ToothGrowth Data Analysis

Pier Lorenzo Paracchini

Overview

The goal is to analyze the ToothGrowth data in the R datasets package, performing some exploratory analysis, and then use confidence intervals and/or hypothesis tests to compare tooth growth by `supp` and `dose`.

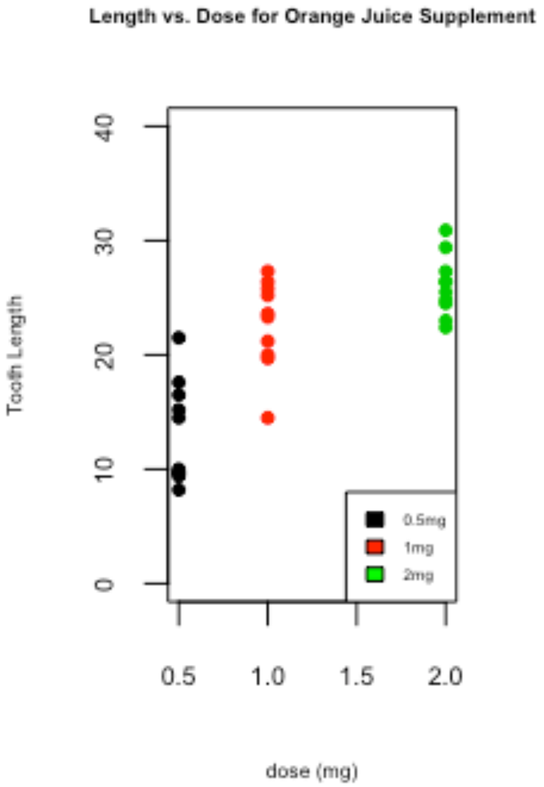
Description of the data from the documentation *"The response is the length of odontoblasts (teeth) in each of 10 guinea pigs at each of three dose levels of Vitamin C (0.5, 1, and 2 mg) with each of two delivery methods (orange juice or ascorbic acid)."*

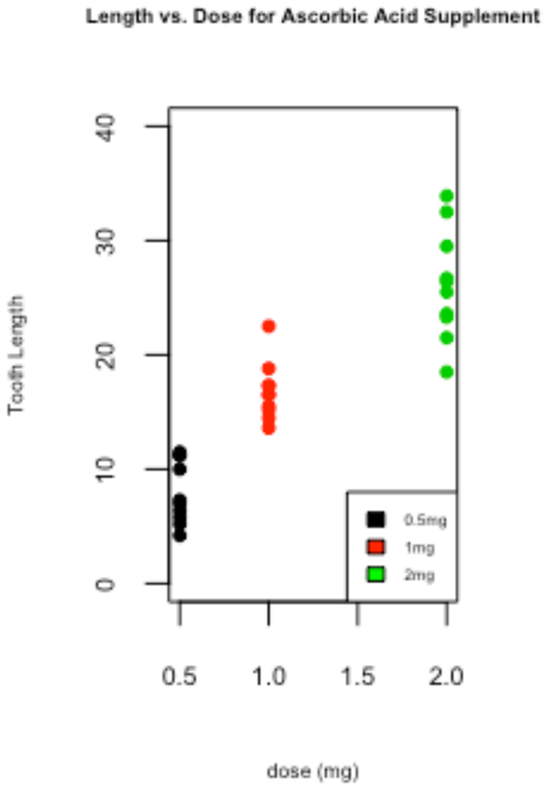
Getting and Exploring the data

```r
require(datasets)
rawData <- ToothGrowth
str(rawData)
```

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

The rawdata includes 60 obs. of 3 features. Features are `len` the tooth length (`numeric`), `supp` the supplement type (`factor`) and finally `dose`, the dose in milligrams (`numeric`). There are 6 possible groups by `supp` and `dose` (see the plot below). For each supplement `supp` ("OJ" and "VC"), there are three different groups based on the `dose` values - 0.5mg, 1mg, 2mg.





And here some basic statics about the sample tooth length for each group.

