Statistical analysis in RStudio

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0.0.1 Abstact

1 INTRODUCTION

The main objective of statistical analysis is to find the correlation and Trends of seal abundance using the serial dataset.

Firstly we will download the data and convert it into a csv file and then import data into R studio after importing data We will read the data and convert the data into data frame Which will import data into rows and columns. If we check the head of data we can find There are 5 columns 210 observations.

- The first column represents the year, each row consists of the year from 2007 to 2010.
- The second column represents the month of a specific year; there are 15 unique variables if it presents the month of a particular Year.
- The third column represents a site which consists of 7 unique variables A,B,C,D,Split and Wall.
- The fourth column represents species which have true unique species Harbour and grey.
- The final column represents the average count of each species in a particular year year and month each variable has a unique count value.

After looking at the column if we check the structure of data,the first four columns represent the character data type, the last column that is average count represents the numerical data type.

After getting familiar with the data set ,the first four column data type should be changed to factor type as in which column the variable of rows are repetitive.

Summer	Year.Month	Site	Species	average.count
summer-2007	2007.Jun	A	HARBOUR	14.1
summer-2007	2007.Jun	B	HARBOUR	0.3

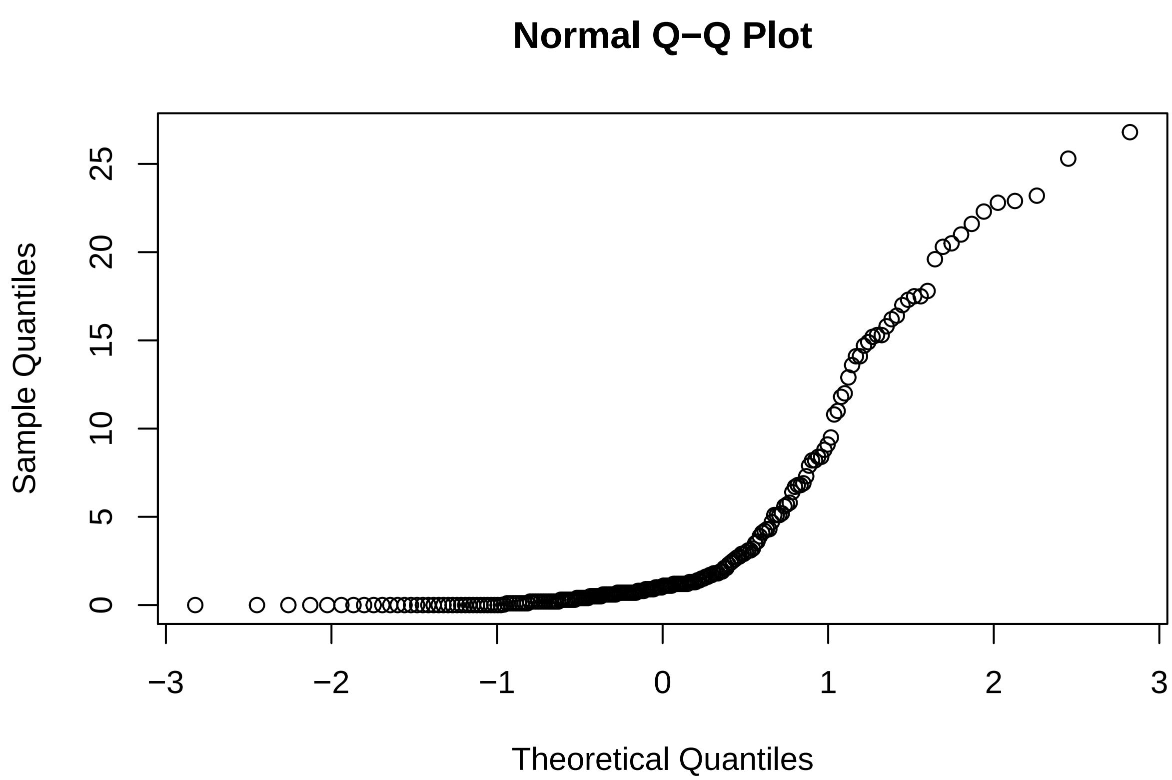
Summer	Year.Month	Site	Species	average.count
summer-2007	2007.Jun	C	HARBOUR	14.7
summer-2007	2007.Jun	Spit	HARBOUR	0.1
summer-2007	2007.Jun	Wall	HARBOUR	0.7
summer-2007	2007.Jun	D	HARBOUR	0.0

```
## 'data.frame':    210 obs. of  5 variables:
##  $ Summer       : chr  "summer-2007" "summer-2007" "summer-2007" "summer-2007" ...
##  $ Year.Month   : chr  "2007.Jun" "2007.Jun" "2007.Jun" "2007.Jun" ...
##  $ Site         : chr  "A" "B" "C" "Spit" ...
##  $ Species      : chr  "HARBOUR" "HARBOUR" "HARBOUR" "HARBOUR" ...
##  $ average.count: num  14.1 0.3 14.7 0.1 0.7 0 0 0.3 0 2.6 ...
```

2 MATERIALS AND METHODS

2.1 QQNORM Test

After checking rows and columns of data, it can be easily identified that only the average.count data column has numerical value. If we check the normality of the average.count column using the qqnorm() function,The Below visualization data represents the relationship between the theoretical and sample quantities which derive the plotted data is distinctly curved and determines that the data is not normal.



While finding out that data is not normal in normality test using qqnorm function, if we run the same test using shapiro.test() function, The p-value is Greater than 0.01 we can say that it then all hypothesis is not rejected Data is not significantly distributed therefore we have to perform non parametric test.

```
##
##  Shapiro-Wilk normality test
##
## data:  data$average.count
## W = 0.67749, p-value < 2.2e-16
```

Since the data is not significant,in order to find out The number of seals are significantly different for each year plot the data of average count of number of seals for each year but before that we have to change the data type of the first four columns into factors.

