

project_tooth

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Info on data:

The response is the length of odontoblasts (cells responsible for tooth growth) in 60 guinea pigs. Each animal received one of three dose levels of vitamin C (0.5, 1, and 2 mg/day) by one of two delivery methods, (orange juice or ascorbic acid (a form of vitamin C and coded as VC)).

Zadání:

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

- Load the ToothGrowth data and perform some basic exploratory data analyses
- Provide a basic summary of the data.
- 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)
- State your conclusions and the assumptions needed for your conclusions.

Some criteria that you will be evaluated on

- Did you perform an exploratory data analysis of at least a single plot or table highlighting basic features of the data?
- Did the student perform some relevant confidence intervals and/or tests?
- Were the results of the tests and/or intervals interpreted in the context of the problem correctly?
- Did the student describe the assumptions needed for their conclusions?

Loading the data

```
# Load libraries
library(dplyr)
library(ggplot2)
library(gridExtra)
library(knitr)

# Load dataset
library(datasets)
data(ToothGrowth)
a<-(ToothGrowth) #give it easily typed name
```

EDA

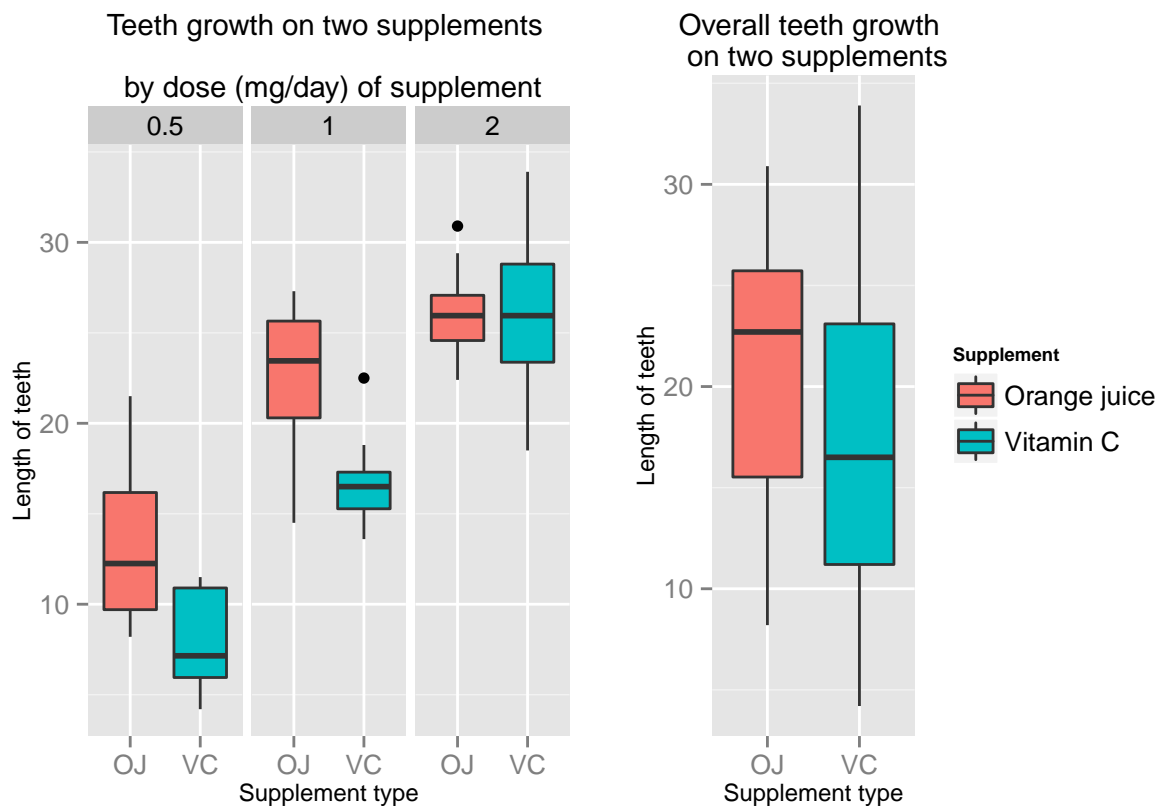
```

p1 <- ggplot(a, aes(y=len, x=as.factor(supp))) +
  geom_boxplot(aes(fill=supp)) +
  guides(fill=FALSE) +
  facet_grid(.~dose) +
  labs(title="Teeth growth on two supplements
  \n by dose (mg/day) of supplement",
  x="Supplement type",
  y="Length of teeth") +
  theme(title = element_text(size = rel(0.75), hjust = 0.5))

p2 <- ggplot(a, aes(x=supp, y=len)) + geom_boxplot(aes(fill=supp)) +
  labs(title="Overall teeth growth \n on two supplements",
  x="Supplement type",
  y="Length of teeth") +
  scale_fill_discrete(name="Supplement",
  labels=c("Orange juice", "Vitamin C")) +
  theme(title = element_text(size = rel(0.75), hjust = 0.5))

# Arrange them:
grid.arrange(p1, p2, ncol=2, nrow=1)

