Exploring the Effect of Vitamin C on Tooth Growth in Guinea Pigs

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Overview

In this report we will explore the ToothGrow dataset included in the default R `datasets` package. This dataset is based on a research study with 10 guinea pigs who were given a vitamin C supplement.

The researchers varied how the supplement was delivered and in what dose. They measured guinea pig tooth length for all 10 guinea pigs for each dose/delivery combination (2 delivery types * 3 doses * 10 guinea pigs = 60 records total).

More information about this dataset is available here.

We will investigate and test the hypotheses that:

1. Tooth length is associated with the manner in which the vitamin C supplement was delivered.
2. Tooth length is associated with the size of vitamin C dose given to a guinea pig.

Load Supporting Resources

We take a moment to load any packages we want to use in this report. These need to be installed and loaded in your R environment if you want to reproduce the report in full.

```r
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
##
## The following object is masked from 'package:stats':
##
##     filter
##
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
library(ggplot2)
library(ggthemes)
```

Load and Explore the Data

We load the data and visualize the key variables of interest.

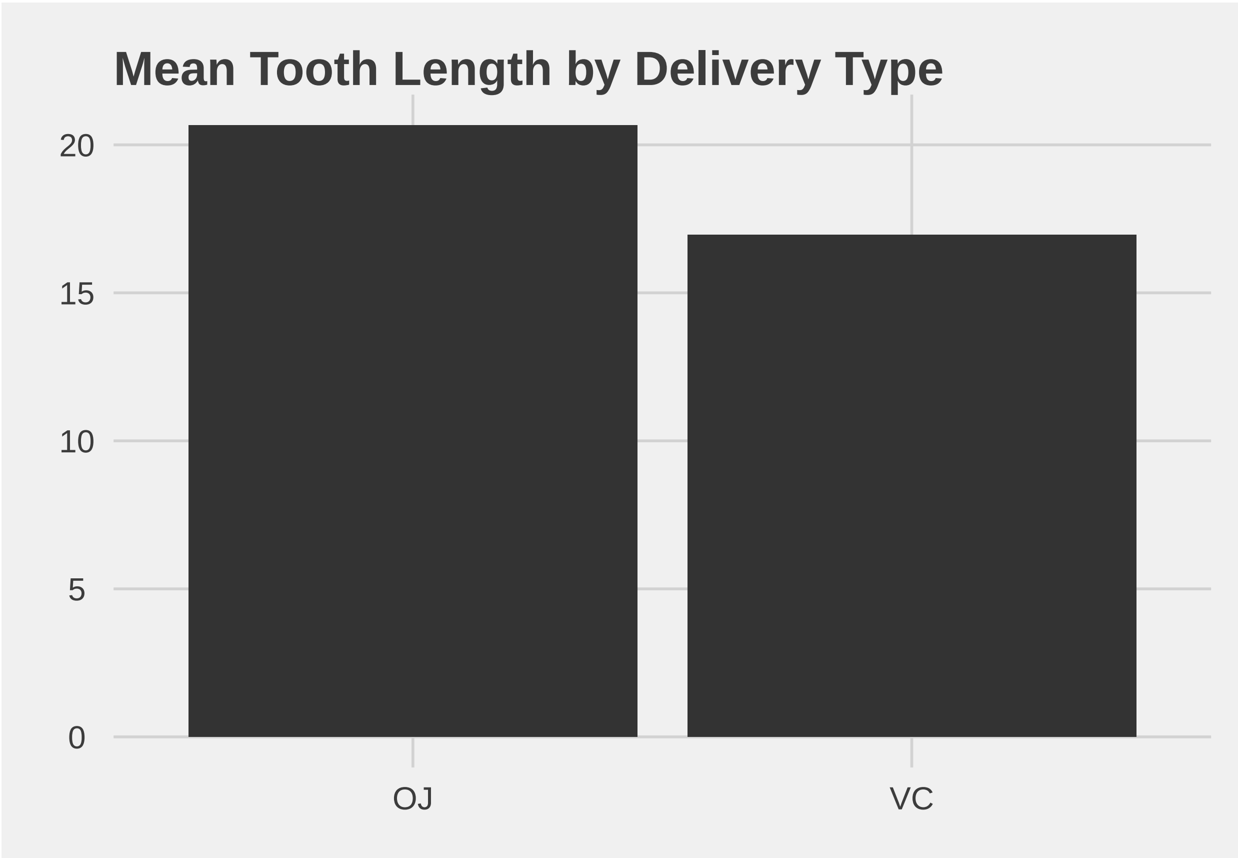
```r
# load the data and then assign the dataset to a shorter name for convenience
# (and in case we want to return to the original data for any reason)
data(ToothGrowth)
tg <- ToothGrowth

# inspect the dataframe
str(tg)
```