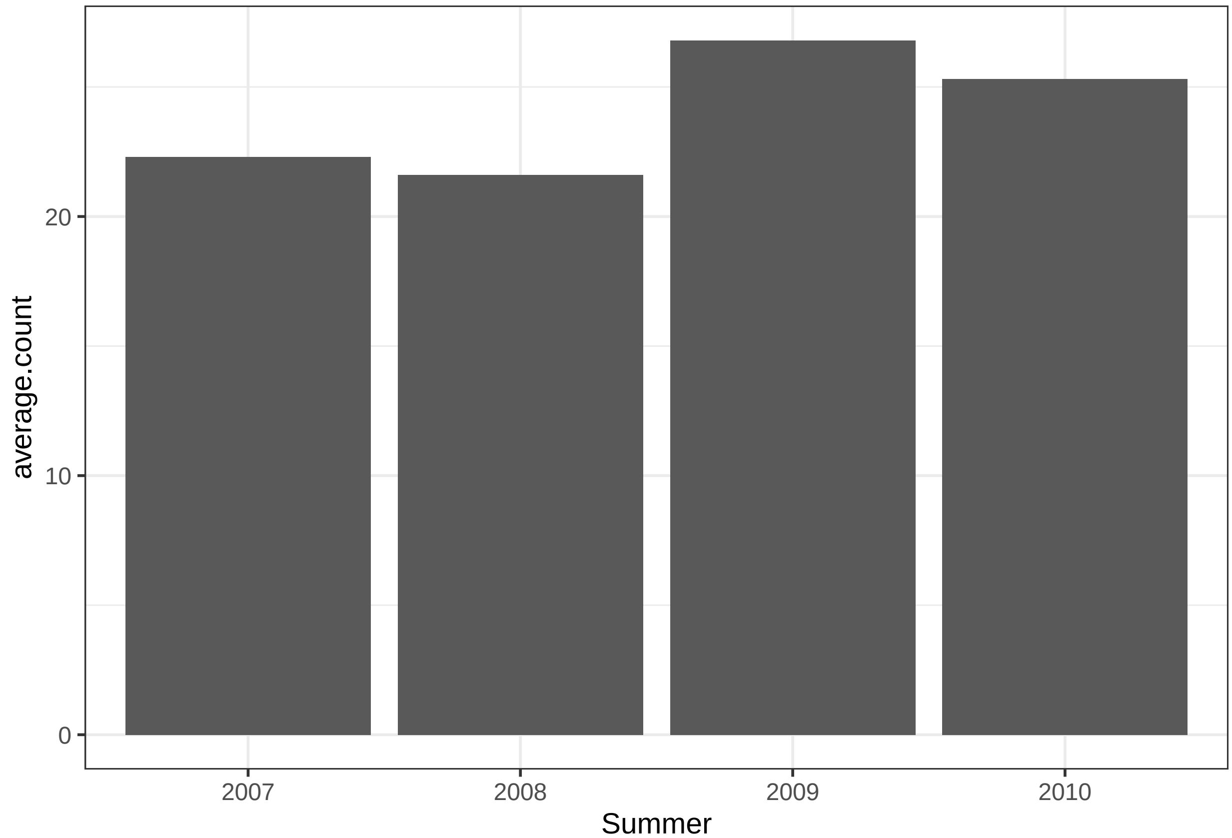
```
## 'data.frame':    210 obs. of  5 variables:
##  $ Summer       : Factor w/ 4 levels "2007","2008",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ Year.Month   : Factor w/ 15 levels "2007.Aug","2007.Jul",..: 3 3 3 3 3 3 3 3 3 3 ...
##  $ Site         : Factor w/ 7 levels "A","B","C","D",..: 1 2 3 6 7 4 5 1 2 3 ...
##  $ Species      : Factor w/ 2 levels "GREY","HARBOUR": 2 2 2 2 2 2 2 1 1 1 ...
##  $ average.count: num  14.1 0.3 14.7 0.1 0.7 0 0 0.3 0 2.6 ...
```

After changing the data type we can find that the summer column has aur factor levels, Year. month column has 15 factor levels, the site column as 7 factor level and and the species column two factor levels.

If we see the data of average count for each year we see that the data is count is increasing for each year but we cannot that the changes are significant or not.

In order to find out this we can transfer some non parametric test like kruskal Wallis rank sum test Which help us to determine the overall correlation and statistical Association for data by providing a chi-squared interpretation and a p-value.

But before if we check the below graph, we can see that the 2009 has highest average count followed by 2010 and the least averge count is 2008.



2.2 Kruskal-Wallis Test

In order to perform the Krukals-wallis test, we need to use the kruskal.test() function.

```
##
##  Kruskal-Wallis rank sum test
##
## data:  data$average.count and data$Summer
## Kruskal-Wallis chi-squared = 6.236, df = 3, p-value = 0.1007
```

Firstly, if we explore the overall difference between all the variables we can see that The P value is greater than 0.01, thus we can say that it There is no significant difference between the groups. In order to explore this into more detail to find out that the pairs of groups are different or not, will use pairwise willox test For comparing different group levels for multiple testing.

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  data$average.count and data$Summer
##
##      2007 2008 2009
## 2008 0.89 -    -
## 2009 0.20 0.43 -
## 2010 0.43 0.64 0.89
```

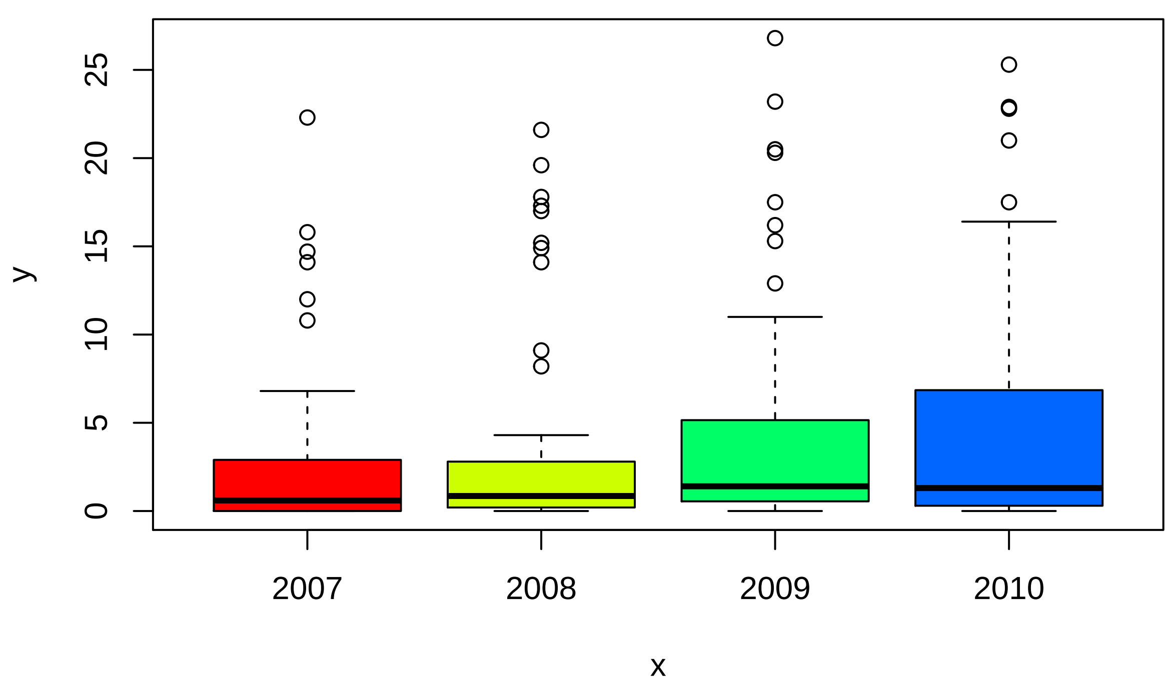
```
##
## P value adjustment method: holm
```

In the above test we can see that the P value for significant years is quite normal. further, providing an adjustment method we can avoid the false positive results in order to see more accuracy.

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  data$average.count and data$Summer
##
##      2007 2008 2009
## 2008 0.54 -    -
## 2009 0.17 0.17 -
## 2010 0.17 0.32 0.75
##
## P value adjustment method: BH
```

