

Appendix_ToothGrowth

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August 21, 2015

An Appendix for Tooth Growth Analysis (R codes and figures)

```
data("ToothGrowth")  
library(ggplot2)  
library(dplyr)
```

```
##  
## 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
```

```
library(knitr)  
  
#group the data by supp and dose  
Tooth_by_Supp_Dose <- ToothGrowth %>%  
  group_by(supp, dose)  
  
#change class of dose into factor  
Tooth_by_Supp_Dose$dose <- as.factor(Tooth_by_Supp_Dose$dose)  
  
Var_By_Supp <- Tooth_by_Supp_Dose %>%  
  group_by(supp, dose) %>%  
  summarise(Variance = var(len))
```

summary of the data

```
str(ToothGrowth)
```

```
## 'data.frame': 60 obs. of 3 variables:
## $ len : num 4.2 11.5 7.3 5.8 6.4 10 11.2 11.2 5.2 7 ...
## $ supp: Factor w/ 2 levels "OJ","VC": 2 2 2 2 2 2 2 2 2 2 ...
## $ dose: num 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 ...
```

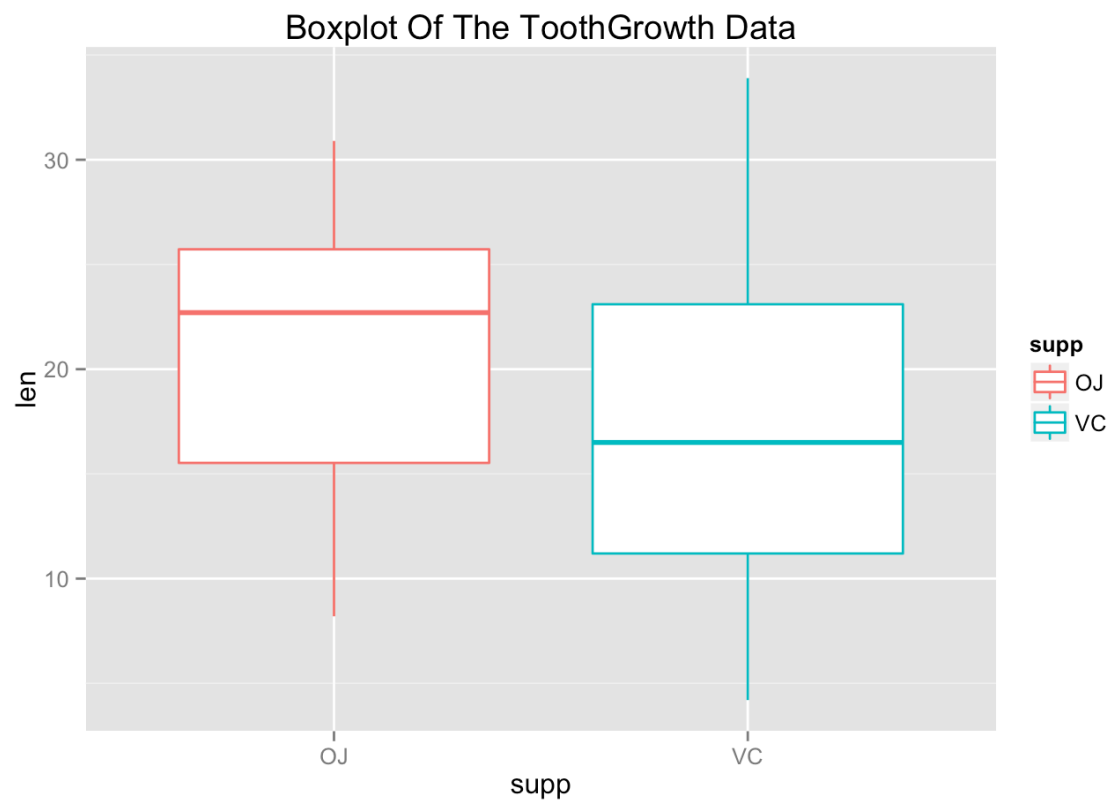
```
summary(ToothGrowth)
```

```
##      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
```

