UNIVERSIDADE FEDERAL FLUMINENSE

Programa de Mestrado e Doutorado em Engenharia de Produção

Multivariate Data Analysis

Lesson: Descriptive Statistics with R

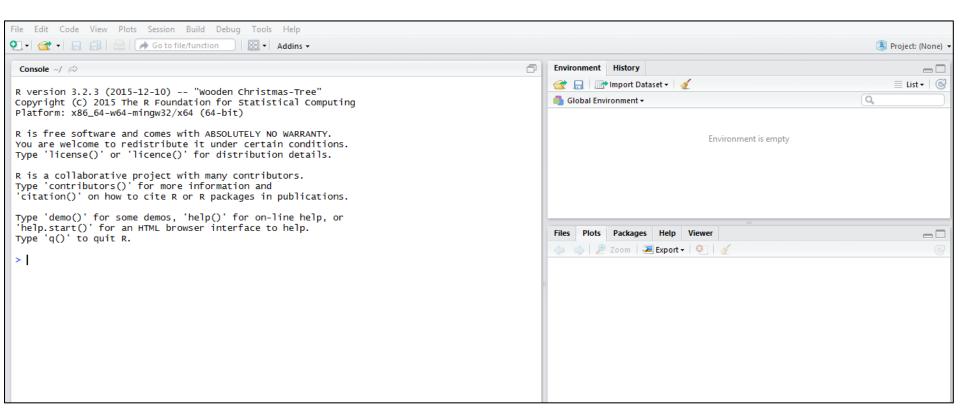
Professor: Valdecy Pereira, D. Sc.

