Statistical Inference

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SYNOPSIS: The Analysis consists of two part

- 1. will investigate the exponential distribution in R and compare it with the Central Limit Theorem
- 2. will analyse the ToothGrowth dataset elucidating on the effect of Supp and dose variables on the len.

Preparing the Workspace

```
rm(list = ls())
if ("ggplot2" %in% row.names(installed.packages()) == FALSE){install.packages("ggplot2")}
if ("grid" %in% row.names(installed.packages()) == FALSE){install.packages("grid")}
if ("gridExtra" %in% row.names(installed.packages()) == FALSE){install.packages("gridExtra")}
library(ggplot2); library(grid); library(gridExtra)
```

Investigating the Exponential Distribution

get the cumulative means and variances

```
mns <- NULL; vars <- NULL; lambda <- 0.2
# simulating 1000 means and variances
for (i in 1:1000){
   mns <- c(mns, mean(rexp(40, lambda)))
   vars <- c(vars, var(rexp(40, lambda)))
}
# getting the mean of the means
cummeans <- cumsum(mns)/(1:1000); cumvar <- cumsum(vars)/(1:1000)</pre>
```

the theoretical values

```
mean.theor <- 1/lambda
var.theor <- (1/lambda)^2
print(paste("theoretical mean: ", mean.theor))

## [1] "theoretical mean: 5"

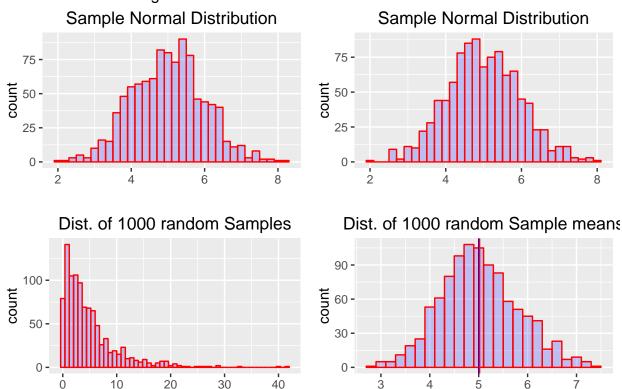
print(paste("theoretical variance: ", var.theor))

## [1] "theoretical variance: 25"</pre>
```

the distribution of means converging to a normal

```
set.seed(100)
#sample normal distribution
p1 <- ggplot(mapping = aes(rnorm(1000, mean = mean.theor)))+
  geom_histogram(binwidth = 0.2, col="red", fill= "blue", alpha=0.2)+
  labs(x = "", title= "Sample Normal Distribution")
#distribution of 1000 random exps; not gaussian
p2 <- ggplot(data.frame(val = rexp(1000, 0.2)), aes(val))+
  geom_histogram(binwidth = 0.8, col="red", fill= "blue", alpha=0.2)+
  labs(x="", title= "Dist. of 1000 random Samples")
# distribution of means
mns.data <- data.frame(mns)</pre>
p3 <- ggplot(mns.data, aes(mns))+
  geom_histogram(binwidth = 0.2, col="red", fill= "blue", alpha=0.2)+
  geom_vline(xintercept = c(mean.theor, mean(mns)), col= c("blue", "red"),
                            size = 0.5) +
 labs(x="", title= "Dist. of 1000 random Sample means")
# arranging plots
set.seed(100)
lay <- rbind(c(1,2),c(3,4))
grid.arrange(p1, p1, p2, p3, layout_matrix= lay,
             top = "checking obedience of the central limit theorem of the mean")
```

checking obedience of the central limit theorem of the mean

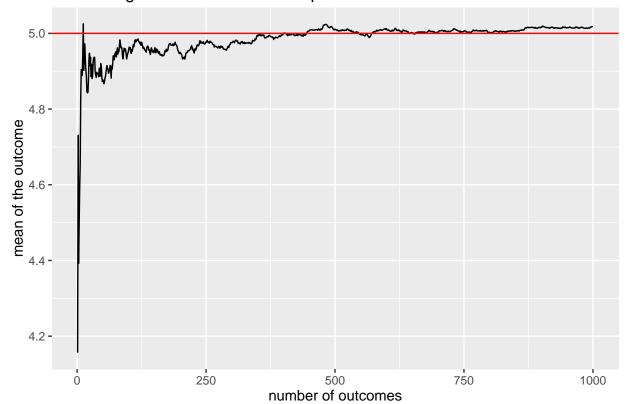


it is observable that the distribution of the means of the exponential distribution (bottom right) converges to

a Normal distibution as compared the distribution of a 1000 exponentials on the bottom left. Thus showing the Central Limit Theorem at work.

showing the convergence of the mean distribution

convergence of the mean of exponential dist. to the theoretical value



we see in the plot above as the mean distribution converges to the theoretical mean, theo.mean (marked by the horizontal line) as the outcomes increase

