## Week4\_Project\_2

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## 2017-March-14th

Title: The report Basic inferential data analysis for ToothGrowth

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Overview:

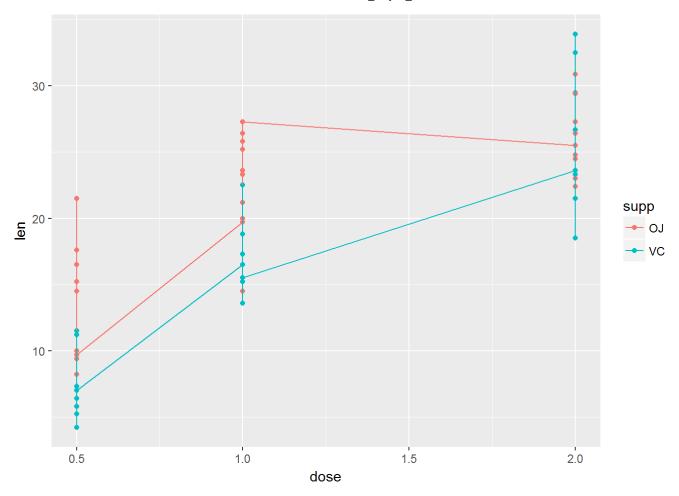
This report use basic exploratory data analysis to check the ToothData The report calculate the following numbers: mean data for each dose/supp pvalue and confidence for supp pvalue and confidence for dose

```
library(ggplot2)
 ## Warning: package 'ggplot2' was built under R version 3.2.5
 library(dplyr)
 ## Warning: package 'dplyr' was built under R version 3.2.5
 ##
 ## Attaching package: 'dplyr'
 ## The following objects are masked from 'package:stats':
 ##
 ##
        filter, lag
 ## The following objects are masked from 'package:base':
 ##
 ##
        intersect, setdiff, setequal, union
 data(ToothGrowth)
Step 1: Load the data and plot the data based on the supp
```

```
head(ToothGrowth)
```

```
## len supp dose
## 1 4.2 VC 0.5
## 2 11.5 VC 0.5
## 3 7.3 VC 0.5
## 4 5.8 VC 0.5
## 5 6.4 VC 0.5
## 6 10.0 VC 0.5
```

```
g1 <- ggplot(ToothGrowth, aes(x=dose, y=len))
g1 + geom_point(aes(colour=supp)) + geom_line(aes(colour=supp))</pre>
```



Step 2: Use groupby method to display the mean of each supp/dose

```
grp <- group_by(ToothGrowth, supp,dose)
summary1 <- summarise(grp, meanlen = mean(len) )
summary1</pre>
```

```
## Source: local data frame [6 x 3]
## Groups: supp [?]
##
##
       supp dose meanlen
##
     <fctr> <dbl>
                    <dbl>
                    13.23
## 1
         OJ
              0.5
## 2
         OJ
              1.0
                    22.70
## 3
         OJ
             2.0
                    26.06
         VC
                     7.98
## 4
              0.5
## 5
         VC
              1.0
                    16.77
         VC
## 6
              2.0
                    26.14
```

## Step 3:

```
# Step 3.1: Compare Supp
test1 <- t.test(ToothGrowth$len ~ ToothGrowth$supp, data = ToothGrowth)
test1$p.value</pre>
```

```
## [1] 0.06063451
```

```
test1$conf.int
```

```
## [1] -0.1710156 7.5710156
## attr(,"conf.level")
## [1] 0.95
```

Because the p-value is greater than 5%, so it will not be included

pdose5\_dose10\_test2\$p.value

```
# Step 3.2: Compare Dose
dose5 <- filter(ToothGrowth, dose==0.5)$len
dose10 <- filter(ToothGrowth, dose==1.0)$len
dose20 <- filter(ToothGrowth, dose==2.0)$len

# Check dose5 and dose10 p-value
pdose5_dose10_test1 <- t.test(dose5, dose10, paired=FALSE, var.equal=TRUE)
pdose5_dose10_test2 <- t.test(dose5, dose10, paired=FALSE, var.equal=FALSE)
pdose5_dose10_test1$p.value</pre>
## [1] 1.266297e-07
```

```
## [1] 1.268301e-07
```

```
pdose5_dose10_test1$conf.int
```

```
## [1] -11.983748 -6.276252
## attr(,"conf.level")
## [1] 0.95
```

```
pdose5_dose10_test2$conf.int
```

```
## [1] -11.983781 -6.276219
## attr(,"conf.level")
## [1] 0.95
```

```
pdose10_dose20_test1 <- t.test(dose10, dose20, paired=FALSE, var.equal=TRUE)
pdose10_dose20_test2 <- t.test(dose10, dose20, paired=FALSE, var.equal=FALSE)
pdose10_dose20_test1$p.value</pre>
```

```
## [1] 1.810829e-05
```

```
pdose10_dose20_test2$p.value
```

```
## [1] 1.90643e-05
```

```
pdose10_dose20_test1$conf.int
```

```
## [1] -8.994387 -3.735613
## attr(,"conf.level")
## [1] 0.95
```

pdose10\_dose20\_test2\$conf.int

```
## [1] -8.996481 -3.733519
## attr(,"conf.level")
## [1] 0.95
```

```
pdose5_dose20_test1 <- t.test(dose5, dose20, paired=FALSE, var.equal=TRUE)
pdose5_dose20_test2 <- t.test(dose5, dose20, paired=FALSE, var.equal=FALSE)
pdose5_dose20_test1$p.value</pre>
```

```
## [1] 2.837553e-14
```

pdose5\_dose20\_test2\$p.value

```
## [1] 4.397525e-14
```

pdose5\_dose20\_test1\$conf.int

```
## [1] -18.15352 -12.83648
## attr(,"conf.level")
## [1] 0.95
```

pdose5\_dose20\_test2\$conf.int

```
## [1] -18.15617 -12.83383
## attr(,"conf.level")
## [1] 0.95
```

Because all p-value are less than 5%, so its clearly stated that the dose has a strong impact on the tooth length

Conclusion: The above report shows that 'dose's increasement can directly impact tooth growth', while supplement does not have impact.