

Statistical Inference Course

second peer graded project

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Basic Inferential Data Analysis

Overview

Now in the second portion of the project, we're going to analyze the ToothGrowth data in the R datasets package.

1. Load the ToothGrowth data and perform some basic exploratory data analyses
2. Provide a basic summary of the data.
3. Use confidence intervals and/or hypothesis tests to compare tooth growth by supp and dose. (Only use the techniques from class, even if there's other approaches worth considering)
4. State your conclusions and the assumptions needed for your conclusions.

1: Data load, exploratory analyses and data summary:

We start by loading the data and storing it into a data frame:

```
data("ToothGrowth")           # Load the data
ToothGrowth <- as.data.frame(ToothGrowth) # Store it on a data frame
```

First thing we do is to check how our data looks like:

```
kable(head(ToothGrowth, n = 4), caption = "First 4 entries on the data set")
```

Table 1: First 4 entries on the data set

len	supp	dose
4.2	VC	0.5
11.5	VC	0.5
7.3	VC	0.5
5.8	VC	0.5

We have three variables; but looking at the head, we cannot grasp the full information on the variables. Thus, and looking for more details on the data set, we go to the package documentation to find the following information on the variables:

- len: a continous variable indicating the lenght of guinea's pigs teeth
- supp: a discrete variable indicating which vitamine C supplement, either orange juice (OJ) or ascorbic acid (VC), was applied
- dose: the dose of supplement (in miligrams/day). The dose could take infinite values being a continous variable, but, since here we only have three defined dose we will considere it as a discrete variable.

Since we consider dose as dicrete variable, we change its attribute on the data frame:

```
ToothGrowth$dose <- as.factor(ToothGrowth$dose) # Change attribute from numeric to factor
```

Thus we could consider if the lenght of the tooth is influnced by the the type of supplemnt (VC or OJ) and the dose (0.5,1,2). Again, the head of the data frame only gives information about the structure of the data frame. We will get more details on how many items of each we have by doing a data summary:

```
kable(summary(ToothGrowth), caption = "Data set summary") # Summary of our data
```

Table 2: Data set summary

len	supp	dose
Min. : 4.20	OJ:30	0.5:20
1st Qu.:13.07	VC:30	1 :20
Median :19.25		2 :20
Mean :18.81		
3rd Qu.:25.27		
Max. :33.90		

For the continous variables (lenght) we obtain the mean, the median and the quantiles. For the discrete variables (supp and dose) we obtain the number of entries. Next step is to see if we have an equal number of entries per each dose and supp:

```
# Table classifying the entries per category
kable(table(ToothGrowth$supp, ToothGrowth$dose), caption = "Number of observations")
```

Table 3: Number of observations

	0.5	1	2
OJ	10	10	10
VC	10	10	10

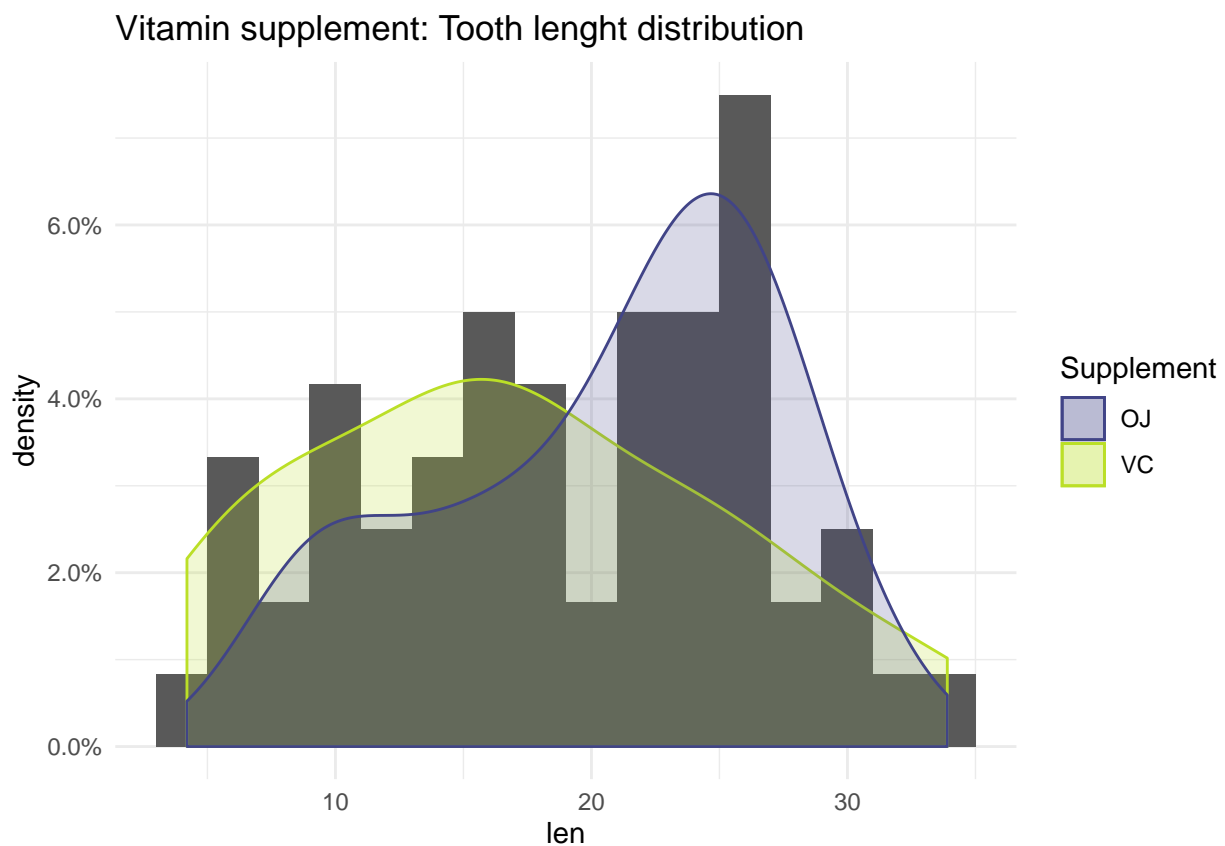
Next would be to look the distribution of our countinuous variable and overlay the density of our discrete variables on it. We start first overlaying the vitamin C supplement data:

```

colours <- viridis_pal(alpha = 1, begin = 0.2, end = 0.9, direction = 1,option = "D")(2)

densityplot_1 <- ggplot(data = ToothGrowth, mapping = aes(x = len))+
  geom_histogram(binwidth = 2,aes(y = ..density..))+
  geom_density(data = ToothGrowth[ToothGrowth$supp == "VC", ],
    aes(color = "VC",
      fill="VC"),
    alpha=.2)+
  geom_density(data = ToothGrowth[ToothGrowth$supp == "OJ", ],
    aes(color = "OJ",
      fill="OJ"),
    alpha=.2)+
  scale_y_continuous(labels = percent_format())+
  scale_colour_manual("Supplement", values = c("OJ" = colours[1],
      "VC" = colours[2]))+
  scale_fill_manual("Supplement", values = c("OJ" = colours[1],
      "VC" = colours[2]))+
  ggtitle("Vitamin supplement: Tooth lenght distribution")+
  theme_minimal()
print(densityplot_1)