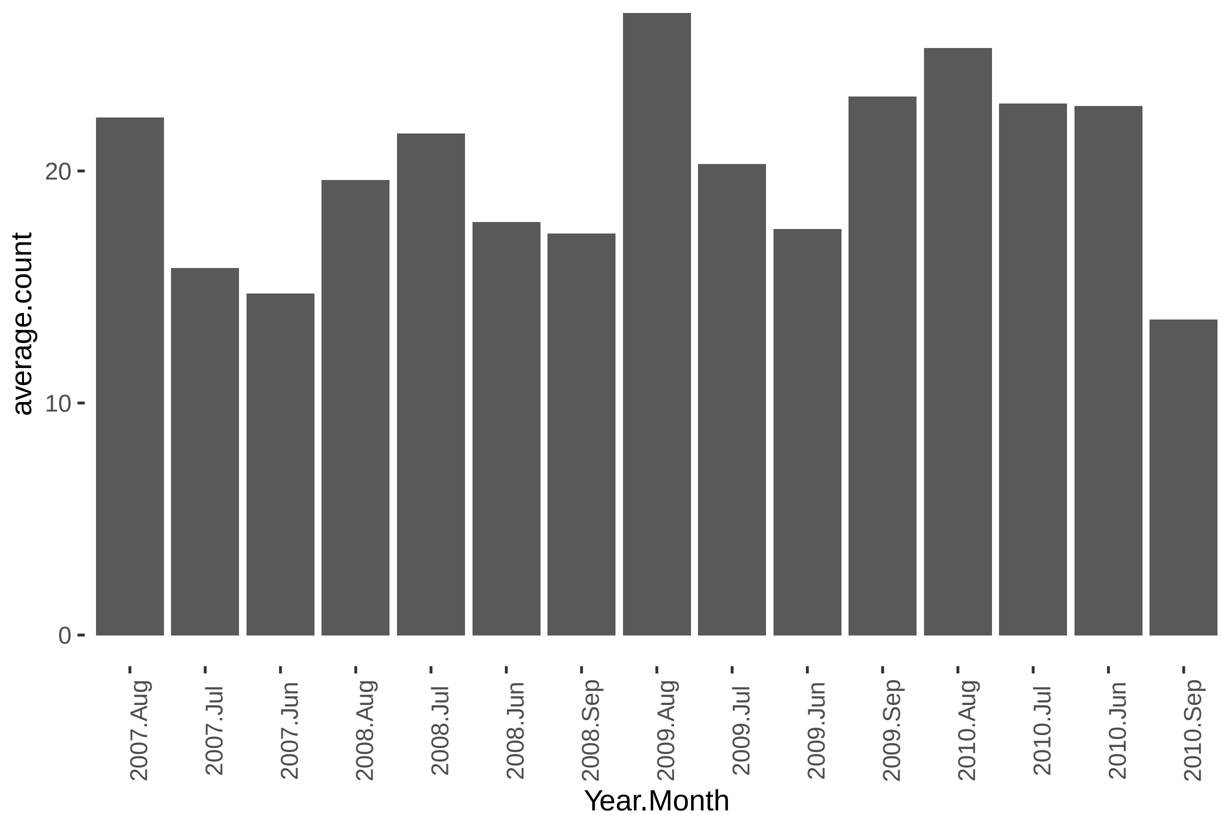
In the above test we can see that the adjusted P value is greater than 0.05, this shows that your value is not significant. In order to understand it with more clarity if we plot our data we can see that there was a significant difference between 2010 and 2007, we can see that the highest number of seals were counted in 2010. Also we can see that in 2007.

There were some high counts of seal, but in the previous bar graph it was suggested that there was a big significant difference between 2007 and 2010. From this we can say that the statistical tests were more accurate and help us to find the significant errors which were present in data.



After this we can check the presence of the seals for each month in a particular year. We might be able to explore the difference for the presence of seals in each month of the year.

The plot below shows the values of average count for each month of particular year.We can see that in 2009 Aug,the number of species were counted the most and in 2010 Sep the species were counted the least. But in order to find significant relationship we need to explore the data and run test accordingly.



2.2.1 Kruskal Test For Each month

If we consider the year 2007, we can see that there is no significant difference between different months.The p-value is greater than 0.05 and the adjusted p value is also greater than 0.05.

```
##
##  Kruskal-Wallis rank sum test
##
## data:  data$average.count[data$Summer == "2007"] and data$Year.Month[data$Summer == "2007"]
## Kruskal-Wallis chi-squared = 1.3113, df = 2, p-value = 0.5191

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  data$average.count[data$Summer == "2007"] and data$Year.Month[data$Summer == "2007"]
##
##          2007.Aug 2007.Jul
## 2007.Jul 0.63     -
## 2007.Jun 0.63     0.63
##
## P value adjustment method: BH
```

