# Statistical Inference Course Project

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```
library(tidyverse)
library(datasets)
```

## Part 1: Simulation Exercise

*In this part we are supposed to generate 1000 averages of 40 random exponentials from a continous exponential distribution with rate lambda = 0.2. We will use this data to test the assumptions of LLN and CLT in practice.*

### Simulation

Declare the simulation parameters

```
set.seed(666)
n <- 1000
lambda <- 0.2
```

Simulated 1000 averages of 40 exponentials from the expponential distribution with the rate lambda = 0.2

```
s.mean = NULL
for (i in 1 : n) { s.mean <- c(s.mean, mean(rexp(40, lambda))) }

head(s.mean)
```

```
## [1] 4.267297 3.640230 5.646912 4.717544 4.463866 4.974047
```

### Theoretical statistics vs. sample statistics

Calculate the theoretical mean and sample mean

```
1/lambda ## Theoretical mean
```

```
## [1] 5
```

```
mean(s.mean) ## Sample mean
```

```
## [1] 4.987818
```

Calculate the theoretical variance and sample variance

```
(1/lambda/sqrt(40))^2 # Theoretical variance
```

```
## [1] 0.625
```

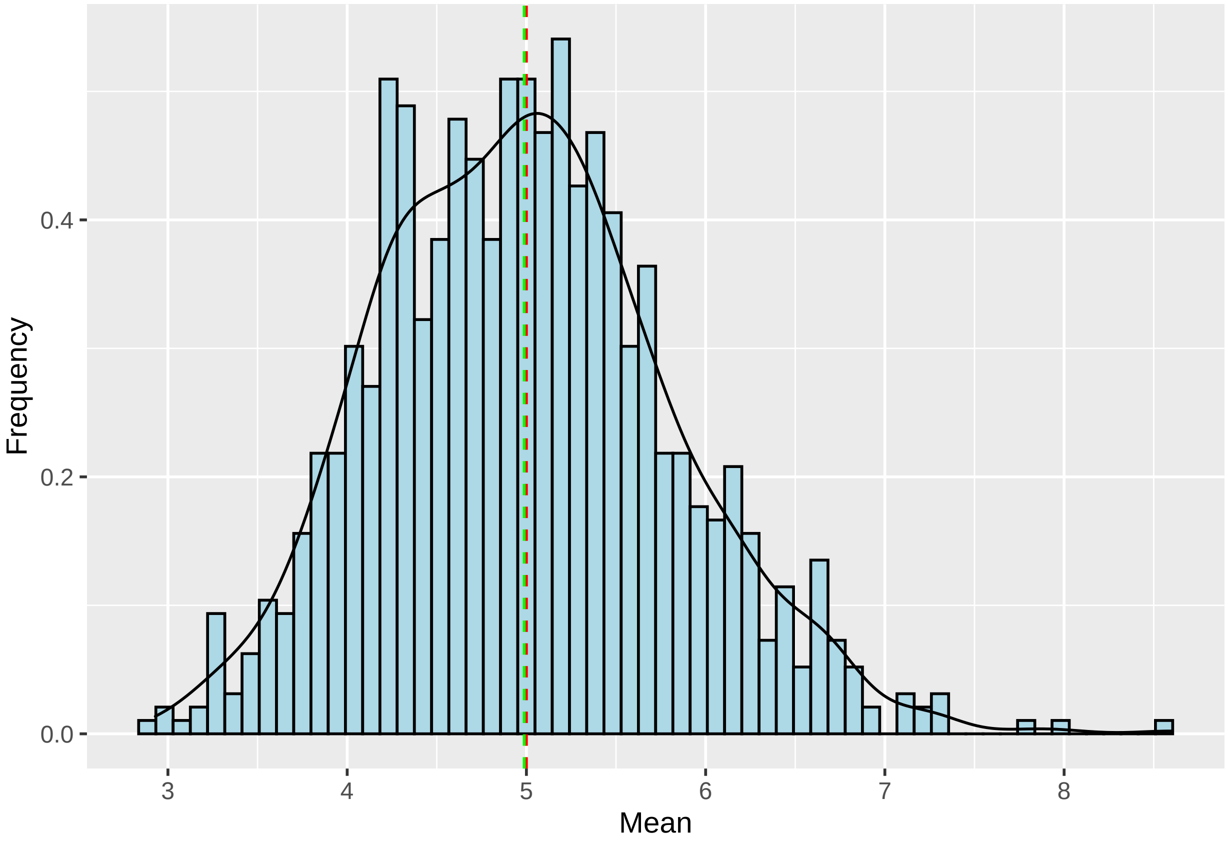
```
var(s.mean) # Sample variance
```