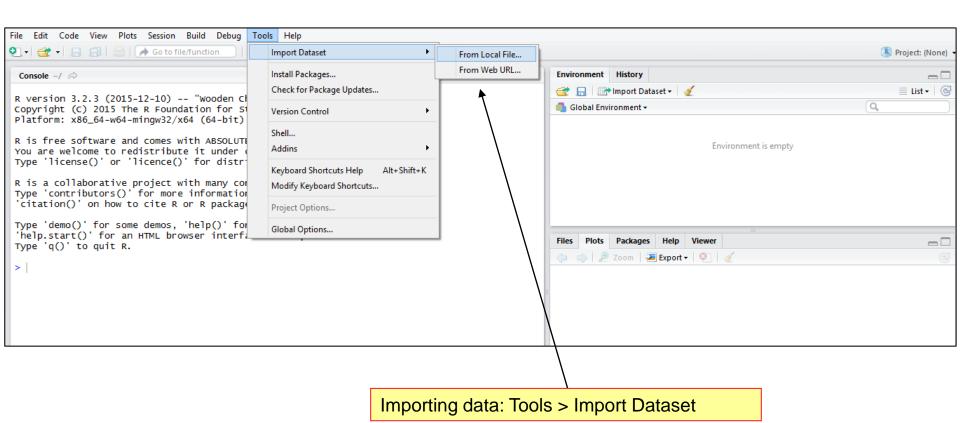
email: valdecy.pereira@gmail.com

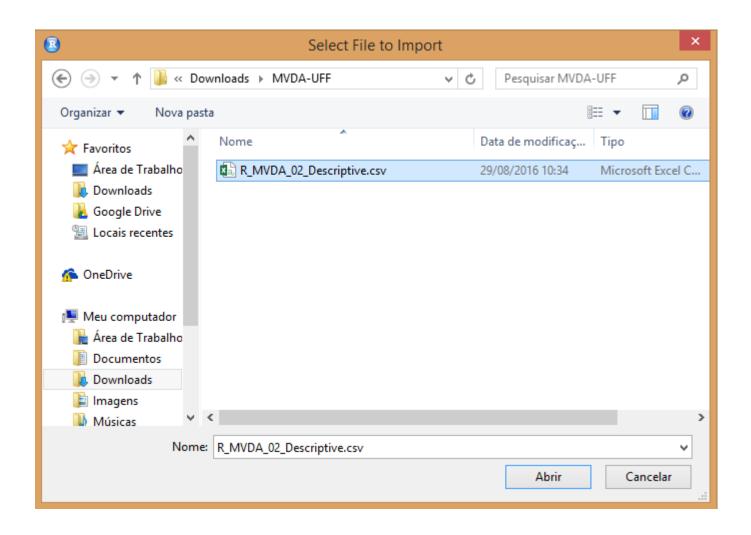
Outline

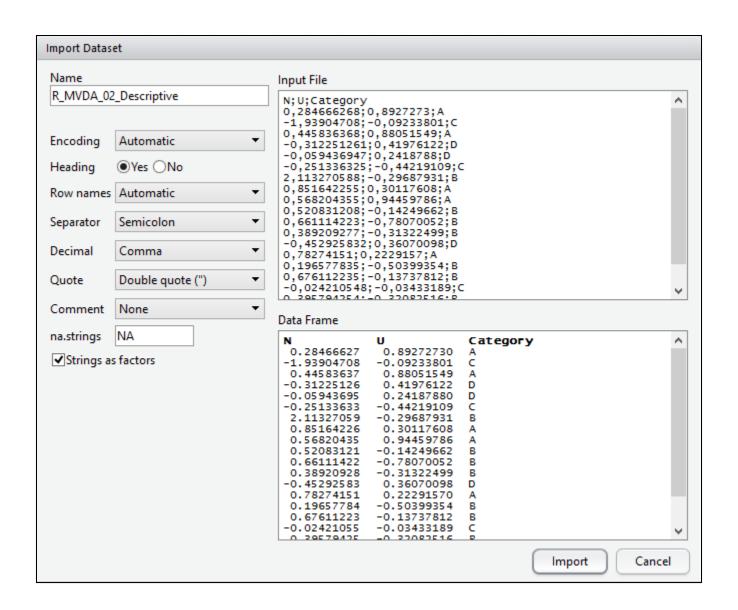
- 1. R-Studio
- 2. Class and Data
 - 3. Packages
- 4. Descriptive Statistics
 - 5. Normal Curve
 - 6. Hypothesis Testing
 - 7. Bibliography

