SI Project 2

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In the second portion of the project, we're going to analyze the ToothGrowth data in the R datasets package.

1.Load the ToothGrowth data and perform some basic exploratory data analyses

```
library(datasets)
data(ToothGrowth)
```

2.Provide a basic summary of the data.

```
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
```

```
dim(ToothGrowth)
```

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

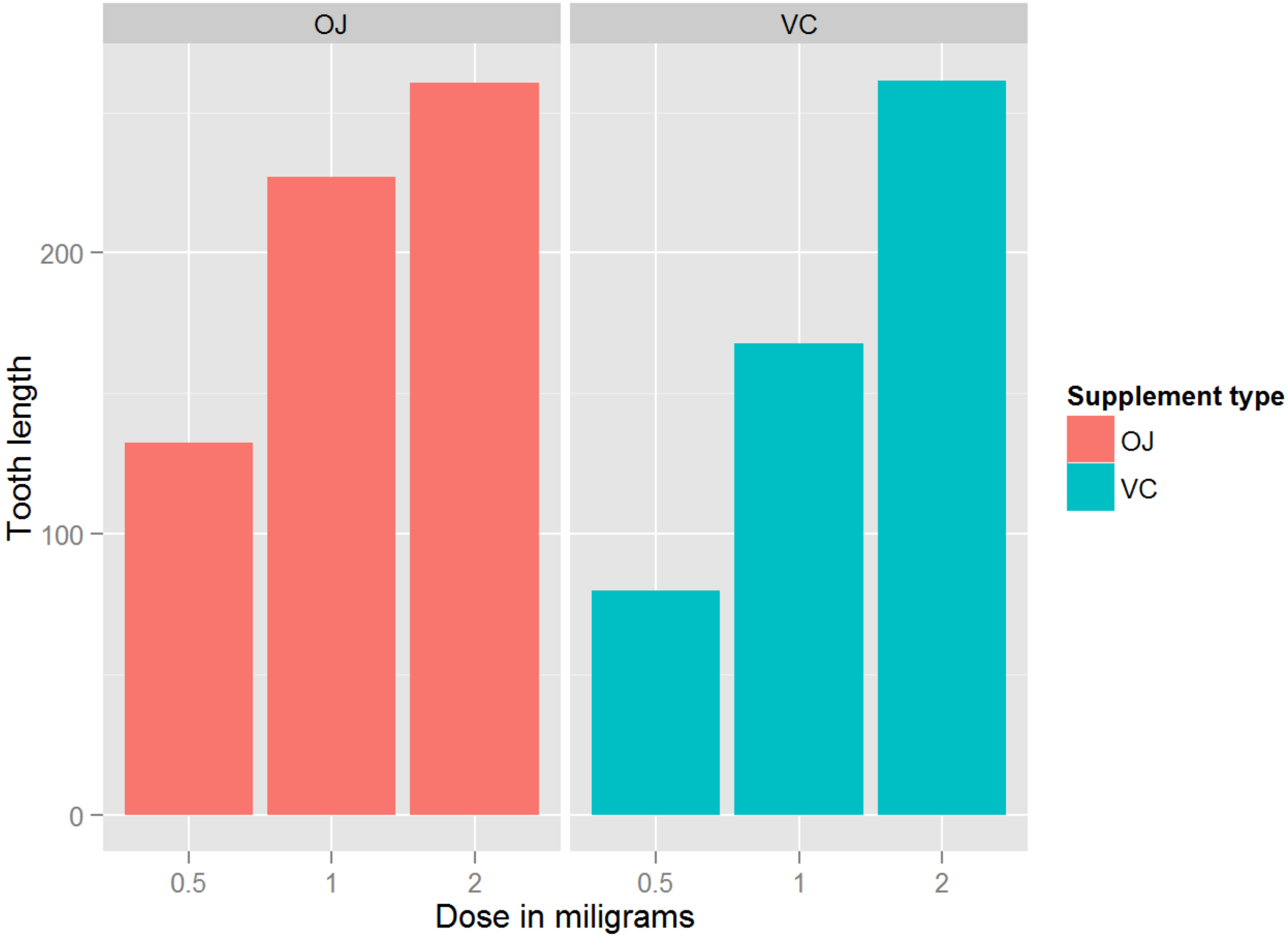
```
summary(ToothGrowth)
```

```
##       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  
```

The data is set of 60 observations, length of odontoblasts (teeth) in each of 10 guinea pigs at each of three dose levels of Vitamin C (0.5, 1 and 2 mg) with each of two delivery methods (orange juice or ascorbic acid).