```



```

a_tab<-group_by(a, supp, dose) %>% summarise(mean(len))
kable(x=a_tab, digits=1, align="c", caption="Summary table of data")

```

Table 1: Summary table of data

supp	dose	mean(len)
OJ	0.5	13.2
OJ	1.0	22.7
OJ	2.0	26.1
VC	0.5	8.0
VC	1.0	16.8
VC	2.0	26.1

Testing

Test hypothesis, that there is a difference between orange juice and vitamin C (all doses together. Test each dose separately for above stated difference => together 4 tests.

Hypotheses

I decide to test the difference in teeth growth between supplementing orange juice (OJ) and vitamin C (VC). I use R function *t.test*. Based on EDA I suppose that orange juice gives better results.

Assumptions for testing: * Guinea pigs were selected randomly and each combination of dose and supplement fed to different group of pigs, thus they form independent groups (*paired=FALSE* as a default of *t.test*) * Lengths of teeth are normal for tested sets of data (see Appendix for testing normality) * No info about variance, thus for sake of correctness (and laziness, I have to admit) is *t.test*'s default *var.equal=FALSE* used

Overall test:

H_0 : there is no difference between OJ and VC

H_a : the OJ has bigger effect than VC

Partial tests for each dose:

H_0 : there is no difference between OJ and VC for set dose level (e.g., 0.5, 1, and 2 mg/day).

H_a : the OJ has bigger effect than VC for set dose level

```
# Prepare table of results:
test_res <- NULL

# Test OJ vs VC overall:
test_res<-cbind(t.test(len ~ factor(supp), data=a, paired=F)$p.value,
  t.test(len ~ factor(supp), data=a, paired=F)$conf.int[1],
  t.test(len ~ factor(supp), data=a, paired=F)$conf.int[2])

# Test OJ vs VC for each dose:
for (i in c(0.5, 1, 2)) {
  test_res <- rbind(test_res,
    cbind(t.test(len ~ factor(supp), data=a[a$dose== i, ],
      paired=F)$p.value,
      t.test(len ~ factor(supp), data=a[a$dose== i, ],
        paired=F)$conf.int[1],
      t.test(len ~ factor(supp), data=a[a$dose== i, ],
```

```

        paired=F)$conf.int[2]
    )
}

# Format table of results:
test_res<-as.data.frame(test_res)
row.names(test_res)<-c("OJ vs VC overall", "OJ vs VC - dose 0.5",
                      "OJ vs VC - dose 1.0", "OJ vs VC - dose 2.0")
colnames(test_res)<-c("p-value", "95% CI (-)", "95% CI (+)")

# Print table of results:
kable(test_res, digits=3, row.names=T, align="c",
      caption="Summary table of test results")

```

Table 2: Summary table of test results

	p-value	95% CI (-)	95% CI (+)
OJ vs VC overall	0.061	-0.171	7.571
OJ vs VC - dose 0.5	0.006	1.719	8.781
OJ vs VC - dose 1.0	0.001	2.802	9.058
OJ vs VC - dose 2.0	0.964	-3.798	3.638

Appendix

```

shapiro.test(a$len[a$supp=="OJ" & a$dose == 0.5]) #norm
shapiro.test(a$len[a$supp=="OJ" & a$dose == 1]) #norm
shapiro.test(a$len[a$supp=="OJ" & a$dose == 2]) #norm
shapiro.test(a$len[a$supp=="VC" & a$dose == 0.5]) #norm
shapiro.test(a$len[a$supp=="VC" & a$dose == 1]) #norm
shapiro.test(a$len[a$supp=="VC" & a$dose == 2]) #norm
shapiro.test(a$len[a$supp=="OJ"]) #norm
shapiro.test(a$len[a$supp=="VC"]) #norm
shapiro.test(a$len) #norm

```