If we consider the year 2008, we can see that there is no significant difference between different months.

```
##
##  Kruskal-Wallis rank sum test
##
## data:  data$average.count[data$Summer == "2008"] and data$Year.Month[data$Summer == "2008"]
## Kruskal-Wallis chi-squared = 0.86061, df = 3, p-value = 0.8349

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  data$average.count[data$Summer == "2008"] and data$Year.Month[data$Summer == "2008"]
##
##          2008.Aug 2008.Jul 2008.Jun
## 2008.Jul 0.93     -        -
## 2008.Jun 0.93     0.93     -
## 2008.Sep 0.93     0.93     0.93
##
## P value adjustment method: BH
```

If we consider the year 2007, we can see that there is no significant difference between different months.

```
##
```

```
##  Kruskal-Wallis rank sum test
##
## data:  data$average.count[data$Summer == "2009"] and data$Year.Month[data$Summer == "2009"]
## Kruskal-Wallis chi-squared = 0.42051, df = 3, p-value = 0.936

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  data$average.count[data$Summer == "2009"] and data$Year.Month[data$Summer == "2009"]
##
##          2009.Aug 2009.Jul 2009.Jun
## 2009.Jul 1        -        -
## 2009.Jun 1        1        -
## 2009.Sep 1        1        1
##
## P value adjustment method: BH
```

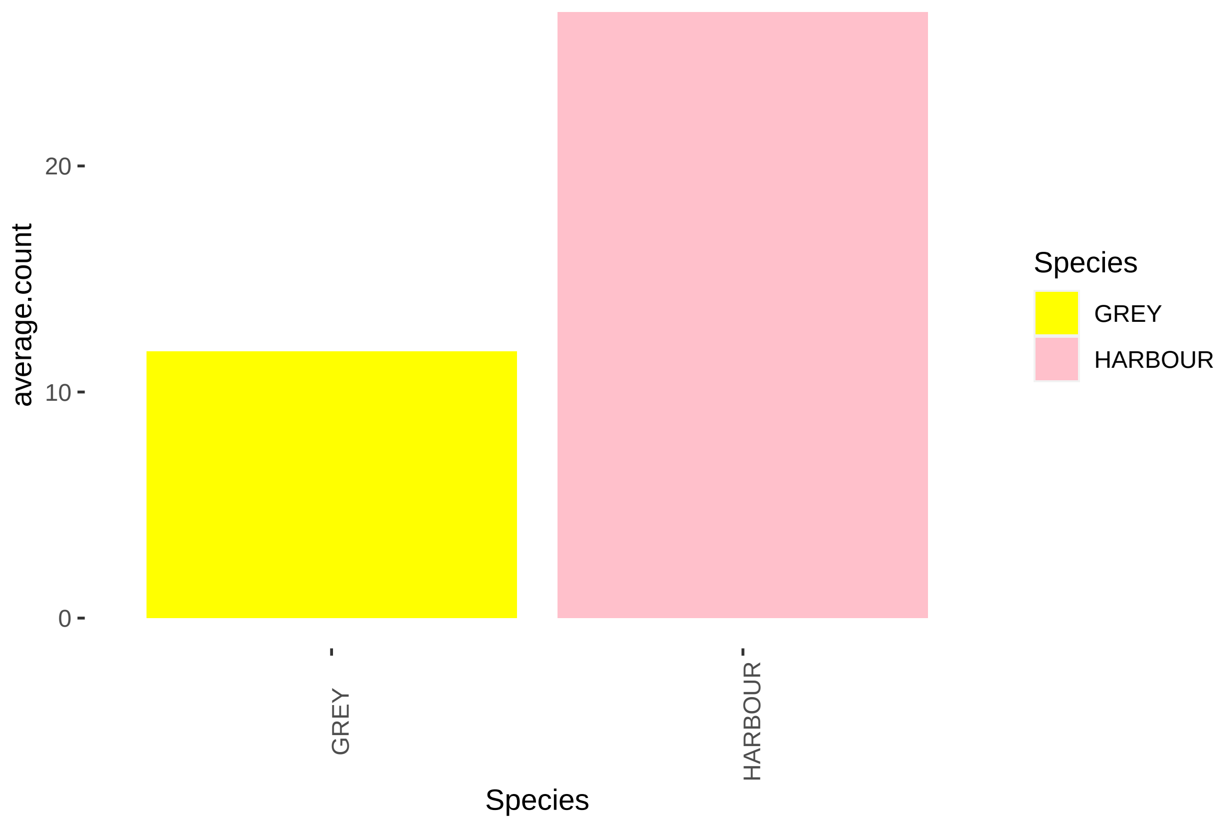
If we consider the year 2010, we can see that there is slight significant difference between different months.

```
##
##  Kruskal-Wallis rank sum test
##
## data:  data$average.count[data$Summer == "2010"] and data$Year.Month[data$Summer == "2010"]
## Kruskal-Wallis chi-squared = 2.5001, df = 3, p-value = 0.4753

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
```

```
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties

## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties


##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  data$average.count[data$Summer == "2010"] and data$Year.Month[data$Summer == "2010"]
##
##          2010.Aug 2010.Jul 2010.Jun
## 2010.Jul 0.75     -        -
## 2010.Jun 0.60     0.96     -
## 2010.Sep 0.96     0.60     0.60
##
## P value adjustment method: BH
```