```



We follow by overlaying the dose supplement data:

```

colours <- viridis_pal(alpha = 1, begin = 0.2, end = 0.9, direction = 1,option = "D")(3)

densityplot_2 <- ggplot(data = ToothGrowth, mapping = aes(x = len))+

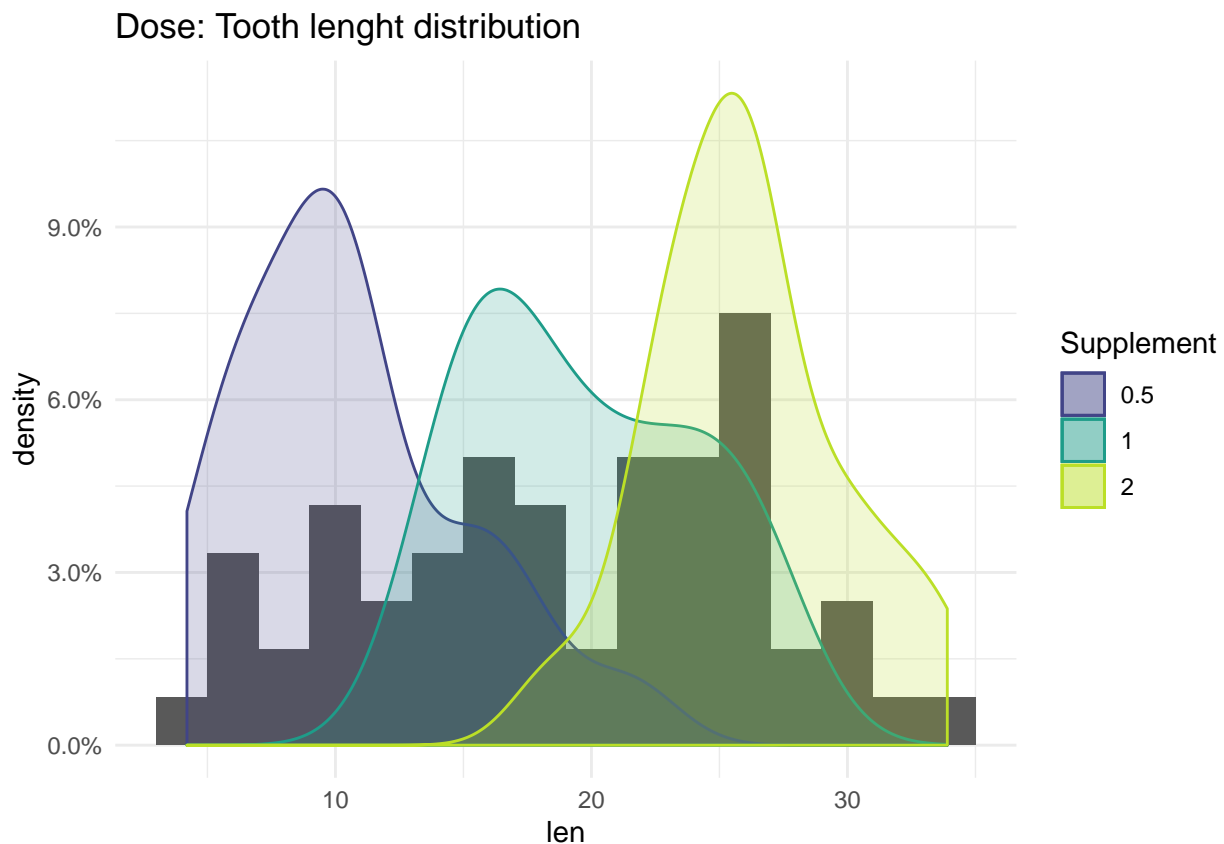
```

```

geom_histogram(binwidth = 2,aes(y = ..density..))+
geom_density(data = ToothGrowth[ToothGrowth$dose == "0.5", ],
             aes(color = "0.5",
                 fill="0.5"),
             alpha=.2)+
geom_density(data = ToothGrowth[ToothGrowth$dose == "1", ],
             aes(color = "1",
                 fill="1"),
             alpha=.2)+
geom_density(data = ToothGrowth[ToothGrowth$dose == "2", ],
             aes(color = "2",
                 fill="2"),
             alpha=.2)+
scale_y_continuous(labels = percent_format())+
scale_colour_manual("Supplement", values = c("0.5" = colours[1],
                                             "1" = colours[2],
                                             "2" = colours[3]))+
scale_fill_manual("Supplement", values = c("0.5" = colours[1],
                                           "1" = colours[2],
                                           "2" = colours[3]))+

ggtitle("Dose: Tooth lenght distribution")+
theme_minimal()
print(densityplot_2)

```



Now that we know how our data looks like, we can start exploring its properties. We start by obtaining the tooth length mean and the variance for the different categorical variables and their combination:

```
# Supplement inferred values:
kable(cbind(tapply(ToothGrowth$len, list(ToothGrowth$supp), mean),
             tapply(ToothGrowth$len, list(ToothGrowth$supp), var)),
      digits = 2,
      caption = "Vitamine C supplement estimate values",
      col.names = c("Mean", "Variance"))
```

Table 4: Vitamine C supplement estimate values

	Mean	Variance
OJ	20.66	43.63
VC	16.96	68.33

```
# Dose inferred values:
kable(cbind(tapply(ToothGrowth$len, list(ToothGrowth$dose), mean),
             tapply(ToothGrowth$len, list(ToothGrowth$dose), var)),
      digits = 2,
      caption = "Dose estimate values",
      col.names = c("Mean", "Variance"))
```

Table 5: Dose estimate values

	Mean	Variance
0.5	10.61	20.25
1	19.73	19.50
2	26.10	14.24

```
# Combined inferred values:
kable(cbind(tapply(ToothGrowth$len, list(ToothGrowth$supp, ToothGrowth$dose), mean),
             tapply(ToothGrowth$len, list(ToothGrowth$supp, ToothGrowth$dose), var)),
      digits = 2,
      caption = "Combined estimate values. Mean followed by variance")
```