As can be seen below, there is a clear positive correlation between the tooth length and the dose levels of Vitamin C, for both delivery methods.

```
library(datasets)
library(ggplot2)
ggplot(data=ToothGrowth, aes(x=as.factor(dose), y=len, fill=supp)) +
    geom_bar(stat="identity",) +
    facet_grid(. ~ supp) +
    xlab("Dose in miligrams") +
    ylab("Tooth length") +
    guides(fill=guide_legend(title="Supplement type"))
```



Confidence Intervals

We first consider a test of average difference between group using VC and OJ. In order to do that, we use unequal variance t test

```
t.test(len ~ supp, paired = F, var.equal = F, data = ToothGrowth)
```

```
## 
##  Welch Two Sample t-test
## 
## data:  len by supp
## t = 1.9153, df = 55.309, p-value = 0.06063
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.1710156  7.5710156
## sample estimates:
## mean in group OJ mean in group VC 
##         20.66333         16.96333
```

As shown in the result, 0 is contained in the 95% confidence interval. Given p-value is 0.06 > 0.05, we cannot reject the null hypothesis that true difference in means is equal to 0

Now we consider dose variable. First we seperate data into different groups:

```
dose12 <- subset(ToothGrowth, dose %in% c(0.5, 1))
dose23 <- subset(ToothGrowth, dose %in% c(1, 2))
dose13 <- subset(ToothGrowth, dose %in% c(0.5, 2))
```

Then we perform unequal variance t test for each of the group:

```
t.test(len ~ dose, paired = FALSE, var.equal = FALSE, data = dose12)
```

```
## 
##  Welch Two Sample t-test
## 
## data:  len by dose
## t = -6.4766, df = 37.986, p-value = 1.268e-07
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -11.983781  -6.276219
## sample estimates:
## mean in group 0.5   mean in group 1 
##            10.605            19.735
```

```
t.test(len ~ dose, paired = FALSE, var.equal = FALSE, data = dose23)
```

```
## 
##  Welch Two Sample t-test
## 
## data:  len by dose
## t = -4.9005, df = 37.101, p-value = 1.906e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -8.996481 -3.733519
## sample estimates:
## mean in group 1 mean in group 2 
##          19.735          26.100
```

```
t.test(len ~ dose, paired = FALSE, var.equal = FALSE, data = dose13)
```

```
## 
##  Welch Two Sample t-test
## 
## data:  len by dose
## t = -11.799, df = 36.883, p-value = 4.398e-14
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -18.15617 -12.83383
## sample estimates:
## mean in group 0.5   mean in group 2 
##            10.605            26.100
```

These results show either 2 groups have significant different means leading to the conclusion that using different dose cause different lens on average.

Regression approach

We could also use simple linear regression to test the relationship between variables:

```
fit <- lm(len ~ dose + supp, data=ToothGrowth)
summary(fit)
```

```
##
## Call:
## lm(formula = len ~ dose + supp, data = ToothGrowth)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -6.600 -3.700  0.373  2.116  8.800
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   9.2725     1.2824   7.231 1.31e-09 ***
## dose          9.7636     0.8768  11.135 6.31e-16 ***
## suppVC       -3.7000     1.0936  -3.383   0.0013 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.236 on 57 degrees of freedom
## Multiple R-squared:  0.7038, Adjusted R-squared:  0.6934
## F-statistic: 67.72 on 2 and 57 DF,  p-value: 8.716e-16
```

```
confint(fit)
```

```
##                 2.5 %    97.5 %
## (Intercept)  6.704608 11.840392
## dose         8.007741 11.519402
## suppVC      -5.889905 -1.510095
```