Computational Stats

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1 0	use the lab computers, the access credentials are: usr: enc pwd: Ecom*2018 Lesson 1			
x <- 3+5 ls()				
## [1] "LatexOrOther" "datasetsDir" "fig_basePath" "x"				
1.1 Start by creating a vector				
y <- c(2,5,9,8) y[1:3]				
## [1] 2 5 9				
y[c(1,3)]				

```
## [1] 2 9
1.1.0.1 Get the elements 1,2,3 from the vector
y[1:3]
## [1] 2 5 9
1.1.0.2 Get the elements 1,3 from the vector
y[c(1,3)]
## [1] 2 9
1.1.0.3 Get an array from 0 to 1, with a 0.001 step
y <- 1:1000/1000
y \le seq(0,1,0.001)
1.1.0.4 Which values are lower than 0.008?
isValueLowerThan <- y < 0.008
y[isValueLowerThan]
## [1] 0.000 0.001 0.002 0.003 0.004 0.005 0.006 0.007
idxs \leftarrow which(y<0.08)
y[idxs]
## [1] 0.000 0.001 0.002 0.003 0.004 0.005 0.006 0.007 0.008 0.009 0.010
## [12] 0.011 0.012 0.013 0.014 0.015 0.016 0.017 0.018 0.019 0.020 0.021
## [23] 0.022 0.023 0.024 0.025 0.026 0.027 0.028 0.029 0.030 0.031 0.032
## [34] 0.033 0.034 0.035 0.036 0.037 0.038 0.039 0.040 0.041 0.042 0.043
## [45] 0.044 0.045 0.046 0.047 0.048 0.049 0.050 0.051 0.052 0.053 0.054
## [56] 0.055 0.056 0.057 0.058 0.059 0.060 0.061 0.062 0.063 0.064 0.065
## [67] 0.066 0.067 0.068 0.069 0.070 0.071 0.072 0.073 0.074 0.075 0.076
## [78] 0.077 0.078 0.079
1.1.0.5 Creating objects by repetition
colors <- c("amarelo","verde","vermelho","azul")</pre>
rep(colors, 5)
## [1] "amarelo" "verde"
                               "vermelho" "azul"
                                                     "amarelo" "verde"
## [7] "vermelho" "azul"
                              "amarelo" "verde"
                                                     "vermelho" "azul"
## [13] "amarelo" "verde"
                              "vermelho" "azul"
                                                     "amarelo" "verde"
```

[1] 10 10 10 10 10

print("===")

[1] "===" rep(10,5)

[19] "vermelho" "azul"

1.2 Now a Matrix!

```
M <- matrix(1:9, ncol=3)</pre>
M
    [,1] [,2] [,3]
## [1,] 1 4 7
       2
## [2,]
             5
## [3,]
         3
                  9
Transposing the Matrix
t(M)
   [,1] [,2] [,3]
##
## [1,] 1 2
## [2,]
       4
              5
                  6
## [3,]
       7
Accessing the Matrix
M[1,2]
## [1] 4
M[1,]
## [1] 1 4 7
M[,2]
## [1] 4 5 6
Matrix Operation
M2 \leftarrow t(M)
M+M2 # valuewise add
## [,1] [,2] [,3]
## [1,] 2 6 10
## [2,]
       6 10
                 14
## [3,]
       10
            14 18
M*M2 # valuewise multiplication
## [,1] [,2] [,3]
## [1,]
       1 8 21
## [2,]
        8
             25
                 48
## [3,]
       21 48 81
M%*%M2 # Matricial Multiplication
## [,1] [,2] [,3]
## [1,] 66 78 90
## [2,]
        78 93 108
## [3,]
       90 108 126
```

1.2.0.1 Joining Matrixes

Matrix Operation

```
cbind(M,M2)
       [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]
               4
        1
                   7
                        1
## [2,]
          2
                             5
                                  6
               5
                        4
                    8
## [3,]
                        7
                                  9
          3
               6
                    9
                             8
rbind(M,M2)
       [,1] [,2] [,3]
## [1,]
         1
               4
                   7
## [2,]
          2
## [3,]
          3
              6
                   9
## [4,]
        1
              2
                   3
## [5,]
        4
             5
                   6
## [6,]
```

