# Inferential Data Analysis

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### Overview

In this project, we are going to explore the ToothGrowth R dataset and do inferential data analysis for our hypotheses

## Setup

```
knitr::opts_chunk$set(echo = TRUE, cache = TRUE, warning = FALSE)
```

### Provide a basic summary of the data

Loading required packages and data set

## **Exploratory Data Analysis**

### Summary of the data

```
means <- data %>%
    group_by(supp, dose) %>%
    summarize(tooth.length = mean(len))

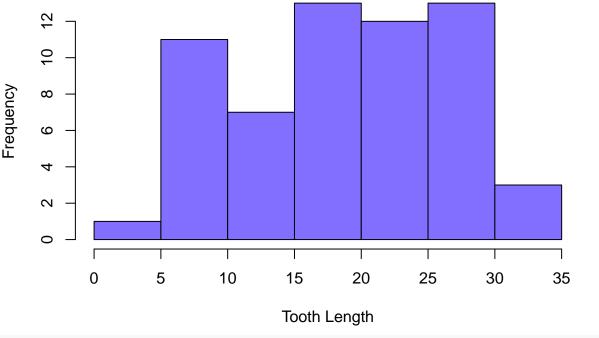
means

## # A tibble: 6 x 3
## # Groups: supp [2]
## supp dose tooth.length
```

```
<fct> <dbl>
##
                          <dbl>
## 1 OJ
             0.5
                          13.2
## 2 OJ
             1
                          22.7
## 3 OJ
             2
                          26.1
## 4 VC
             0.5
                          7.98
## 5 VC
             1
                          16.8
## 6 VC
                          26.1
```

```
# Classes
nclass = round(sqrt(length(data$len)))
hist(data$len, col = "slateblue1", main = "Histogram of Tooth Length", xlab = "Tooth Length", nclass = :
```

## **Histogram of Tooth Length**



```
# DJ - orange juice
# VC - vitamin C
```

## Inferential Analysis

Use confidence intervals and/or hypothesis tests to compare tooth growth by supp and dose

## Hypotesis 1 - Relation between tooth length and the supplement used

```
# Separate value vectors for analysis
supp = data$supp

len_by_OJ = data$len[supp == "OJ"] # Mean
len_by_VC = data$len[supp == "VC"]

# T-test: non-paired, variance based on approx of df, t < mean
t.test(len_by_VC, len_by_OJ, conf.level = .95, var.equal = FALSE, paired = FALSE, alternative = "less")</pre>
```

```
##
##
   Welch Two Sample t-test
##
## data: len_by_VC and len_by_OJ
## t = -1.9153, df = 55.309, p-value = 0.03032
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
          -Inf -0.4682687
##
## sample estimates:
## mean of x mean of y
   16.96333 20.66333
```

The p-value shows strong evidence to reject the null hypothesis (pval < 0.05), indicating there is correlation between the tooth length and the supplement used.

### **Hypothesis Conclusion**

We can confirm with a 95% confidence interval that the tooth length by using Vitamin C across all dosages is less than that of Orange Juice, implying that the tooth length is directly affected by the supplement used.

### Hypothesis 2 - Comparing tooth growth by dose

## t = 4.9005, df = 37.101, p-value = 9.532e-06

```
# Separate value vectors for analysis
half = data$len[data$dose == .5]
one = data$len[data$dose == 1] # Mean
two = data$len[data$dose == 2]
# Dose one is considered the mean sample for testing
# T-test, non-paired, var by approx of df, t < mean
t.test(half, one, alternative = "less", paired = FALSE, var.equal = FALSE, conf.level = .95)
##
##
   Welch Two Sample t-test
##
## data: half and one
## t = -6.4766, df = 37.986, p-value = 6.342e-08
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
##
         -Inf -6.753323
## sample estimates:
## mean of x mean of y
      10.605
                19.735
The p-value shows strong evidence to reject the null hypothesis (pval < 0.05), indicating there is correlation
between lower supplement doses and tooth length.
\# T-test, non-paired, var by approx of df, t > mean
t.test(two, one, alternative = "greater", paired = FALSE, var.equal = FALSE, conf.level = .95)
##
##
   Welch Two Sample t-test
## data: two and one
```

```
## alternative hypothesis: true difference in means is greater than 0
## 95 percent confidence interval:
## 4.17387    Inf
## sample estimates:
## mean of x mean of y
## 26.100    19.735
```

The p-value shows strong evidence to reject the null hypothesis (pval < 0.05), indicating there is correlation between higher supplement doses and tooth length.

### **Hypothesis Conclusion**

We can confirm with a 95% confidence interval that the supplement dosage rate interferes with tooth growth.

We can visualize this statement as the plot shows:

```
ggplot(data, aes(dose, len, group = supp, fill = supp)) +
    geom_bar(stat = "identity", position = "dodge", color = "white") +
    labs(
        x = "Dose",
        y = "Tooth Length",
        fill = "Supplement"
    ) +
    coord_flip() +
    theme_minimal()
```

