Tootgrowth Analysis

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analysis of tooth growth data

Generic analysis of toothgrowth data

processing data

Loading data

```
library(UsingR)
## Loading required package: MASS
## Loading required package: HistData
## Loading required package: Hmisc
## Loading required package: grid
## Loading required package: lattice
## Loading required package: survival
## Loading required package: Formula
## Loading required package: ggplot2
##
## Attaching package: 'Hmisc'
## The following objects are masked from 'package:base':
##
       format.pval, round.POSIXt, trunc.POSIXt, units
##
##
##
## Attaching package: 'UsingR'
##
## The following object is masked from 'package:ggplot2':
##
##
       movies
##
## The following object is masked from 'package:survival':
##
##
       cancer
data(ToothGrowth)
```

Initial analysis of tooth growth

```
dim(ToothGrowth)
```

```
## [1] 60 3
```

Contains 3 dimensions and 60 findings in total

```
names(ToothGrowth)
## [1] "len" "supp" "dose"
```

"len", "supp", and "dose" are column names

Getting a summary

```
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
```

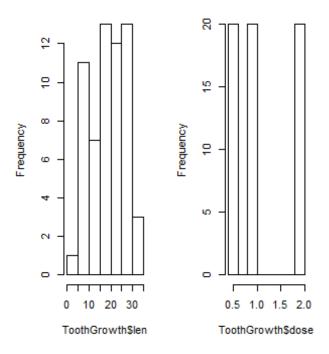
There are 2 levels on the Supplement

histograms

Seeing a histogram of the values

```
par(mfrow = c(1, 3))
hist(ToothGrowth$len)
hist(ToothGrowth$dose)
```

listogram of ToothGrowthistogram of ToothGrowth!



Looks like dose is discrete as well

```
unique(ToothGrowth$dose)
## [1] 0.5 1.0 2.0
```

We see there are 3 unique values here.

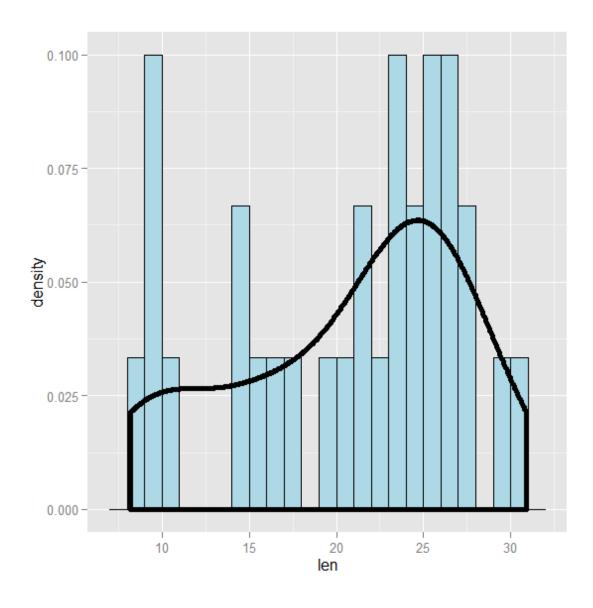
Looks like the data uses 2 segments for treatment with a supplement and having 3 doses on each. lets see each one separate as a confidence interval ##Confidence and p-values

```
#treatment on OJ
X0<-ToothGrowth[ToothGrowth$supp=="0]",c(1,3)]</pre>
#treatment on VC
Y0<-ToothGrowth[ToothGrowth$supp=="VC",c(1,3)]
summary(lm(X0$len ~ X0$dose))
##
## Call:
## lm(formula = X0$len ~ X0$dose)
##
## Residuals:
       Min
                1Q Median
##
                                3Q
                                       Max
  -7.2557 -3.7979 -0.0643 3.3521 7.9386
##
## Coefficients:
               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 11.550
                             1.722 6.708 2.79e-07 ***
```

```
## X0$dose
                 7.811
                            1.302 6.001 1.82e-06 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 4.446 on 28 degrees of freedom
## Multiple R-squared: 0.5626, Adjusted R-squared: 0.547
## F-statistic: 36.01 on 1 and 28 DF, p-value: 1.825e-06
summary(lm(Y0$len ~ Y0$dose))
##
## Call:
## lm(formula = Y0$len ~ Y0$dose)
##
## Residuals:
##
      Min
               1Q Median
                               3Q
                                      Max
## -8.2264 -2.6029 0.0814 2.2288 7.4893
##
## Coefficients:
              Estimate Std. Error t value Pr(>|t|)
##
## (Intercept)
                 3.295
                            1.427
                                    2.309
                                            0.0285 *
## Y0$dose
                11.716
                            1.079 10.860 1.51e-11 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 3.685 on 28 degrees of freedom
## Multiple R-squared: 0.8082, Adjusted R-squared: 0.8013
## F-statistic: 117.9 on 1 and 28 DF, p-value: 1.509e-11
```

Both show very small p values hence without knowing what the supplement was I can say that there is very little support for this study to take the supplement for growth of teeth.

Plot of supplement "OJ"



Plot of supplement "VC"