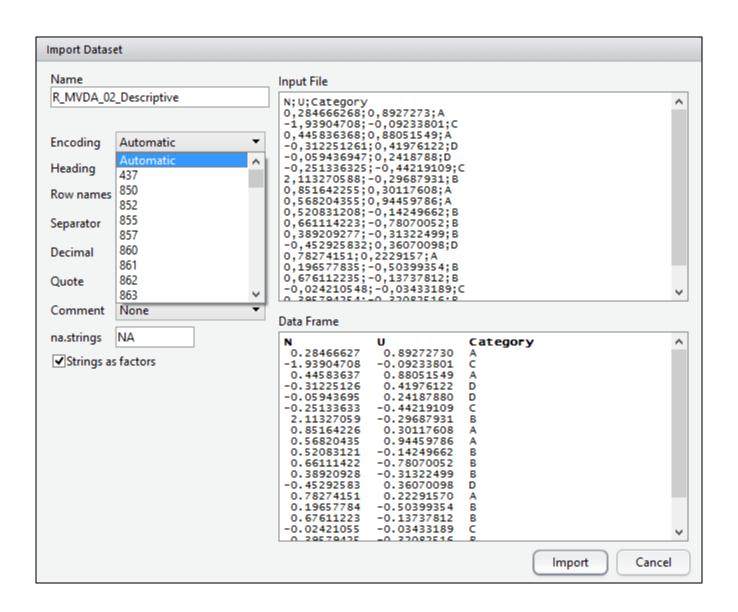
R-Studio

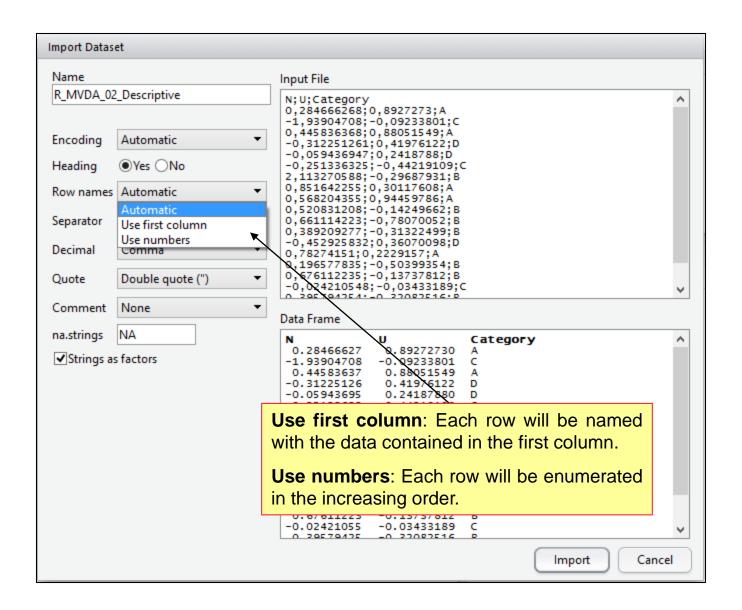


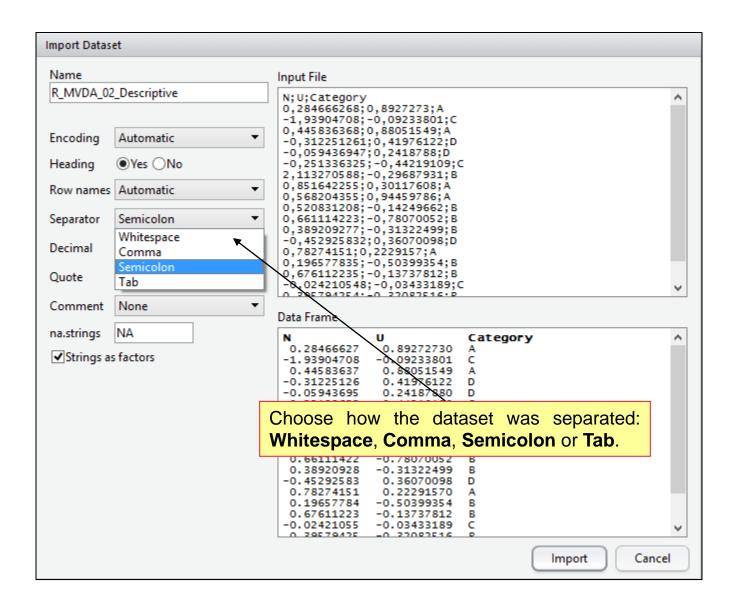


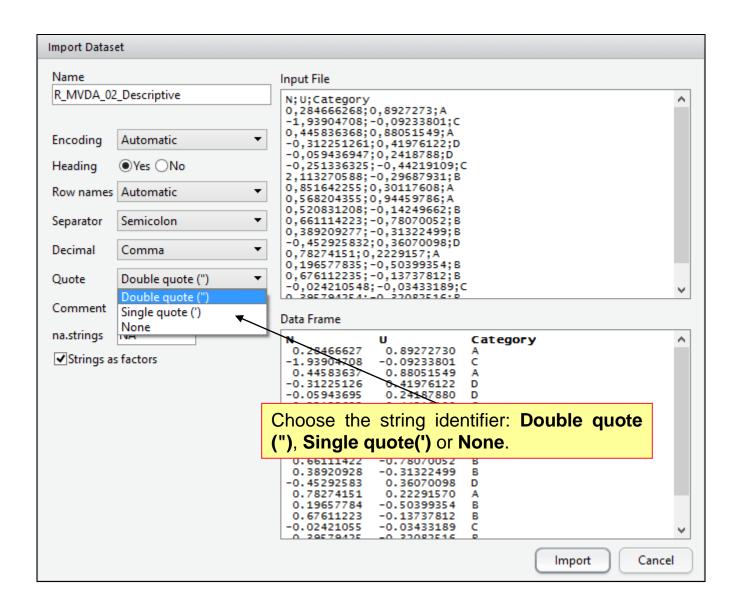


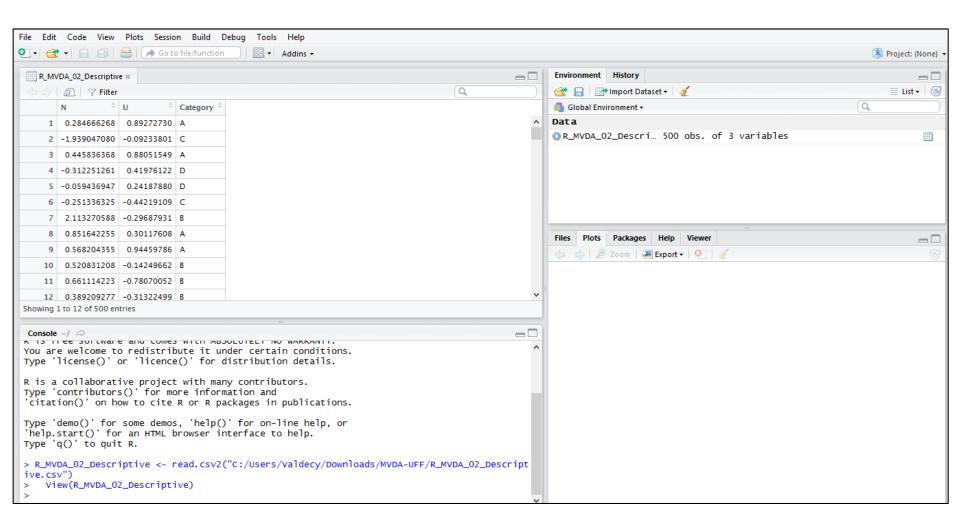


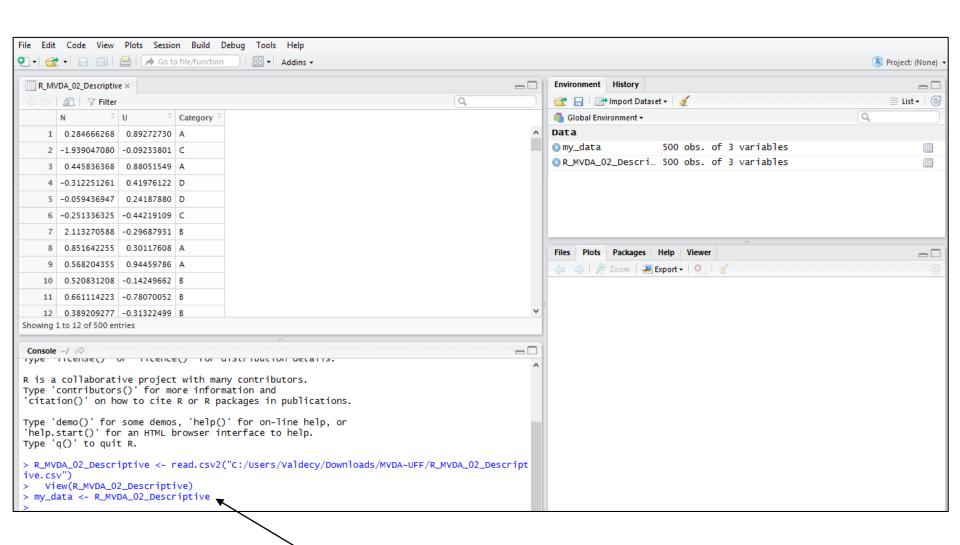




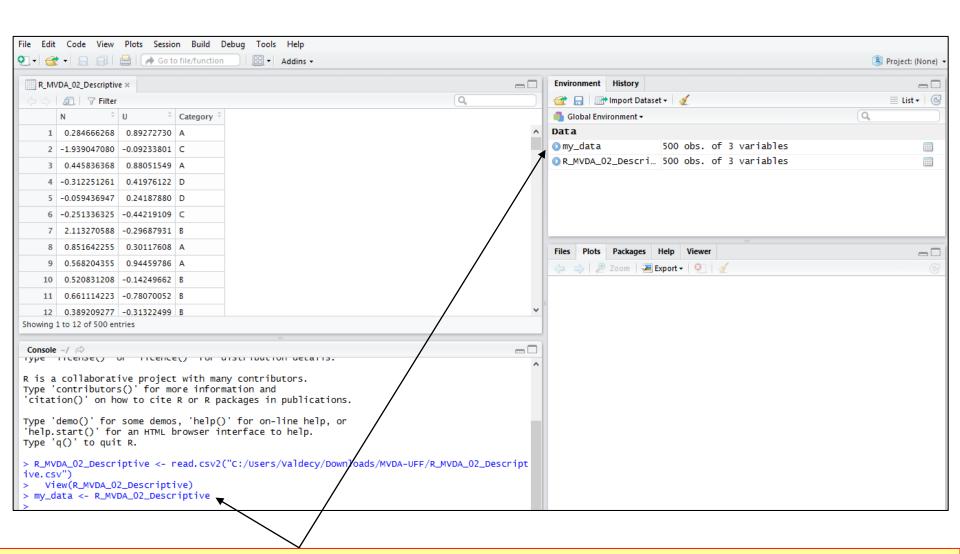








my_data <- R_MVDA_02_Descriptive



my_data <- R_MVDA_02_Descriptive

Class Type - Vector

A *VECTOR* is a collection of ordered homogeneous elements.

```
# Numeric Vector
a < -c(1, 3.33, 8.87, 6, -2, 7)
# To retrieve the elements of vector use []
a [ c (2,4) ]
[1] 3.33 6.00
a [ c (1:4) ]
[1] 1.00 3.33 8.87 6.00
# Character (String) Vector
b <- c("alpha", "bravo")
# Logical Vector
c <- c(TRUE, TRUE, TRUE, FALSE, TRUE, FALSE) # or # c <- c (T, T, T, F, T, F)
length(a)
[1] 6
names(a) <- c("A", "B", "C", "D", "E", "F")
  A B C D E F
1.00 3.33 8.87 6.00 -2.00 7.00
```

Class Type - Matrix

A *MATRIX* is a *VECTOR* with two-dimensional shape. The information contained must be of the same type (numeric, character or logic).

```
# Matrix 5 x 4 (5 rows and 4 columns) with a sequence of numbers from 1 to 20.
matrix(1:20, nrow = 5, ncol = 4, byrow = FALSE)
    [.1] [.2] [.3] [.4]
[1,]
[2,]
   2 7 12 17
[3,]
   3 8 13 18
[4,] 4 9 14 19
[5,] 5 10 15 20
matrix(1:20, nrow = 5, ncol = 4, byrow = TRUE)
[1,]
   5 6 7 8
[2,]
[3,]
   9 10 11 12
    13 14 15 16
```

17 18 19

[5,]

```
