label to which ecological group they belong.

Using this data we will be preparing this data for classification, analysing results of different classification algorithms and see how to use the data for classification.

We will be looking into Random Forest and IBk as classification algorithms. Random Forest is tree / decision based and IBk is a K-nearest neighbour classifier (lazy). As IBk is lazy we have to be cautious because there might form a bias towards groups with bigger data values.

After we have decided what classification algorithm to use we can use this research to create a Java wrapper application to make use of this classifier in the future if we want to study an unknown fossil and see what the possible ecological group is.

Research Question

Are there bones in a bird that are more important for classification using machine learning? Or should we take all available information into account if we are creating a classification algorithm using machine learning. And then what algorithm should we use?

Data

Data received from:

Birds' Bones and Living Habits, Kaggle dataset

Bone measurements were measured from a skeleton collection of Natural History Museum of Los Angeles County, provided by Dr. D. Liu of Beijing Museum of Natural History

Exploratory Data Analyses

The data contains 420 bird samples where the bone lengths and diameters have been measured. The birds are separated in 6 different groups:

- Swimming Birds, SW
- Wading Birds, W
- Terrestrial Birds, T
- Raptors, R
- Scansorial Birds, P
- Singing Birds, SO

Most samples have data for:

- Length and Diameter of the Humerus
- Length and Diameter of the Ulna

- Length and Diameter of the Femur
- Length and Diameter of the Tibiotarsus
- Length and Diameter of the Taesometatarsus

I'm creating a graph which displays the bonelengths on y axis and the Id on x colorcoded by their ecological group. by evaluating this we can see if some groups have overall larger or smaller bones and we see if there are big outliers.

```
# this omits several ggplot2 errors retaining to missing values
BirdBones.noNA <- BirdBones[complete.cases(BirdBones),]
# Displaying the data frame structure and a small summary
str(BirdBones)
```

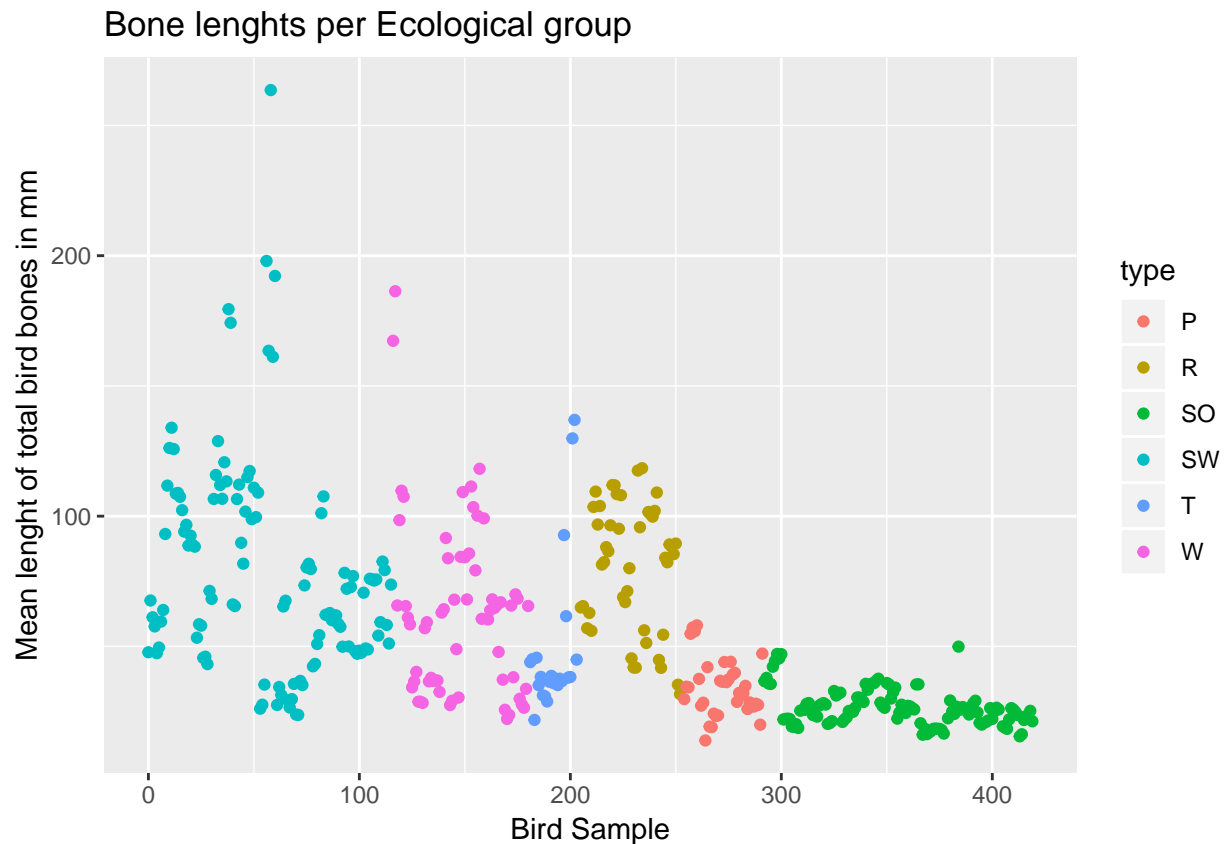
```
## 'data.frame': 420 obs. of 12 variables:
## $ id : int 0 1 2 3 4 5 6 7 8 9 ...
## $ huml : num 80.8 88.9 80 77.7 62.8 ...
## $ humw : num 6.68 6.63 6.37 5.7 4.84 ...
## $ ulnal: num 72 80.5 69.3 65.8 52.1 ...
## $ ulnaw: num 4.88 5.59 5.28 4.77 3.73 3.47 4.5 4.55 6.13 7.05 ...
## $ feml : num 41.8 47 43.1 40 34 ...
## $ femw : num 3.7 4.3 3.9 3.52 2.72 4.41 3.41 3.78 5.45 7.44 ...
## $ tibl : num 5.5 80.2 75.3 69.2 56.3 ...
## $ tibw : num 4.03 4.51 4.04 3.4 2.96 2.73 3.56 3.81 5.58 7.31 ...
## $ tarl : num 38.7 41.5 38.3 35.8 31.9 ...
## $ tarw : num 3.84 4.01 3.34 3.41 3.13 2.83 3.64 3.81 4.37 6.34 ...
## $ type : Factor w/ 6 levels "P","R","SO","SW",...: 4 4 4 4 4 4 4 4 4 4 ...
```

```
summary(BirdBones)
```

```
##           id           huml           humw           ulnal
## Min.      : 0.0   Min.      : 9.85   Min.      : 1.140   Min.      : 14.09
## 1st Qu.:104.8   1st Qu.: 25.17   1st Qu.: 2.190   1st Qu.: 28.05
## Median :209.5   Median : 44.18   Median : 3.500   Median : 43.71
## Mean      :209.5   Mean      : 64.65   Mean      : 4.371   Mean      : 69.12
## 3rd Qu.:314.2   3rd Qu.: 90.31   3rd Qu.: 5.810   3rd Qu.: 97.52
## Max.      :419.0   Max.      :420.00   Max.      :17.840   Max.      :422.00
##           NA's      :1           NA's      :1           NA's      :3
##           ulnaw           feml           femw           tibl
## Min.      : 1.000   Min.      : 11.83   Min.      : 0.930   Min.      : 5.50
## 1st Qu.: 1.870   1st Qu.: 21.30   1st Qu.: 1.715   1st Qu.: 36.42
## Median : 2.945   Median : 31.13   Median : 2.520   Median : 52.12
## Mean      : 3.597   Mean      : 36.87   Mean      : 3.221   Mean      : 64.66
## 3rd Qu.: 4.770   3rd Qu.: 47.12   3rd Qu.: 4.135   3rd Qu.: 82.87
## Max.      :12.000   Max.      :117.07   Max.      :11.640   Max.      :240.00
## NA's      :2           NA's      :2           NA's      :1           NA's      :2
##           tibw           tarl           tarw           type
## Min.      : 0.870   Min.      : 7.77   Min.      : 0.660   P : 38
## 1st Qu.: 1.565   1st Qu.: 23.04   1st Qu.: 1.425   R : 50
## Median : 2.490   Median : 31.74   Median : 2.230   SO:128
## Mean      : 3.182   Mean      : 39.23   Mean      : 2.930   SW:116
## 3rd Qu.: 4.255   3rd Qu.: 50.25   3rd Qu.: 3.500   T : 23
## Max.      :11.030   Max.      :175.00   Max.      :14.090   W : 65
## NA's      :1           NA's      :1           NA's      :1
```

there are 420 total measurements, and by using complete cases i found that there are 413 measurements which are complete and do not contain missing values, aka > there are 7 measurements that contain missing values.

```
library(ggplot2)
library(reshape)
source("../scripts/BoneMeans.R")
BirdBones.noNA <- BoneMeans(data = BirdBones.noNA, length = length, diameter = diameter)
ggplot(data = BirdBones.noNA, aes(id, length.mean, colour = type)) +
  ggtitle("Bone lengths per Ecological group") +
  ylab("Mean length of total bird bones in mm") +
  xlab("Bird Sample") +
  geom_point()
```



As seen above swimming birds have the biggest bones, but also shown is that there are a lot more samples in that group where there is a lot of variation. I can look into cleaning up the data and removing the biggest outliers in this group. Singing birds also have a lot of samples but there is much less variation and so more certainty.

