

Statistical Inference: Analysis of ToothGrowth Data

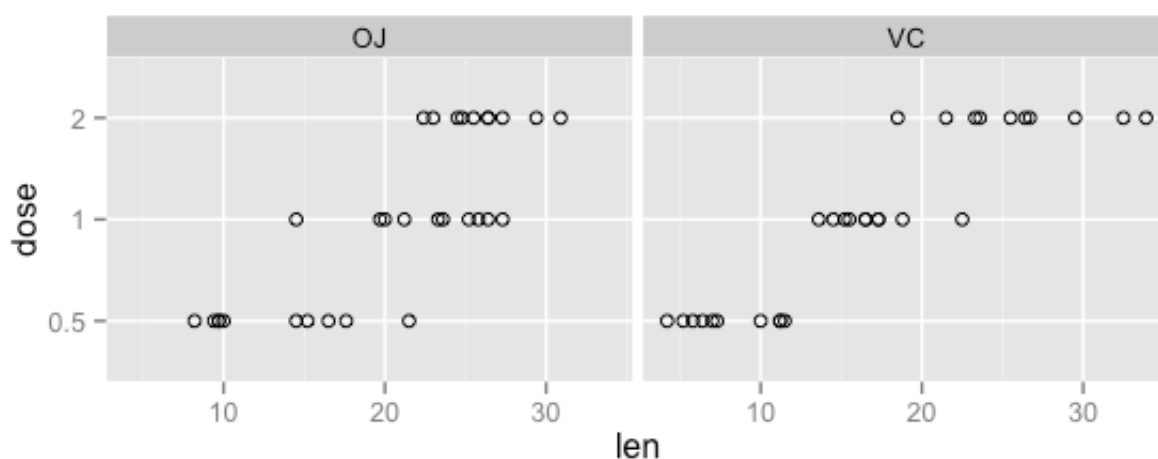
Sheldon White (sheldonwhite@comcast.net (<mailto:sheldonwhite@comcast.net>))

Data Summary

The ToothGrowth data-set is a set of 60 observations describing the measured tooth growth in Guinea Pigs (which will be referred to as “subjects”). Each subject apparently received supplemental Vitamin C at 0.5, 1.0 or 2.0 milligram levels, either in Orange Juice or pure Vitamin C. The units of the length values are not specified.

We start by a basic plot of the data, segregating the data by supplement type.

```
library(ggplot2)
data(ToothGrowth)
ToothGrowth$dose = as.factor(ToothGrowth$dose)
ggplot(ToothGrowth, aes(x=len, y=dose)) + geom_point(shape=1) + facet_grid(. ~ supp)
```



Superficially, it looks like for each supplement type, increasing dosages are matched by increasing tooth length values. Let’s also look at the variances of the different test groups:

```
variances = data.frame(supplement = character(0), dosage = character(0), variance = numeric(0))
for (s in c('OJ', 'VC')) {
  for (d in c(0.5, 1, 2)) {
    row = data.frame(s, d, var(subset(ToothGrowth, supp == s & dose == d)$len))
    colnames(row) = c("suppliment", "dosage", "variance")
    variances = rbind(variances, row)
  }
}
knitr::kable(variances, align = 1)
```

suppliment	dosage	variance
OJ	0.5	19.889
OJ	1.0	15.296
OJ	2.0	7.049
VC	0.5	7.544
VC	1.0	6.327
VC	2.0	23.018

Definitely some differences in the variance of the different test groups. The smaller variance values can be visually matched with a tighter grouping of values in the plot (for instance, VC at 1 milligram).

Hypothesis Tests

We can use t-confidence intervals to perform a series of comparisons between the different sets of subjects. Each test will be framed as a 95% confidence interval for (lengthOfGroup1 - lengthOfGroup1).

The assumptions I make in this analysis:

- Each set of 10 Guinea Pigs for a dose/supplement combination are distinct. (Each pig received a single supplement at a single dosage.) A total population of 60 subjects is assumed.
- Each population variance is assumed to be different.