# Another example
my_matrix <- matrix(c(1, 2, 3, 4), nrow = 2, ncol = 2, byrow = TRUE)
rownames(my_matrix) <- c ("1st_row", "2nd_row")</pre>
colnames(my_matrix) <- c ("column_A", "column_B")</pre>
              column_A column_B
1st row
2nd row
my_matrix[2,1]
[1] 3
length(my_matrix)
[1] 4
dim(my_matrix)
[1] 2 2
my_matrix[ -1, ]
column A column B
    3
```

```
my_matrix <- cbind(my_matrix, c(5, 6))
colnames(my_matrix)[ 3 ] <- c("column_C")
             column A column B column C
1st_row
                                         5
2nd row
my_matrix <- rbind(my_matrix, c(7, 8, 9))
rownames(my_matrix)[ 3 ] <- c("3rd_row")</pre>
             column A column B column C
                                         5
1st row
2nd row
                                         6
3rd row
```

Class Type - Data Frame

A *DATA-FRAME* is a general form of a *MATRIX*, and the information contained can be from different types (numeric, character or logic).

```
my_data_frame <- data.frame (c (1, 2, 3, 4), c ("one", "two", "five", "ten"), c (T, T, T, F))
colnames(my_data_frame) <- c("A", "B", "C")
rownames(my_data_frame) <- c("r1", "r2", "r3", "r4")

A
B
C
r1
1
one
TRUE
r2
2
two
TRUE
r3
3
five
TRUE
r4
4
ten
FALSE
```

my_data_frame [,1]; my_data_frame\$A or my_data_frame["A"] returns the values from the first column

To add, remove or name rows and columns in a *DATA-FRAME*, consult *MATRIX* commands for the same purpose.