1.2.0.2 Inverting a matrix

```
#solve(M) # M must not be singular
```

1.3 DataFrames

```
y <- 1:10
y2 <- 11:20
y3 <- letters[1:10]
d1 <- data.frame(y,y2,y3)</pre>
d1
##
      y y2 y3
      1 11 a
## 1
## 2
      2 12 b
## 3
      3 13 c
## 4
      4 14 d
## 5
      5 15 e
## 6
      6 16 f
      7 17 g
## 7
      8 18 h
## 8
## 9
      9 19 i
## 10 10 20 j
```

1.4 Reading a Tab Separated File

```
emp <- read.table(file.path(datasetsDir,"empresas.txt"), header=F)
knitr::kable(head(emp))

V1
V2
V3</pre>
```

```
V4
V5
Soflor
2
5
10
3
Florinha
3
10
22
7
Flora
5
30
55
18
Floflo
2
5
12
4
Fazflor
3
15
28
Comercflor
10
18
5
dim(emp)
## [1] 40 5
names(emp) <- c("nome","n.socios","c.social","vmm","n.emp")
knitr::kable(head(emp))</pre>
```

nome

 ${\rm n.socios}$

 ${\it c.} {\it social}$

vmm

n.emp

Soflor

Florinha

Flora

Floflo

 ${\it Fazflor}$

Comercflor

```
emp$n.socios
## [1] 2 3 5 2 3 2 3 4 6 5 2 3 2 3 2 3 2 5 2 2 3 3 2 2 2 2 4 4 3 2 2 4 2 2
## [36] 2 3 3 3 2
emp[,2]
## [1] 2 3 5 2 3 2 3 4 6 5 2 3 2 3 2 3 2 5 2 2 3 3 2 2 2 2 4 4 3 2 2 4 2 2
## [36] 2 3 3 3 2
1.5
     Generating data
set.seed(5)
emp$ant <- round(rnorm(dim(emp)[1],10,1))</pre>
     Getting insights
1.6
summary(emp)
                      n.socios
                                    c.social
##
           nome
                                                     vmm
## Alecrim
            : 1
                         :2.00 Min.
                                       : 5.00
                                                Min. : 5.00
                   Min.
## Beijaflor : 1
                                                1st Qu.: 11.00
                   1st Qu.:2.00
                                1st Qu.: 5.00
                                                Median : 19.00
## Caflor
                  Median:3.00
                               Median:10.00
             : 1
## Comercflor: 1
                   Mean :2.85
                                 Mean :11.72
                                                Mean
                                                      : 24.48
                                                3rd Qu.: 31.00
## Cravinho : 1
                   3rd Qu.:3.00
                                 3rd Qu.:15.00
## Cravo
             : 1
                   Max.
                         :6.00
                                 Max. :50.00
                                                Max. :100.00
## (Other)
             :34
       n.emp
                         ant
                          : 8
## Min. : 2.000
                   Min.
  1st Qu.: 3.000
                   1st Qu.: 9
## Median : 5.500
                   Median:10
## Mean : 6.225
                    Mean
                         :10
## 3rd Qu.: 9.000
                    3rd Qu.:11
        :18.000
## Max.
                    Max.
##
mean(emp$n.socios)
## [1] 2.85
sd(emp$n.socios)
## [1] 1.051251
tapply(emp$vmm, emp$n.emp, mean) # vmm mean by number of employes
##
           2
                      3
                                           5
                                                     6
                                                                7
##
    8.714286 10.875000 12.666667
                                   18.000000
                                             22.000000 23.000000
```

11

32.250000 45.000000 61.000000 45.000000 100.000000

14

10

##

##

##

28.000000

16 18 55.000000 55.000000 tapply(emp\$vmm, emp\$n.emp, sd) # vmm sd by number of employes

5 NA 1.500000 ## 2.627691 1.457738 1.154701 0.000000 1.414214 1.414214 ## 10 11 14 15 16 18 NA 1.414214 NANANA ## NA

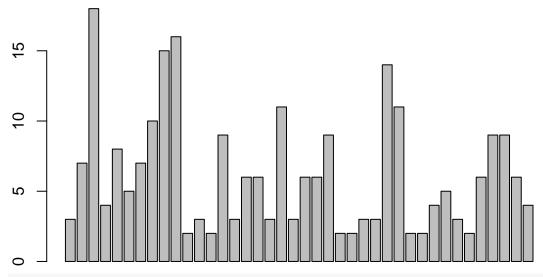
$$\overline{X} = \frac{1}{N} \sum_{i=1}^{N} X_i$$

$$S^{2} = \frac{1}{N} \sum_{i=1}^{N} (X_{i} - \overline{X})^{2}$$
 (1)