```
## [1] 0.6646822
```

**Conclusion: both sample mean and variance are very close to the predicted theoretical parameters. This result is in accordance with Law of Large Numbers**

### Normality of the sampling distribution of the sampling mean

Plot the histogram of the sampling distribution of the mean. The red dashed line corresponds to the theoretical mean and the grean one to the sample mean.



Test with Shapiro–Wilk test for normality

```
shapiro.test(s.mean$s.mean)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  s.mean$s.mean
## W = 0.99187, p-value = 2.584e-05
```

**Conclusion: Under the CLT we can assume that the sampling distribution of the mean is approximately normal. However, our specific sample does not pass Shapiro–Wilk test so the normality assumtion is not valid.**

## Part 2 Basic Inferential Data Analysis

_In this part we will use the ToothGrowth dataset studying the impact of dose and delivery method of Vitamin C on tooth growth in guiney pig. I will perform an exploratory analysis, look at the summary of the data and do some basic hyptotheis testing.

### Loading the data

```
data("ToothGrowth")
```

### Exploratory analysis

Look at the structure of the data and the summary statistics

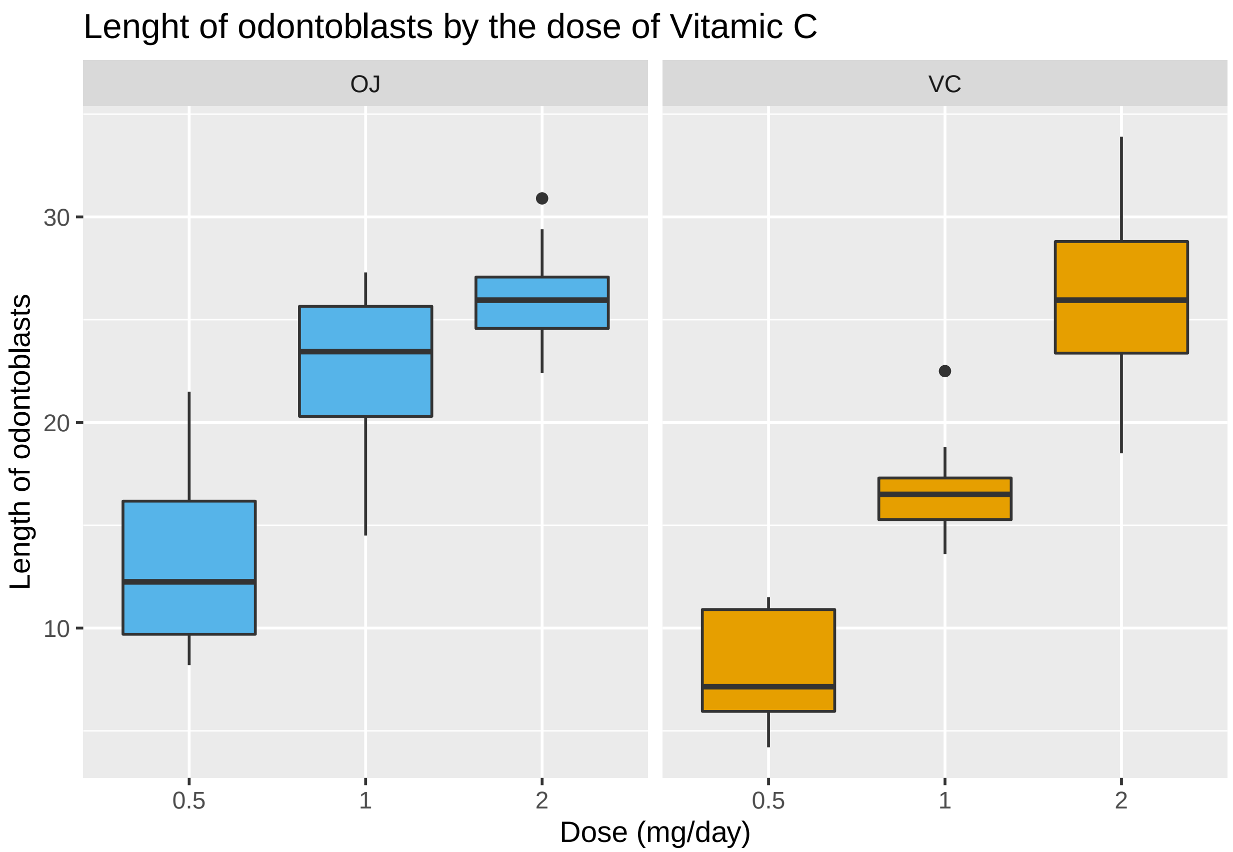
```
str(ToothGrowth)
```

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