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

```r
# add a factored version of dose for cases where we might want to treat this
# as a grouping variable (e.g. plotting)
tg$dose_level <- factor(tg$dose)

# observe the mean tooth length and standard deviation for each delivery type
sum_supp <- summarise(group_by(tg, supp),
                      mean_length = mean(len),
                      sd_length = sd(len))

# observe the mean tooth length and standard deviation for each dose combination
sum_dose <- summarise(group_by(tg, dose_level),
                      mean_length = mean(len),
                      sd_length = sd(len))

# for each dose/delivery combination
sum_combo <- summarise(group_by(tg, supp, dose_level),
                       mean_length = mean(len),
                       sd_length = sd(len))

# print the summaries along with a visualization of each
sum_supp
```

```
## Source: local data frame [2 x 3]
##
##   supp mean_length sd_length
## 1   OJ    20.66333  6.605561
## 2   VC    16.96333  8.266029
```

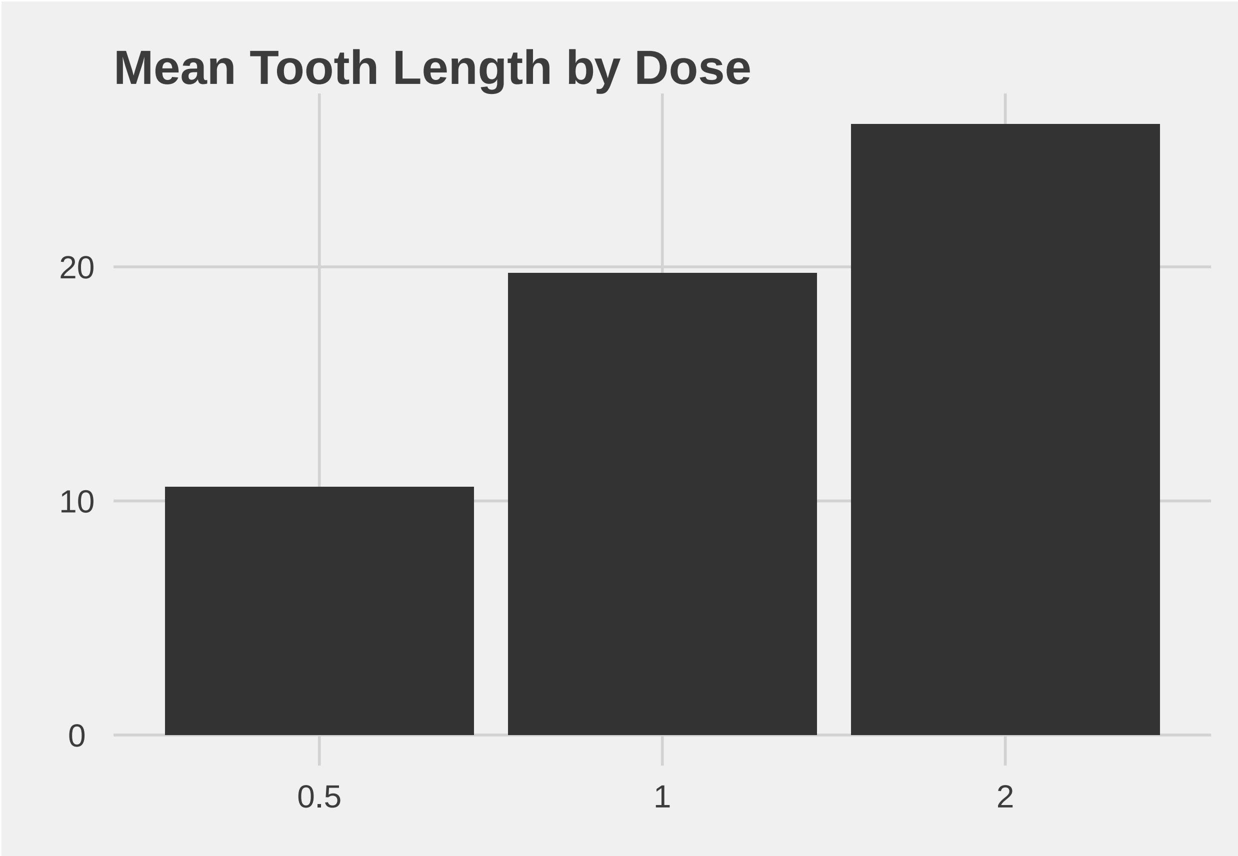
```r
ggplot(sum_supp, aes(x = supp, y = mean_length)) +
    geom_bar(stat = "identity") +
    labs(title = "Mean Tooth Length by Delivery Type") +
    theme_fivethirtyeight()
```




```
sum_dose
```

```
## Source: local data frame [3 x 3]
##
##   dose_level mean_length sd_length
## 1        0.5      10.605  4.499763
## 2          1      19.735  4.415436
## 3          2      26.100  3.774150
```