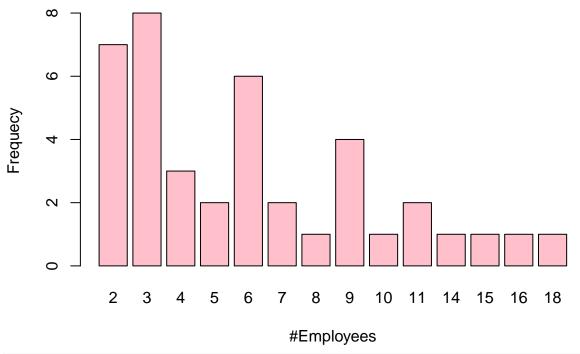
table(emp\$n.emp) #first line are values, second line is frequency

2 3 4 5 6 7 8 9 10 11 14 15 16 18 ## 7 8 3 2 6 2 1 4 1 2 1 1 1 1

 ${\tt barplot(emp\$n.emp)}$ # each company is a bin in x label, y is the number of employees

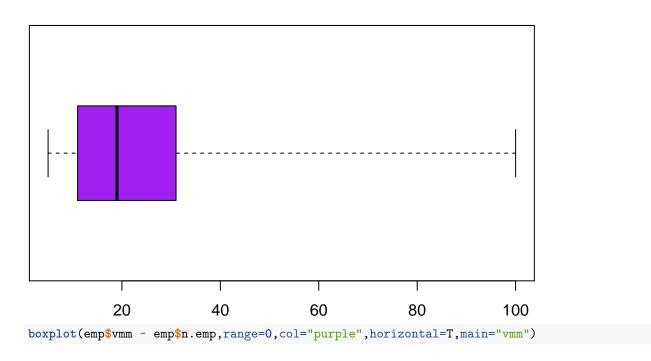


barplot(table(emp\$n.emp), xlab="#Employees", ylab="Frequecy", col="pink")

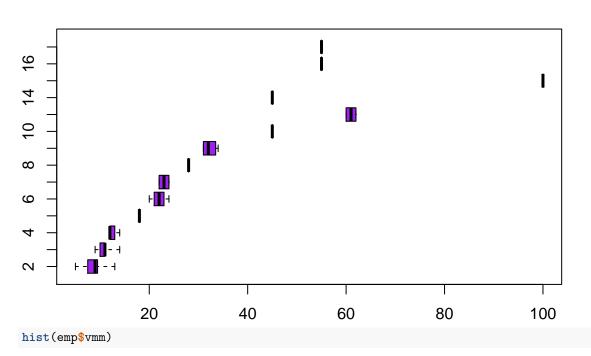


boxplot(emp\$vmm,range=0,col="purple",horizontal=T,main="vmm")

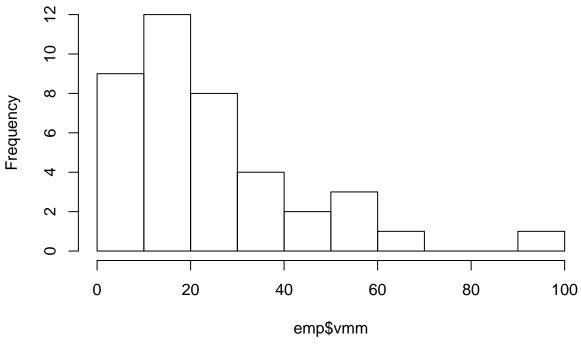
vmm





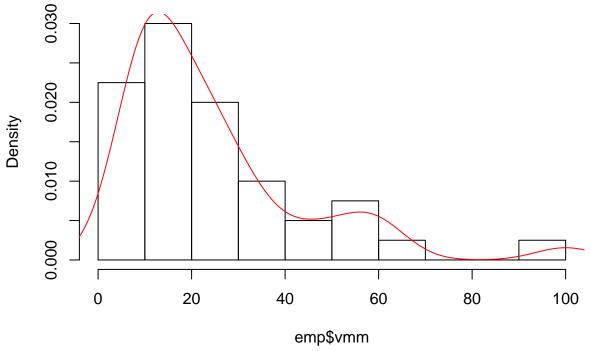


Histogram of emp\$vmm



hist(emp\$vmm, freq=F)
lines(density(emp\$vmm),col=2)