2.3 Specices Abundance

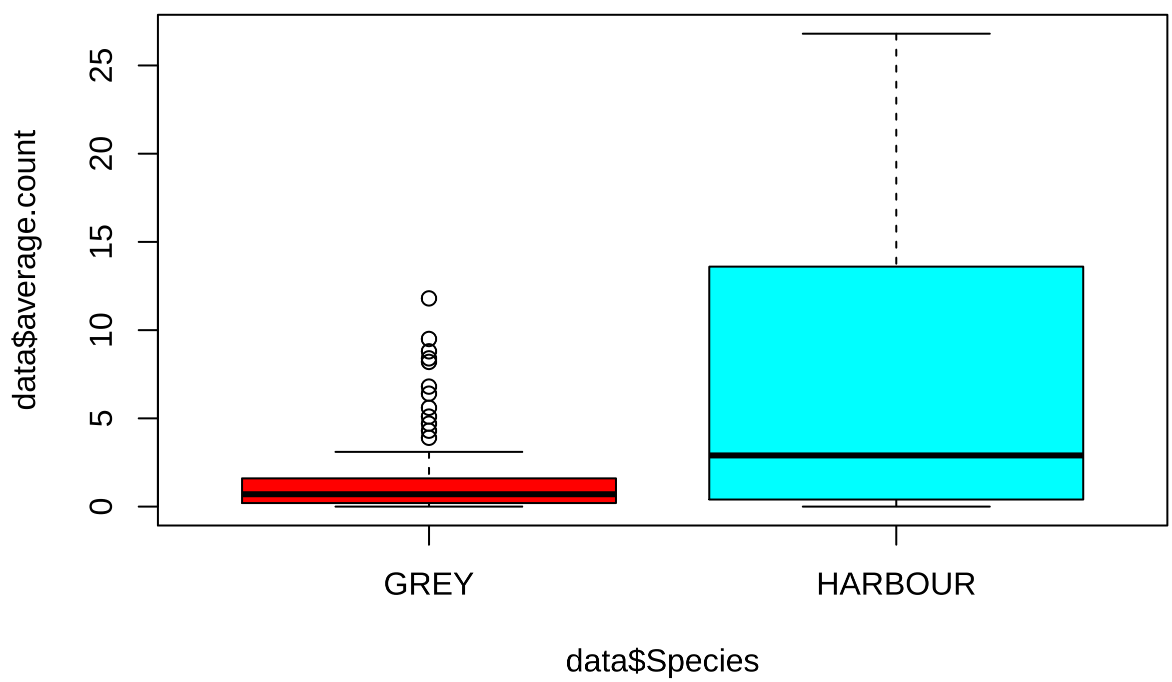
Considering the data and previous stats we found that there were no significant difference for each month but in order to get detailed information about the species we can check the count of each type of species and find out the non-significant relationship of the data .



As we had seen the above graph about the average count is increasing over year to year, using the kruskal test we can find out the difference between each species.

```
##
##  Kruskal-Wallis rank sum test
##
## data:  data$average.count and data$Species
## Kruskal-Wallis chi-squared = 18.66, df = 1, p-value = 1.562e-05
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  data$average.count and data$Species
##
##         GREY
## HARBOUR 1.6e-05
##
## P value adjustment method: BH
```



After performing the test we can easily see the p values is greater than 0.01 and after plotting the below graph we can say that the Harbour seals population are more comparatively grey. In other way, it can be derived that the harbor seals are more significantly common than the grey species.

Also, we can explore data in more detailed way in order to find out significant difference of species for each year.

If we look at the below stats, we can clearly see the p-value for 2007 year is greater than 0.05 and adjusted p-value is is also greater than 0.05 which derives there is slightest significance difference in the Species

```
##
##  Kruskal-Wallis rank sum test
##
## data:  data$average.count[data$Summer == "2007"] and data$Species[data$Summer == "2007"]
## Kruskal-Wallis chi-squared = 3.2976, df = 1, p-value = 0.06938
```

```
## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  data$average.count[data$Summer == "2007"] and data$Species[data$Summer == "2007"]
##
##         GREY
## HARBOUR 0.071
##
## P value adjustment method: BH
```

Again, If we look at the below stats, we can clearly see the p-value for 2008 year is greater than 0.05 and adjusted p-value is is also greater than 0.05 which derives there is slightest significance difference in the Species.

```
##
##  Kruskal-Wallis rank sum test
##
## data:  data$average.count[data$Summer == "2008"] and data$Species[data$Summer == "2008"]
## Kruskal-Wallis chi-squared = 2.727, df = 1, p-value = 0.09866
```

```
## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  data$average.count[data$Summer == "2008"] and data$Species[data$Summer == "2008"]
##
##         GREY
## HARBOUR 0.1
##
## P value adjustment method: BH
```

Again, If we look at the below stats, we can clearly see the p-value for 2009 year is below to 0.05 and adjusted p-value is is also less than 0.05 which derives there is significance difference in the Species.

```
##
##  Kruskal-Wallis rank sum test
##
## data:  data$average.count[data$Summer == "2009"] and data$Species[data$Summer == "2009"]
## Kruskal-Wallis chi-squared = 10.332, df = 1, p-value = 0.001307
```

```
## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  data$average.count[data$Summer == "2009"] and data$Species[data$Summer == "2009"]
##
##         GREY
## HARBOUR 0.0013
##
## P value adjustment method: BH
```

Finally, If we look at the below stats, we can clearly see the p-value for 2010 year is below to 0.05 and adjusted p-value is is also less than 0.05 which derives there is significance difference in the Species.

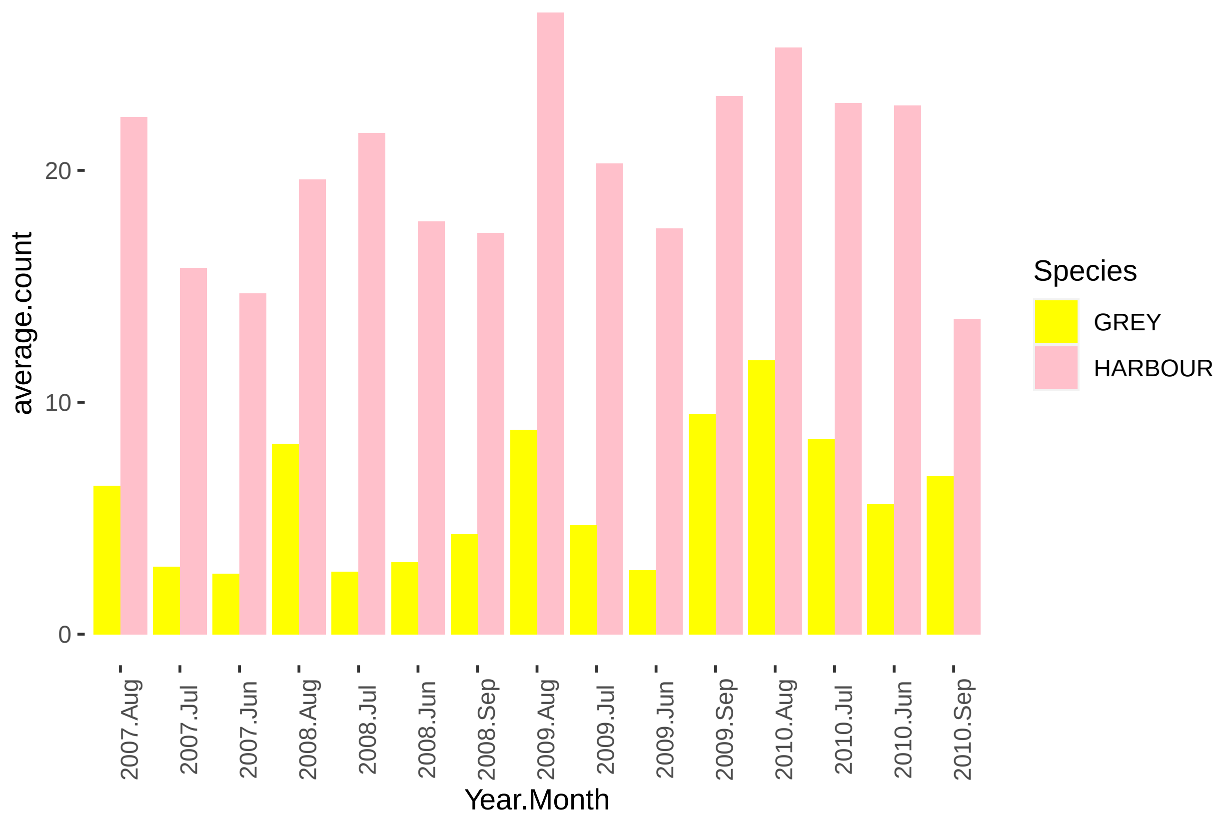
```
##
##  Kruskal-Wallis rank sum test
##
## data:  data$average.count[data$Summer == "2010"] and data$Species[data$Summer == "2010"]
## Kruskal-Wallis chi-squared = 4.1213, df = 1, p-value = 0.04235
```

```
## Warning in wilcox.test.default(xi, xj, paired = paired, ...): cannot compute
## exact p-value with ties
```

```
##
##  Pairwise comparisons using Wilcoxon rank sum test with continuity correction
##
## data:  data$average.count[data$Summer == "2010"] and data$Species[data$Summer == "2010"]
##
##         GREY
## HARBOUR 0.043
##
## P value adjustment method: BH
```

