Tooth Growth Analysis

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Overview

In the ToothGrowth dataset that comes standard in the R repository, the response variable is the length of odontoblasts (cells responsible for tooth growth) in 60 guinea pigs split into 6 groups of (we assume independently chosen) 10, each group receiving one of three dose levels of Vitamin C (0.5, 1.0, and 2.0 mg) with one of two delivery methods (orange juice [OJ] or an aqueous solution of ascorbic acid [VC]).[1]

[1] See Edward Kuns description here

In this paper, we do an exploratory analysis of the data, then run through some *t-test* to confirm what we see that:

- At lower dosages (0.5, 1), OJ seems to have better growth characteristics
- At highest dosage (2), OJ flattens out a bit and looks similar to VC.

Exploratory Data Analysis

Note that all the code required to reproduce all the analysis is provided in an appendix after the expository portion of this paper. We look first at the structure of the *ToothGroth* dataset:

```
## '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 ...
```

And now look at the breakdown of Supplement and Dose:

```
##
##      0.5  1  2
##   OJ  10 10 10
##   VC  10 10 10
```

Since **dose** has 3 discrete levels, we make it a factor, then produce a conditioning plot (Figure 1) for initial exploratory purposes. We see that for both supplement type (OJ, VC) increasing dosage gives increased length. At lower dosages (0.5, 1), OJ seems to have better growth characteristics, while at highest dosage (2), OJ flattens out a bit and looks similar to VC.

We now produce a table of summary statistics for each of the breakouts of supplement by dose:

Table 1: Summary Statistics

	OJ.0.5	VC.0.5	OJ.1	VC.1	OJ.2	VC.2
nbr.val	10.00	10.00	10.00	10.00	10.00	10.00
min	8.20	4.20	14.50	13.60	22.40	18.50
max	21.50	11.50	27.30	22.50	30.90	33.90
range	13.30	7.30	12.80	8.90	8.50	15.40
sum	132.30	79.80	227.00	167.70	260.60	261.40
median	12.25	7.15	23.45	16.50	25.95	25.95
mean	13.23	7.98	22.70	16.77	26.06	26.14
SE.mean	1.41	0.87	1.24	0.80	0.84	1.52
CI.mean.0.95	3.19	1.96	2.80	1.80	1.90	3.43
var	19.89	7.54	15.30	6.33	7.05	23.02
std.dev	4.46	2.75	3.91	2.52	2.66	4.80
coef.var	0.34	0.34	0.17	0.15	0.10	0.18

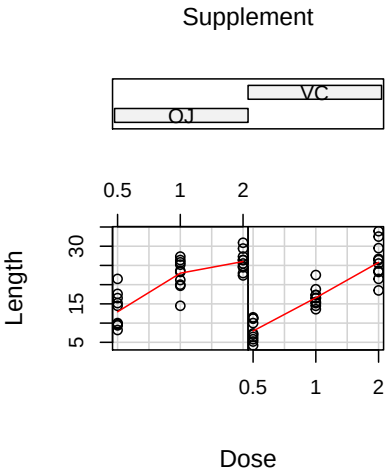

Figure 1: ToothGrowth: length vs dose, by supplement type

Table 1 seems to corroborate what our picture tells us, so now lets get a bit more into the statistical analysis aspect of this study.

Key Assumptions

We assume that the Guinea Pigs are of same/similar stock, and randomly assigned into which of the 6 buckets (OJ vs VC, dosage 0.5, 1. 2) and remain within that group for study duration (hence paired = FALSE in the t-tests). We further assume that for each bucket the distribution of tooth length is fairly normal, though we do not assume same variation (hence var.equal = FALSE in the t-tests).

Hypothesis Tests: T-test's and the EDA Confirmation

So next we run a series of *t-test* pitting each supplement at each corresponding dosage level. For all the tests we will use the following hypothesis:

- $H_0 : \mu_{OJ} = \mu_{VC}$, the means of type delivery are the same (at appropriate dosage)

- $H_a : \mu_{OJ} > \mu_{VC}$, since our EDA indicates this may be appropriate for some levels

Table 2 shows the selected statistics we derive from each *t-test* (again see the appendix for the gory details).

