Tooth Growth Dataset Exploration

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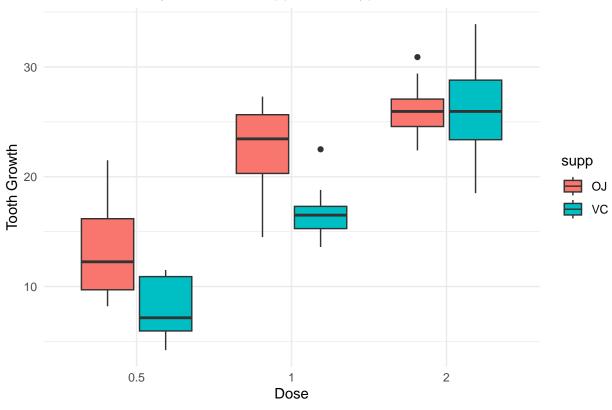
Data Loading

```
data("ToothGrowth")
head(ToothGrowth)
##
     len supp dose
## 1 4.2
           VC 0.5
## 2 11.5
           VC 0.5
## 3 7.3
          VC 0.5
## 4 5.8
          VC 0.5
## 5 6.4
           VC 0.5
## 6 10.0
           VC 0.5
```

Visualization

```
ggplot(ToothGrowth, aes(x=factor(dose), y=len, fill=supp)) +
  geom_boxplot() +
  labs(x = "Dose", y = "Tooth Growth", title = "Tooth Growth by Dose and Supplement Type") +
  theme_minimal()
```

Tooth Growth by Dose and Supplement Type



Statistical Analysis

```
t_test_results <- lapply(unique(ToothGrowth$dose), function(dose_level) {</pre>
  data_subset <- subset(ToothGrowth, dose == dose_level)</pre>
  t.test(len ~ supp, data = data_subset)
print(t_test_results)
## [[1]]
##
##
    Welch Two Sample t-test
##
## data: len by supp
## t = 3.1697, df = 14.969, p-value = 0.006359
## alternative hypothesis: true difference in means between group OJ and group VC is not equal to O
## 95 percent confidence interval:
## 1.719057 8.780943
## sample estimates:
## mean in group OJ mean in group VC
##
              13.23
                                 7.98
##
##
## [[2]]
```

```
##
## Welch Two Sample t-test
##
## data: len by supp
## t = 4.0328, df = 15.358, p-value = 0.001038
## alternative hypothesis: true difference in means between group OJ and group VC is not equal to O
## 95 percent confidence interval:
## 2.802148 9.057852
## sample estimates:
## mean in group OJ mean in group VC
              22.70
                               16.77
##
##
## [[3]]
##
## Welch Two Sample t-test
##
## data: len by supp
## t = -0.046136, df = 14.04, p-value = 0.9639
## alternative hypothesis: true difference in means between group OJ and group VC is not equal to O
## 95 percent confidence interval:
## -3.79807 3.63807
## sample estimates:
## mean in group OJ mean in group VC
##
              26.06
                               26.14
```

Normality Check

Shapiro-Wilk normality test

W = 0.93134, p-value = 0.1639

data: data_subset\$len

##

[[3]]

```
shapiro_test_results <- lapply(unique(ToothGrowth$dose), function(dose_level) {
   data_subset <- subset(ToothGrowth, dose == dose_level)
   shapiro.test(data_subset$len)
})
print(shapiro_test_results)

## [[1]]
##
## Shapiro-Wilk normality test
##
## data: data_subset$len
## W = 0.94065, p-value = 0.2466
##
##
##
## [[2]]</pre>
```

```
## Shapiro-Wilk normality test
##
## data: data_subset$len
## W = 0.97775, p-value = 0.9019
```