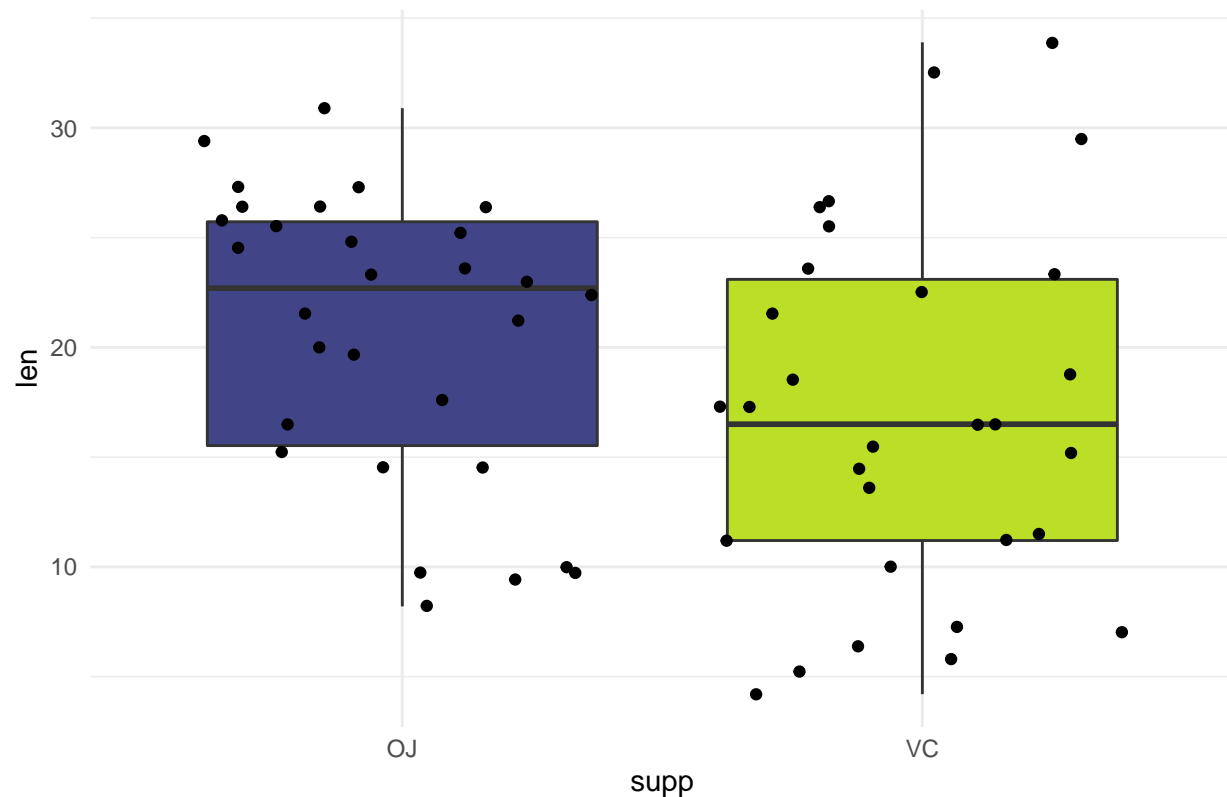
Table 6: Combined estimate values. Mean followed by variance

	0.5	1	2	0.5	1	2
OJ	13.23	22.70	26.06	19.89	15.30	7.05
VC	7.98	16.77	26.14	7.54	6.33	23.02

A better way to visualize the quantiles and means of our data is via graphical exploration. We start by plotting boxplots of the lenght depending on the vitamine C supplement:

```
boxplot_1 <- ggplot(data = ToothGrowth, mapping = aes(x = supp, y = len, fill = supp))+
  geom_boxplot()+
  geom_jitter()+
  scale_fill_viridis(discrete = T, option = "D", end = 0.9, begin = 0.2)+
  ggtitle("Tooth lenght vs. vitamine C supplement")+
  theme_minimal()+
  theme(legend.position = "none")
print(boxplot_1)
```

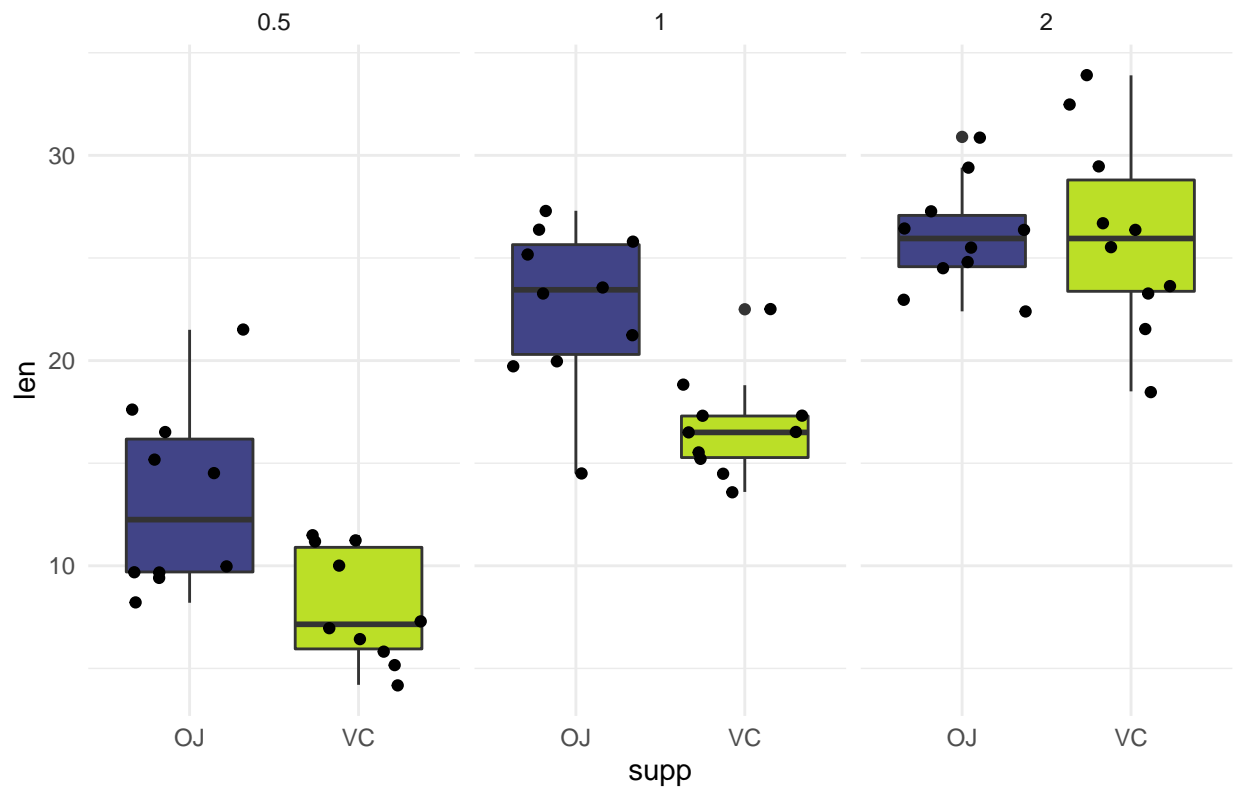
Tooth lenght vs. vitamine C supplement



We can also visualize how the dose of each supplement influences:

```
boxplot_2 <- ggplot(data = ToothGrowth, mapping = aes(x = supp, y = len, fill = supp))+  
  facet_wrap( ~ dose)+  
  geom_boxplot()+  
  geom_jitter()+  
  scale_fill_viridis(discrete = T, option = "D", end = 0.9, begin = 0.2)+  
  ggtitle("Tooth lenght vs. vitamine C supplement (dose dependant)")+  
  theme_minimal()+  
  theme(legend.position = "none")  
print(boxplot_2)
```