Note: this plot does not show a perfect classifier, this data is sorted.

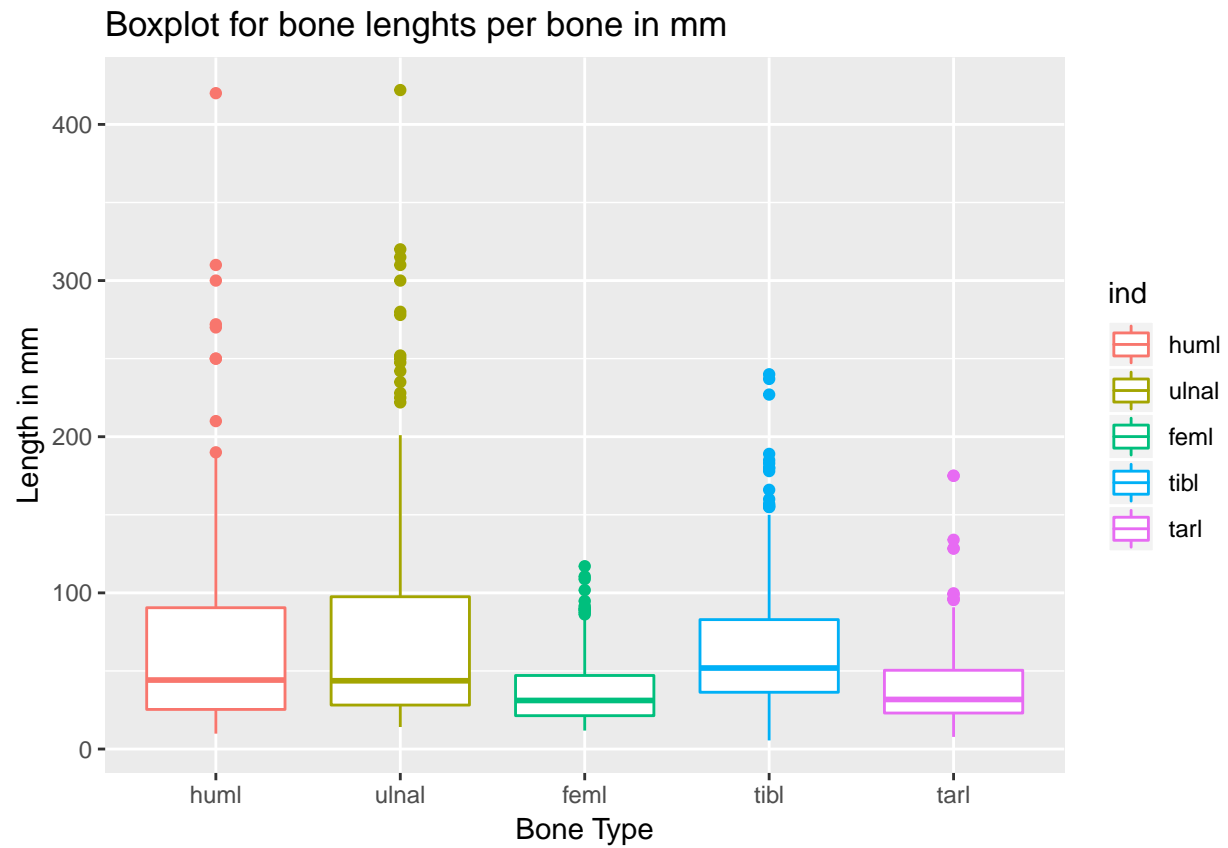
For the rest of the birds there are not a lot of sample so maybe we could try and normalizing the data so there is an even amount of samples per group.

There are also 7 samples that contain missing values, we could just straight out not use these samples because 4 of these are part of the biggest group of samples. and the others are not part of the smallest groups.

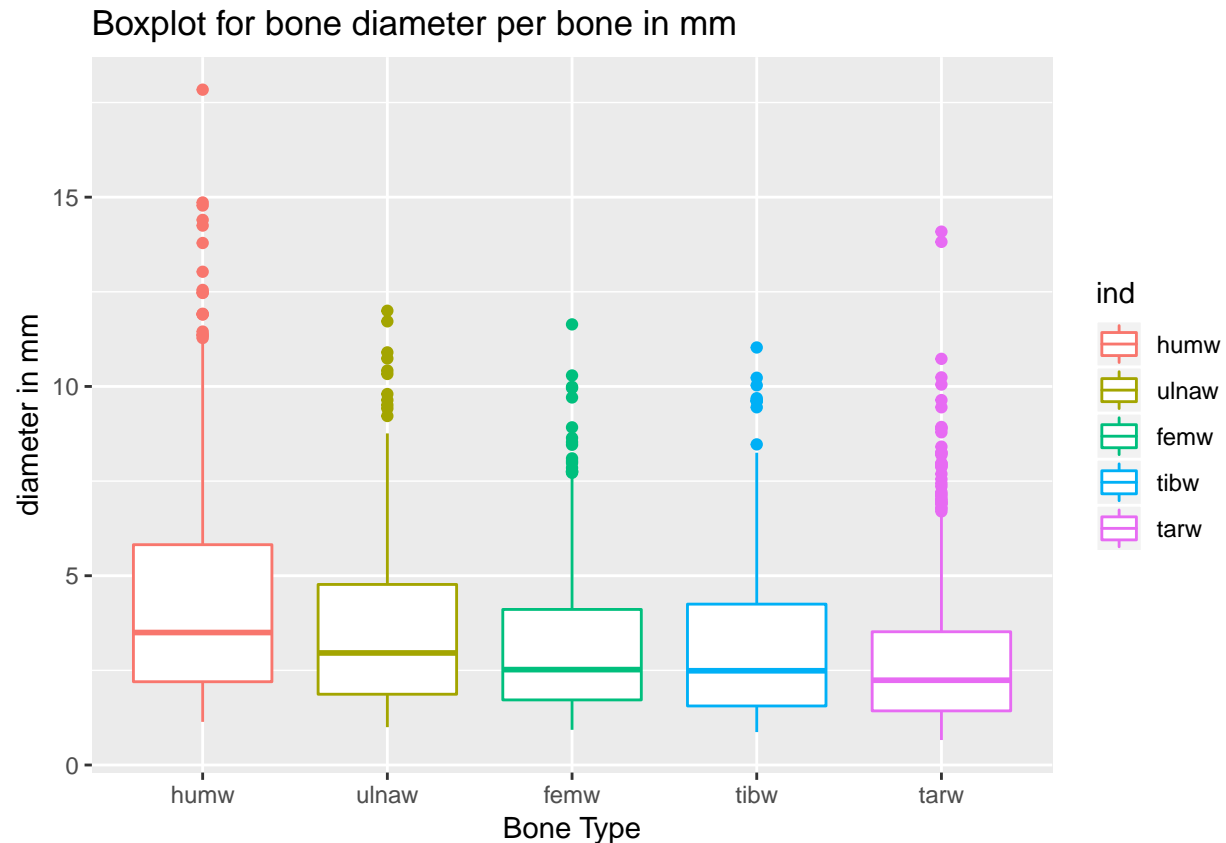
```
library(ggplot2)

ggplot(stack(BirdBones.noNA[length]), aes(x = ind, y = values, color = ind)) +
  geom_boxplot() +
  ggtitle("Boxplot for bone lengths per bone in mm") +
```

```
xlab("Bone Type")+
ylab("Length in mm")
```



```
ggplot(stack(BirdBones.noNA[diameter]), aes(x = ind, y = values, color = ind)) +
  geom_boxplot()+
  ggtitle("Boxplot for bone diameter per bone in mm")+
  xlab("Bone Type")+
  ylab("diameter in mm")
```



What we see above is that there are a considerable amount of outliers between the bones themselves, but this was expected as they are from different groups and the different groups don't have the same amount of measurements. Below I will do a comparison between the group bone mean lengths which will show outliers in their respective group. Using the above boxplots we can maybe see which bones are not very important > see if they don't differ at all which means we don't need them that much for classification.

