Statistical Inference Week 2, Part 2: Basic Inferential Data Analysis Instructions

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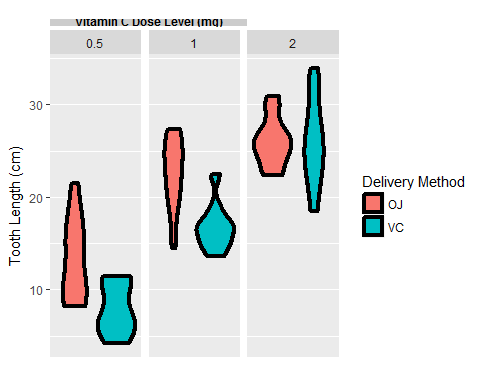
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# Overview of ToothGrow Dataset

The data used in the following analysis is from the ToothGrow dataset in the default datasets package. The title of the dataset is *The Effect of Vitamin C on Tooth Growth in Guinea Pigs*. The description of the dataset is as follows:

*The response is the 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).*

# Basic Exploratory Data Analysis



By charting out violin plots for each dose and delivery method combination, we can consider the hypothesis that the dose level is correlated with tooth length regardless of delivery method. We can also see that the delivery method has an impact, though the impact becomes less pronounced as the dose level increases.

# Confidence Intervals and Hypothesis Testing

To assess if our insights drawn from our graphical analysis are statistically valid, we perform T-Tests for the tooth length as the outcome predicted by three separate vectors.

1. Delivery method as the predictor
2. Dose level as predictor
3. Delivery method and dose as predictors

The approach is outlined in the first t-test and replicated for each additional test.

## Comparing outcomes across delivery methods

For this test, we ignore dosage and consider only the delivery method (either orange juice and ascorbic acid) as a predictor of tooth length. We consider the following hypotheses:

: Tooth length is not affected by delivery method.

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

##   
## 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 the p-value is greater than 0.05 and confidence interval crosses 0 (-7.571, 0.171), we can not reject within a 95% confidence interval. This indicated that there is not strong evidence pointing to a significant difference in tooth length between delivery methods.

## Comparing outcomes across delivery methods

For this test, we ignore delivery methods and consider only the dose level as a predictor of tooth length. We consider the following hypothesis:

: Tooth length is not affected by dose level

We assess this hypothesis by performing three t-tests, with tooth length predicted by dose level, between each combination of dose levels (i.e. 0.5 ~ 1.0, 0.5 ~ 2.0, 1.0 ~ 2.0).

As the p-value is less than 0.05 and confidence interval does not cross 0 for any of the combinations, we can reject with at least a 95% confidence interval. This indicates that there is strong evidence pointing to a significant difference in tooth length between dose levels.

## Comparing outcomes across delivery methods and dose levels

Finally, we consider the effect of delivery method while also considering dose level. For this, we consider the following hypotheses:

: Tooth length is not affected by delivery method at a 0.5mg dose

: Tooth length is not affected by delivery method at a 1.0mg dose

: Tooth length is not affected by delivery method at a 2.0mg dose

We assess this hypothesis by performing three t-tests, with tooth length predicted by delivery method level combination at each dose levels. The primary results from these tests are summarized in the chart below.

We can take away the following for this table:

* **For and** : Because the p-value is less than 0.05 and because the confidence interval does not cross 0 for either test, we can reject and with at least a 95% confidence interval.
* **For** : Because the p-value is greater than 0.05 and because the confidence interval crosses 0 (-7.571, 0.171), we can not reject the : within a 95% confidence interval.

# Conclusions and Assumptions

## Conclusions

Based on the insights drawn from the analysis performed, we can conclude the following:

* There is not strong evidence indicating that tooth length varies based on delivery methods independent of dose level ; however, there is evidence showing that it varies when the dose level is contolled at either 0.5mg or 1.0 mg.
* There is strong evidence indicating that tooth length varies based on dose levels.

## Assumptions

To arrive at these conclusions, we assume the following for our data and analysis:

* Populations of guinea pigs were independent (i.e.  60 guinea pigs with similar tooth lengths each randomly assigned)
* Variances across groups are NOT equal (as such, we set var.equal = F in our T Tests)
* Acurate and consistent data collection and measurement methodologies were used in compiling the dataset.

