

Course Project: Part 2

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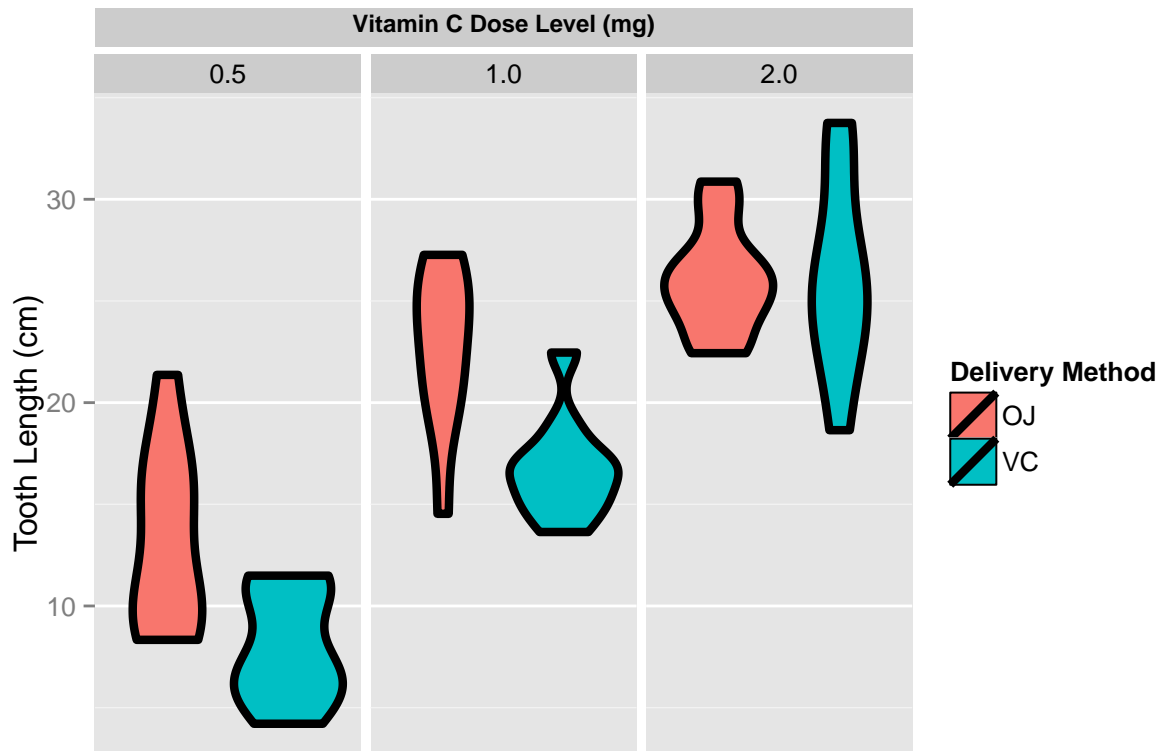
November 23, 2014

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, as quoted from the accompanying documentation 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 already start to consider the hypothesis that the dose level is correlated with tooth length regardless of delivery method. We can also see that the delivery method also has an impact, though the impact becomes less pronounced as the dose level increases.

Confidence Intervals and Hypothesis Testing

In order 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 will be outlined in the first t-test and replicated for each additional test (albeit with code suppressed for readability).

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:

H_0 : 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
```

Because the p-value is greater than 0.05 and because the confidence interval crosses 0 (-7.571, 0.171), we can not reject H_0 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:

H_0 : 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). The primary results from these tests are summarized in the chart below.

Because the p-value is less than 0.05 and because the confidence interval does not cross 0 for any of the combinations, we can reject H_0 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.

	dose.levels	t.statistic	p.value	conf.int.lower	conf.int.upper
1	0.5mg-1.0mg	-6.48	0.00	-11.98	-6.28
2	0.5mg-2.0mg	-11.80	0.00	-18.16	-12.83
3	1.0mg-2.0mg	-4.90	0.00	-9.00	-3.73

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:

H_0 : Tooth length is not affected by delivery method at a 0.5mg dose

H_1 : Tooth length is not affected by delivery method at a 1.0mg dose

H_2 : 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.

	dose.level	t.statistic	p.value	conf.int.lower	conf.int.upper
1	0.5mg	3.17	0.01	1.72	8.78
2	1.0mg	4.03	0.00	2.80	9.06
3	2.0mg	-0.05	0.96	-3.80	3.64

We can take away the following for this table:

- **For H_0 and H_1 :** Because the p-value is less than 0.05 and because the confidence interval does not cross 0 for either test, we can reject H_0 and H_1 with at least a 95% confidence interval.
- **For H_2 :** 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 H_2 : 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

In order to arrive at these conclusions, we assume the following about our data and analysis:

- Populations of guinea pigs were independent (i.e. there were 60 guinea pigs with similar tooth lengths which were each randomly assigned to a condition)
- 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)

```