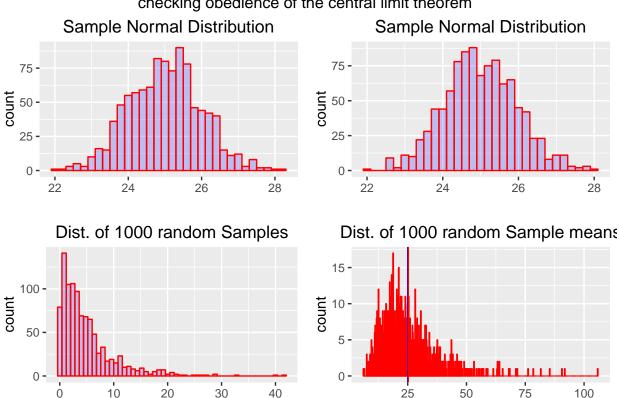
the distribution of variances converging to normal

```
#sample normal distribution
p5 <- ggplot(mapping = aes(rnorm(1000, mean = var.theor)))+
  geom_histogram(binwidth = 0.2, col="red", fill= "blue", alpha=0.2)+
  labs(x = "", title= "Sample Normal Distribution")

# distribution of variances
p6 <- ggplot(mapping= aes(vars))+</pre>
```

```
geom_histogram(binwidth = 0.2, col="red", fill= "blue", alpha=0.2)+
  geom_vline(xintercept = c(var.theor, mean(vars)), col= c("blue", "red"),
             size = 0.5)+
  labs(title= "Dist. of 1000 random Sample means", x= "")
set.seed(100)
lay2 <- rbind(c(1, 2),</pre>
              c(3, 4))
grid.arrange(p5,p5, p2, p6, layout_matrix= lay2,
             top= "checking obedience of the central limit theorem")
```

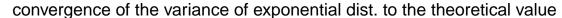
checking obedience of the central limit theorem

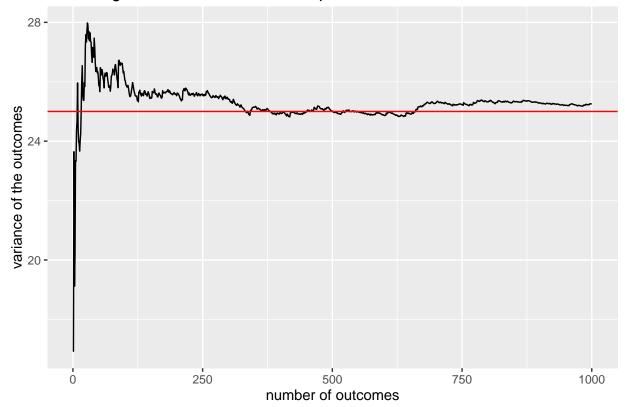


it is observable that the distribution of the variances of the exponential distribution (bottom right) converges to a Normal distibution as compared the distribution of a 1000 exponentials on the bottom left. Thus showing the Central Limit Theorem at work.

showing the convergence of the mean variances

```
ggplot(mapping = aes(1:1000, cumvar))+
  geom_line()+
  geom_hline(yintercept = var.theor, col= "red")+
  labs(x = "number of outcomes", y = "variance of the outcomes",
       title= "convergence of the variance of exponential dist. to the theoretical value")
```





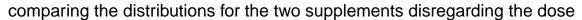
we see in the plot above as the mean distribution converges to the theoretical variance theor.var (marked by the horizontal line) as the outcomes increase.

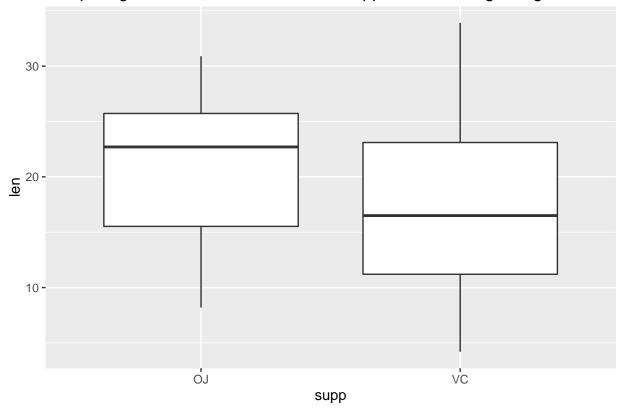
2. The analysis of the ToothGrowth dataset

The dataset consists of 60 rows and 3 columns. It looks intuitive that the observations are paired by the supp variable so we would consider this case.