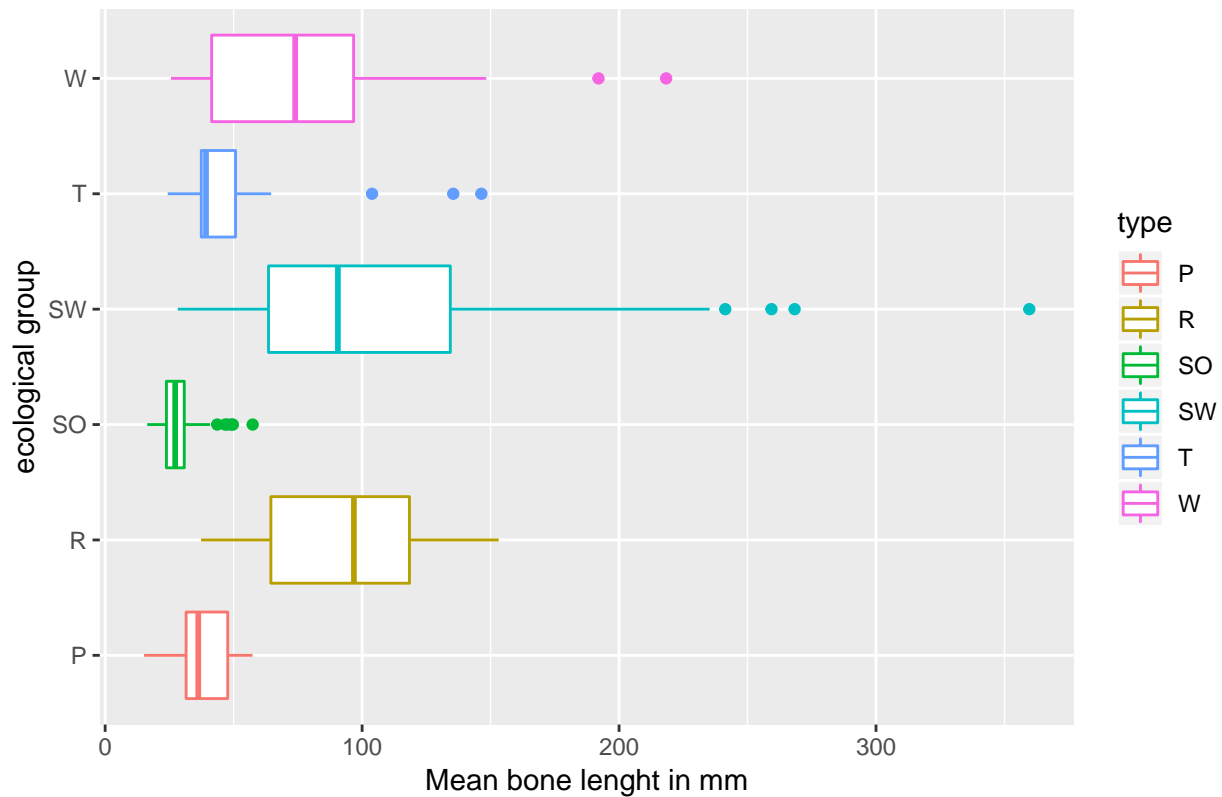
As we can see the femur length and tarsometatarsus length do not contain a lot of variation and maybe are candidates for exclusion from analysis.

```
# diameter & length indexes for only the longer bones.
length.long <- c(2, 4, 8)
diameter.long <- c(3, 5, 9)
BirdBones.noNA.long <- BoneMeans(BirdBones.noNA, length.long, diameter.long)
```

```
library(ggplot2)

ggplot(BirdBones.noNA.long, aes(x = type, y = length.mean, color = type)) +
  geom_boxplot() +
  coord_flip() +
  ggtitle("Boxplot for each ecological group's mean bone length") +
  ylab("Mean bone length in mm") +
  xlab("ecological group")
```

Boxplot for each ecological group's mean bone lenght

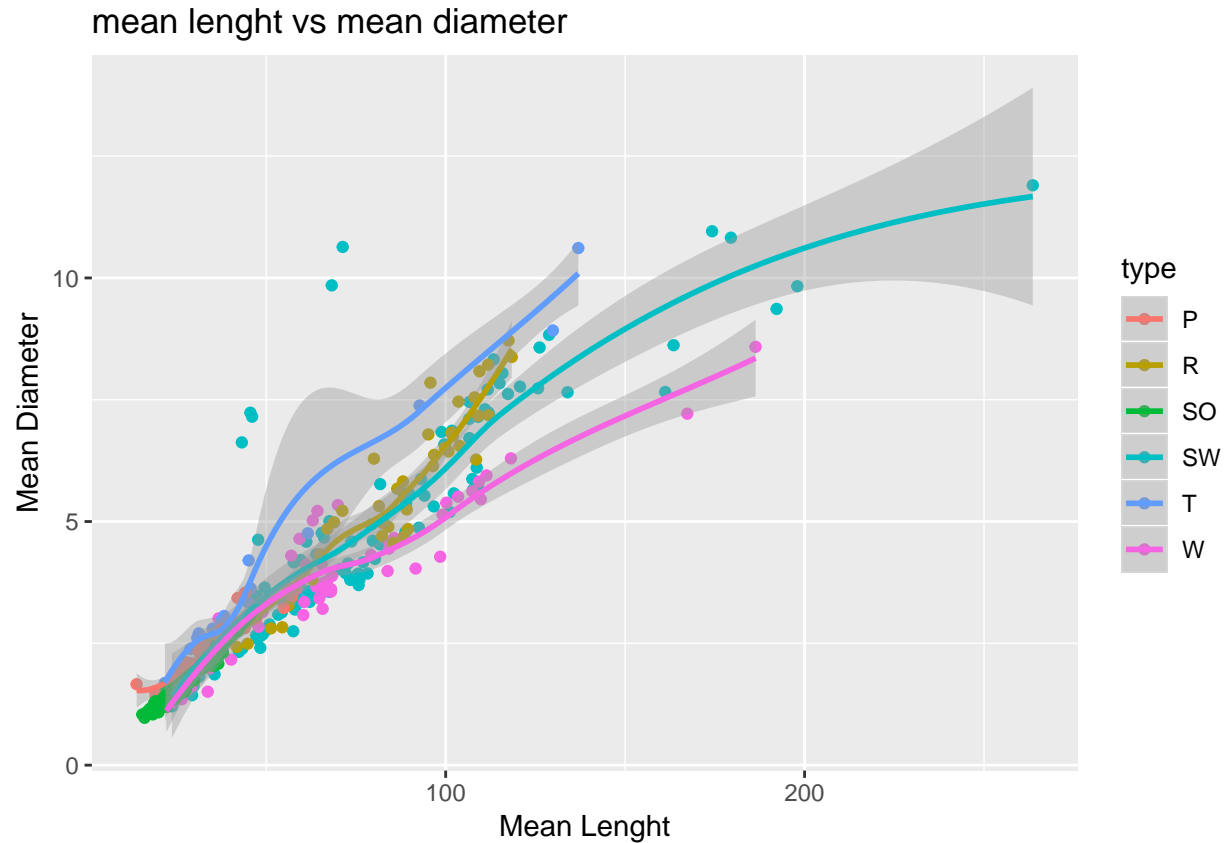


As you can see there are quite a few outliers in all groups except in group R, The raptors. but we saw in the above boxplot that there were loads of outliers between all bones, yet here that is significantly reduced. so if we are going to inspect the data we have to look at them per group and NOT by bone type.

What we can also see in these plots are which birds are most likely the largest, as seen above color cyan or SW or Swimming Birds are the biggest of them all closely followed by W or Wading Birds

```
ggplot(BirdBones.noNA, aes(x=length.mean, y=diameter.mean, color=type)) +
  geom_point() +
  geom_smooth() +
  ggtitle("mean lenght vs mean diameter") +
  xlab("Mean Lenght") +
  ylab("Mean Diameter")
```

