Coursera Data Science Project: Statistical Inference (Part 2)

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August 23, 2015

Introduction

This is the project for the statistical inference class. In it, I will use simulation to explore inference and do some simple inferential data analysis. The project consists of two parts:

1. A simulation exercise.
2. Basic inferential data analysis (this report)

Basic Inferential Data Analysis

Load and explore data

```
library(datasets)
data("ToothGrowth")
ToothGrowth_tbl <- tbl_df(ToothGrowth)
glimpse(ToothGrowth_tbl)
```

```
## Observations: 60
## Variables:
## $ len  (dbl) 4.2, 11.5, 7.3, 5.8, 6.4, 10.0, 11.2, 11.2, 5.2, 7.0, 16....
## $ supp (fctr) VC, VC, VC, VC, VC, VC, VC, VC, VC, VC, VC, VC, VC, VC, ...
## $ dose (dbl) 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 1.0, 1....
```

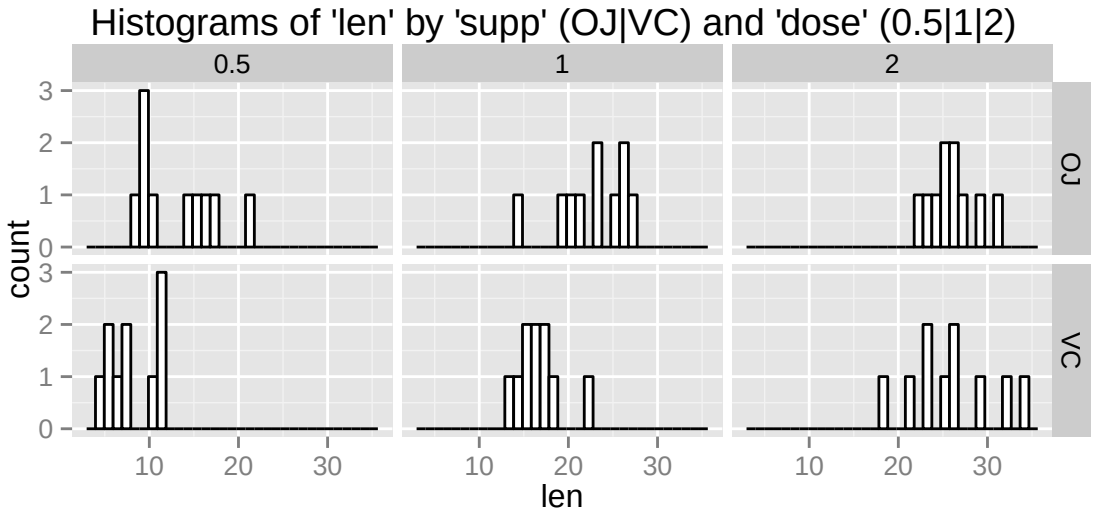
Some inspection of the ToothGrowth data indicates it has 60 observations of 3 values: len, supp, dose. The 'supp' value is a factor with only 2 levels: OJ, VC. The 'dose' value, although a number, actually has only 3 values: 0.5, 1, 2. For processing, this value was converted to a factor.

```
ToothGrowth_tbl$dose <- as.factor(ToothGrowth_tbl$dose)
```

Data Summary

A faceted set of histograms

```
ggplot(ToothGrowth_tbl, aes(x=len)) +
  geom_histogram(color="black", fill="white") +
  facet_grid(supp ~ dose) +
  ggtitle("Histograms of 'len' by 'supp' (OJ|VC) and 'dose' (0.5|1|2) ")
```



The basic question is: **"Is ToothGrowth 'len' affected by 'supp' or 'dose'?"**
The mean, sd, and count of values of 'len' are:

```
summaryLen <- ToothGrowth_tbl %>% group_by(supp, dose) %>%
              summarize (mean = mean(len), sd=sd(len), n=n())
print(summaryLen)
```