boxplot

```
summary_plot <- ggplot(data=ToothGrowth, aes(x=supp, y=len)) +
  geom_boxplot(aes(color = supp)) +
  ggtitle("Boxplot Of The ToothGrowth Data")

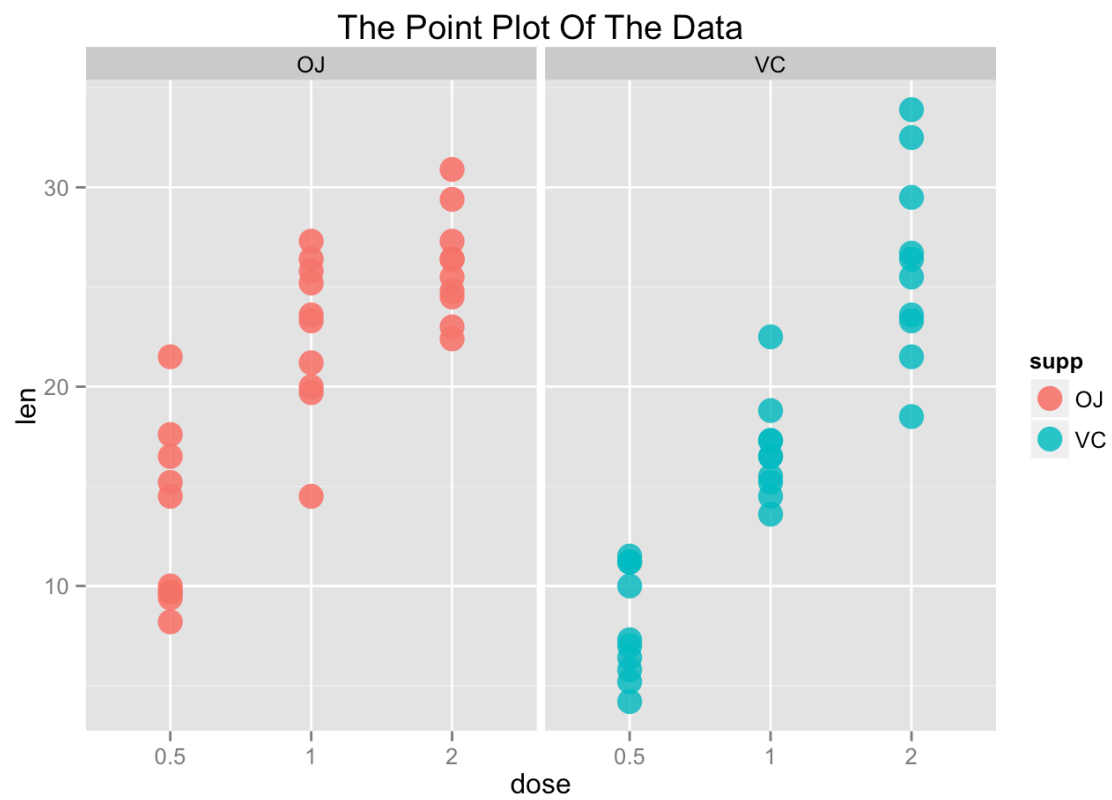
summary_plot
```



