Statistical Inference: Peer Graded Assigment - Part 2

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OVERVIEW

Part 2 Basic Inferential Data Analysis: This part of the analysis uses the ToothGrowth data in the R datasets library and compares tooth growth across dosage and delivery methods. The specific instructions of this assignemnt are to "Use confidence intervals and/or hypothesis tests to compare tooth growth by supp and dose"

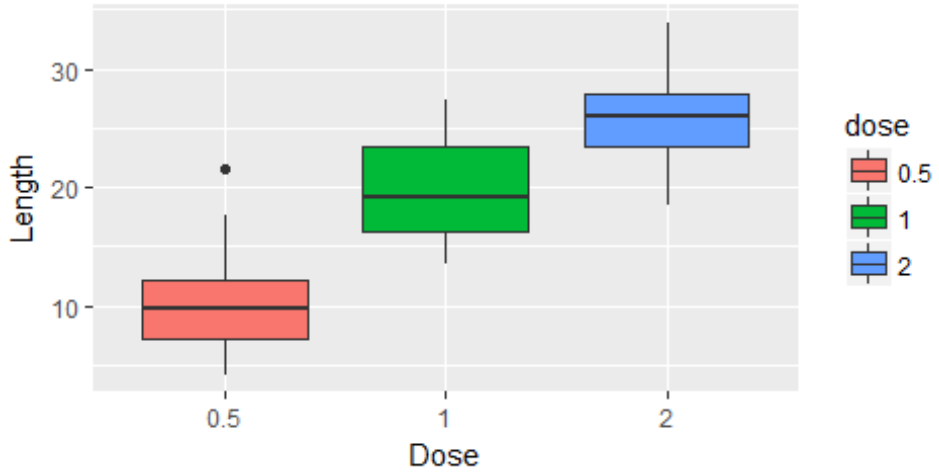
Description of the data

The response is the length of odontoblasts (cells responsible for tooth growth) in 60 guinea pigs. Each animal received one of three dose levels of vitamin C (0.5, 1, and 2 mg/day) by one of two delivery methods, orange juice coded as OJ or ascorbic acid a form of vitamin C and coded as VC.

EXPLORATORY ANALYSIS

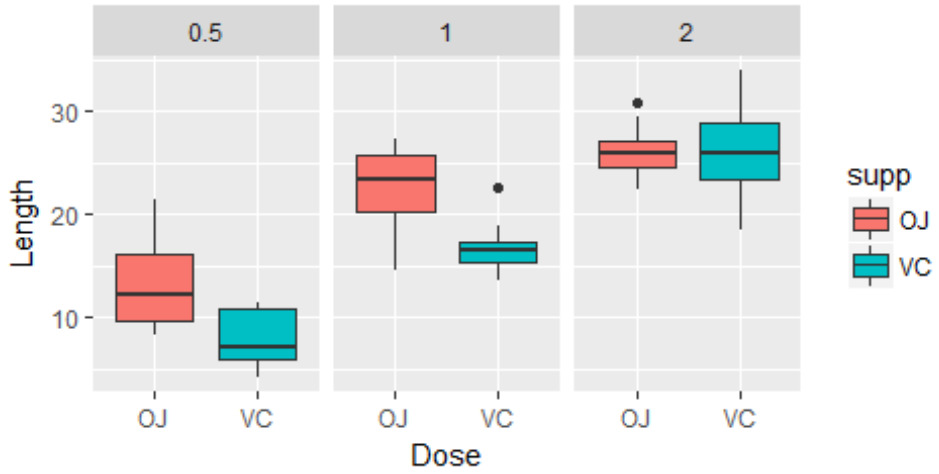
Average Tooth Growth Increases with Dose

Figure 1



For Lower Doses, Average Growth is Higher for OJ

Figure 2



Summary of Exploratory Analysis

1. The data indicate there maybe a strong relationship between an increase in tooth length and dose. Figure 1 on Left
2. The data indicate there maybe a difference in effectiveness between Orange Juice and Vitamin C supplements. Figure 2 on Right

HYPOTHESIS TESTING

Hypothesis Test 1: Over all dosage levels, with 95% confidence is Orange Juice a more effective delivery method than Vitamin C supplements

Assumptions: Tooth growth is normally distributed

Approach: Use Permutation testing to find percentage of results that produce a more extreme difference in averages than was measured

Ho: `There is no significant difference in tooth growth between Orange Juice and Vitamin C`

Ha: `Average tooth growth is greater for Orange Juice`

```
y <- ToothGrowth$len
group <- ToothGrowth$supp
testStat <- function(l, g) mean(l[g == "OJ"]) - mean(l[g == "VC"])  # test statistic difference of means between groups
observedStat <- testStat(y, group)  # test statistic for real observations
permutations <- sapply(1:10000, function(i) testStat(y, sample(group)))  # test statistics for permutations
observedStat

## [1] 3.7

mean(permutations > observedStat)  # percentage of permutations that have a more extreme result than was observed

## [1] 0.0282
```