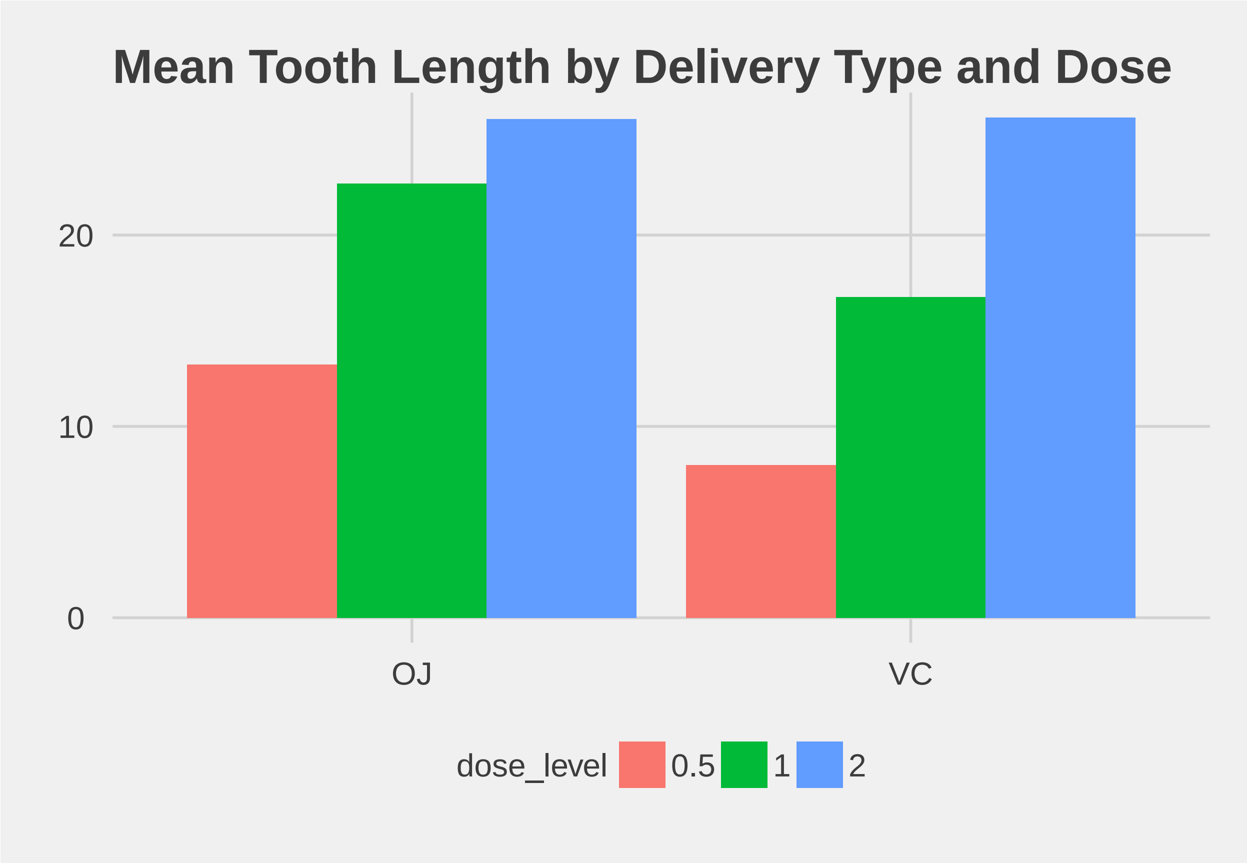
```
ggplot(sum_dose, aes(x = dose_level, y = mean_length)) +
    geom_bar(stat = "identity") +
    labs(title = "Mean Tooth Length by Dose") +
    theme_fivethirtyeight()
```




```
sum_combo
```

```
## Source: local data frame [6 x 4]
## Groups: supp
##
##   supp dose_level mean_length sd_length
## 1   OJ        0.5       13.23  4.459709
## 2   OJ          1       22.70  3.910953
## 3   OJ          2       26.06  2.655058
## 4   VC        0.5        7.98  2.746634
## 5   VC          1       16.77  2.515309
## 6   VC          2       26.14  4.797731
```

```
ggplot(sum_combo, aes(x = supp, y = mean_length, fill = dose_level)) +
    geom_bar(stat = "identity", position = "dodge") +
    labs(title = "Mean Tooth Length by Delivery Type and Dose") +
    theme_fivethirtyeight()
```



Hypothesis Testing

Here we perform the calculations needed to assess whether our observed data support our hypotheses or are insufficient to draw clear conclusions.