point plot

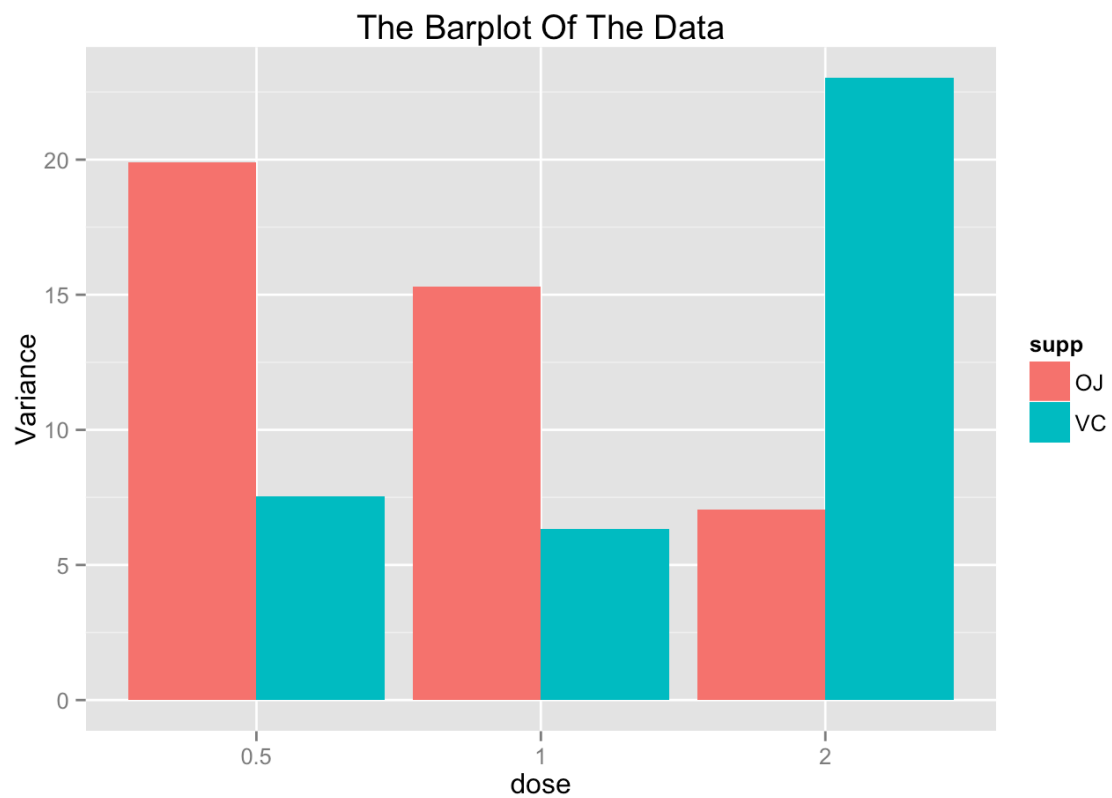
```
Growth_Plot <- ggplot(data = Tooth_by_Supp_Dose, aes(x=dose, y=len))  
+  
  geom_point(aes(color=supp), alpha=0.9, size = 5) +  
  facet_grid(.~ supp) +  
  ggtitle("The Point Plot Of The Data")
```