Histogram of emp\$vmm



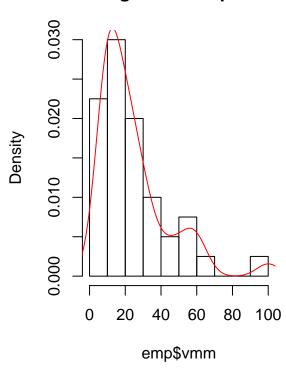
```
par(mfrow=c(1,2))
hist(emp$vmm)

hist(emp$vmm, freq=F)
lines(density(emp$vmm),col=2)
```

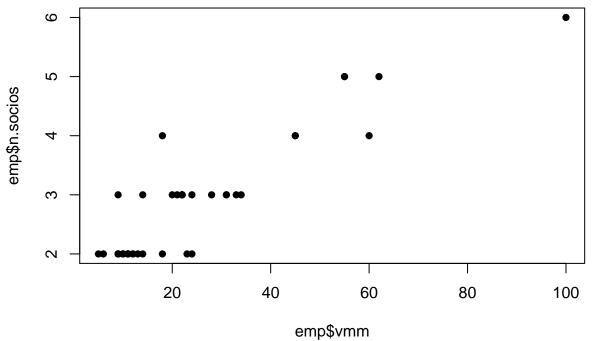
Histogram of emp\$vmm

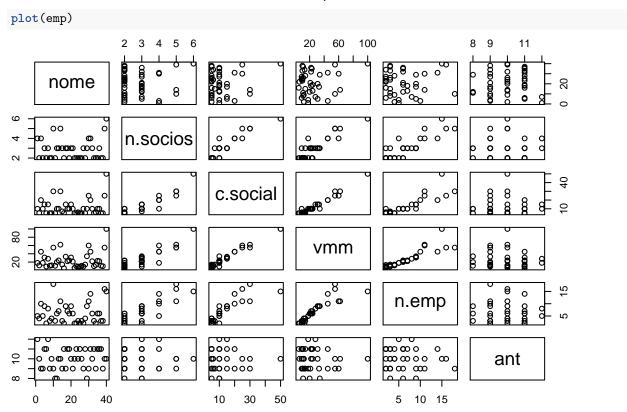
Frequency 0 20 40 60 80 100 emp\$vmm

Histogram of emp\$vmm









```
1.7 Lists
uma.lista <- list(</pre>
 um.vector=1:10,
 uma.palavra="olá",
 uma.matrix=M,
 outra.lista=list(
   a="flor",
   b=rep(3,5)
  )
)
uma.lista["um.vector"]
## $um.vector
## [1] 1 2 3 4 5 6 7 8 9 10
uma.lista$um.vector
## [1] 1 2 3 4 5 6 7 8 9 10
uma.lista[1]
## $um.vector
## [1] 1 2 3 4 5 6 7 8 9 10
1.8 Functions
desconto <- function(price, discount=25){</pre>
  #Discount is a number between 0 and 100
  #calcula o desconto de um preço
 newPrice <- price*(1-discount/100)</pre>
 discount <- price - newPrice</pre>
 list(
   novo.preco=newPrice,
    desconto=discount)
}
desconto(1000,20)
## $novo.preco
## [1] 800
```

```
## $novo.preco
## [1] 800
##
## $desconto
## [1] 200
```

desconto(1000,25)

```
## $novo.preco
## [1] 750
##
## $desconto
## [1] 250
```

This is how you function

2 Lessons 2

2.1 Random Variables and Vectors

2.1.1 Elements of probability

A random variable X is a function that takes an event space and return a value:

$$X:\Omega \to {\rm I\!R}$$

2.1.2 Expected value

3 Lesson 3

```
g <- function(x){
  exp(x^2)
}

#create sample from uniform distribution
sample <- runif(10000)
sample.length <- length(sample)

mean(g(sample))</pre>
```