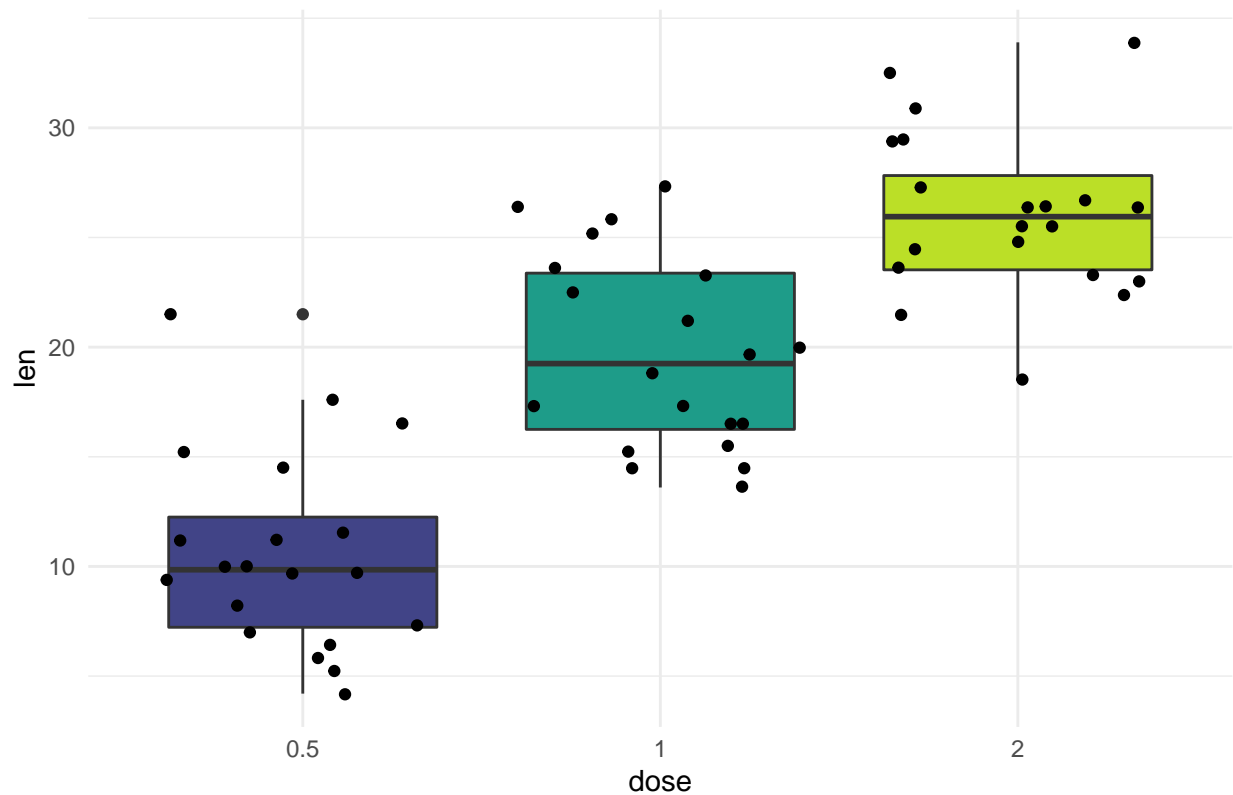
Tooth lenght vs. vitamine C supplement (dose dependant)



We now do the same showing the lenght depending on the dose:

```
boxplot_1 <- ggplot(data = ToothGrowth, mapping = aes(x = dose, y = len, fill = dose))+
  geom_boxplot()+
  geom_jitter()+
  scale_fill_viridis(discrete = T, option = "D", end = 0.9, begin = 0.2)+
  ggtitle("Tooth lenght vs. dose")+
  theme_minimal()+
  theme(legend.position = "none")
print(boxplot_1)
```

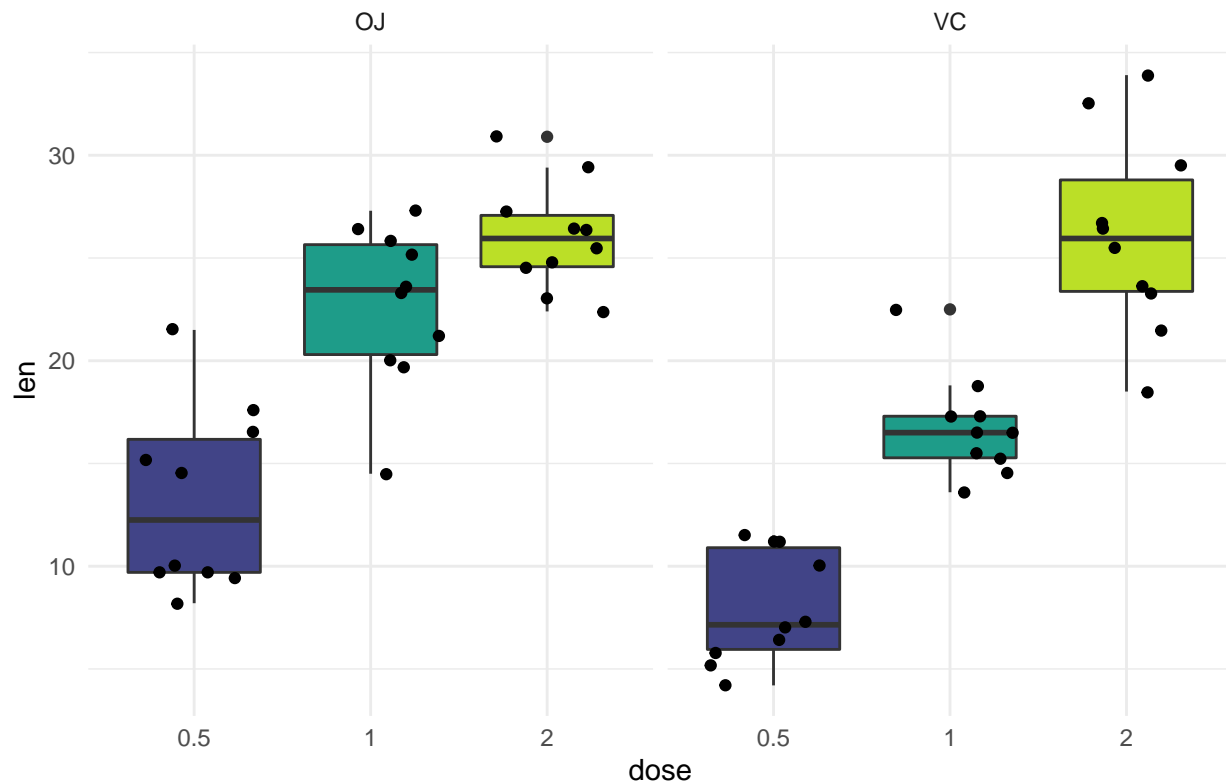
Tooth lenght vs. dose



And finally, showing the supplement influence:

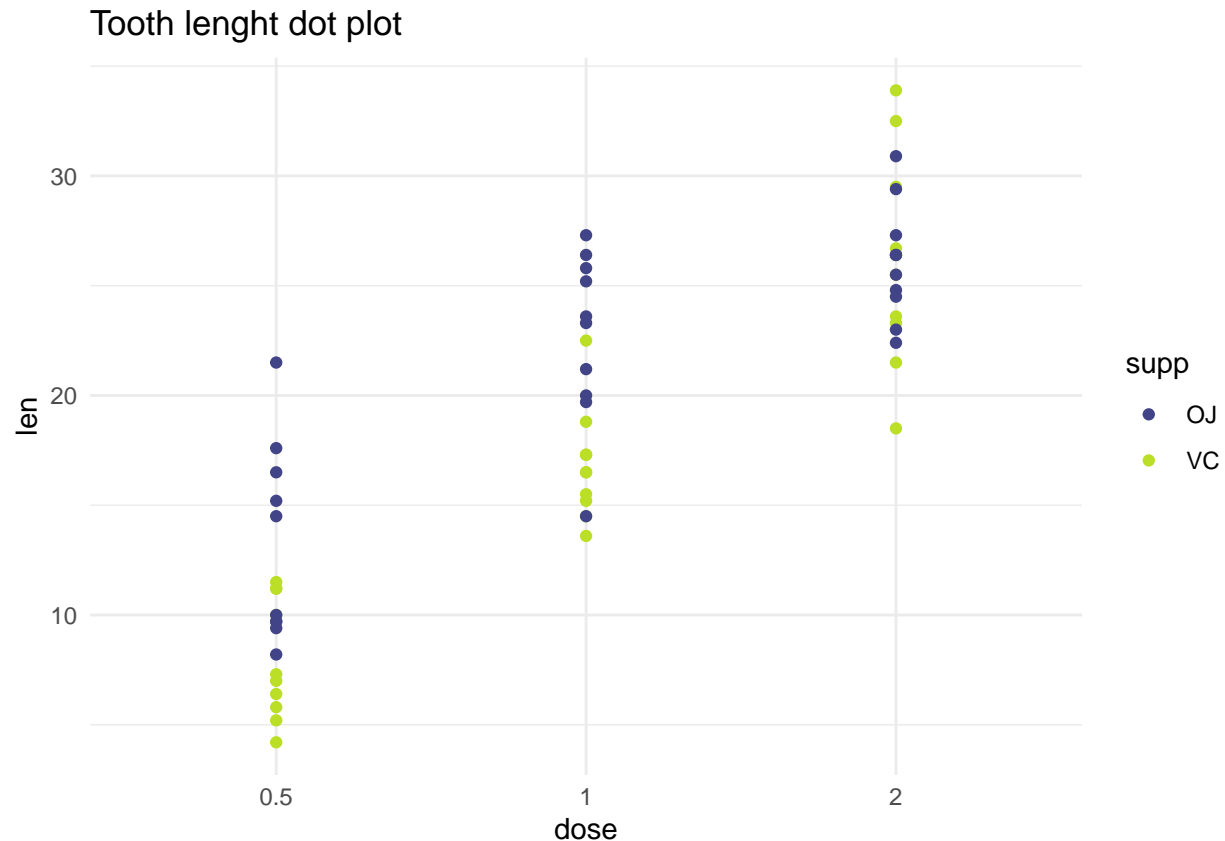
```
boxplot_2 <- ggplot(data = ToothGrowth, mapping = aes(x = dose, y = len, fill = dose))+
  facet_wrap( ~ supp)+
  geom_boxplot()+
  geom_jitter()+
  scale_fill_viridis(discrete = T, option = "D", end = 0.9, begin = 0.2)+
  ggtitle("Tooth lenght vs. dose (vitamine C supplement dependant)")+
  theme_minimal()+
  theme(legend.position = "none")
print(boxplot_2)
```


Tooth lenght vs. dose (vitamine C supplement dependant)



Overall, we observe that both the supplement and the dose change the shape of the distribution of tooth length. This is supported by different tooth length means and all the graphical visual exploration, and can be summarized on a dot plot:

```
dotplot <- ggplot(ToothGrowth, aes(x= dose, y= len)) +
  geom_point(aes(color=supp))+
  scale_color_viridis(discrete = T, option = "D", end = 0.9, begin = 0.2)+
  ggtitle("Tooth lenght dot plot")+
  theme_minimal()
print(dotplot)
```



But are those differences significant? We will test that on the following block.

2: Testing for differences on tooth lenght:

We first define what will be the hypotesis we will be testing:

$$H_0 : \mu_1 = \mu_2$$

$$H_a : \mu_2 \neq \mu_1$$

We assume that the distribution follows normality and that there is no equality on the variances (Although none are true; but we have to stick to class techniques).

Supplement type effect:

We want to assess wteher the means change on each particular comparisons. We will test either we can accept or reject our null hypothesis with confidences intervals and p-values resulting from t-test. First we compute the confidence intervals:

```
quantile = 0.975 # is 95% with 2.5% on both sides of the range

n_y <- nrow(ToothGrowth[ToothGrowth$supp == "OJ", ]) # observations of OJ
n_x <- nrow(ToothGrowth[ToothGrowth$supp == "VC", ]) # observations of VC
```

```

var_y <- var(ToothGrowth[ToothGrowth$supp == "OJ", ]$len) # variance of OJ
var_x <- var(ToothGrowth[ToothGrowth$supp == "VC", ]$len) # variance of VC

mean_y <- mean(ToothGrowth[ToothGrowth$supp == "OJ", ]$len) # mean of OJ
mean_x <- mean(ToothGrowth[ToothGrowth$supp == "VC", ]$len) # mean of VC

# calculate pooled standard deviation

sd_p <- sqrt(((n_x - 1) * var_x + (n_y - 1) * var_y) / (n_x + n_y - 2))

confidenceInterval <- mean_y - mean_x + c(-1, 1) *
  qt(quantile, df=n_y+n_x-2) * sd_p * (1 / n_x + 1 / n_y)^.5

round(confidenceInterval, 2)

## [1] -0.17  7.57

```

Then we perform a t. test:

```

t.test(len ~ supp,
       data = ToothGrowth,
       paired = 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

```

We observe that the confidence intervals provided are the same that we computed. Thus, from now on we will **rely on the confidence intervals from the t-test**. Let's explore what both results tell us:

- 0 is included in our confidence interval
- The obtained p-value is larger than 0.05

This results indicate that the **difference on the mean of tooth lenght does not rely only on the type of supplement**.