Table 2: T-test Results

X vs Y	Mean X	Mean Y	p-value	(Conf Int	Conf Int)
OJ.0.5 vs VC.0.5	13.23	7.98	0.0064	1.7191	8.7809
OJ.1 vs VC.1	22.7	16.77	0.001	2.8021	9.0579
OJ.2 vs VC.2	26.06	26.14	0.9639	-3.7981	3.6381
All OJ vs All VC	20.6633	16.9633	0.0606	-0.171	7.571

Conclusion

From this we see that for smaller individual dosage levels (0.5, 1.0) the null hypothesis ($H_0 : \mu_{OJ} = \mu_{VC}$) can be discounted due to the corresponding confidence intervals do not contain 0 and associated p-value indicate strong confidence, leaving the alternate hypothesis ($H_a : \mu_{OJ} > \mu_{VC}$)[2]. However, looking at the highest dosage level (2.0), and at the *t-test* looking at only supplement regardless of dosage, we cannot discount H_0 as 0 is included in the confidence intervals, and the p-values are large.

[2] Greater than because the confidence interval lies strictly positive.

Appendix

```
library(tufte)
# invalidate cache when the tufte version changes
knitr::opts_chunk$set(tidy = FALSE, cache.extra = packageVersion('tufte'))
options(htmltools.dir.version = FALSE)
```

Get the Data and Look at it

```
## we use the Tufte feature of R Markdown to produce the desired style  Render with:
## render("Part 2 - ToothGrowth.Rmd", output_format = "tufte_handout")

library(knitr, quietly = TRUE, warn.conflicts = FALSE) ## for "spread" function
library(tidyr, quietly = TRUE, warn.conflicts = FALSE) ## for "spread" function
library(dplyr, quietly = TRUE, warn.conflicts = FALSE) ## manipulate the data
library(pastecs, quietly = TRUE, warn.conflicts = FALSE) ## we want to use the "stat.desc" function

data(ToothGrowth)
str(ToothGrowth)

table(ToothGrowth$supp, ToothGrowth$dose)
```

What Does it Look Like?

```
ToothGrowth$dose <- as.factor(ToothGrowth$dose) ## convert to a factor as only 3 levels

coplot(len ~ dose | supp, data = ToothGrowth, panel = panel.smooth, xlab = c("Dose", "Supplement"),
       ylab = "Length")

## turn 2-column into 1-column. E.g. "OC" "1.0" becomes "OC1.0"
ToothGrowth$treat <- with(ToothGrowth, interaction(supp, dose))

## reduce the dataset down to one column of 10 obs for each of 6 different treatments
growth <- ToothGrowth %>%
  select(len, treat) %>%
  group_by(treat) %>%
  mutate(row = 1:n()) %>%
  spread(treat, len) %>%
  select(-row)

stats <- stat.desc(growth)
stats <- round(stats, 2)
kable(stats[c(1, 4:14),], caption = "Summary Statistics")
```

The Tests

```
tt <- NULL

tt <- rbind(tt, c("OJ.0.5 vs VC.0.5",
                  round(
                    unlist(
                      t.test(growth$OJ.0.5, growth$VC.0.5, var.equal = FALSE, paired = FALSE)[
                        c("estimate","p.value","conf.int")]),
                    4)))

tt <- rbind(tt, c("OJ.1 vs VC.1",
                  round(
                    unlist(
                      t.test(growth$OJ.1, growth$VC.1, var.equal = FALSE, paired = FALSE)[
                        c("estimate","p.value","conf.int")]),
                    4)))

tt <- rbind(tt, c("OJ.2 vs VC.2",
                  round(
                    unlist(
                      t.test(growth$OJ.2, growth$VC.2, var.equal = FALSE, paired = FALSE)[
                        c("estimate","p.value","conf.int")]),
                    4)))


## for comparing all OJ vs VC we just hit up the original dataset
tt <- rbind(tt, c("All OJ vs All VC",
                  round(
                    unlist(
                      t.test(ToothGrowth[ToothGrowth$supp == "OJ",1],
                             ToothGrowth[ToothGrowth$supp == "VC",1],
                             var.equal = FALSE, paired = FALSE)[
                      c("estimate","p.value", "conf.int")]),
                    4)))

colnames(tt) <- c("X vs Y", "Mean X", "Mean Y", "p-value", "(Conf Int", "Conf Int)")

kable(tt, caption = "T-test Results")
```