Supp	Dose	No of Sample	Sample mean	Sample SD
"OJ"	0.5	10	13.23	4.46
"OJ"	1.0	10	22.7	3.911
"OJ"	2.0	10	26.06	2.655
---	---	---	---	---
"VC"	0.5	10	7.98	2.747
"VC"	1.0	10	16.77	2.515
"VC"	2.0	10	26.14	4.798

Confidence Intervals & Hypothesis Testing

Basic Assumptions

Having **each group has a limited number of sample (10 sample)** then **`t distribution`** and **`t confidence intervals`** are going to be used. Being the guinea pigs used for each measurement distinct from each other within a group and between the groups then the **groups can be considered independent from each other** and each guinea pig can be considered **iid**. Finally looking at the **sample**

standard deviation for the different groups the assumption can be made to consider the **diffent variances as equals**.

Independent group t confidence intervals

Group1	Group2	t confidence interval (g1, g2)
OJ, 1.0	**OJ, 0.5**	5.5291857, 13.4108143 **(1)**
OJ, 2.0	**OJ, 1.0**	0.2194983, 6.5005017 **(2)**
---	---	---
VC, 1.0	**VC, 0.5**	6.3156545, 11.2643455 **(3)**
VC, 2.0	**VC, 1.0**	5.7710402, 12.9689598 **(4)**
---	---	---
OJ, all	**VC, all**	-0.1670064, 7.5670064 **(5)**
---	---	---
OJ, 0.5	**VC, 0.5**	6.3156545, 11.2643455 **(6)**
OJ, 1.0	**VC, 1.0**	14.4871567, 21.8328433 **(7)**
OJ, 2.0	**VC, 2.0**	5.7710402, 12.9689598 **(8)**

Interpretation

- **Supplement `OJ` only**, since the intervals (1)(2) are entirely above zero it suggest that groups with a higher dose have more tooth length than groups with a lower dose (at 95% confidence). The same cosideration can be done considering **supplement `VC` only** see (3)(4).

- Comparing the **supplement `OJ` vs. `VC`**
  - **overall** data, the confidence interval (5) contains zero (with most on the interval above zero) and makes it difficult to interpret the data
  - **data** for the same `dose` level (e.g 0.5 mg `OJ` vs. 0.5 mg `VC`), the intervals (6)(7)(8) are entirely above zero suggesting again that groups treated with `OJ` have more tooth length than groups treated with `VC` (at 95% confidence)

Hypothesis Testing

Lets perform (two sided) hypothesis testing focusing on the comparison of the 2 different supplements `OJ vs VC` and considering the following hypothesis

- $H_0: \mu_1 = \mu_2$
- $H_1: \mu_1 \neq \mu_2$

Group1	Group2	t	df	p-value
OJ, all	**VC, all**	1.9152683	58	0.0603934
---	---	---	---	---
OJ, 0.5	**VC, 0.5**	7.4634301	18	6.492264610^{-7}
OJ, 1.0	**VC, 1.0**	10.3877952	18	4.957285710^{-9}
OJ, 2.0	**VC, 2.0**	5.4698137	18	3.397577910^{-5}

Interpretation
Remember the **p-value** represents the probability of seeing evidence as extreme or more extreme than the one obtained under H_0.

- Comparing the **supplement `OJ` vs. `VC`**
  - **overall** data, the __t__value is relevant so **"the** H_0 **hypothesis can be rejected"** with a **p-value** around 6%.
  - **data** for the same `dose` level (e.g 0.5 mg `OJ` vs. 0.5 mg `VC`), **t** values are quite big so it could be said that **"the** H_0 **hypothesis can be rejected"** and the **p-values** are very very low therefore a very unlikely event has been observed or, again, the **"the** H_0 **hypothesis is false"**.