[1] 1.46525

3.0.1 Estimating pi

```
g <- function(x){
    sqrt(1-x^2)
}

#create sample from uniform distribution
sample <- runif(100000000)

mean(g(sample))*4

## [1] 3.141693

gIndicatriz <- function(x,y){
    ifelse((x^2 + y^2) <= 1, 1, 0)
}

sampleX <- runif(1000000)
sampleY <- runif(1000000)
mean(gIndicatriz(sampleX,sampleY))*4</pre>
```

[1] 3.141924

3.1 Hypothesis Testing

A statistical hypothesis is some conjecture about the distribution of one or more random variables. For each hypothesis designated by null hypothesis and denoted by H0, there is always an alternative hypothesis denoted by H1. We start the test by believing that H0 is true, and during the test we can discard that hypothesis only if the data points there.

Moreover, we can see these hypothesis testing as:

- A statistical hypothesis is some statement about the parameters of one or more populations (parametric tests) or about the distribution of the population (non-parametric tests).
- The goal of a test is to use the information of a data sample to decide (reject or no reject) about a conjecture over unknown aspects of a given population.

3.1.1 Types of error while infering through hypothesis testing

There are always some risk associated to statistical inference:

- *** Type 1 error ***: reject H0 when H0 is true (rejecting error, aka False Negative in ML nomenclature)
- *** Type 2 error ***: accept H0 when H0 is false (no rejecting error, aka False Positive in ML nomenclature)

3.1.2 Defining α to reduce a type of error

$$\alpha = P(Type1Err) = P(RejectingH0|H0istrue)$$

So, we define α as being the probability that we want for the Type 1 error - or how much are we willing to be prone to this type of error.

Therefore, α is called **significance level** of the test (a test that is very prone to errors is not very significant, right?)

In general, we assign a very small value to the probability of type I error (0.05 ou 0.01).

On the other end of the error spectrum, we define β as

$$\beta = P(Type2Err) = P(AcceptingH0|H0isfalse)$$

where $1 - \beta$ is called power of the test. The insight here is that the lower the β , the more "power" this test have.

3.1.3 Procedure to make a test using p-value

3.1.3.1 Wait, what is p-value?

(WIP)

3.1.4 Estimating test stats

The hypothesis being tested is the following:

We have a sample (the variable popSample below) of independent observations from a random variable that we know follows an exponencial distribution, with unknown parameter λ .

We want to test if $\lambda = 3$.

```
popSample \leftarrow c(0.2, 1.2, 2.9, 1.2, 0.1, 0.1, 0.4, 0.1, 0.7, 0.1, 0.9, 0.3, 0.6, 0.1, 0.2, 0.1, 0.4, 0.1, 0.3, 1.4)
lambdaEstimator <- function(sample){</pre>
  1/mean(sample)
}
parameter <- 3
testStatsEstimator <- function(sample,hypothesisLambda, estimatedLambda){</pre>
  sampleMean <- mean(sample)</pre>
  sampleLength <- length(sample)</pre>
  return(
    (
       1/((sampleMean*hypothesisLambda)^sampleLength))
       (exp(
         sampleLength*
           hypothesisLambda*sampleMean -1)
     )
  )
}
tobs <- testStatsEstimator(popSample,parameter,lambdaEstimator(popSample))</pre>
```

Here, we will do the following 1000 times:

- we get a random sample from an exponential with $\lambda=3$
- we obtain the estimated test statistic for this sample

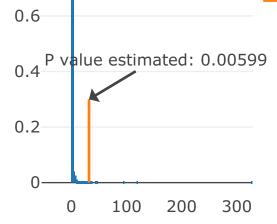
By the end of this process, we will get 1000 values that represente possible values of the Test Statistic Function

```
empiricDistTestStats <- sapply(1:1000,function(idx){</pre>
  sampleTest <- rexp(length(popSample),parameter)</pre>
  testStatsEstimator(sampleTest,parameter,lambdaEstimator(sampleTest))
})
empiricDistTestStats <- c(empiricDistTestStats,tobs)</pre>
empiricDistTestStats.df <- as.data.frame(empiricDistTestStats)</pre>
names(empiricDistTestStats.df) <- c("values")</pre>
empiricFrequency <- empiricDistTestStats.df %% dplyr::group_by(values) %% dplyr::summarise(n=n())
p_value_estimated <- sum(empiricFrequency[empiricFrequency$values >= tobs,]$n)/sum(empiricFrequency$n)
a <- list(
 text = paste0("P value estimated: " , round(p_value_estimated,5)),
 x = tobs,
 y = 0.3,
 xref = "x",
 yref = "y",
 ax = 50
```

```
plotly::plot_ly(
    x = empiricDistTestStats
    , type="histogram"
    , histnorm = "probability"
    , name = "Empiric Frequency") %>%
plotly::add_segments(
    x = tobs, xend = tobs, y = 0, yend = 0.3, name = "T obs"
) %>% plotly::layout(annotations=a)

0.8

Empiric Frequency
    T obs
```