Supplement type effect (at each particular dose):

Let's test the supplement type effect at each particular dose level:

```

ToothGrowth_Dose1 <- ToothGrowth[ToothGrowth$dose == "0.5",]
t.test(len ~ supp,
       data = ToothGrowth_Dose1,
       paired = FALSE)

##
## 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 is not equal to 0
## 95 percent confidence interval:
## 1.719057 8.780943
## sample estimates:
## mean in group OJ mean in group VC
## 13.23 7.98
```

```
ToothGrowth_Dose2 <- ToothGrowth[ToothGrowth$dose == "1",]
t.test(len ~ supp,
       data = ToothGrowth_Dose2,
       paired = FALSE)
```

```
##
## 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 is not equal to 0
## 95 percent confidence interval:
## 2.802148 9.057852
## sample estimates:
## mean in group OJ mean in group VC
## 22.70 16.77
```

```
ToothGrowth_Dose3 <- ToothGrowth[ToothGrowth$dose == "2",]
t.test(len ~ supp,
       data = ToothGrowth_Dose3,
       paired = FALSE)
```

```
##
## 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 is not equal to 0
## 95 percent confidence interval:
## -3.79807 3.63807
## sample estimates:
## mean in group OJ mean in group VC
## 26.06 26.14
```

Let's explore these results tell us:

- 0 is not included in our confidence interval for doses **0.5** and **1**
- The obtained p-value is lower than 0.05 for doses **0.5** and **1**

We can visualize this results as barplot of $-\log_{10}(\text{p-values})$:

```
pval1 <- t.test(len ~ supp,
               data = ToothGrowth_Dose1,
               paired = FALSE)$p.val
pval2 <- t.test(len ~ supp,
               data = ToothGrowth_Dose2,
               paired = FALSE)$p.val
pval3 <- t.test(len ~ supp,
```

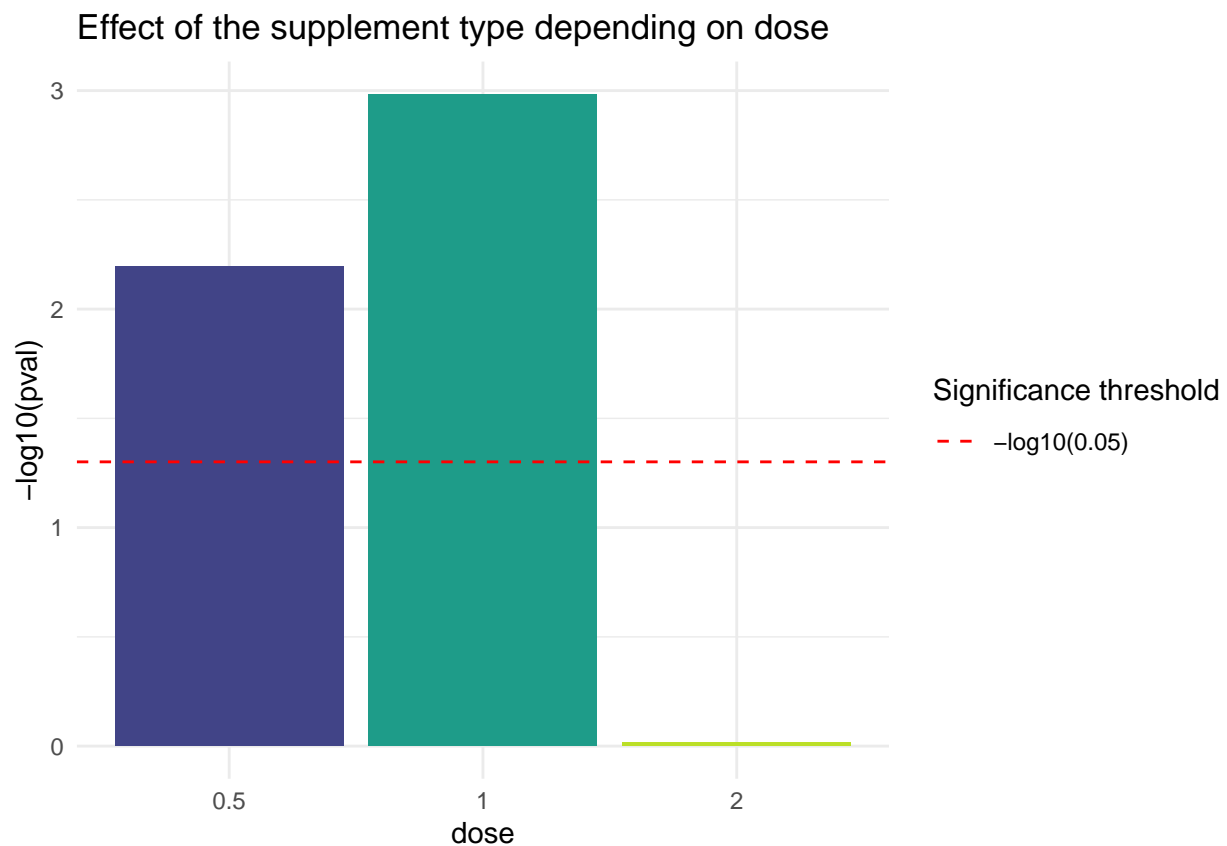
```

data = ToothGrowth_Dose3,
paired = FALSE)$p.val

dose <- c("0.5", "1", "2")
pval <- c(-log10(pval1), -log10(pval2), -log10(pval3))
df <- data.frame(dose, pval)

barplot <- ggplot(data = df, aes(x = dose, y = pval, fill = dose))+
  geom_bar(stat = "identity", show.legend = F)+
  scale_fill_viridis(discrete = T, option = "D", end = 0.9, begin = 0.2)+
  geom_hline(aes(yintercept = -log10(0.05),
    linetype = "-log10(0.05)",
    color = "red")+
  scale_linetype_manual(name = "Significance threshold", values = c(2, 2),
    guide = guide_legend(override.aes = list(color = c("red"))))+
  ggtitle("Effect of the supplement type depending on dose")+
  ylab("-log10(pval)")+
  theme_minimal()
print(barplot)

```



This results indicate that the **difference on the mean of tooth lenght relies on the type of supplement for the lower doses (0.5 and 1)**. When the dose is 2 mg/day, the type of supplement **does not significantly change the mean of tooth length**.

Dose effect (at OJ supplement type):

So now we can explore if the dose itself makes the mean of tooth length to change. We start exploring whether this is true for the **orange juice (OJ)** supplement:

```
ToothGrowth_OJ_Dose_1and2 <- ToothGrowth[ToothGrowth$dose != "2" &
                                           ToothGrowth$supp == "OJ",]

t.test(len ~ dose,
       data = ToothGrowth_OJ_Dose_1and2,
       paired = FALSE)

##
##  Welch Two Sample t-test
##
## data:  len by dose
## t = -5.0486, df = 17.698, p-value = 8.785e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -13.415634  -5.524366
## sample estimates:
## mean in group 0.5    mean in group 1
##           13.23           22.70

ToothGrowth_OJ_Dose_1and3 <- ToothGrowth[ToothGrowth$dose != "1" &
                                           ToothGrowth$supp == "OJ",]

t.test(len ~ dose,
       data = ToothGrowth_OJ_Dose_1and3,
       paired = FALSE)

##
##  Welch Two Sample t-test
##
## data:  len by dose
## t = -7.817, df = 14.668, p-value = 1.324e-06
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -16.335241  -9.324759
## sample estimates:
## mean in group 0.5    mean in group 2
##           13.23           26.06

ToothGrowth_OJ_Dose_2and3 <- ToothGrowth[ToothGrowth$dose != "0.5" &
                                           ToothGrowth$supp == "OJ",]

t.test(len ~ dose,
       data = ToothGrowth_OJ_Dose_2and3,
       paired = FALSE)

##
##  Welch Two Sample t-test
##
## data:  len by dose
## t = -2.2478, df = 15.842, p-value = 0.0392
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -6.5314425 -0.1885575
## sample estimates:
```

```
## mean in group 1 mean in group 2
##      22.70      26.06
```