Class Type - List

A *LIST* is an ordered collection of objects.

```
my_list <- list(my_matrix, my_data_frame, b)</pre>
[[1]]
               column A column B column C
 1st row
                    1
                                              5
                    3
 2nd_row
                                             6
 3rd_row
                                             9
[[2]]
[1] "alpha" "bravo"
my_list[[2]]
[[2]]
[1] "alpha" "bravo"
my_list[[2]][1]
[1] "alpha"
```

Scales

Scale	Туре	R
Nominal	Non-Metric	Factor
Ordinal	Non-Metric	Factor
Interval	Metric	Numeric
Ratio	Metric	Numeric

- Non-metric data are attributes, characteristics or categories that identify or describe an observation.
- Metric data are precision measures and the differences between scale points can be made.

NOMINAL

 The numbers serve as labels to name, identify, classify and (or) categorize data on persons, objects, events or facts.

 Ex: Vehicle plate. The numbers have no meaning unless identify the person or number associated with the object.

Descriptive Statistics: Mode.

```
# Strings are converted automatically in factors
factor(c("small", "medium", "large"), levels = c("small", "medium", "large"))
[1] small medium large
Levels: small medium large
```

ORDINAL

- It represents an order relation between objects. An ordinal scale is one in which the numbers are in addition to name, identify, classify, also to order, according to a comparison process, people, objects or events in a certain characteristic.
- Ex: Rank 1st place, 2nd place, 3rd place, etc.
- Descriptive Statistics: Mode and Median.

```
# Orders are created from the lowest to the greater attribute.
ordered(c("small", "medium", "large"), levels = c("small", "medium", "large"))
[1] small medium large
Levels: small < medium < large
```

INTERVAL

- Numbers sort the objects such that the distance (range) between them correspond to the distances between objects, people or events in the characteristic being measured, although there is an arbitrary zero.
- Ex: Celsius, Fahrenheit, etc.
- Descriptive Statistics: Mode, Median and Mean.

RATIO

- They have the same characteristics as the INTERVAL scale, with the advantage of having absolute zero.
- Ex: Age, income, sales of a product, market share, cost, number of consumers, weight, height, distance, etc.
- Descriptive Statistics: Mode, Median and Mean.

Packages

MVDA – Packages

Packages are a set of functions made by R users or companies, having as the main objective, extending the capabilities of R.

```
# Downloading and installing a Package install.packages("package name")
```

Accessing a Package library("package name")

Useful Codes

MVDA – Codes

structure of an object

transform to list

list objects

head(object) # object's first 6 rows tail(object) # object's last 6 rows summary(object) # summarize an object sort(object) # sort an object help(command) # help as.numeric(object) # transform to numeric as.factor(object) # transform to factor as.matrix(object) # transform to matrix as.vector(object) # transform to vector as.data.frame(object) # transform to data frame

rm(object) # delete an object fix(object) # edit object

str(object)

as.list(object)

ls()

View(object) # View object in a window

MVDA - Codes

```
# For for (i in 1:3){ print(i) } [1] 1 [1] 2 [1] 3
```

```
# If-then-else
x <- 0
if (x < 0) {
    print("Negative number")
} else if (x > 0) {
    print("Positive number")
} else
    print("Zero")
[1] "Zero"
```

```
# While
x <- 1
while(x < 5) {
    x <- x + 1
    print(x)
}
[1] 2
[1] 3
[1] 4</pre>
```

MVDA - Codes

Logic Operate	or Description
<	# less than
<=	# less than or equal to
>	# greater than
>=	# greater than or equal to
==	# exactly equal to
<u>!</u> =	# not equal to
!x	# not x
x y	# x OR y
x & y	# x AND y

Descriptive Statistics

MVDA - Mean

The **Arithmetic Mean**, **Mean** or **Average** is the sum of a collection of numbers divided by the number of members of the same collection. It is often used to report <u>central tendencies</u>, however it is not a robust statistic, meaning that it is greatly influenced by <u>outliers</u>.

$$Mean = \frac{\sum x}{n}$$

```
# Arithmetic mean for dataset that holds a sequence from 1 to 100 sum(1:100)/length(seq(1:100))
[1] 50.5

mean(x = 1:100) # mean(1:100) also works!
```

[1] 50.5

MVDA - Mean

In the **Weighted Mean** each element of the set may have different importance (weight), and in this case the calculation should take into account the weights of each element.