First we create a function to perform a T test on a specified subset of the ToothGrowth data, returning the results in a convenient format. (By default t.test() assumes a non-paired test and unequal variances, which is what we want here.)

```
generateInterval = function(label, supp1, dose1, supp2, dose2) {
  p = with(ToothGrowth, t.test(len[supp == supp1 & dose == dose1],
                              len[supp == supp2 & dose == dose2]))
  row = data.frame(label, p$conf.int[1], p$conf.int[2], p$conf.int[2] - p$conf.int[1])
  colnames(row) = c("comparison", "low", "high", "range")
  row
}
```

First, we'll compare equal dosages of the two supplements. Each row addresses the hypothesis "A given dosage of OJ causes greater tooth length than the same dosage of VC." A range that's completely positive confirms the hypothesis, but a range that include the zero point tells us that the conclusion cannot be inferred by the data.

```
resultsSupp = data.frame(comparison = character(0), low = numeric(0), high = numeric(0), range = numeric(0))
resultsSupp = rbind(resultsSupp, generateInterval("OJ:0.5 - VC:0.5", 'OJ', 0.5, 'VC', 0.5))
resultsSupp = rbind(resultsSupp, generateInterval("OJ:1.0 - VC:1.0", 'OJ', 1, 'VC', 1))
resultsSupp = rbind(resultsSupp, generateInterval("OJ:2.0 - VC:2.0", 'OJ', 2, 'VC', 2))
knitr::kable(resultsSupp, align = 1)
```

comparison	low	high	range
------------	-----	------	-------

OJ:0.5 - VC:0.5	1.719	8.781	7.062
OJ:1.0 - VC:1.0	2.802	9.058	6.256
OJ:2.0 - VC:2.0	-3.798	3.638	7.436

We can see that at a dosage of 0.5 and 1 milligrams, the T Confidence intervals are completely greater than zero and we are justified in claiming a greater tooth length from the OJ supplements. At the dosage level of 2 milligrams, the range is basically centered around zero and we can't conclude anything from this data.

Next, we'll compare different dosages of a single supplement. Each row addresses the hypothesis "A larger dosage of a supplement causes greater tooth length than a lesser dosage of the same supplement." A range that's completely positive confirms the hypothesis, but a range that include the zero point tells us that the conclusion cannot be inferred by the data.

```
resultsDose = data.frame(label = character(0), low = numeric(0), high = integer(0))
resultsDose = rbind(resultsDose, generateInterval("OJ:1.0 - OJ:0.5", 'OJ', 1, 'OJ', 0.5))
resultsDose = rbind(resultsDose, generateInterval("OJ:2.0 - OJ:1.0", 'OJ', 2, 'OJ', 1))
resultsDose = rbind(resultsDose, generateInterval("OJ:2.0 - OJ:0.5", 'OJ', 2, 'OJ', 0.5))
resultsDose = rbind(resultsDose, generateInterval("VC:1.0 - VC:0.5", 'VC', 1, 'VC', 0.5))
resultsDose = rbind(resultsDose, generateInterval("VC:2.0 - VC:1.0", 'VC', 2, 'VC', 1))
resultsDose = rbind(resultsDose, generateInterval("VC:2.0 - VC:0.5", 'VC', 2, 'VC', 0.5))
knitr::kable(resultsDose, align = 1)
```

comparison	low	high	range
OJ:1.0 - OJ:0.5	5.5244	13.416	7.891
OJ:2.0 - OJ:1.0	0.1886	6.531	6.343
OJ:2.0 - OJ:0.5	9.3248	16.335	7.011
VC:1.0 - VC:0.5	6.3143	11.266	4.951
VC:2.0 - VC:1.0	5.6857	13.054	7.369
VC:2.0 - VC:0.5	14.4185	21.901	7.483

In all cases, a larger dosage appears to result in greater tooth growth. The most questionable case is comparing OJ at 2 milligrams versus OJ at 1 milligram. Here the lower bound of the range is very close to zero and we probably have the least confidence about this prediction.

```
sessionInfo()
```

```
## R version 3.1.0 (2014-04-10)
## Platform: x86_64-apple-darwin13.1.0 (64-bit)
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] ggplot2_1.0.0
##
## loaded via a namespace (and not attached):
## [1] colorspace_1.2-4 digest_0.6.4     evaluate_0.5.5  formatR_0.10
## [5] grid_3.1.0      gtable_0.1.2    htmltools_0.2.4 knitr_1.6
## [9] labeling_0.2    MASS_7.3-33     munsell_0.4.2  plyr_1.8.1
## [13] proto_0.3-10    Rcpp_0.11.2     reshape2_1.4   rmarkdown_0.2.49
## [17] scales_0.2.4    stringr_0.6.2   tools_3.1.0    yaml_2.1.13
```