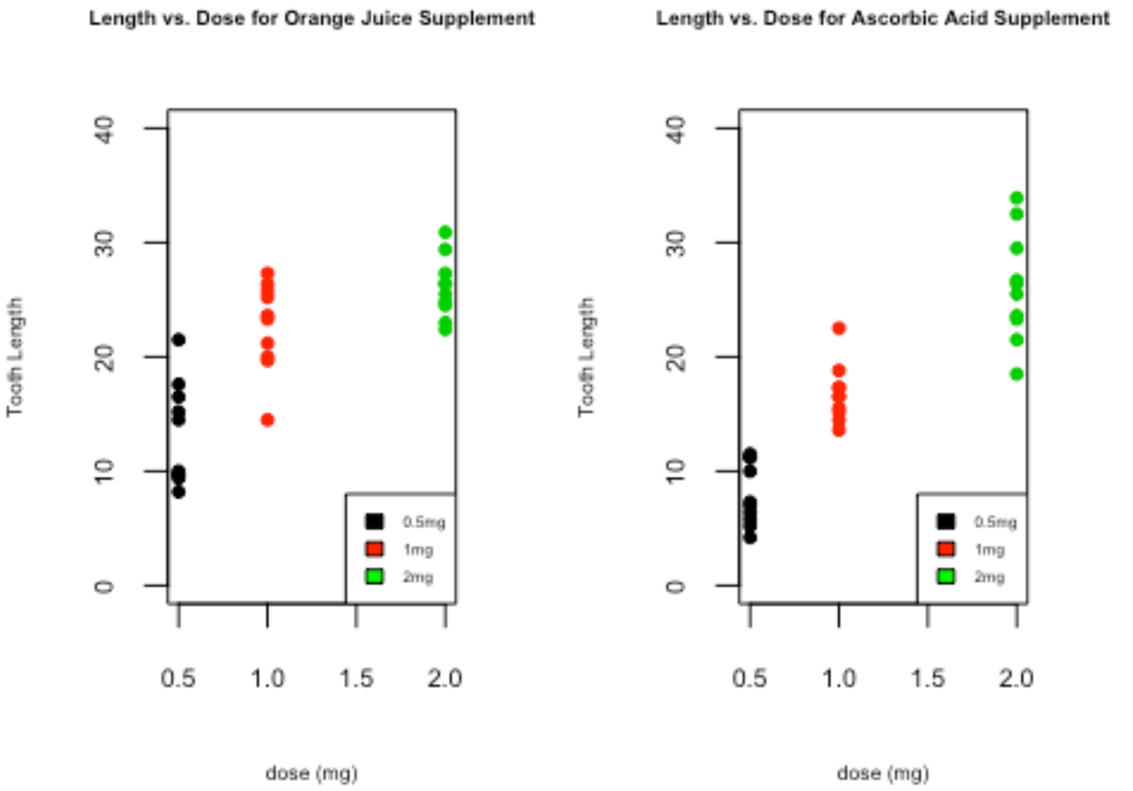
Appendix

Code used to create the basic plot to visualize basic information of the rawData.

```
require(graphics)
rawData_OJ <- rawData[rawData$supp == "OJ",]
rawData_OJ$doseF <- as.factor(rawData_OJ$dose)
rawData_VC <- rawData[rawData$supp == "VC",]
rawData_VC$doseF <- as.factor(rawData_VC$dose)

par(ps = 8, cex.lab = 0.8, mfcol = c(1,2))
plot(rawData_OJ$dose, rawData_OJ$len, col = c(rawData_OJ$doseF), pch = 20, main ="Length vs. Dose
for Orange Juice Supplement", xlab = "dose (mg)", ylab ="Tooth Length", ylim=c(0, 40), cex.main =
0.8)
legend("bottomright",cex = 0.6, fill = c("black","red","green"), legend = c("0.5mg","1mg","2mg"))

plot(rawData_VC$dose, rawData_VC$len, col = c(rawData_VC$doseF), pch = 20, main ="Length vs. Dose
for Ascorbic Acid Supplement", xlab = "dose (mg)", ylab ="Tooth Length", , ylim=c(0, 40), cex.main
= 0.8)
legend("bottomright",cex = 0.6, fill = c("black","red","green"), legend = c("0.5mg","1mg","2mg"))
```