Growth_Plot



barplot

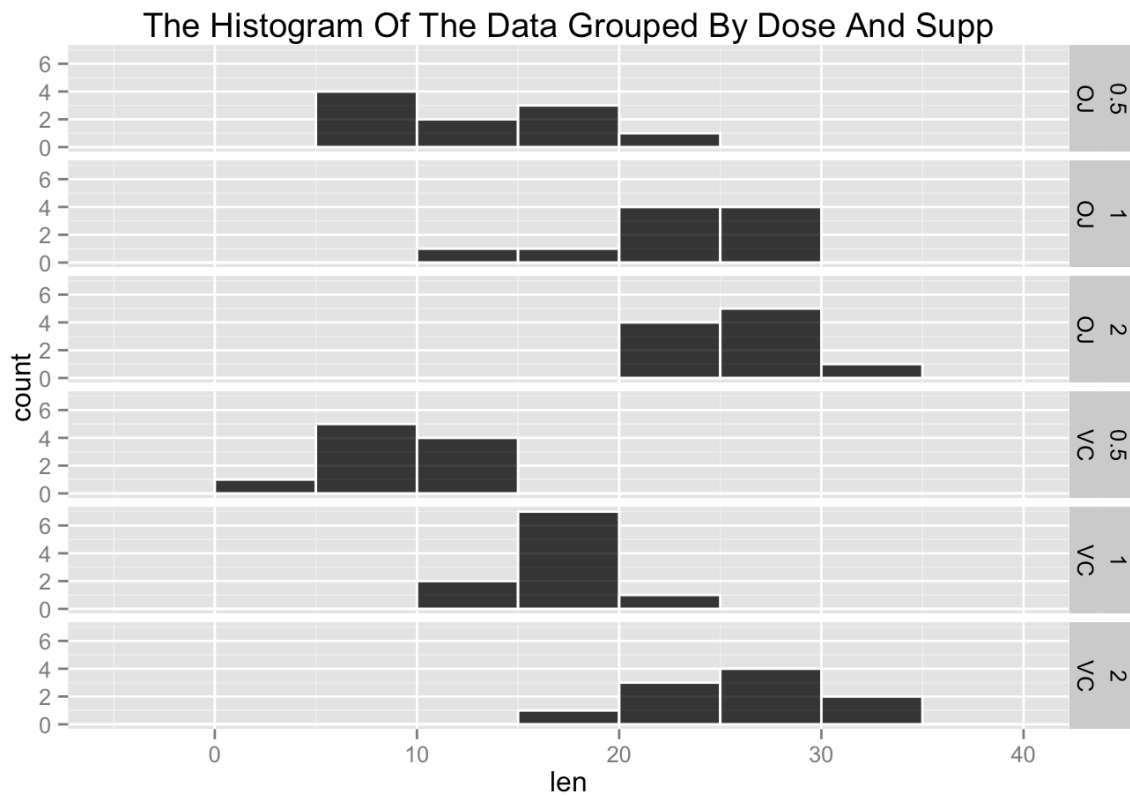
```
Bar_Plot <- ggplot(data=Var_By_Supp,aes(x=dose, y = Variance)) +
  geom_bar(aes(fill = supp), position = "dodge", stat="identity")
+
  ggtitle("The Barplot Of The Data")
Bar_Plot
```



histogram of variances

```
#So variances are unequal.
Hist_Plot <- ggplot(data= Tooth_by_Supp_Dose, aes(len)) +
  geom_histogram(binwidth=5,colour = "white",fill = "black",alpha=
0.8) +
  facet_grid(supp + dose ~ .) +
  ggtitle("The Histogram Of The Data Grouped By Dose And Supp")

Hist_Plot
```



#the assumption that the data distributed in the shape of mound is acceptable, since each unite of observations is identical and randomly chosen.

The t test on the group (OJ, 0.5) and the group (VC, 0.5):

```
Dose_0.5 <- filter(ToothGrowth, dose == 0.5)
test_0.5 <- t.test(len ~ supp, paired = FALSE, var.equal = FALSE, data = Dose_0.5)
test_0.5
```

```
##
## Welch Two Sample t-test
##
## data: len by supp
## t = 3.1697, df = 14.969, p-value = 0.006359
## alternative hypothesis: true difference in means is not equal to
0
## 95 percent confidence interval:
## 1.719057 8.780943
## sample estimates:
## mean in group OJ mean in group VC
##          13.23          7.98
```

The t test on the group (OJ, 1) and the group (VC, 1):

```
Dose_1.0 <- filter(ToothGrowth, dose == 1.0)
test_1.0 <- t.test(len ~ supp, paired = FALSE, var.equal = FALSE, da
ta = Dose_1.0)
test_1.0
```

```
##
## Welch Two Sample t-test
##
## data: len by supp
## t = 4.0328, df = 15.358, p-value = 0.001038
## alternative hypothesis: true difference in means is not equal to
0
## 95 percent confidence interval:
## 2.802148 9.057852
## sample estimates:
## mean in group OJ mean in group VC
##          22.70          16.77
```

The t test on the group (OJ, 2) and the group (VC, 2):

```
Dose_2.0 <- filter(ToothGrowth, dose == 2.0)
test_2.0 <- t.test(len ~ supp, paired = FALSE, var.equal = FALSE, da
ta = Dose_2.0)
test_2.0
```

```
##
##  Welch Two Sample t-test
##
## data:  len by supp
## t = -0.046136, df = 14.04, p-value = 0.9639
## alternative hypothesis: true difference in means is not equal to
0
## 95 percent confidence interval:
##  -3.79807  3.63807
## sample estimates:
## mean in group OJ mean in group VC
##           26.06           26.14
```