Inferential Data Analysis on Tooth-Growth

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Date: Sunday, May 17, 2015

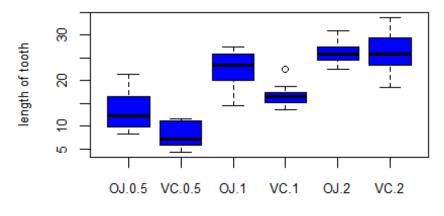
Overview: In this report, I will make a fundamental data exploration onto the dataset of Tooth-Growth and use confidence interval/hypothesis test to research the realtionship between growth length and supp as well as dose

Section I: Basic Exploratory Data Analysis

```
library(datasets); data(ToothGrowth); x<-ToothGrowth; summary(x)</pre>
##
         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
```

Next I can explore the data distribution via combinations by supp and dose

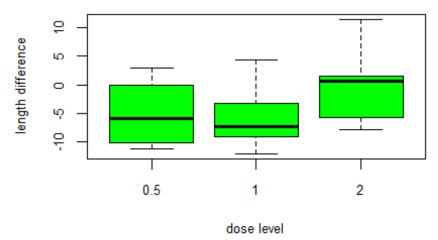
Tooth Growth Distribution



combination of supp and dose

From this plot, I found that distributions of different combinations are various, even for the same supp, different dose can lead to various mean level. Next I can explore the length difference between VC and OJ under the same dose level, in order to view the mean value level.

Length Difference by Supp



```
rm(y.vc,y.oj)
```

We can see that mean values of difference are obviously not zero (except dose=2), so supp should be a significant dominat variable to tooth length

Section II: Hypothesis test on growth length

Firstly, we can test the significance between different dose level under the same supp group. For example, we can test dose levels of .5 and 1 within VC. Because tooth growth data split by different supp or dose have the same size and are not independent, so we can use pair comparison, which is the assumption of test.

- +H0: Difference in means is equal to 0
- +Ha: Difference in means is not equal to 0

```
g1<-subset(x,as.character(supp)=="VC" & as.numeric(as.character(dos
e))==.5)$len
g2<-subset(x,as.character(supp)=="VC" & as.numeric(as.character(dos</pre>
```

```
e))==1)$len
t.test(g1,g2,paired=TRUE)$conf;t.test(g1,g2,paired=TRUE)$p.value
## [1] -12.030399 -5.549601
## attr(,"conf.level")
## [1] 0.95
## [1] 0.0001715165
```

We can see the p-value is far less than 5% and confidence interval doesn't include 0. Then we can reject H0 and accept Ha, means of different dose level are significantly not equal. Using the similar way, I found the differences are significant except the comparison that dose levels are 1 vs 2 within OJ (p.value=0.08384, failed to reject H0). Secondly, I can test difference in means between VC and OJ within the same dose level.

+H0: Difference in means is equal to 0 +Ha: Difference in means is not equal to 0

```
y.cmp<-subset(y,dose==.5)
t.test(y.cmp$len.vc,y.cmp$len.oj,paired=TRUE)$conf;
## [1] -9.236542 -1.263458
## attr(,"conf.level")
## [1] 0.95
t.test(y.cmp$len.vc,y.cmp$len.oj,paired=TRUE)$p.value;
## [1] 0.01547205</pre>
```

We can see the p-value is less than 5% and confidence level doesn't include 0. Then we can reject H0 and accept Ha. Similarly we can test dose levels of 1&2. Dose Level = 1

```
## [1] -9.908089 -1.951911
## attr(,"conf.level")
## [1] 0.95
## [1] 0.008229248
```

Dose Level = 2

```
## [1] -4.168976  4.328976
## attr(,"conf.level")
## [1] 0.95
## [1] 0.9669567
```

Now, we can see difference in means under dose level of 0.5 and 1 are significantly not equal to 0, but not at the level of 2.(p.value=0.97)

Our conclusion is that supp and dose are both dominant factors to length of tooth-growth, but the dominance is not significant under few situations.