Tests	Grade	Weigth
T1	80	0.30
T2	90	0.30
T3	96	0.40

$$\overline{x}_p = \frac{\sum_{i=1}^n x_i p_i}{\sum_{i=1}^n p_i}$$

Weighted mean for dataset in the example weighted.mean(x = c(80, 90, 96), w = c(0.3, 0.3, 0.4)) [1] 89.4

MVDA - Mean

The **Trimmed Mean** is obtained by eliminating the data set the "m" largest and "m" lower values. Usually "m" corresponds from 2.5% to 5% of the observed values that may be considered as outliers.

```
# Trimmed mean for data set that holds a sequence from 1 to 100 and the value 5897 as an outlier mean(x = c(1:100, 5897))
[1] 108.39

mean(x = c(1:100, 5897), trim = 0.10) # Both sides are trimmed
[1] 51

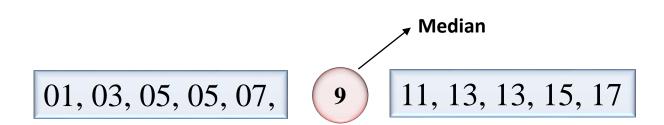
mean(x = 2:100) # This is the same as reducing de data from 2 to 100
```

[1] 51

MVDA - Median

The **Median** of a set of values is the middle value of this set when they are in increasing order, dividing it in half.

```
# Median median(x = c(3, 7, 5, 5, 1, 9, 15, 13, 17, 13, 11))
[1] 9
```



MVDA - Mode

The **Mode** of a data set is the one which is has the higher frequency. It can not exist, or it may not be unique.

```
# Mode

mode_table <- table(c(3, 7, 5, 5, 1, 9, 15, 13, 17, 13, 17))

1  3  5  7  9  13  15  17

1  1  2  1  1  2  1  2

names(mode_table)[mode_table == max(mode_table)]

[1] "5" "13" "17"
```

MVDA - Dispersion

The **Variance** and the **Standard Deviation** are the most widely used measures of dispersion. The **Standard Deviation** is most commonly used because its result is in the same unit of the studied variable, while the **Variance** results are squared.

x_i	\bar{x}	$(x_i - \bar{x})^2$
2	6	16
4	6	4
6	6	0
8	6	4
10	6	16

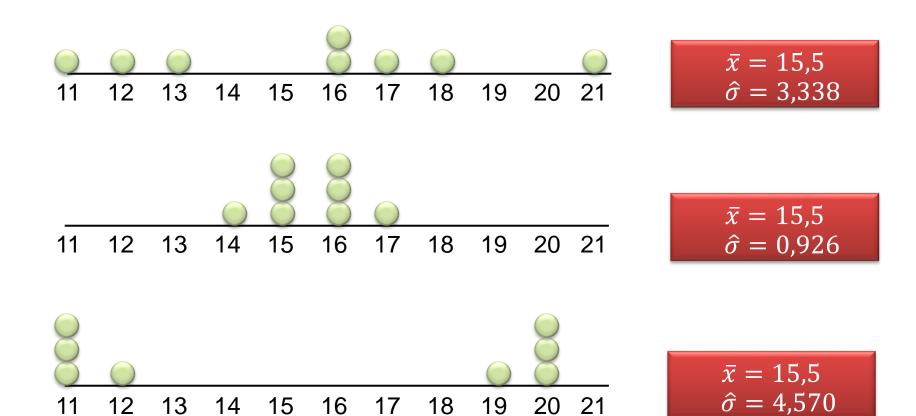
$$\hat{\sigma}^2 = \frac{\sum_{i=1}^{n} (x_i - \bar{x})^2}{n - 1}$$

$$\hat{\sigma} = \sqrt{\hat{\sigma}^2}$$

```
# Variance
var(c(2, 4, 6, 8, 10))
[1] 10
```

```
# Standart Deviation sd(c(2, 4, 6, 8, 10)) [1] 3.16
```

MVDA - Dispersion



A **Normal Distribution** is fully described by its mean and standard deviation parameters, that is, knowing these values any probability can be determined in a normal distribution. Also **Central Limit Theorem** states that the sum of independent random variables is approximately Normally limited, provided that the number of variables of the sum is large enough (≥ 50).

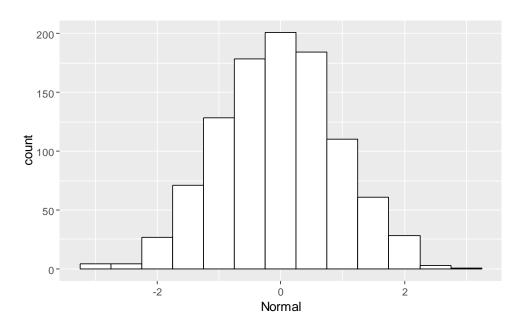
Generate a data set with 1000 observations with mean 0 and standart deviation 1.

```
set.seed(101)
n_data <- as.data.frame(rnorm(1000, 0, 1)) # or n_data <- as.data.frame(rnorm(n = 1000, mean = 0, sd = 1))

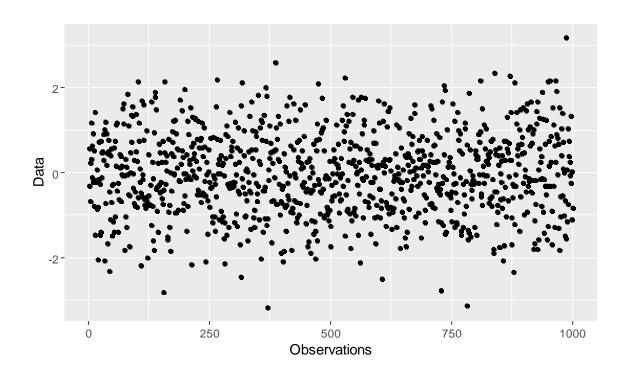
# Central Limit Theorem
cl <- data.frame(runif(500))
for (i in 1:50) {
    cl[ , i] <- data.frame(runif(500))
}
cl$Sum <- rowSums(cl)

library("ggplot2")
ggplot(data = cl, aes( x = Sum)) + geom_density() + xlab("Normal")</pre>
```