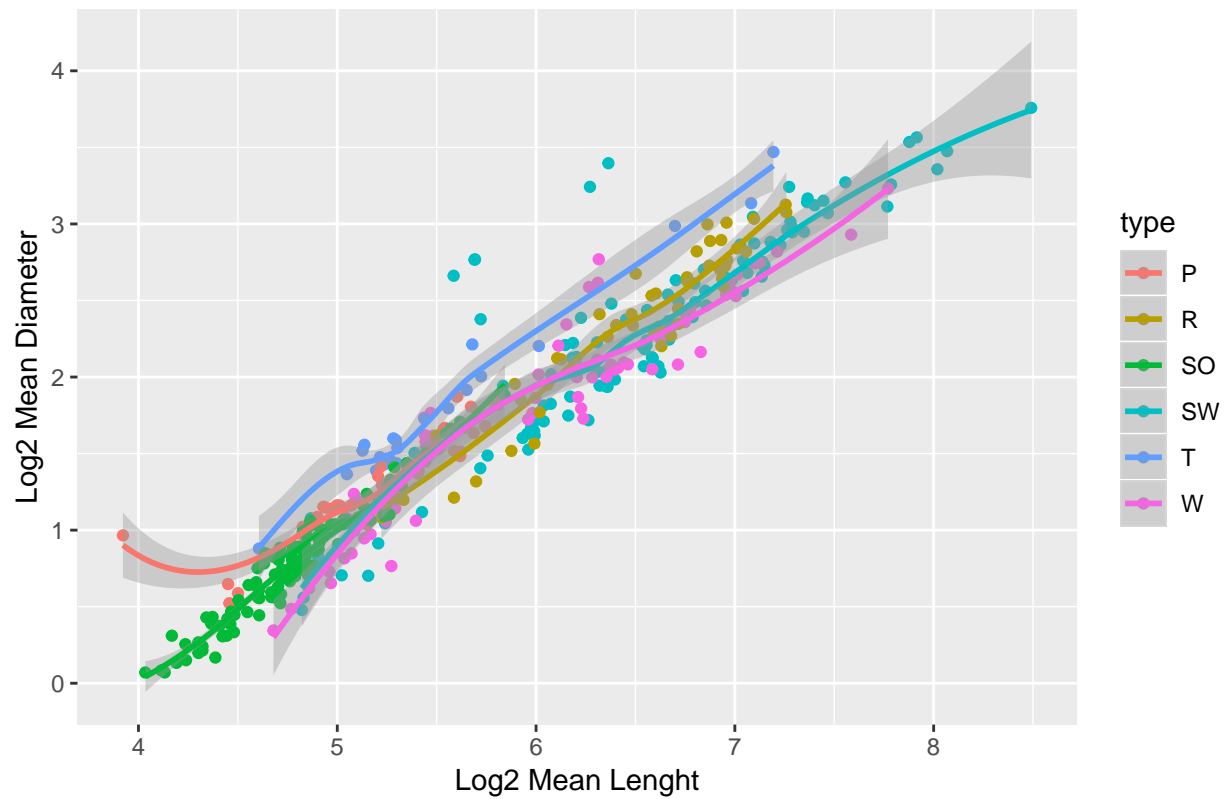
```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



Untransformed datapoints separated by group, again here we can see which birds are the biggest, but for smaller birds this plot is not very readable. we do see something odd, where T has a climbing line around length 50, other birds have a decreasing line. also Swimming Birds have some results that are very different from their mean line.

```
ggplot(BirdBones.noNA.long, aes(x=log2(length.mean), y=log2(diameter.mean), color=type)) +
  geom_point() +
  geom_smooth(method = loess) +
  xlab("Log2 Mean Length") +
  ylab("Log2 Mean Diameter") +
  labs(title = "Log2 transformed data")
)
```

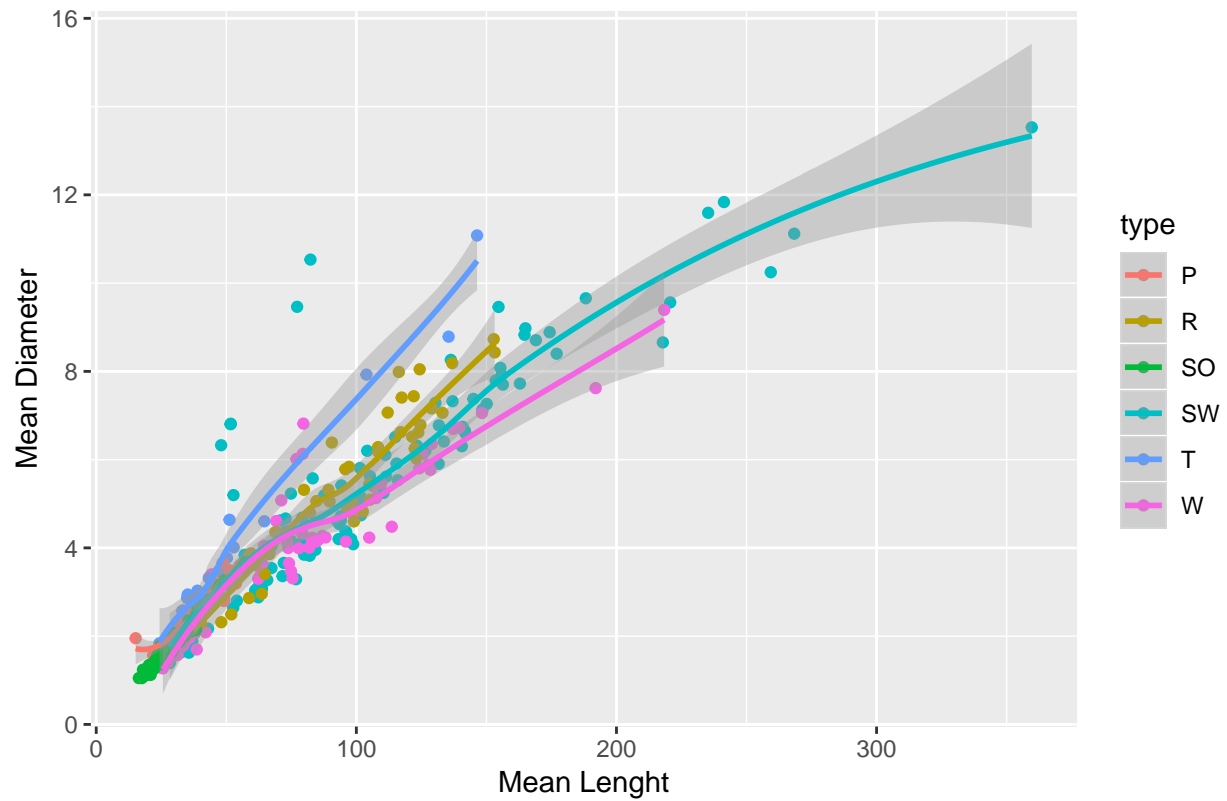
Log2 transformed data



```
ggplot(BirdBones.noNA.long,aes(x=length.mean,y=diameter.mean,color=type))+
  geom_point()+
  geom_smooth()+
  ggtitle("mean lenght vs mean diameter For Humerus, Ulna and Tibiotarsus")+
  xlab("Mean Lenght")+
  ylab("Mean Diameter")

## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```

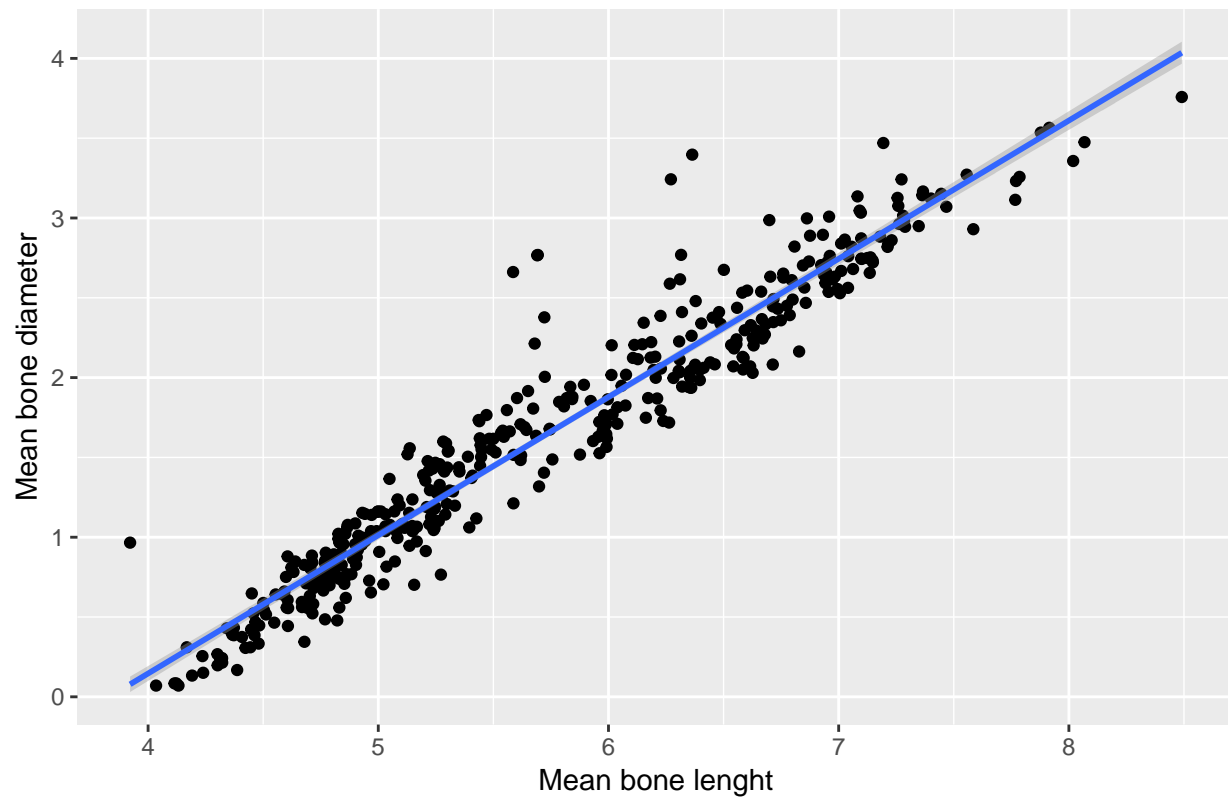

mean lenght vs mean diameter For Humerus, Ulna and Tibiotarsus



```
BirdBones.noNA.long$log2length <- log2(BirdBones.noNA.long$length.mean)
BirdBones.noNA.long$log2diameter <- log2(BirdBones.noNA.long$diameter.mean)

library(ggplot2)
ggplot(BirdBones.noNA.long, aes(x = log2length, y = log2diameter)) +
  geom_point() +
  geom_smooth(method = lm) +
  ggtitle("Log2 transformed Corelation between bone diameter & bone length") +
  xlab("Mean bone lenght") +
  ylab("Mean bone diameter")
```