```
summary(ToothGrowth)
```

```
##       len        supp         dose      
##  Min.   : 4.20   OJ:30   Min.   :0.500  
##  1st Qu.:13.07   VC:30   1st Qu.:0.500  
##  Median :19.25           Median :1.000  
##  Mean   :18.81           Mean   :1.167  
##  3rd Qu.:25.27           3rd Qu.:2.000  
##  Max.   :33.90           Max.   :2.000  
```

Plot of the Lenght of the odontoblasts by the method of delivery: VC - ascorbic acid, OJ - orange juice.



### Hypothesis Testing

Test if there is a difference in tooth growth between the group that was given ascorbic acid and orange juice.

```
t.test(ToothGrowth$len ~ ToothGrowth$supp)
```

```
##
##  Welch Two Sample t-test
##
## data:  ToothGrowth$len by ToothGrowth$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 95% confidence interval contains the difference between the means of two groups so we cannot reject the null hipothesis*

Test if there is difference in tooth growth between the group that was given low (0.5) and high (2) dose of Vitamin C.

```
ToothGrowth.sub <- filter(ToothGrowth, dose  %in% c(.5, 2))
t.test(ToothGrowth.sub$len ~ ToothGrowth.sub$dose)
```

```
##
##  Welch Two Sample t-test
##
## data:  ToothGrowth.sub$len by ToothGrowth.sub$dose
## 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
```

*The observed p-value is very low, much lower than alpha = 0.05. Based on this fact we cannot assume that the means of the populations are equal. We reject the null hypthesis*

### Conclusions

Given the data we analyzed we can conclude that:

1. The method of delivery does not impact the tooth growth in guinea pig
2. The dose impacts the tooth growth in guinea pig

### Assumptions

1. The samples come from independent identicaly distributed populations
2. The samples are representative of the population

## Apendix

### Code for plot 1

```
s.mean <- as.data.frame(s.mean)
plot1 <- ggplot(s.mean, aes(s.mean)) +
        geom_histogram(aes(y=..density..), bins = 60,
                       colour = "black", fill = "lightblue")+
        geom_density()+
        geom_vline(aes(xintercept=c(1/lambda)),
                   color="red", linetype="dashed",
                   size = 0.5)+
        geom_vline(aes(xintercept=mean(s.mean)),
                   color="green", linetype="dashed",
                   size = 0.5)+
        xlab("Mean") + ylab("Frequency")
```

**Code for plot 2**

```
plot2 <- ggplot(ToothGrowth, aes(x = as.factor(dose), y = len)) +
        geom_boxplot(aes(fill=supp)) +
        scale_fill_manual(values=c("#56B4E9", "#E69F00"))+
        facet_wrap(.~supp)+
        labs(title = "Lenght of odontoblasts by the dose of Vitamic C") +
        xlab("Dose (mg/day)") +
        ylab("Length of odontoblasts") +
        theme(legend.position = "none")
```