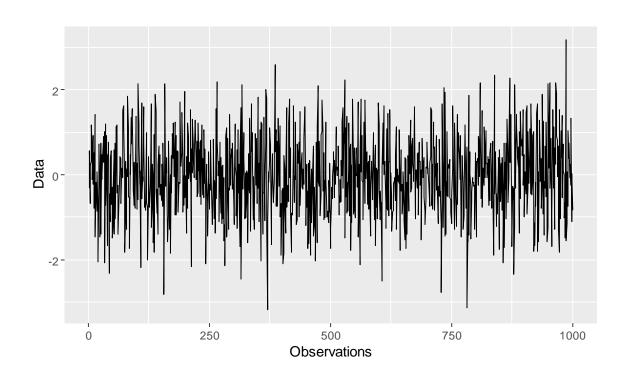
```
# histogram library("ggplot2") ggplot(data = n_{as}(x = n_{as}(x
```



```
# scatter plot library("ggplot2") ggplot(data = n_{data}, aes( x = 1:1000, y = n_{data}, 1)) + geom_point() + xlab("Observations") + ylab("Data")
```

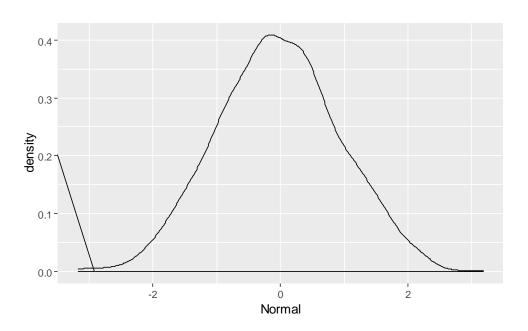


```
# line plot library("ggplot2") ggplot(data = n_{as}(x = 1:1000, y = n_{as}(1)) + geom_line() + xlab("Observations") + ylab("Data")
```

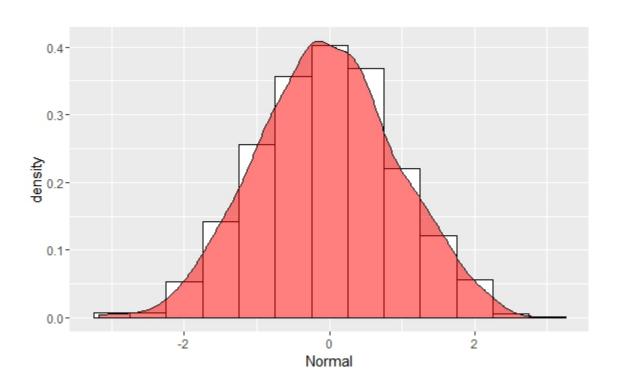


A **probability density function** (**PDF**) describes the relative likelihood of a random variable to assume a value (Integral of the function over a range). The integral over the entire space is always equal to one.

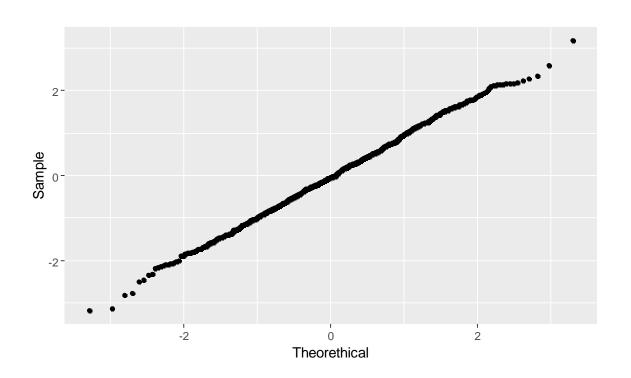
```
# density curve
ggplot(data = n_data, aes( x = n_data[,1])) + geom_density() + xlab("Normal")
```