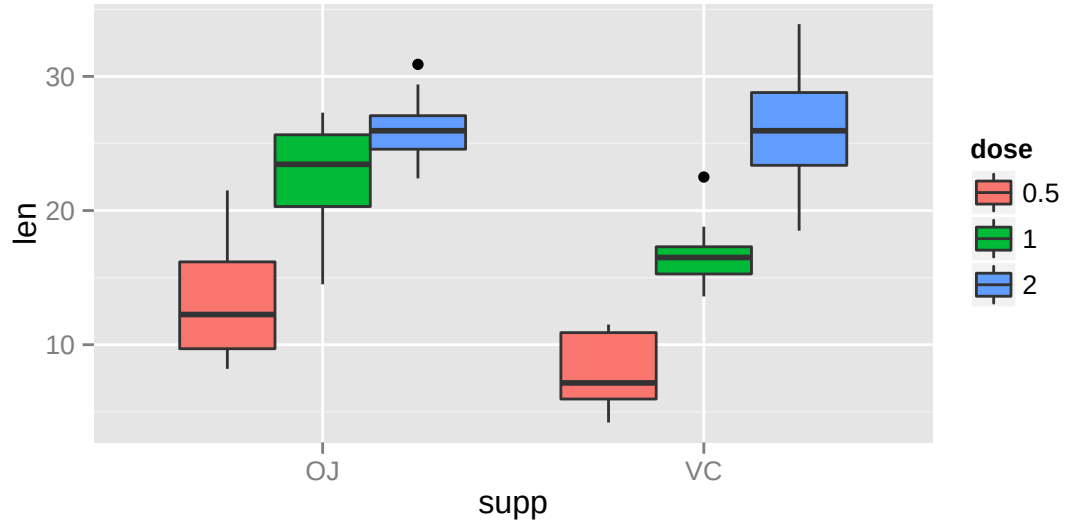
```
## Source: local data frame [6 x 5]
## Groups: supp
##
##   supp dose  mean       sd  n
## 1   OJ  0.5 13.23 4.459709 10
## 2   OJ    1 22.70 3.910953 10
## 3   OJ    2 26.06 2.655058 10
## 4   VC  0.5  7.98 2.746634 10
## 5   VC    1 16.77 2.515309 10
## 6   VC    2 26.14 4.797731 10
```

Compare tooth growth by supp and dose

Different doses of supp will be compared using a t-test. To aid understanding about what is being tested, the figure below contains two sets of box plots; one for each of the the 'sup': 'OJ' and 'VC. Each set contains 3 box plots, one for each of the doses: '0.5', '1', and '2'. The null hypothesis is: **There is no difference in the means of samples**

```
supp_by_dose <- tbl_df(data.frame(matrix(ncol=4, nrow=6)))
colnames(supp_by_dose) <- c("supp", "dose1", "dose2", "pvalue")
supp_by_dose[1,] = c("OJ", ".5", "1",
    t.test(len~dose, data=droplevels(filter(ToothGrowth_tbl, supp=="OJ" & dose!=2)))[3]$p.value)
supp_by_dose[2,] = c("OJ", ".5", "2",
    t.test(len~dose, data=droplevels(filter(ToothGrowth_tbl, supp=="OJ" & dose!=1)))[3]$p.value)
supp_by_dose[3,] = c("OJ", "1", "2",
    t.test(len~dose, data=droplevels(filter(ToothGrowth_tbl, supp=="OJ" & dose!=0.5)))[3]$p.value)
```

```
supp_by_dose[4,] = c("VC", ".5", "1",
    t.test(len~dose, data=droplevels(filter(ToothGrowth_tbl, supp=="VC" & dose!=2)))[3]$p.value)
supp_by_dose[5,] = c("VC", ".5", "2",
    t.test(len~dose, data=droplevels(filter(ToothGrowth_tbl, supp=="VC" & dose!=1)))[3]$p.value)
supp_by_dose[6,] = c("VC", "1", "2",
    t.test(len~dose, data=droplevels(filter(ToothGrowth_tbl, supp=="VC" & dose!=0.5)))[3]$p.value)
supp_by_dose$pvalue <- round(as.numeric(supp_by_dose$pvalue), 4)
supp_by_dose <- mutate(supp_by_dose, H0 = ifelse(pvalue > 0.05, "Accept", "Reject"))
ggplot(ToothGrowth_tbl, aes(x=supp, y=len, fill=dose)) + geom_boxplot()
```




```
print(supp_by_dose)
```