Log2 transformed Correlation between bone diameter & bone length

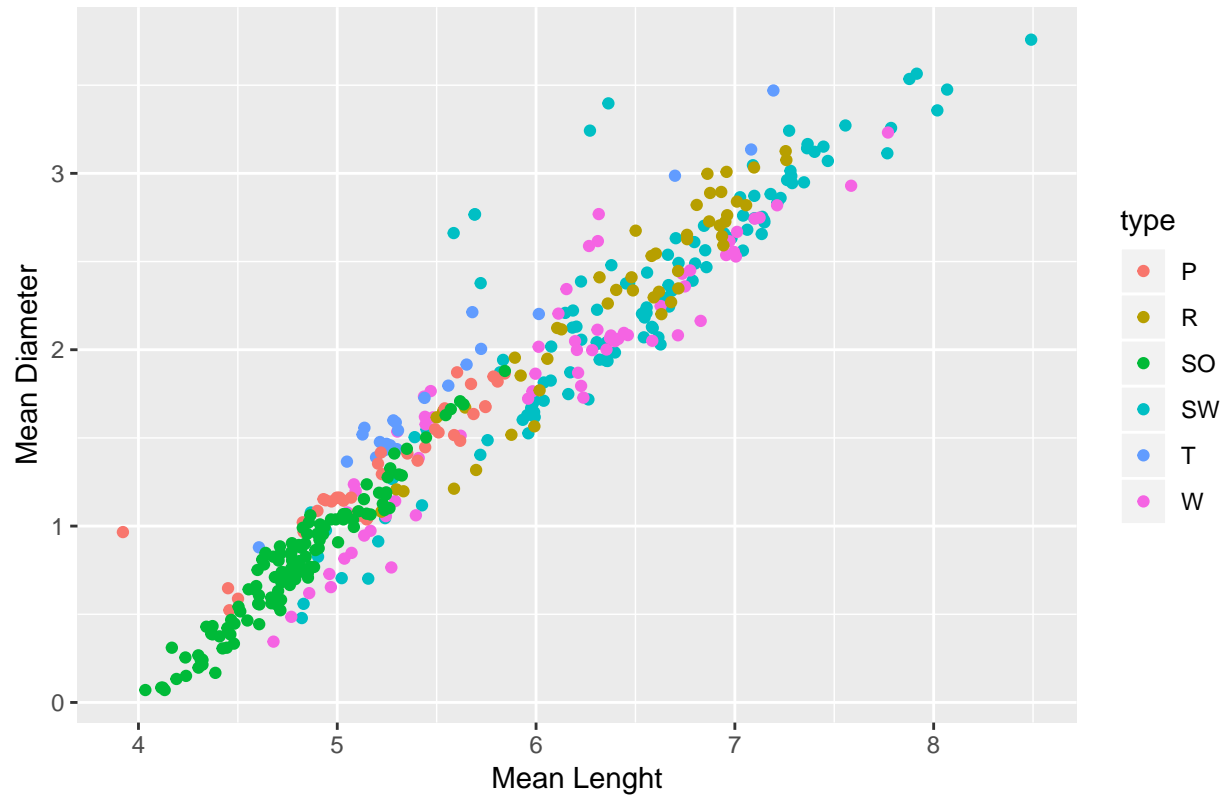


As expected there is a correlation between the bone length and bone diameter, you can see this because the plot gives a linear line. It does make a lot of sense if you have longer bones there you will most likely also have thicker bones (bigger diameters).

We can also see a couple of outliers in the scatter plot above. We can try and isolate these samples and take a closer look.

```
ggplot(BirdBones.noNA.long, aes(x=log2length, y=log2diameter, color=type)) +  
  geom_point() +  
  ggtitle(" Log2 transformed mean lenght vs mean diameter For Humerus, Ulna and Tibiotarsus") +  
  xlab("Mean Lenght") +  
  ylab("Mean Diameter")
```

Log2 transformed mean length vs mean diameter For Humerus, Ulna and Ti



Same plot as above but colorcoded so we can see to which group the outliers belong.

```
# m <- as.matrix(BirdBones.noNA$length.mean, ncol=2)
# 6 groups so 6 clusters is assumed
# cl <- kmeans(m, 6)
#
# ...
# ```{r}
# BirdBones.noNA$cluster <- factor(cl$cluster)
# centers <- as.data.frame((cl$centers))
# ...
# ```{r}
# library(ggplot2)
#
#
# ggplot(data=BirdBones.noNA, aes(x=length.me43an, y=id, color=type )) +
#   geom_point() +
#   geom_point(data=centers, aes(x=V1,y=V2, color='Center')) +
#   geom_point(data=centers, aes(x=V1,y=V2, color='Center'), size=50, alpha=.4, legend=FALSE)

# library(ggplot2)
# library(pheatmap)
# df.hum <- data.frame(log2(BirdBones.noNA$huml), log2(BirdBones.noNA$humw))
# kmeans.hum <- kmeans((df.hum), 6)
#
# dm.len <- data.matrix(BirdBones.noNA[length])
# dm.dia <- data.matrix(BirdBones.noNA[diameter])
```

```
#
# pheatmap(dm.len, kmeans_k = 6)
# pheatmap(dm.dia, kmeans_k = 6)
# plot(kmeans.hum$cluster)
# plot(kmeans.hum$centers)

# Removed these as they dont really add much value to the research
```

For data cleaning we already have a dataset without NA's(BirdBones.NoNA). now we need to remove the found outliers and discard the unneeded bones.

```
huml.3rd.q <- 90.31
huml.1st.q <-25.17

out <- huml.1st.q - 1.5*(huml.3rd.q - huml.1st.q)
out.large <- huml.3rd.q + 1.5*(huml.3rd.q - huml.1st.q)
outliers <- subset(BirdBones.noNA, huml > out.large | huml < out)
Birdbones.Clean <- BirdBones.noNA[! BirdBones.noNA$id %in% outliers$id, ]
```

```
summary(Birdbones.Clean)
```

```
##          id          huml          humw          ulnal
## Min.      : 0.0    Min.      : 9.85    Min.      : 1.140    Min.      : 14.09
## 1st Qu.:108.8    1st Qu.: 25.04    1st Qu.: 2.188    1st Qu.: 28.00
## Median :213.5    Median : 42.49    Median : 3.440    Median : 42.74
## Mean      :211.3    Mean      : 60.20    Mean      : 4.177    Mean      : 64.13
## 3rd Qu.:314.2    3rd Qu.: 88.93    3rd Qu.: 5.702    3rd Qu.: 95.17
## Max.      :419.0    Max.      :188.00    Max.      :14.780    Max.      :280.00
##          ulnaw          feml          femw          tibl
## Min.      : 1.000    Min.      : 11.83    Min.      : 0.930    Min.      : 5.50
## 1st Qu.: 1.867    1st Qu.: 21.23    1st Qu.: 1.690    1st Qu.: 36.05
## Median : 2.910    Median : 30.43    Median : 2.475    Median : 51.06
## Mean      : 3.473    Mean      : 35.76    Mean      : 3.106    Mean      : 62.38
## 3rd Qu.: 4.615    3rd Qu.: 45.40    3rd Qu.: 4.050    3rd Qu.: 80.27
## Max.      :12.000    Max.      :117.07    Max.      :11.640    Max.      :227.00
##          tibw          tarl          tarw          type
## Min.      : 0.870    Min.      : 7.77    Min.      : 0.660    P : 38
## 1st Qu.: 1.540    1st Qu.: 23.01    1st Qu.: 1.417    R : 48
## Median : 2.440    Median : 31.43    Median : 2.210    S0:124
## Mean      : 3.059    Mean      : 38.09    Mean      : 2.836    SW:108
## 3rd Qu.: 4.122    3rd Qu.: 48.28    3rd Qu.: 3.353    T : 23
## Max.      :10.030    Max.      :175.00    Max.      :14.090    W : 63
##          length.mean          diameter.mean
## Min.      : 13.90    Min.      : 0.972
## 1st Qu.: 27.26    1st Qu.: 1.753
## Median : 39.53    Median : 2.709
## Mean      : 52.11    Mean      : 3.330
## 3rd Qu.: 69.18    3rd Qu.: 4.359
## Max.      :167.32    Max.      :10.636
```

```
long.bones <- c(1, 2,3, 4,5,8,9, 12)
Birdbones.Clean <- Birdbones.Clean[,long.bones ]
```

```
write.csv(Birdbones.Clean, "../data/CleanData.csv")
```

After creating the csv file im going to use weka to create an arff, i know there is a write.arff function but i

can't get that to install properly.