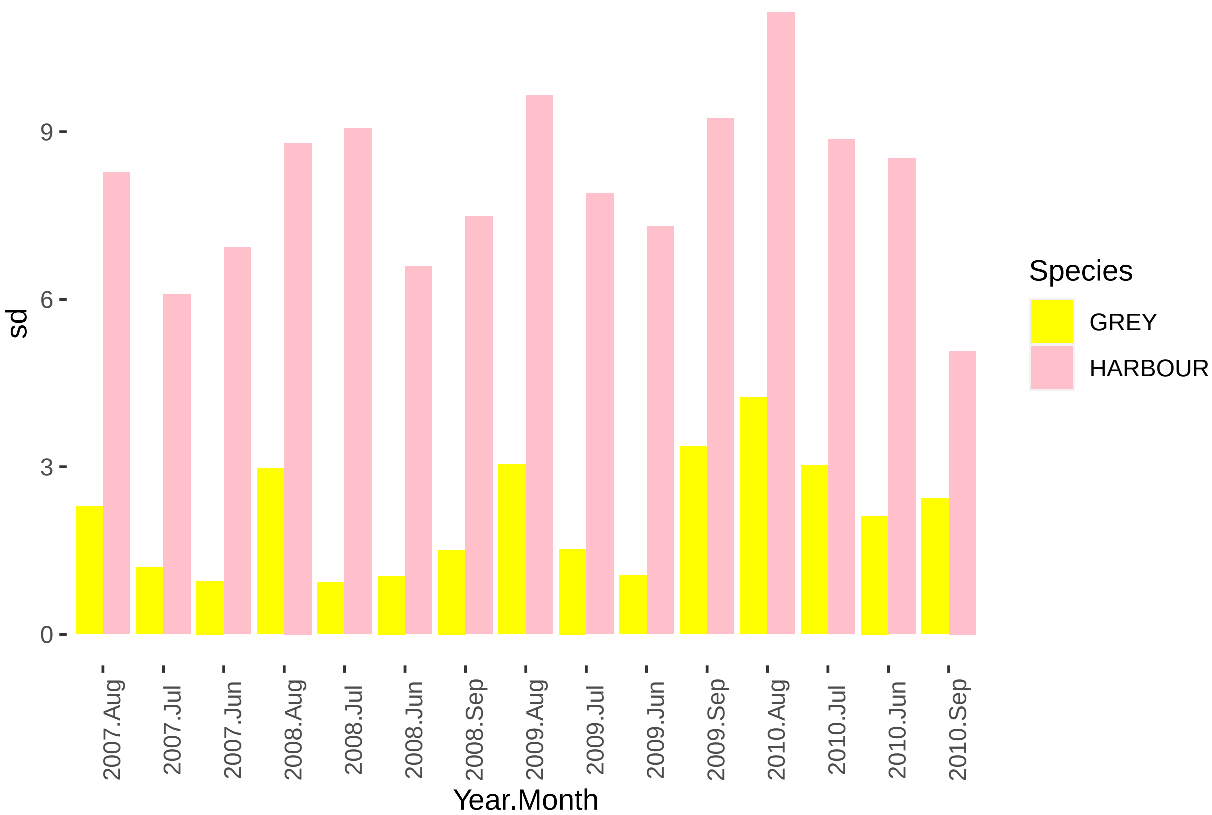
From this we can easily say that in 2007 and 2008 the population of species were not significantly different where as in 2009 and 2010 we can say that the population is significantly different from other.