Let's explore these results tell us:

- 0 is not included in our confidence interval for **all doses**
- The obtained p-value is lower than 0.05 for doses **all doses**

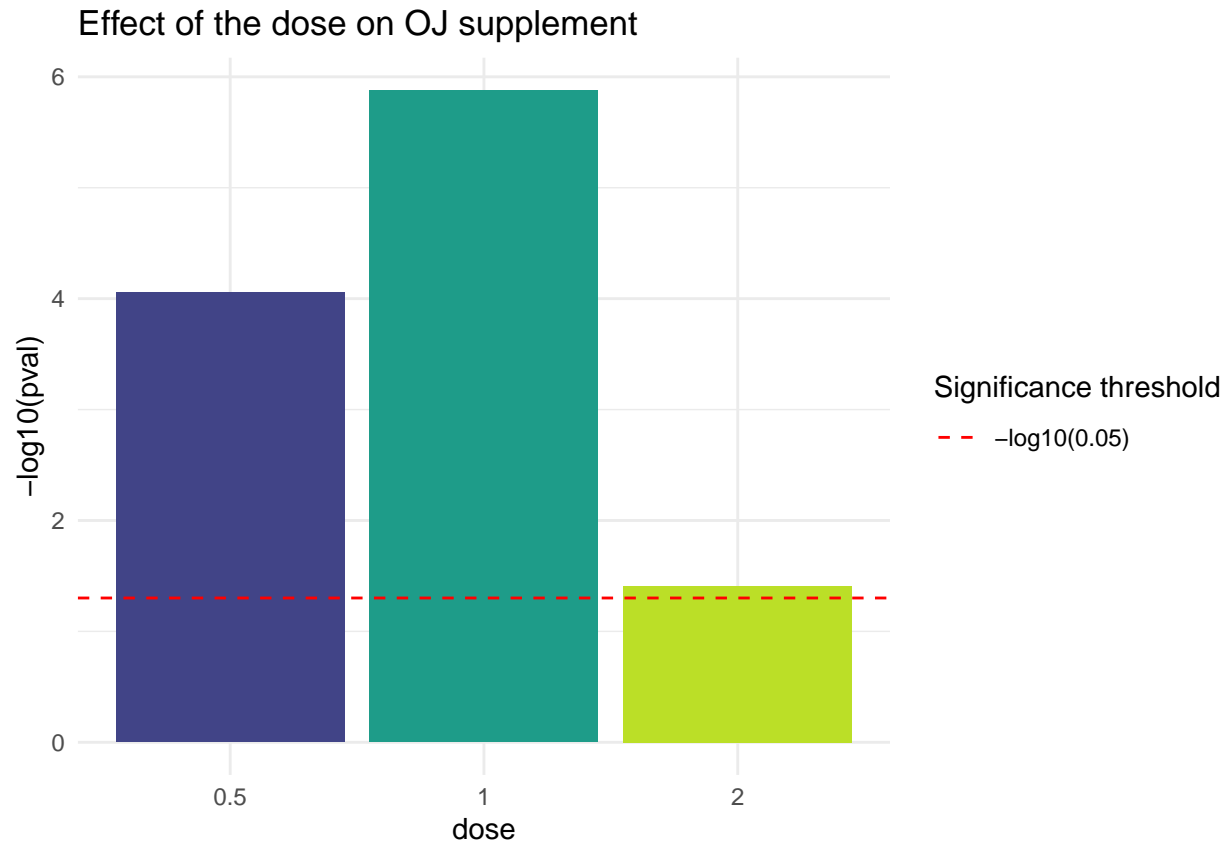
We can visualize this results as barplot of $-\log_{10}(\text{p-values})$:

```
pval1 <- t.test(len ~ dose,
  data = ToothGrowth_OJ_Dose_1and2,
  paired = FALSE)$p.val
pval2 <- t.test(len ~ dose,
  data = ToothGrowth_OJ_Dose_1and3,
  paired = FALSE)$p.val
pval3 <- t.test(len ~ dose,
  data = ToothGrowth_OJ_Dose_2and3,
  paired = FALSE)$p.val

comparison <- c("0.5-1", "0.5-2", "1-2")
pval <- c(-log10(pval1), -log10(pval2), -log10(pval3))
df <- data.frame(dose, pval)

barplot <- ggplot(data = df, aes(x = dose, y = pval, fill = dose))+
  geom_bar(stat = "identity", show.legend = F)+
  scale_fill_viridis(discrete = T, option = "D", end = 0.9, begin = 0.2)+
  geom_hline(aes(yintercept = -log10(0.05),
    linetype = "-log10(0.05)"),
    color = "red")+
  scale_linetype_manual(name = "Significance threshold", values = c(2, 2),
    guide = guide_legend(override.aes = list(color = c("red"))))+
  ggtitle("Effect of the dose on OJ supplement")+
  ylab("-log10(pval)")+
  theme_minimal()

print(barplot)
```



This results are telling that there are **significant changes in the mean of tooth lenght** when comparing **all doses** on OJ supplement. We can see that an **increase** of dose leads to an **increase** of tooth lenght.

Dose effect (at VC supplement type):

So now we can explore if the dose itself makes the mean of tooth lenght to change. We start exploring wether this is true for the **orange juice (VC)** supplement:

```

ToothGrowth_VC_Dose_1and2 <- ToothGrowth[ToothGrowth$dose != "2" &
                                           ToothGrowth$supp == "VC",]

t.test(len ~ dose,
       data = ToothGrowth_VC_Dose_1and2,
       paired = FALSE)

##
##  Welch Two Sample t-test
##
## data:  len by dose
## t = -7.4634, df = 17.862, p-value = 6.811e-07
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -11.265712  -6.314288
## sample estimates:
## mean in group 0.5    mean in group 1
##           7.98         16.77

```



```

ToothGrowth_VC_Dose_1and3 <- ToothGrowth[ToothGrowth$dose != "1" &
                                          ToothGrowth$supp == "VC",]

t.test(len ~ dose,
       data = ToothGrowth_VC_Dose_1and3,
       paired = FALSE)

##
## Welch Two Sample t-test
##
## data: len by dose
## t = -10.388, df = 14.327, p-value = 4.682e-08
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -21.90151 -14.41849
## sample estimates:
## mean in group 0.5 mean in group 2
## 7.98 26.14

ToothGrowth_VC_Dose_2and3 <- ToothGrowth[ToothGrowth$dose != "0.5" &
                                          ToothGrowth$supp == "VC",]

t.test(len ~ dose,
       data = ToothGrowth_VC_Dose_2and3,
       paired = FALSE)

##
## Welch Two Sample t-test
##
## data: len by dose
## t = -5.4698, df = 13.6, p-value = 9.156e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -13.054267 -5.685733
## sample estimates:
## mean in group 1 mean in group 2
## 16.77 26.14

```

Let's explore these results tell us:

- 0 is not included in our confidence interval for **all doses**
- The obtained p-value is lower than 0.05 for doses **all doses**

We can visualize this results as barplot of $-\log_{10}(\text{p-values})$:

```

pval1 <- t.test(len ~ dose,
               data = ToothGrowth_VC_Dose_1and2,
               paired = FALSE)$p.val
pval2 <- t.test(len ~ dose,
               data = ToothGrowth_VC_Dose_1and3,
               paired = FALSE)$p.val
pval3 <- t.test(len ~ dose,
               data = ToothGrowth_VC_Dose_2and3,
               paired = FALSE)$p.val

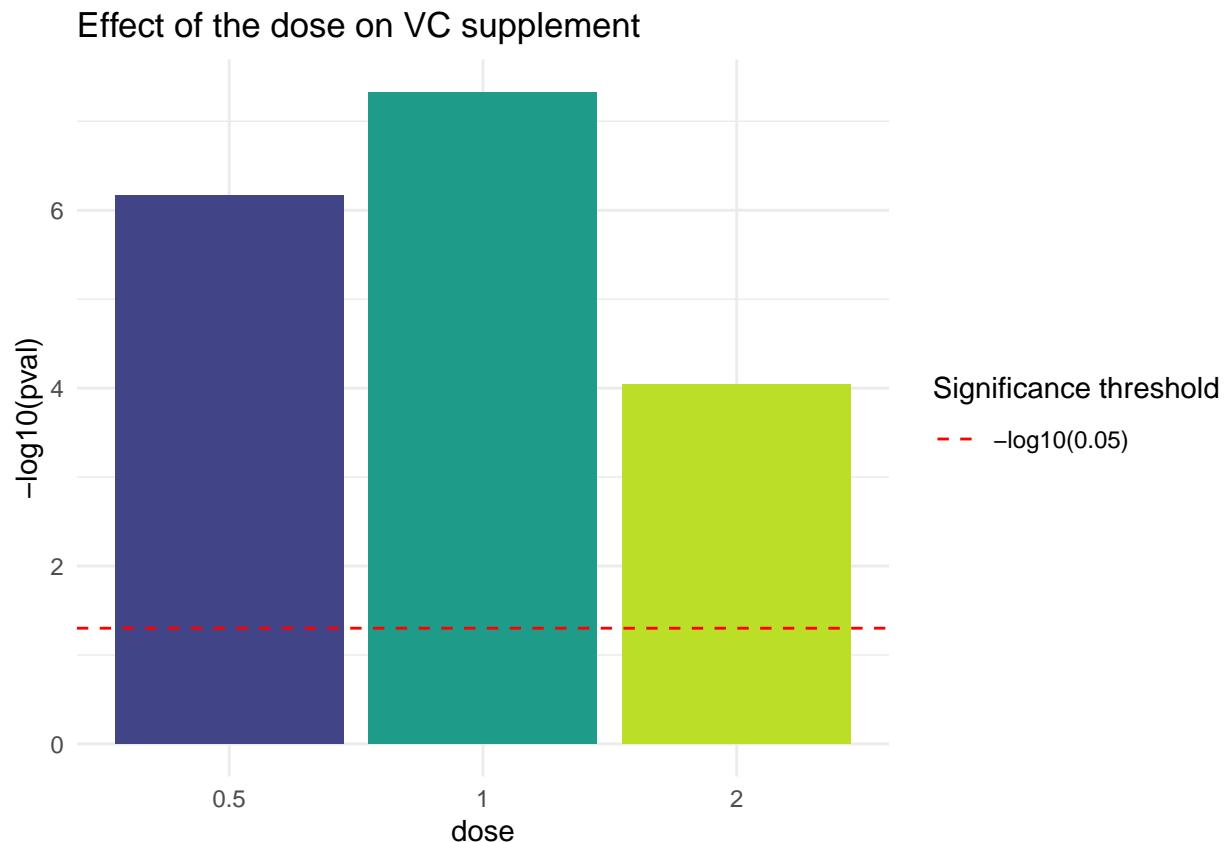
comparison <- c("0.5-1", "0.5-2", "1-2")
pval <- c(-log10(pval1), -log10(pval2), -log10(pval3))
df <- data.frame(dose, pval)

```

```

barplot <- ggplot(data = df, aes(x = dose, y = pval, fill = dose))+
  geom_bar(stat = "identity", show.legend = F)+
  scale_fill_viridis(discrete = T, option = "D", end = 0.9, begin = 0.2)+
  geom_hline(aes(yintercept = -log10(0.05),
    linetype = "-log10(0.05)"),
    color = "red")+
  scale_linetype_manual(name = "Significance threshold", values = c(2, 2),
    guide = guide_legend(override.aes = list(color = c("red"))))+
  ggtitle("Effect of the dose on VC supplement")+
  ylab("-log10(pval)")+
  theme_minimal()
print(barplot)

```



This results are telling that there are **significant changes in the mean of tooth lenght** when comparing **all doses** on VC supplement. We can see that an **increase** of dose leads to an **increase** of tooth lenght.

3: Conclusions:

To sum up, we can conclude the following statements:

- We reject the null hypotesis for all doses comparisons in both supplement types. This means that tooth length significantly increases, regardless of supplement method, as we increase the dose.
- At lower doses (0.5 mg and 1.0 mg) the are significant differences between the OJ and VC supplement type, being OJ the one that leads to more tooth growth.

- At the higher dose (2.0 mg), there is no significant difference between the OJ and VC supplement methods.

This conclusions are only valid under the following assumptions:

- The distribution of the means is normal.
- The variance is not equal
- The measurements are not paired.
- The populations are independent.
- The guinea pigs were truly selected at random avoiding conflating factors to influence the results.

Session info:

```
print(sessionInfo(), locale = F)

## R version 3.5.1 (2018-07-02)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 18363)
##
## Matrix products: default
##
## attached base packages:
## [1] stats      graphics  grDevices utils      datasets  methods   base
##
## other attached packages:
## [1] reshape2_1.4.3    viridis_0.5.1      viridisLite_0.3.0 knitr_1.27
## [5] scales_1.1.0      ggplot2_3.2.1
##
## loaded via a namespace (and not attached):
## [1] Rcpp_1.0.3        pillar_1.4.3       compiler_3.5.1     plyr_1.8.5
## [5] highr_0.8         tools_3.5.1        digest_0.6.23     evaluate_0.14
## [9] lifecycle_0.1.0   tibble_2.1.3       gtable_0.3.0      pkgconfig_2.0.3
## [13] rlang_0.4.3       yaml_2.2.0         xfun_0.12         gridExtra_2.3
## [17] withr_2.1.2       dplyr_0.8.3        stringr_1.4.0     grid_3.5.1
## [21] tidyselect_0.2.5  glue_1.3.1         R6_2.4.1          rmarkdown_2.1
## [25] farver_2.0.3      purrr_0.3.3        magrittr_1.5      htmltools_0.4.0
## [29] assertthat_0.2.1  colorspace_1.4-1   labeling_0.3       stringi_1.4.5
## [33] lazyeval_0.2.2    munsell_0.5.0      crayon_1.3.4
```