Analyzing the Tooth Growth under some supplements

Taha Bakhouch.

Summary of data

In this project , we will study the data available in the dataFrame ToothGrowth.
Using the summary R command we get :

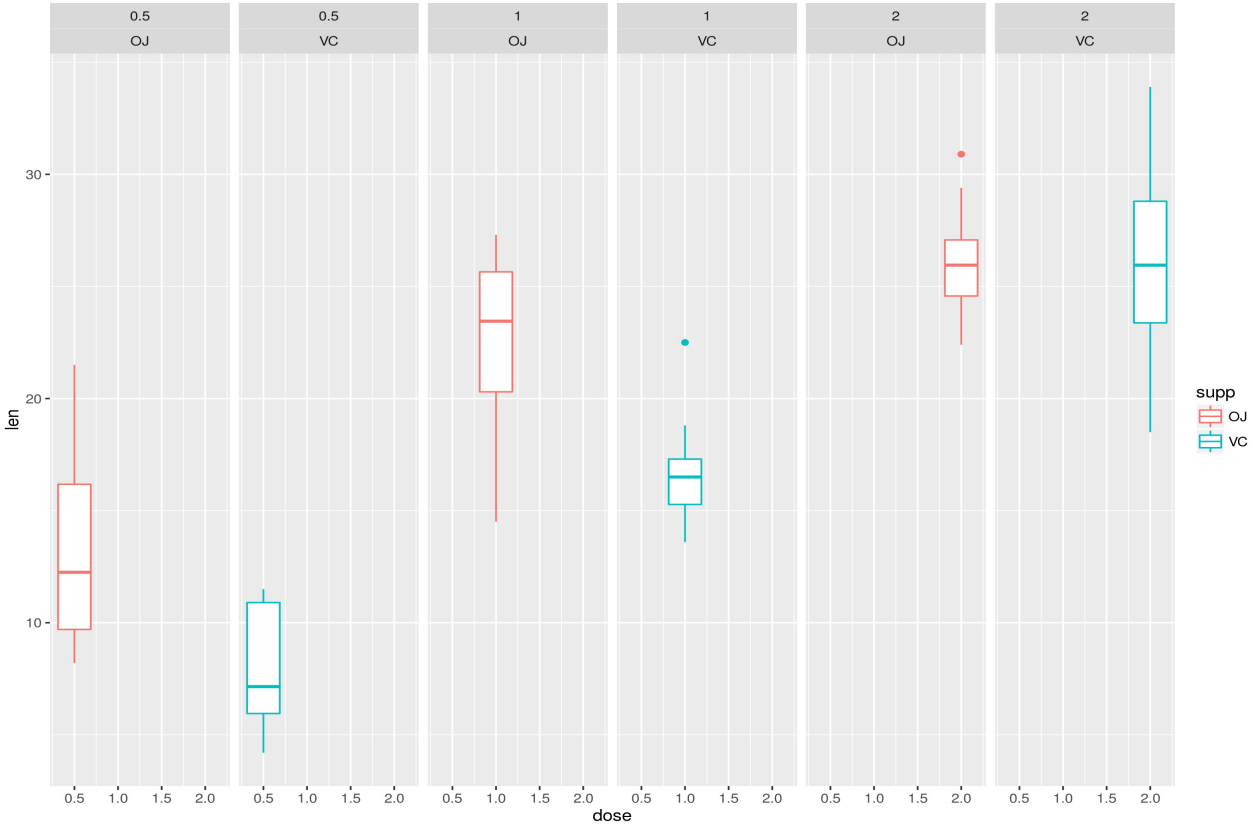
```
> summary(ToothGrowth)
       len        supp         dose
 Min.   : 4.20   OJ:30   Min.   :0.500
 1st Qu.:13.07   VC:30   1st Qu.:0.500
 Median :19.25           Median :1.000
 Mean   :18.81           Mean   :1.167
 3rd Qu.:25.27           3rd Qu.:2.000
 Max.   :33.90           Max.   :2.000

TootGrowth contains 3 columns :
-length : the length of a tooth of the pig
-supp : supplement used on that pig
-dose : the dose of the supplement used on the pig
```