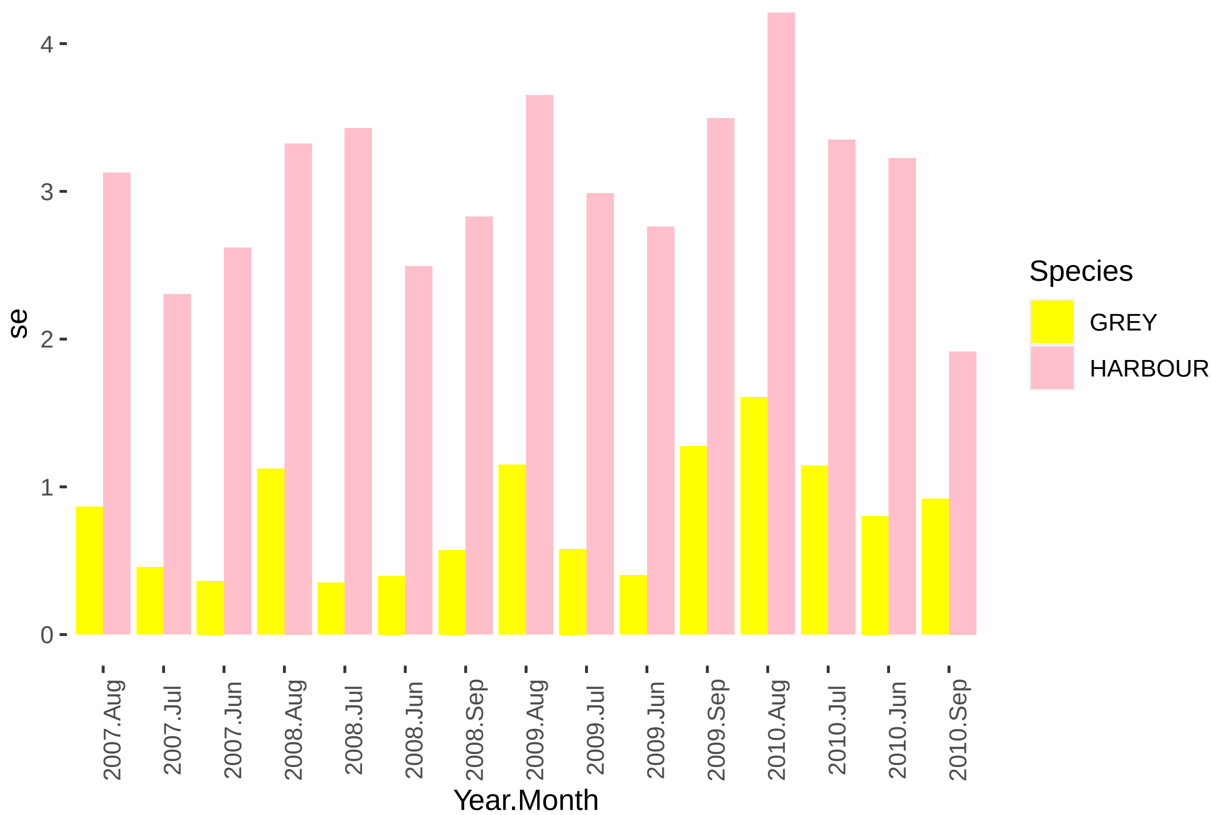
Therefore from here we need to calculate the error in order to find the out better results and improve the performance but before that we can check the population of individual species for particular month and further we can develop the error bars after calculating the error .



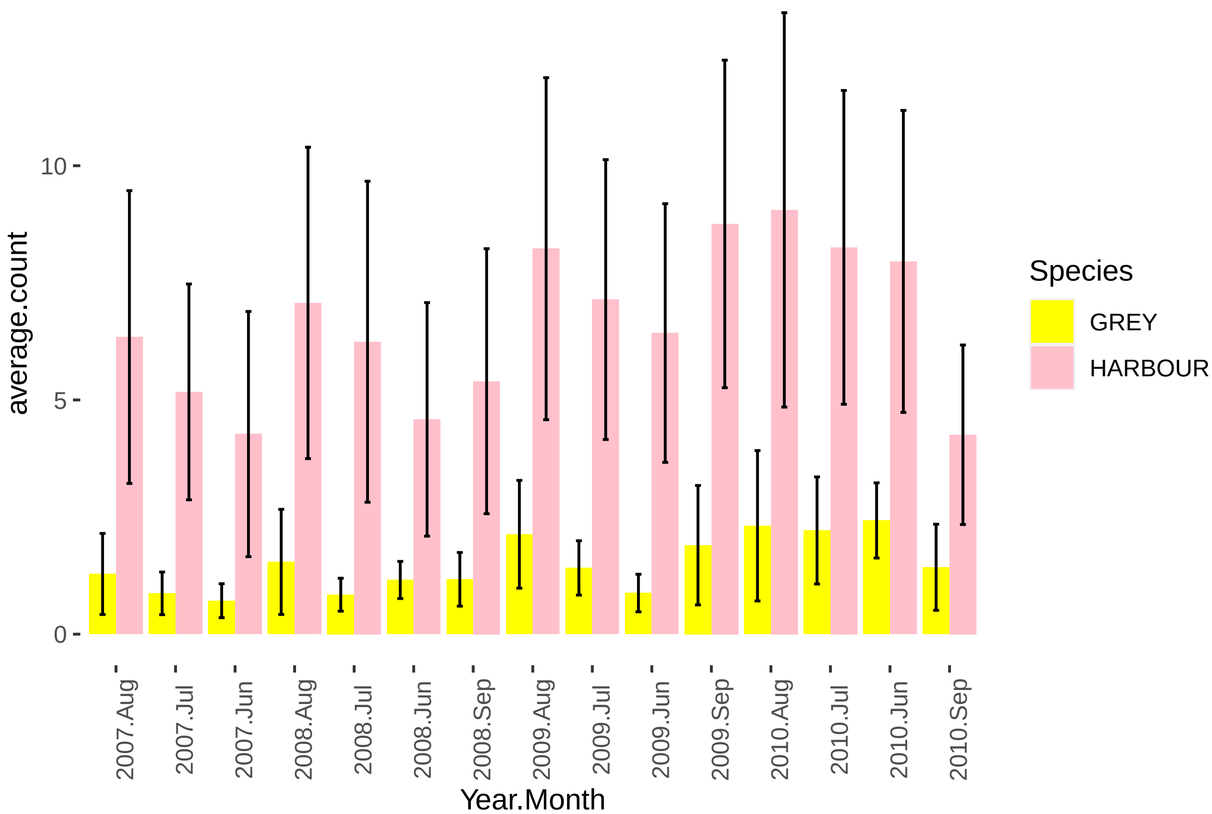
If you look at the graph of average count of each species in a particular month everywhere we can see that the existence of herbal species are way more than the gray species. Therefore we can say that the herbal species are more common than the gray species.In order to find the significant differences between the species we need to find the error species for particular month in each year using SummarySE() function.