Weka Analysis

For this classification we want the accuracy to be as high as possible, as wrongly classified fossils dont have that big of an impact as if someones health is on the line.

Using ZeroR We get 30% guessed correctly. It looks for the values with the largest sample count which is SO and guesses that its most likely that any bird is that bird. Zero R : Zero Rules.

ZeroR predicts class value: SO

- Correctly Classified Instances 124 30.6931 %
- Incorrectly Classified Instances 280 69.3069 %

```
conf.matrix <-
  rbind(
    c(0,0,0,0,0,108),
    c(0,0,0,0,0,63),
    c(0,0,0,0,0,23),
    c(0,0,0,0,0,48),
    c(0,0,0,0,0,38),
    c(0,0,0,0,0,124))
colnames(conf.matrix) <- c("SW", "W", "T", "R", "P", "SO")
rownames(conf.matrix) <- c("SW", "W", "T", "R", "P", "SO")

conf.matrix

##      SW W T R P  SO
## SW   0 0 0 0 0 108
## W    0 0 0 0 0  63
## T    0 0 0 0 0  23
## R    0 0 0 0 0  48
## P    0 0 0 0 0  38
## SO   0 0 0 0 0 124
```

Using One R without any changes gives a model that is overfitted. what i would want from one R is 6 different classifiers each for 1. With a default bucket size of 6 we get 15 different classifiers.

with bucket size 12 we get 7 classifiers, and 15 we get 3.

```
conf.matrix <-
  rbind(
    c(70,10,0,14,8,6),
    c(24,13,1,10,11,4),
    c(1,7,5,2,5,3),
    c(23,8,0,11,6,0),
    c(0,5,4,1,14,14),
    c(0,1,3,0,12,108))
colnames(conf.matrix) <- c("SW", "W", "T", "R", "P", "SO")
rownames(conf.matrix) <- c("SW", "W", "T", "R", "P", "SO")

conf.matrix

##      SW W T R P  SO
## SW  70 10 0 14  8  6
## W   24 13 1 10 11  4
## T    1  7 5  2  5  3
```

```
## R 23 8 0 11 6 0
## P 0 5 4 1 14 14
## S0 0 1 3 0 12 108
```

One R with bucket size 11 seems to give us 6 different classifiers which is what i want. But the accuracy of the One R model is not very high.

One R Classifier model with bucket size 11

huml:

```
< 29.71 -> S0
< 34.31 -> T
< 45.64 -> P
< 108.105 -> SW
< 126.94 -> R
>= 126.94 -> SW
```

Correctly Classified Instances 208 51.4851 %

Incorrectly Classified Instances 196 48.5149 %

```
conf.matrix <-
  rbind(
    c(69,11,1,10,8,9),
    c(35,2,4,4,10,8),
    c(4,1,4,2,8,4),
    c(29,5,1,6,6,1),
    c(5,0,7,0,16,10),
    c(2,0,3,0,10,109))
colnames(conf.matrix) <- c("SW", "W", "T", "R", "P", "S0")

row.names(conf.matrix) <- c("SW", "W", "T", "R", "P", "S0")

conf.matrix
```

```
## SW W T R P S0
## SW 69 11 1 10 8 9
## W 35 2 4 4 10 8
## T 4 1 4 2 8 4
## R 29 5 1 6 6 1
## P 5 0 7 0 16 10
## S0 2 0 3 0 10 109
```

We get a lower accuracy but from the first run we were sure that the rule was overfitted

Next i tried Naive Bayes but it has almost the same result and not a lot of options to change:

Correctly Classified Instances 209 51.7327 % Incorrectly Classified Instances 195 48.2673 %

=== Confusion Matrix ===

a b c d e f <- classified as 35 33 1 23 8 8 | a = SW 10 20 1 8 11 13 | b = W 2 4 0 1 15 1 | c = T 7 7 0 25 8 1
| d = R 0 4 0 0 18 16 | e = P 0 1 0 0 12 11 | f = S0

```
conf.matrix <-
  rbind(
    c(35,33,1,23,8,8),
    c(10,20,1,8,11,13),
    c(2,4,0,1,15,1),
    c(7,7,0,25,8,1),
```

```

c(0,4,0,0,18,16),
c(0,1,0,0,12,11))
colnames(conf.matrix) <- c("SW", "W", "T", "R", "P", "SO")

row.names(conf.matrix) <- c("SW", "W", "T", "R", "P", "SO")

conf.matrix

##      SW  W  T  R  P  SO
## SW 35 33 1 23  8  8
## W  10 20 1  8 11 13
## T   2  4 0  1 15  1
## R   7  7 0 25  8  1
## P   0  4 0  0 18 16
## SO  0  1 0  0 12 11

```

With using Random.Forest i have done 3 diffrent runs, Becouse this accuracy is already much higher than the one & zero R performance. one with 10 max depht, 15 max depht and 20 max depht.

Simple logistic also gives promising results with default settings:

Correctly Classified Instances 304 75.2475 % Incorrectly Classified Instances 100 24.7525 %

=== Confusion Matrix ===

a b c d e f <- classified as 78 17 2 5 0 6 | a = SW 24 33 0 0 0 6 | b = W 0 0 11 3 8 1 | c = T 4 3 0 35 5 1 | d = R 0 6 1 1 25 5 | e = P 0 0 1 1 0 122 | f = SO

SMO with default settings gives very close results to One R:

Correctly Classified Instances 217 53.7129 % Incorrectly Classified Instances 187 46.2871 %

=== Confusion Matrix ===

a b c d e f <- classified as 94 0 0 0 0 14 | a = SW 41 0 0 0 0 22 | b = W 7 0 0 0 0 16 | c = T 41 0 0 0 0 7 | d = R 9 0 0 0 0 29 | e = P 1 0 0 0 0 123 | f = SO

Nearest neighbour IBk gives very promising results and we might look into the future:

Correctly Classified Instances 336 83.1683 % Incorrectly Classified Instances 68 16.8317 %

=== Confusion Matrix ===

a b c d e f <- classified as 91 8 0 4 0 5 | a = SW 12 44 1 1 3 2 | b = W 0 1 16 2 2 2 | c = T 2 1 0 43 0 2 | d = R 0 0 1 1 28 8 | e = P 6 1 0 1 2 114 | f = SO

j48 with default settings gives us medioker results and mighnt not be very interesting to use in the future:

Correctly Classified Instances 271 67.0792 % Incorrectly Classified Instances 133 32.9208 %

=== Confusion Matrix ===

a b c d e f <- classified as 68 23 2 11 1 3 | a = SW 18 30 2 4 4 5 | b = W 3 3 11 1 1 4 | c = T 8 5 0 31 3 1 | d = R 1 2 4 2 23 6 | e = P 5 4 5 1 1 108 | f = SO

Tester: weka.experiment.PairedCorrectedTTester -G 4,5,6 -D 1 -R 2 -S 0.05 -result-matrix "weka.experiment.ResultMatrixPlainT
-mean-prec 2 -stddev-prec 2 -col-name-width 0 -row-name-width 25 -mean-width 2 -stddev-width 2 -sig-width
1 -count-width 5 -print-col-names -print-row-names -enum-col-names" Analysing: Percent_correct Datasets:
1 Resultsets: 8 Confidence: 0.05 (two tailed) Sorted by: - Date: 10/6/18, 7:59 PM

Dataset (1) rules.Ze | (2) rules (3) trees (4) trees (5) funct (6) funct (7) bayes (8) lazy.

CleanData (100) 30.69 | 53.39 v 66.84 v 79.14 v 74.54 v 53.52 v 50.67 v 83.32 v

(v/ /*) | (1/0/0) (1/0/0) (1/0/0) (1/0/0) (1/0/0) (1/0/0) (1/0/0) (1/0/0)

Key: (1) rules.ZeroR ‘ 48055541465867954 (2) rules.OneR’-B 11’ -3459427003147861443 (3) trees.J48 ‘-C 0.25 -M 2’ -217733168393644444 (4) trees.RandomForest ‘-P 100 -I 100 -num-slots 1 -K 0 -M 1.0 -V 0.001 -S 1 -depth 15’ 1116839470751428698 (5) functions.SimpleLogistic ‘-I 0 -M 500 -H 50 -W 0.0’ 7397710626304705059 (6) functions.SMO ‘-C 1.0 -L 0.001 -P 1.0E-12 -N 0 -V -1 -W 1 -K "functions.supportVector.PolyKernel -E 1.0 -C 250007" -calibrator "functions.Logistic -R 1.0E-8 -M -1 -num-decimal-places 4"’ -6585883636378691736 (7) bayes.NaiveBayes ‘ 5995231201785697655 (8) lazy.IBk’-K 1 -W 0 -A "weka.core.neighboursearch.LinearNNSearch -A \"weka.core.EuclideanDistance -R first-last\"” -3080186098777067172

So from our experimentation with different classification algorithms we conclude that Random.Forest and IBk ran the best of them all.