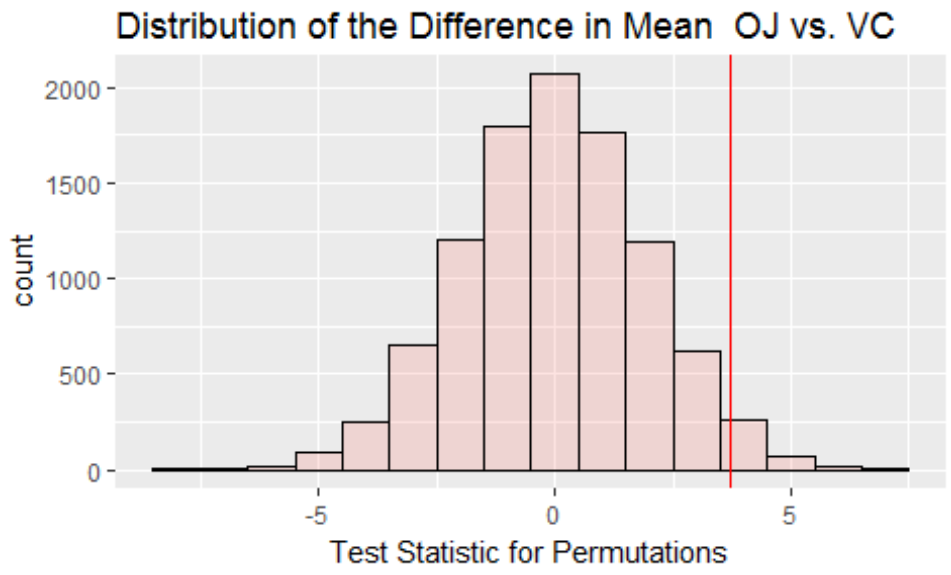


Figure 3: Permutations Analysis

Conclusion for Hypothesis 1

Based on the very low probability of finding a more extreme example, we should **REJECT the null hypothesis Ho:** `There is no significant difference in tooth growth between Orange Juice and Vitamin C`

Hypothesis Test 2: At low dose (0.5), with 95% confidence is Orange Juice a more effective delivery method than Vitamin C supplements

Assumptions: Tooth growth is normally distributed

Ho: `There is no difference in average growth`

Ha: `Average tooth growth is greater for Orange Juice`

```
lenOJ <- ToothGrowth$len[ToothGrowth$dose == 0.5 & ToothGrowth$supp ==
    "OJ"]
lenVC <- ToothGrowth$len[ToothGrowth$dose == 0.5 & ToothGrowth$supp ==
    "VC"]
t.test(lenOJ, lenVC, alternative = "greater", paired = FALSE, var.equal =
TRUE)$p.value

## [1] 0.002651831
```

Conclusion for Hypothesis 2

Based on the Student's T Test, we should **REJECT the null Hypothesis Ho:** `There is no difference in average growth`

3. At high dose (2.0), with 95% confidence is Orange Juice a more effective delivery method than Vitamin C supplements

Assumptions: Tooth growth is normally distributed

Ho: `There is no difference in average growth`

Ha: `Average tooth growth is greater for Orange Juice`

```
lenOJ <- ToothGrowth$len[ToothGrowth$dose == 2 & ToothGrowth$supp ==
    "OJ"]
lenVC <- ToothGrowth$len[ToothGrowth$dose == 2 & ToothGrowth$supp ==
    "VC"]
t.test(lenOJ, lenVC, alternative = "greater", paired = FALSE, var.equal =
TRUE)$p.value

## [1] 0.5181451
```

Conclusion for Hypothesis 3

Based on the Student's T Test, we should **ACCEPT the null Hypothesis Ho:** `There is no difference in average growth`

APPENDIX

Code for Figure 1

```
createFig1

## function() {
##         g <- ggplot(data=ToothGrowth, aes(y=len, x=dose, fill=dose)) +
geom_boxplot()
##         g <- g + labs(title = "Average Tooth Growth Increases with Dose",
x="Dose", y="Length", subtitle="Figure 1")
##         print(g)
## }
```

Code for Figure 2

```
createFig2

## function() {
##         g <- ggplot(data=ToothGrowth, aes(y=len, x=supp, fill=supp)) +
geom_boxplot()
##         g <- g + facet_grid(. ~ dose)
##         g <- g + labs(title = "For Lower Doses, Average Growth is Higher
for OJ", x="Dose", y="Length", subtitle="Figure 2")
##         print(g)
## }
```

Code for Figure 3

```
createFig3

## function() {
##         dat <- data.frame(x=permutations)
##         g <- ggplot(dat, aes(x = x, fill="red"))
##         g <- g + geom_histogram(alpha = .20, binwidth=1, color = "black")
##         g <- g + geom_vline(xintercept=observedStat, color='red') +
theme(legend.position="none")
##         g <- g + labs(title="Distribution of the Difference in Mean  OJ
vs. VC", x="Test Statistic for Permutations")
##         print(g)
## }
```