# Appendix I: Coding Reference

## Loading the Data

First, we load the data and set the supp column in the dataset as a two-level factor variable, with a level representing Ascorbic Acid and Orange Juice respectively.

data(ToothGrowth)  
ToothGrowth$supp <- factor(ToothGrowth$supp, levels = c("VC", "OJ"), labels = c("Ascorbic Acid", "Orange Juice"))

## Basic Exploratory Data Analysis

library(ggplot2)  
library(gtable)  
library(grid)  
library(dplyr)  
library(knitr)  
  
xlab <- "Delivery Method"  
ylab <- "Tooth Length (cm)"  
flab <- "Vitamin C Dose Level (mg)"  
g <- ggplot(data = ToothGrowth, aes(x = factor(supp), y = len, fill = supp)) + scale\_fill\_discrete(name = xlab)  
g <- g + geom\_violin(col = "black", size = 1.5) + facet\_wrap(~ dose) + scale\_x\_discrete(breaks=NULL)  
g <- g + xlab("") + ylab(ylab)  
z <- ggplotGrob(g)  
z <- gtable\_add\_rows(z, unit(1, "lines"), pos = 0)  
z <- gtable\_add\_grob(z, list(rectGrob(gp = gpar(col = NA, fill = gray(0.8), size = .5)), textGrob(flab, vjust = .27,   
 gp = gpar(cex = .75, fontface = "bold", col = "black"))), 2, 4, 2, 10, name = c("a", "b"))  
z <- gtable\_add\_rows(z, unit(2/10, "line"), 2)  
grid.newpage()  
grid.draw(z)

## Comparing outcomes across delivery methods

data(ToothGrowth)  
teeth\_05\_10 <- filter(ToothGrowth, dose == 0.5 | dose == 1.0)  
teeth\_05\_20 <- filter(ToothGrowth, dose == 0.5 | dose == 2.0)  
teeth\_10\_20 <- filter(ToothGrowth, dose == 1.0 | dose == 2.0)  
  
ttest\_05\_10 <- t.test(len ~ dose, data = teeth\_05\_10, paired = F, var.equal = F)  
ttest\_05\_20 <- t.test(len ~ dose, data = teeth\_05\_20, paired = F, var.equal = F)  
ttest\_10\_20 <- t.test(len ~ dose, data = teeth\_10\_20, paired = F, var.equal = F)  
  
library(xtable)  
sumtable <- data.frame(dose.levels = c("0.5mg-1.0mg", "0.5mg-2.0mg", "1.0mg-2.0mg"),   
 t.statistic = c(ttest\_05\_10$statistic, ttest\_05\_20$statistic, ttest\_10\_20$statistic),   
 p.value = c(ttest\_05\_10$p.value,ttest\_05\_20$p.value,ttest\_10\_20$p.value),   
 conf.int.lower = c(ttest\_05\_10$conf.int[1], ttest\_05\_20$conf.int[1], ttest\_10\_20$conf.int[1]),   
 conf.int.upper = c(ttest\_05\_10$conf.int[2], ttest\_05\_20$conf.int[2], ttest\_10\_20$conf.int[2]))  
print(xtable(sumtable), comment=F)

## Comparing outcomes across delivery methods and dose levels

data(ToothGrowth)  
teeth\_05 <- filter(ToothGrowth, dose == 0.5)  
teeth\_10 <- filter(ToothGrowth, dose == 1.0)  
teeth\_20 <- filter(ToothGrowth, dose == 2.0)  
  
ttest\_05 <- t.test(len ~ supp, data = teeth\_05, paired = F, var.equal = F)  
ttest\_10 <- t.test(len ~ supp, data = teeth\_10, paired = F, var.equal = F)  
ttest\_20 <- t.test(len ~ supp, data = teeth\_20, paired = F, var.equal = F)  
sumtable <- data.frame(dose.level = c("0.5mg", "1.0mg", "2.0mg"),   
 t.statistic = c(ttest\_05$statistic, ttest\_10$statistic, ttest\_20$statistic),  
 p.value = c(ttest\_05$p.value, ttest\_10$p.value, ttest\_20$p.value),   
 conf.int.lower = c(ttest\_05$conf.int[1], ttest\_10$conf.int[1], ttest\_20$conf.int[1]),   
 conf.int.upper = c(ttest\_05$conf.int[2], ttest\_10$conf.int[2], ttest\_20$conf.int[2]))  
print(xtable(sumtable), comment=F)