Random.Forest

First i have changed the max depth value and tested 10, 15, 20. in this testing using the experimenter i concluded that a max depth of 15 gives the best results.

Trees.Ra(Max 10) : 78.85%

Trees(Max 15) : 79.14%

Trees(Max 20) : 79.09%

```
conf.matrix <-
  rbind(
    c(87,11,0,4,0,6),
    c(17,34,0,2,4,6),
    c(2,0,12,2,4,3),
    c(7,1,0,37,3,0),
    c(0,0,1,1,30,6),
    c(0,0,1,1,1,121))
colnames(conf.matrix) <- c("SW", "W", "T", "R", "P", "SO")

row.names(conf.matrix) <- c("SW", "W", "T", "R", "P", "SO")

conf.matrix
```

```
##      SW  W  T  R  P  SO
## SW  87 11  0  4  0  6
## W   17 34  0  2  4  6
## T    2  0 12  2  4  3
## R    7  1  0 37  3  0
## P    0  0  1  1 30  6
## SO   0  0  1  1  1 121
```

Changing other settings only gives worse results.

IBk, Nearest Neighbour

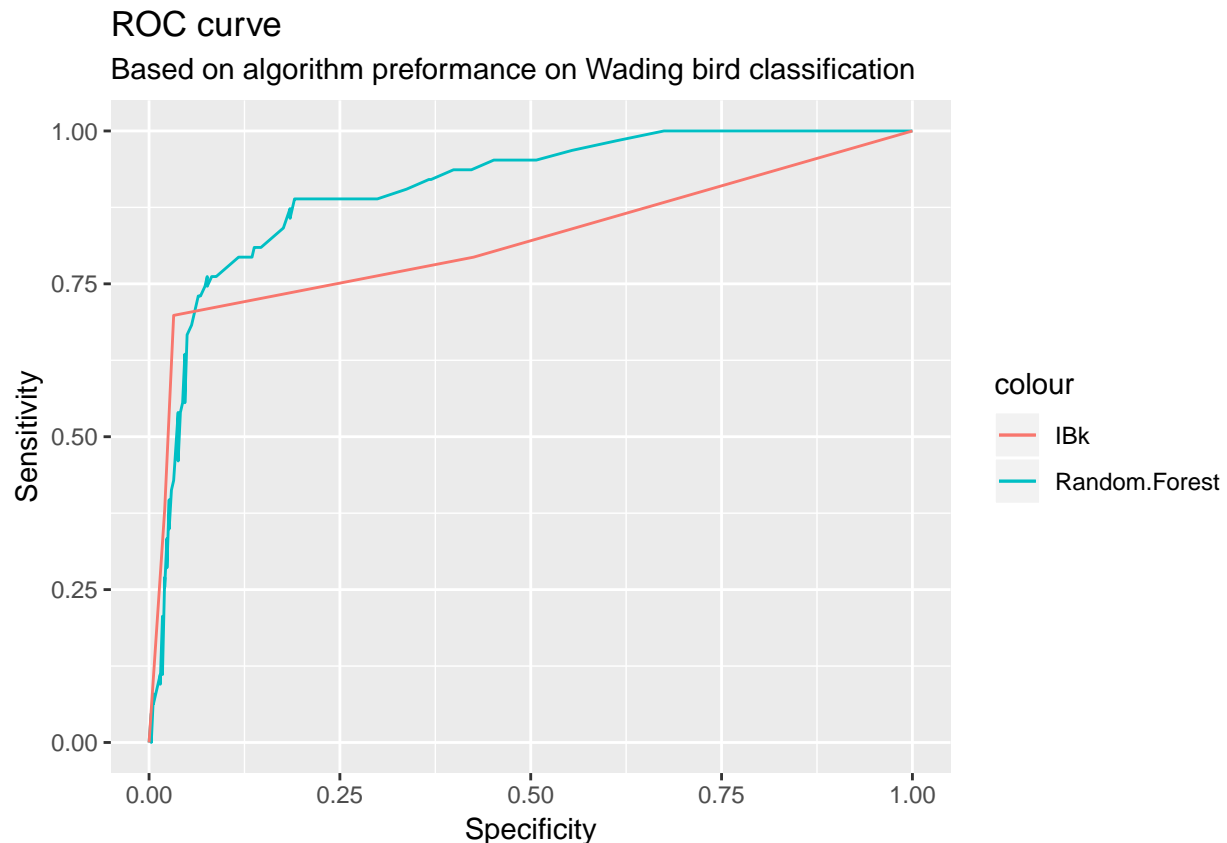
It seems that it doesn't really matter what settings are used for this algorithm as it gives them all the same accuracy. and if accuracy is the only metric we really want to maximize we can use default settings.

```

rocdataW <- read.csv("../data/RocWading.arff", header = F, comment.char = "@", na.strings = "?")
rocdataWibk <- read.csv("../data/RocWadingIbk.arff", header = F, comment.char = "@", na.strings = "?")

library(ggplot2)
ggplot()+
  geom_line(aes(x = rocdataW$V6, y = rocdataW$V7, color="Random.Forest"))+
  geom_line(aes(x = rocdataWibk$V6, y = rocdataWibk$V7, color="IBk"))+
  labs(x = "Specificity",
       y = "Sensitivity",
       title = "ROC curve",
       subtitle = "Based on algorithm performance on Wading bird classification"
  )

```



Learning Curve

To analyse the learning curve for these algorithms i am gradually removing more data and trying to classify the data with the algorithm. This can be done by using the weka experimenter, using *InstancesResultListener* -O *weka_experiment.arff* as a destination, *CrossValidationResultProducer* with *splitEvaluator: Classifier-SplitEvaluator* with classifier: *FilteredClassifier*, filter: *RemovePercentage* and classifier set to *random.forest maxdepth 15* or *IBk*

Results For Random.Forest

Dataset (1) meta.Fil | (2) meta. (3) meta. (4) meta. (5) meta. (6) meta. (7) meta. (8) meta. (9) meta.

CleanData (100) 22.07 | 23.27 25.17 26.82 v 29.17 v 32.59 v 35.48 v 39.24 v 47.05
v

(v/ /*) | (0/1/0) (0/1/0) (1/0/0) (1/0/0) (1/0/0) (1/0/0) (1/0/0) (1/0/0)

Results For IBk

Dataset (1) meta.Fil | (2) meta. (3) meta. (4) meta. (5) meta. (6) meta. (7) meta. (8) meta. (9) meta.

CleanData (100) 18.26 | 19.08 20.63 23.01 v 25.26 v 28.52 v 31.58 v 35.75 v 45.99
v

(v/ /*) | (0/1/0) (0/1/0) (1/0/0) (1/0/0) (1/0/0) (1/0/0) (1/0/0) (1/0/0)

```
RemovedPercentage <- c(10, 20, 30, 40, 50, 60, 70, 80, 90)
Random.Forest <- c(22.07, 23.27, 25.17, 26.82, 29.17, 32.59, 35.48, 39.24, 47.05)
IBk <- c(18.26, 19.08, 20.63, 23.01, 25.26, 28.52, 31.58, 35.75, 45.99)
```