Year.Month	Species	N	average.count	sd	se	ci
2007.Aug	GREY	7	1.2857143	2.2886885	0.8650430	2.1166839
2007.Aug	HARBOUR	7	6.3428571	8.2679818	3.1250034	7.6466079
2007.Jul	GREY	7	0.8714286	1.2051477	0.4555030	1.1145757
2007.Jul	HARBOUR	7	5.1714286	6.0939080	2.3032807	5.6359249
2007.Jun	GREY	7	0.7142857	0.9599107	0.3628121	0.8877693
2007.Jun	HARBOUR	7	4.2714286	6.9254878	2.6175883	6.4050079

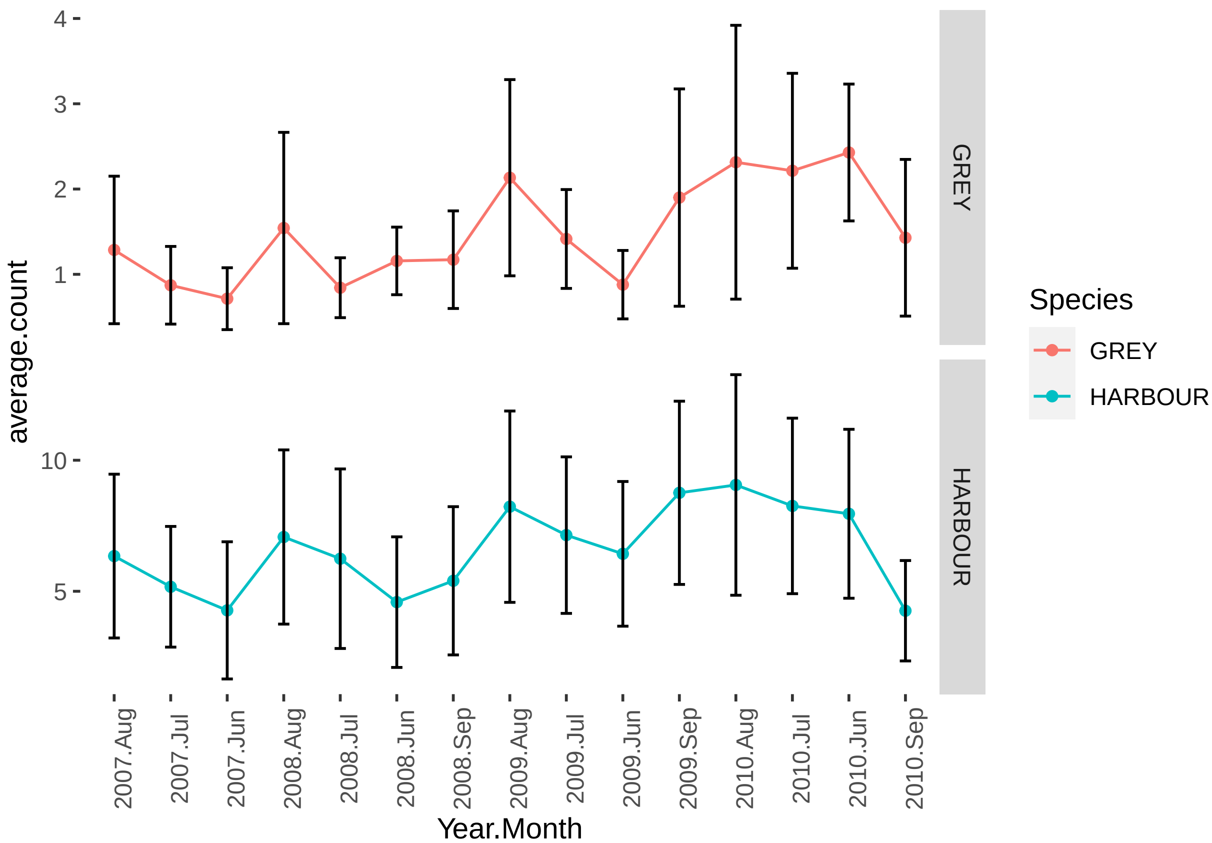

9
6
3
0
sd
2007.Aug
2007.Jul
2007.Jun
2008.Aug
2008.Jul
2008.Jun
2008.Sep
2009.Aug
2009.Jul
2009.Jun
2009.Sep
2010.Aug
2010.Jul
2010.Jun
2010.Sep
Year.Month
Species
GREY
HARBOUR


se
4
3
2
1
0
Year.Month
2007.Aug
2007.Jul
2007.Jun
2008.Aug
2008.Jul
2008.Jun
2008.Sep
2009.Aug
2009.Jul
2009.Jun
2009.Sep
2010.Aug
2010.Jul
2010.Jun
2010.Sep
Species
GREY
HARBOUR

If we check summary data we can find that the date of it consists of count, mean, standard deviation, standard error of mean and confidence interval. in order to find more detailed information we can plot the significant errors graph using ggplot2 in order to find significant difference between each species



Considering the above graph clearly shows that the graph provides an error bar which significantly shows how each species is using standard error. This clearly signifies difference species for a particular month.



3 RESULTS

In the above test, we have analysed the significant difference between the species and the count values. We have different nominal variables and only one measure of variables, however we are able to identify non-significant values of the population of seals over time.
Moreover, when comparing data according to the year wise, we found out that the highest seal was obtained in 2010 and there were high counts in summer 2007. But they also found out that the levels of variance in the data particularly word not explored. Therefore we started exploring data for each month in a year in order to find out the presence of seals, but the test suggested that there is no significant difference and different months for each year. Moreover, Started analysing particular species for each year. Initially we had seen that the harbour seals species are more common than grey sea species, after that we found out 2009 and 10 the data appeared to be more significant 2007 and 2008 the data was slightly significant. After that, we calculated the standard error, and visualised the data which represented how the variables are using standard errors.

By summing up, we can say that the data is well explored, analysed and ready to be processed for modelling which will help to give better results for prediction.

4 DISCUSSION

In the above data, We were able to successfully explore and analyse and find out the normality distribution of existence for both the species. According to the non parametric test, the most common use of Kruskal Wallis Test is when the data has one nominal variable and one measurement variable but test does not assume that a data han is well distributed and completely align for two parameters which can be mean and standard deviation and also it is called as one way anova(Biostathandbook, One Way Annovas). also this test assumes that the null hypothesis of mean groups are same. therefore if distribution groups are same, the Kruskal wallis test will not show a significant difference in their distribution. Yet, the test does not considered that the data are normally distributed, which can be a big advantage but 800 data has different groups different variants the test will give inaccurate result. Therefore, if the distribution is different and variant is different we can use anova test for accurate results

4.0.1 REFERENCES

The Kruskal-Wallis One-way Ananysis of Variance by Ranks –Analysis of k-Between-Group Data with a Quantitative Response Variable. Available from : https://psych.unl.edu/psycrs/handcomp/hckw.PDF. [Accessed at 20th December 2020] Biostathandbook.com, http://www.biostathandbook.com/kruskalwallis.html [Accessed at 23d December 2020]