Code used to prepare the data of the different groups

```
len_OJ <- rawData[rawData$supp == "OJ",]$len
len_OJ_05 <- rawData[rawData$supp == "OJ" & rawData$dose == 0.5,]$len
len_OJ_10 <- rawData[rawData$supp == "OJ" & rawData$dose == 1.0,]$len
len_OJ_20 <- rawData[rawData$supp == "OJ" & rawData$dose == 2.0,]$len
```

```
len_VC <- rawData[rawData$supp == "VC",]$len
len_VC_05 <- rawData[rawData$supp == "VC" & rawData$dose == 0.5,]$len
len_VC_10 <- rawData[rawData$supp == "VC" & rawData$dose == 1.0,]$len
len_VC_20 <- rawData[rawData$supp == "VC" & rawData$dose == 2.0,]$len
```

Code used to calculate basic statistics for the different groups

```
getStatistics <- function(data){
  return (list(n = length(data), mean = mean(data), sd = round(sd(data),digits = 3)))
}

##OJ Statistics
stats_OJ_05 <- getStatistics(len_OJ_05)
stats_OJ_10 <- getStatistics(len_OJ_10)
stats_OJ_20 <- getStatistics(len_OJ_20)

##VC Statistics
stats_VC_05 <- getStatistics(len_VC_05)
stats_VC_10 <- getStatistics(len_VC_10)
stats_VC_20 <- getStatistics(len_VC_20)
```

Code used to calculate t test data (confidence intervals and hypothesis testing) between the different groups

```
t.testOJ_10_vs_05 <- t.test(len_OJ_10, len_OJ_05, paired = FALSE, var.equal = TRUE)
t.testOJ_20_vs_05 <- t.test(len_OJ_20, len_OJ_05, paired = FALSE, var.equal = TRUE)
t.testOJ_20_vs_10 <- t.test(len_OJ_20, len_OJ_10, paired = FALSE, var.equal = TRUE)

t.testVC_10_vs_05 <- t.test(len_VC_10, len_VC_05, paired = FALSE, var.equal = TRUE)
t.testVC_20_vs_05 <-t.test(len_VC_20, len_VC_05, paired = FALSE, var.equal = TRUE)
t.testVC_20_vs_10 <-t.test(len_VC_20, len_VC_10, paired = FALSE, var.equal = TRUE)

t.testOJ_05_vs_VC_05 <- t.test(len_OJ_05, len_VC_05, paired = FALSE, var.equal = TRUE)
t.testOJ_10_vs_VC_10 <- t.test(len_OJ_10, len_VC_10, paired = FALSE, var.equal = TRUE)
t.testOJ_20_vs_VC_20 <- t.test(len_OJ_20, len_VC_20, paired = FALSE, var.equal = TRUE)

t.testOJ_vs_VC <- t.test(len_OJ, len_VC, paired = FALSE, var.equal = TRUE)
```

Markdown used for the generation of the different tables

Note in the following markdown the ` has been changed to ' in the inline code, in order to be able to show the code itself.

Table of Sample statistics

```
Supp | Dose | No of Sample | Sample mean | Sample SD
---- | ---- | ---- | ---- | ----
"OJ" | 0.5 | 'r stats_OJ_05$n' | 'r stats_OJ_05$mean' | 'r stats_OJ_05$sd'
...
```

Table of Confidence Intervals

```
__Group1__ | __Group2__ | __t confidence interval (g1, g2)__
---- | ---- | ----
__OJ, 1.0__ | __OJ, 0.5__ | 'r t.testOJ_10_vs_05$conf' __(1)__
...
```

Table of Hypothesis Testing

```
__Group1__ | __Group2__ | __t__ | __df__ | __p-value__
---- | ---- | ---- | ---- | ----
__OJ, all__ | __VC, all__ | 'r t.testOJ_vs_VC$statistic' | 'r t.testOJ_vs_VC$parameter' | 'r
t.testOJ_vs_VC$p.value'
```