4 Deliverables

5 Deliveable 1

5.1 Exercise 1

1. Consider the continuous random variable X with pdf:

$$f(x) = \begin{cases} \frac{4}{3}(x^3 + x) & 0 < x < 1\\ 0, & \text{for all others } x \text{ values} \end{cases}$$

Now consider the random variable Y = g(X), where $g(x) = log(x^2 + 4)$. Estimate P(1.3 < Y < 1.5) using the Monte Carlo Method, as well as the estimator standard deviation.

$$P(1.3 < Y < 1.5) \quad = \quad P(1.3 < g(x) < 1.5) \quad = \quad P(1.3 < \log(x^2 + 4) < 1.5)$$

Given that x only present values between 0 < x < 1, that imples:

- the minimum value of $log(x^2 + 4)$ is log(4)
- the maximum value of $log(x^2+4)$ is log(5)

Therefore, we know that:

$$P(1.3 < log(x^2 + 4) < log(4)) = 0$$

With this taken into consideration, the probability that we want to calculate is:

$$P(log(4) < log(x^2 + 4) < 1.5)$$

Which we can know expand into:

$$P(\log(4) < \log(x^2 + 4) < 1.5) \quad = \quad P(4 < x^2 + 4 < e^{1.5}) \quad = \quad P(0 < x^2 < e^{1.5} - 4) \quad = \quad P(0 < x < \sqrt{e^{1.5} - 4})$$

So, we now know that the probability we want to calculate can be obtain by the following integral:

$$\int_0^{\sqrt{e^{1.5} - 4}} \frac{4}{3} (x^3 + x) dx \tag{2}$$

```
mc <- function(t){
    k <- sqrt(exp(1.5)-4)
    return ( (4/3) * ((k*t)^3 + k*t) *k )
}

#t follows an uniform

sample <- runif(100000)
pEst <- mean(mc(sample))

varEstimator <- (1/(length(sample)^2))*sum((mc(sample)-pEst)^2)
df <- data.frame(
    probEstimated = pEst,
    varianceMC = varEstimator
)

knitr::kable(df, format = knitr:::pandoc_to())</pre>
```

probEstimated	varianceMC
0.397763	7e-07

5.2 Exercise 2

5.2.1 2.1

5.2.2 2.2

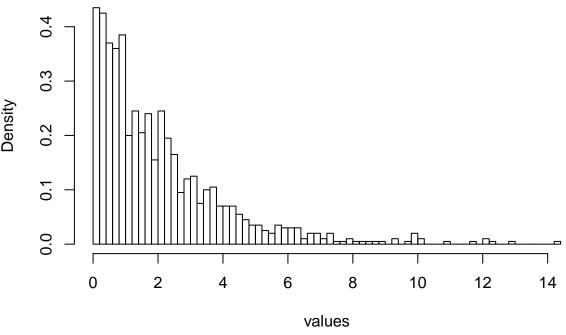
```
lambda <- 0.5
samples <- runif(1000)

inverseExp <- function(u, lambda){
   -(1/lambda)*log(1-u)</pre>
```

```
values <- inverseExp(samples, lambda)

hist(values, breaks=100, freq = F)
</pre>
```

Histogram of values



```
g <- function(x){
    exp(sqrt(x))*(2/(sqrt(2*pi)))*x^(-1/2)
}

X <- runif(10000)
Y <- runif(10000)

EX <- mean(g(inverseExp(X, lambda)))
EY <- mean(g(inverseExp(Y, lambda)))</pre>
```