Exploratory Analysis :

In the following figure, we can see boxplots that represent the lengths of Tooths under a particular dose (0,5 - 1 or 2) of a particular supplement (OJ or VC).
We can remark two type of relations :

- For the same quantity of the dose, it seems that the length of tooths of OJ suppliment are bigger that the length of tooths of PJ suppliment .
- Using the same supplement , we can see for highier dose : It seems , we get bigger length



```
> groupedData<-group_by(ToothGrowth,supp)
> qplot(dose, len,data = groupedData,geom = c("boxplot"),facets = .~dose*supp, colour=supp)
```

let's extract data before testing hypotheses .

```
##extracting data
ToothOneDose<-ToothGrowth[ToothGrowth$dose==0.5,]
Oj1<-ToothOneDose[ToothOneDose$supp=="OJ",]
Vc1<-ToothOneDose[ToothOneDose$supp=="VC",]
ToothTwoDose<-ToothGrowth[ToothGrowth$dose==1.0,]
Oj2<-ToothTwoDose[ToothTwoDose$supp=="OJ",]
Vc2<-ToothTwoDose[ToothTwoDose$supp=="VC",]
ToothTreeDose<-ToothGrowth[ToothGrowth$dose==2,]
Oj3<-ToothTreeDose[ToothTreeDose$supp=="OJ",]
Vc3<-ToothTreeDose[ToothTreeDose$supp=="VC",]
```

Testing : Highier Dose => More Growth ?

To test this hypothese , we will perform the student test under the following hypotheses :

H0 : Mean(d1(supplement_i)) = Mean(d2(supplement_i))

Ha : Mean(d1(supplement_i)) = Mean(d2(supplement_i))

where d1(supplement_i) is the sample of tooths that mesured with supplement_i and dose 0,5 . supplement_ i can be either OJ or VC.

The results of computing the p-values ,using R :

	OJ	VC
Dose from 0,5 to 1	4.39246e-05	3.405509e-07

So we can reject the H0 hypotheses under 5% of risk1 and accept that by increasing the dose from 0,5 to 1 , we have bigger tooths

```
>t.test(x=Oj1$len ,y= Oj2$len,paired = FALSE ,alternative = c("less"))$p.value
>t.test(x=Vc1$len ,y= Vc2$len,paired = FALSE ,alternative = c("less"))$p.value
```

We do the same thing, comparing the doses of 1 and 2 , we get :

	OJ	VC
Dose : from 1 to 2	0.01959757	4.577802e-05

The experiences confirm that more dose implies more more growth.

```
>t.test(x=Oj2$len ,y= Oj3$len,paired = FALSE ,alternative = c("less"))$p.value
>t.test(x=Vc2$len ,y= Vc3$len,paired = FALSE ,alternative = c("less"))$p.value
```

Testing: Highier OJ => More VC?

For this test , we will try to see if the data can confirm that OJ is better than VC

We will realize the test for each dose.

The null hypotheses are : OJ has the same effect as VC.the alternative hypotheses are that OJ mean are better that VC.

Dose	0,5	1	2
p_Value	0.003179303	0.0005191879	0.5180742

For dose of 0,5 or 1 , p values are too lows , we can reject the null hypotheses and accept the fact of that OJ is better VC.

However , for the dose = 2 , p value is too high , we can't reject the null hypothese.

```
## for 0.5 of dose
t.test(x=Oj1$len ,y= Vc1$len,paired = FALSE ,alternative = c("greater"))$p.value
## for 1 of dose
t.test(x=Oj2$len ,y= Vc2$len,paired = FALSE ,alternative = c("greater"))$p.value
## for 2 of dose
t.test(x=Oj3$len ,y= Vc3$len,paired = FALSE ,alternative = c("greater"))$p.value
```