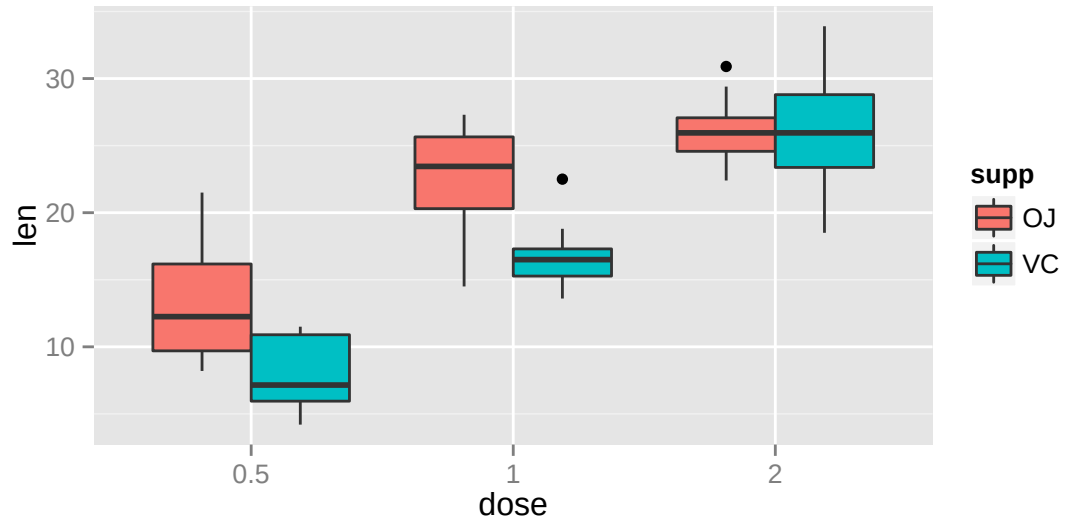
```
## Source: local data frame [6 x 5]
##
##   supp dose1 dose2 pvalue     H0
## 1   OJ    .5     1 0.0001 Reject
## 2   OJ    .5     2 0.0000 Reject
## 3   OJ     1     2 0.0392 Reject
## 4   VC    .5     1 0.0000 Reject
## 5   VC    .5     2 0.0000 Reject
## 6   VC     1     2 0.0001 Reject
```

As can be seen graphically, and confirmed by the p-values and rejection of the null hypothesis: *For each supplement, the amount of the 'dose' does indeed have a statistically different effect on the mean of the 'len'.*

Different 'supp' at each 'dose' will be compared using a t-test. To aid understanding about what is being tested, the figure below contains three sets of box plots; one for each of the the 'dose': '0.5', '1', and '2'. Each set contains 2 box plots, one for each of the 'sup' : 'OJ' and 'VC: . The null hypothesis is: **There is no difference in the means of samples**

```
dose_by_supp <- tbl_df(data.frame(matrix(ncol=4, nrow=3)))
colnames(dose_by_supp) <- c("dose", "supp1", "supp2", "pvalue")
dose_by_supp[1,] <- c(".5", "OJ", "VC",
```

```
  t.test(len~supp, data=droplevels(filter(ToothGrowth_tbl,  dose==.5)))[3]$p.value)
dose_by_supp[2,] <- c("1", "OJ", "VC",
  t.test(len~supp, data=droplevels(filter(ToothGrowth_tbl,  dose==1)))[3]$p.value)
dose_by_supp[3,] <- c("2", "OJ", "VC",
  t.test(len~supp, data=droplevels(filter(ToothGrowth_tbl,  dose==2)))[3]$p.value)
dose_by_supp$pvalue <- round(as.numeric(dose_by_supp$pvalue), 4)
dose_by_supp <- mutate(dose_by_supp, H0 = ifelse(pvalue > 0.05, "Accept", "Reject"))
ggplot(ToothGrowth_tbl, aes(x=dose, y=len, fill=supp)) + geom_boxplot()
```




```
print(dose_by_supp)
```

```
## Source: local data frame [3 x 5]
##
##   dose supp1 supp2 pvalue     H0
## 1   .5    OJ    VC 0.0064 Reject
## 2    1    OJ    VC 0.0010 Reject
## 3    2    OJ    VC 0.9639 Accept
```

As can be seen graphically, and confirmed by the p-values and rejection or acception of the null hypothesis: *For the 'doses' 0.5 and 1, the 'supp' does indeed have a statistically different effect on the mean of the 'len'. for the dose of 2, there is no difference.*

Conclusions

The only case where changing the supp or the dose does not affect the len is when the dose for each supp==2 (p-vale=0.96). In all other cases the p-value is less than 0.05, and thus the null hypothesis is rejected.