Visualising the data showing some plots

```
ggplot(data = ToothGrowth)+
  geom_boxplot(mapping = aes(x=supp, y= len) ) +
  labs(title= "comparing the distributions for the two supplements disregarding the dose")
```

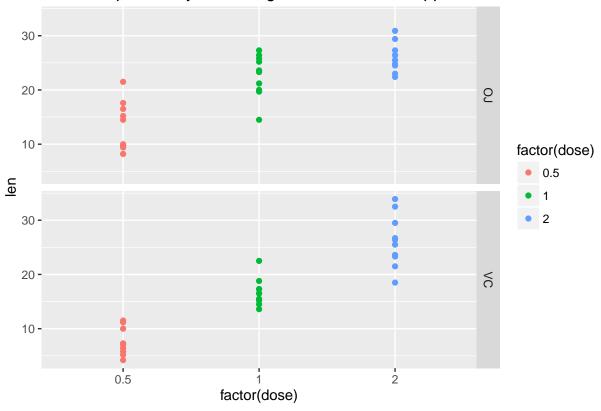




Here we observe the distribution of the len variable with respect to the supp variable

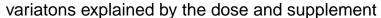
```
# var explained by dose, grid by supp
ggplot(ToothGrowth)+
  geom_point(mapping = aes(x=factor(dose), y=len, col= factor(dose)))+
  facet_grid(supp~.)+
  labs(title= "variatons explained by the dosage for each of the supplement")
```

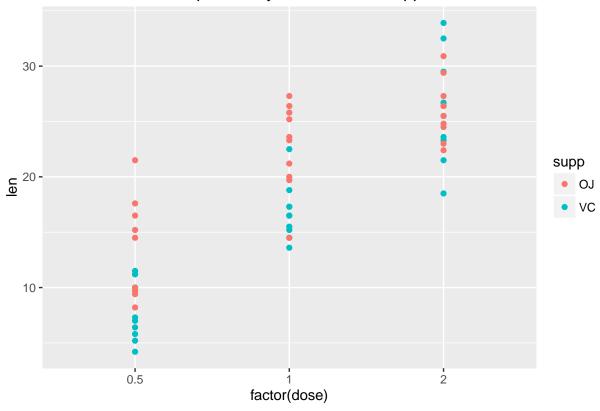




It is obvious from the above, the effect of the dose on the outcome of the len for both categories of supp variable

```
#exploring variations due to all factors
ggplot(ToothGrowth)+
  geom_point(mapping = aes(x=factor(dose), y=len, col= supp))+
  labs(title= "variatons explained by the dose and supplement")
```





from the above plot, we observe an increase in the OJ supp for the first two dose (0.5 and 1). It becomes unclear the effect of the different supplements ### Assuming paired observation

```
data("ToothGrowth"); n <- nrow(ToothGrowth)/2

#divison alongn supp variable
g1 <- ToothGrowth$len[1:30]; g2 <- ToothGrowth$len[31:60]

# showing the confidence interval (Assuming paired observations)
mn <- mean(g2-g1); s <- sd(g2-g1)
mn + c(-1, 1)*qt(0.975, n-1)*s/sqrt(n)</pre>
```

[1] 1.408659 5.991341

we see the interval (95% confidence interval) here does not contain zero which implies that we could confidently reject the hypothesis of a zero mean difference. This implies that the variability due to the supp variable is indeed significant and could not have happened by chance. ### Assuming unpaired observation

```
t.test(x= g2, y = g1, paired = FALSE)$conf

## [1] -0.1710156  7.5710156
## attr(,"conf.level")
## [1] 0.95
```

the unpaired test however shows an interval that contains zero and so we do not have enough evidence to reject the hypothesis of a 0 mean difference

implementing the permutation method

```
#implement the permutation test
cal.diff <- function(value, group){</pre>
  # function to get the mean different for a list
  # differentiated by groups (another column)
  divs <- levels(group)</pre>
  meandiff <- mean(value[group == divs[1] ]) - mean(value[group == divs[2]])</pre>
  meandiff
}
observation <- cal.diff(ToothGrowth$len, ToothGrowth$supp)
permutations <- NULL
for (i in 1:1000){
  permutations <- c(permutations, cal.diff(ToothGrowth$len,
                                             sample(ToothGrowth$supp)))
print(paste("the observed mean difference: ", observation))
## [1] "the observed mean difference: 3.7"
### check fraction of permutation greater than the observation
mean(permutations > observation)
## [1] 0.028
we see a low percentage of the permutations greater than the observation
```

```
quantile(permutations, c(0.025,0.975))

## 2.5% 97.5%
## -3.848167 3.746833
```

we see it is highly unlikely to have gotten this value if it were left to randomness.

```
quantile(permutations, 0.95)
## 95%
## 3.195
```

the 95% quantile is also less than the observation indication our observation is very unlikely due to chance. hence there is a difference in the len is associated with the supp. Particularly, the mean difference is of the len is not zero in favour of the OJ supp category.

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