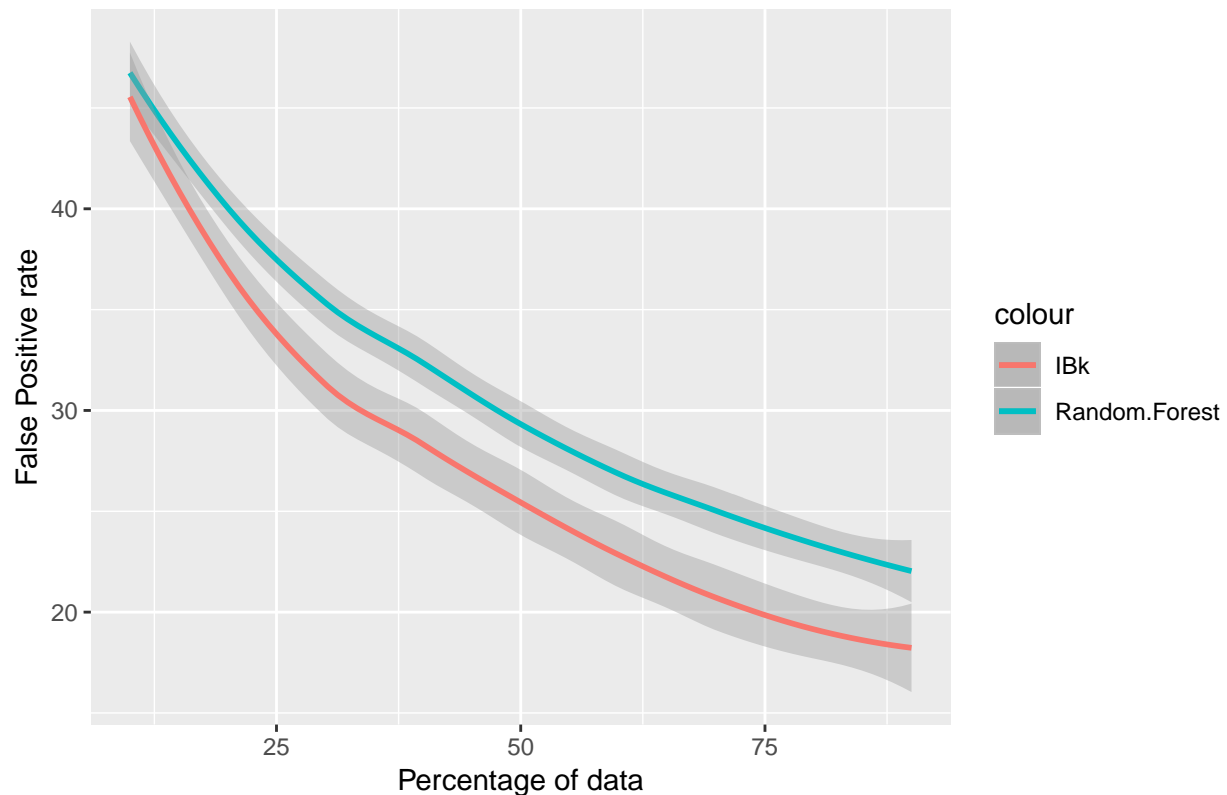
```
# reversing data because of small mistake in my understanding of learning curves & how weka handles the
dataf <- data.frame(rev(RemovedPercentage), Random.Forest, IBk)
dataf <- dataf[seq(dim(dataf)[1],1),]
dataf
```

```
## rev.RemovedPercentage. Random.Forest IBk
## 9 10 47.05 45.99
## 8 20 39.24 35.75
## 7 30 35.48 31.58
## 6 40 32.59 28.52
## 5 50 29.17 25.26
## 4 60 26.82 23.01
## 3 70 25.17 20.63
## 2 80 23.27 19.08
## 1 90 22.07 18.26
```

```
library(ggplot2)
ggplot(dataf)+
  geom_smooth(aes(x = RemovedPercentage, y = Random.Forest, color="Random.Forest"))+
  geom_smooth(aes(x = RemovedPercentage, y = IBk, color="IBk"))+
  ggtitle("Learning curve for Random.Forest & IBk")+
  xlab("Percentage of data")+
  ylab("False Positive rate")
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```

Learning curve for Random.Forest & IBk



Because our learning data is not very large (404), it is not really easy to determine the minimum amount of data needed for classification and we can assume that 400 samples is necessary.

```
experimenter_data <- read.csv("../data/AlgorithmPerformance.csv", header = T, sep = ",")
```

From my analyses im going to choose Random.Forest as classifier algorithm. although IBk gives a higher accuracy because we haven't normalised the data using nearest neighbour isn't reliable and thats why we shouldn't use it.

To give an answer to the research question we need to run a few more weka experiments with Random forest. We want to see what bone in the birds have te most impact on classification accuracy.

```
# New Clean dataset with all bones.
Birdbones.Clean.All <- BirdBones.noNA[! BirdBones.noNA$id %in% outliers$id, ]

write.csv(Birdbones.Clean.All, "../data/CleanDataAll.csv")
```

Base Results with all bones:

Accuracy : 84.6535 %

Removed humurus: huml & humw collums:

Accuracy: 82.1782 %

Difference: -2.4753 %

Removed ulnal & ulnaw collums:

Accuracy: 83.1683 %

Difference: -1.4852 %

Removed feml & femw collums:

Accuracy: 80.4455 %

Diffrence: -4.208 %

Removed tibl & tibw collums:

Accuracy: 84.4059 %

Diffrence: -0.2476 %

Removed tarl & tarw collums:

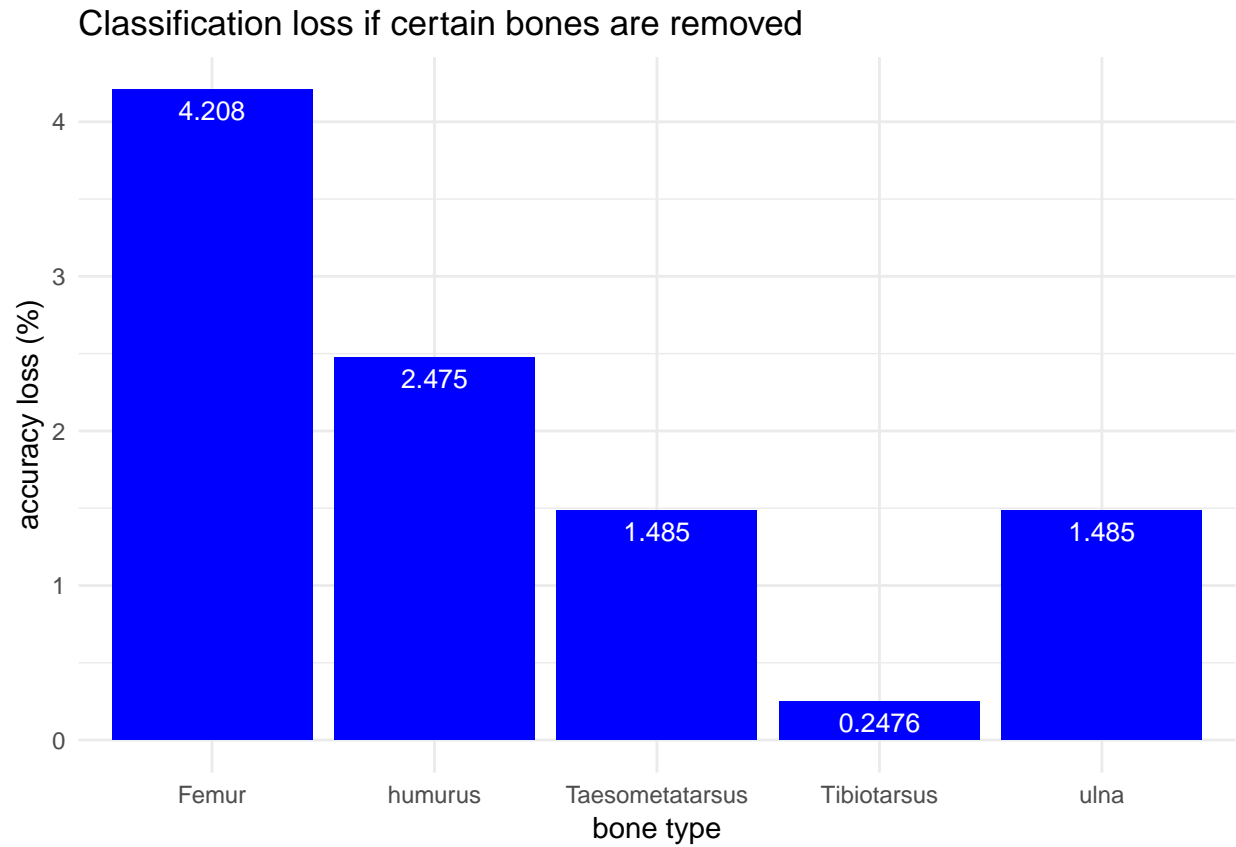
Accuracy: 83.1683 %

Diffrence: -1.4852 %

```
humurus <- signif(84.6535 - 82.1782, 4)
ulna <- signif(84.6535 -83.1683, 4)
Femur <- signif(84.6535 -80.4455, 4)
Tibiotarsus <- signif(84.6535 - 84.4059, 4)
Taesometatarsus <- signif(84.6535-83.1683, 4)

loss <- data.frame(Bone=c("humurus", "ulna", "Femur", "Tibiotarsus", "Taesometatarsus"),
                   Classify_loss=c(humurus, ulna, Femur, Tibiotarsus, Taesometatarsus))

library(ggplot2)
ggplot(data=loss, aes(x=Bone, y=Classify_loss)) +
  geom_bar(stat="identity", fill = "blue")+
  geom_text(aes(label=Classify_loss), vjust=1.6, color="white", size=3.5)+
  theme_minimal()+
  labs(x = "bone type",
       y = "accuracy loss (%)",
       title = "Classification loss if certain bones are removed"
  )
```



above we see the difference it makes per bone what the classification accuracy is. The Femur seems to be the most important bone for the functioning in bird species.