The most appropriate approach would be test the overall delivery type ~ dosage relationship using a multi-way ANOVA. However, assignment directions dictate that we only make use of techniques discussed in the current course.

As a result, we will simply test the hypotheses associated with our main effects and we will simply employ t-tests to explore the relevant pairwise comparisons.

Hypothesis 1: Delivery Type ~ Tooth Length

Is tooth length associated with the manner in which the vitamin C supplement was delivered?

```
# we use a conservative t-test: two-sided, assuming unequal variance
# since we don't have pairing information, we treat the groups as independent
t.test(len ~ supp,
       data = tg,
       alternative = "two.sided",
       var.equal = FALSE
       )
```

```
##
```

```
##  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
```

The null hypothesis we are tested is that the difference between our sample means is 0 (aka - the samples have the same means).

The observed p-value suggests marginal significance - we don't make the classic $p < 0.05$ cut-off, but we're close. We can see this marginal significance echoed in the 95% confidence interval - the majority of likely distributions of differences between the means include values larger than 0.

I would treat this as weak evidence that the delivery type may be associated with tooth length, with OJ being associated with longer teeth.

Hypothesis 2: Dosage ~ Tooth Length

Is tooth length associated with the size of the vitamin C dosage?

Ideally, we would test this with an ANOVA. However, per assignment directions, we will restrict our analysis to those presened in the course and will instead treat the results as being three pairwise comparisons.

```r
# as before, we use conservative t-tesst: two-sided, assuming unequal variance
# since we don't have pairing information, we treat the groups as independent

# 0.5 v 1.0
tg_05_10 <- tg[tg$dose_level == "0.5" | tg$dose_level == "1", ]
t.test(len ~ dose_level,
       data = tg_05_10,
       alternative = "two.sided",
       var.equal = FALSE
       )
```

```
##
##  Welch Two Sample t-test
##
## data:  len by dose_level
## t = -6.4766, df = 37.986, p-value = 1.268e-07
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -11.983781  -6.276219
## sample estimates:
## mean in group 0.5   mean in group 1
##            10.605            19.735
```

```r
# 0.5 v 2.0
tg_05_20 <- tg[tg$dose_level == "0.5" | tg$dose_level == "2", ]
t.test(len ~ dose_level,
```

```
       data = tg_05_20,
       alternative = "two.sided",
       var.equal = FALSE
       )
```

```
##
##  Welch Two Sample t-test
##
## data:  len by dose_level
## t = -11.799, df = 36.883, p-value = 4.398e-14
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -18.15617 -12.83383
## sample estimates:
## mean in group 0.5   mean in group 2
##            10.605            26.100
```

```
# 1.0 v 2.0
tg_10_20 <- tg[tg$dose_level == "1" | tg$dose_level == "2", ]
t.test(len ~ dose_level,
       data = tg_10_20,
       alternative = "two.sided",
       var.equal = FALSE
       )
```

```
##
##  Welch Two Sample t-test
##
## data:  len by dose_level
## t = -4.9005, df = 37.101, p-value = 1.906e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -8.996481 -3.733519
## sample estimates:
## mean in group 1 mean in group 2
##          19.735          26.100
```

All comparisons were statistically significant. That is, the observed p-values and confidence intervals suggest that it is unlikely the true distribution of differences between sample means includes "0" (no differences between the samples) for any of the comparisons.

This supports the hypothesis that there is an association between dosage and tooth length. The magnitude of the dosages and the observed tooth lengths suggest that tooth length tends to increase with dosage.

Assumptions and Conclusions

For purpose of this report, we have assumed that it is acceptable to treat our comparison groups as independent. Given that we know the data came from the same guinea pigs (i.e., the comparison are within-group rather than between), this is not ideal. However, independent groups t-tests tend to have less power than paired t-tests and we were conservative about the kinds of t-tests we ran.

To avoid an explosion in the number of pairwise comparison we needed to conduct, we also restricted our analyses to only investigating main effects. It is possible, however, that interactions between independent variables can make interpreting main effects problematic. Thus, we also assumed that any main effects we observed would hold even in the presence of possible delivery type ~ dosage interaction.

With the above assumptions in mind, we observed weak evidence that delivery type is associated with tooth length (OJ being associated with longer teeth than ascorbic acid) and reasonable evidence that dosage size is associated with tooth length (larger doses being associated with longer teeth.

It would appear that delivery type and dosage should be considered if trying to understand or influence tooth length in guinea pigs.