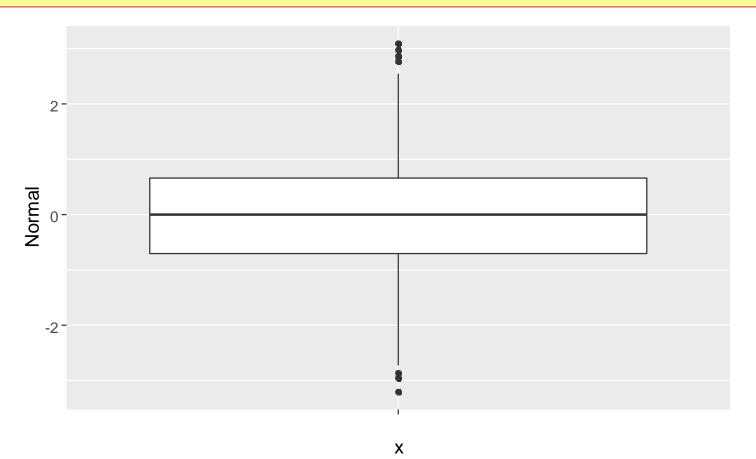
```
# both curves ggplot(data = n_{as}(x = n_{
```



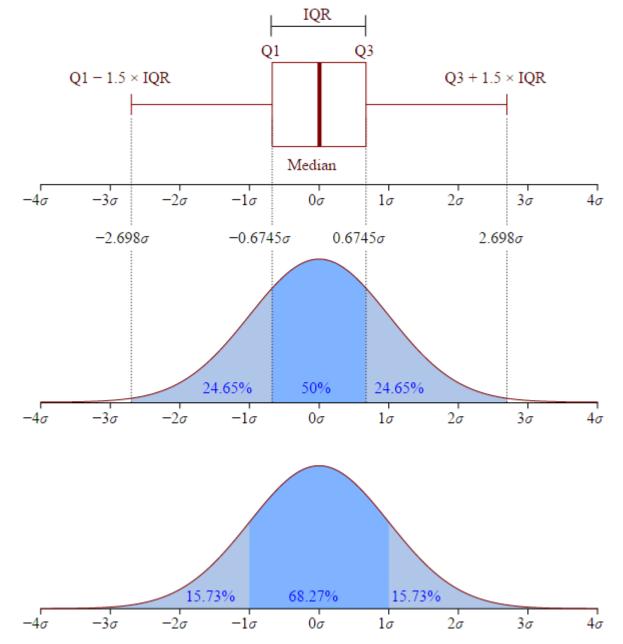
```
# qq plot
ggplot(data = n_data, aes( sample = n_data[ ,1])) + stat_qq()+ xlab("Theorethical") +
ylab("Sample")
```



```
# box plot ggplot(data = n_data, aes(x = " ", y = n_data[ ,1])) + geom_boxplot() + ylab("Normal") # Q1 - 1.5IQR, Q1, Q2, Q3, Q3 + 1.5IQR boxplot.stats(n_data[,1])stats [1] -2.5069914 -0.6919844 -0.0543911 0.5855897 2.3370023
```

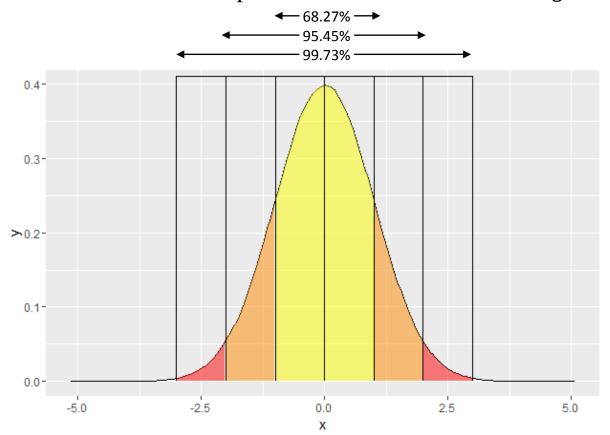


52



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The yellow area is within one standard deviation (σ) of the mean, representing 68.27% of the total number of observations. Within two standard deviations from the mean (orange and yellow areas) represents 95.45% of the total number of observations, and finally, within three standard deviations (yellow, orange and red areas) covers 99.73% of the total number of observations. This fact is known as empirical rule or the rule of the 3-sigmas.



```
# Normal Plot
 set.seed(101)
 n_data <- as.data.frame(rnorm(900000, 0, 1))
 density_n_data <- density(n_data[, 1])
 df d <- data.frame(density n data$x, density n data$y)
 colnames(df_d) <- c ("x", "y")
 ggplot(data = df_d, aes(x = x, y = y)) + geom_line() + geom_ribbon(data = subset(df_d, x >= -1 &
x \le 1), aes(ymax = y), ymin = 0, fill= "yellow", colour = NA, alpha=0.5) + geom_ribbon(data = y)
 subset(df_d, x \ge -2 & x < -1), aes(ymax = y), ymin = 0, fill = "darkorange", colour = NA, alpha = -1
 0.5) + geom_ribbon(data = subset(df_d, x >= 1 & x < 2), aes(ymax = y), ymin = 0, fill =
  "darkorange", colour = NA, alpha=0.5) + geom_ribbon(data = subset(df_d, x \ge -3 \& x < -2), aes(
  ymax = y), ymin = 0, fill = "red", colour = NA, alpha=0.5) + geom_ribbon(data = subset(df_d, x >= 2)
 & x < 3), aes(ymax = y), ymin = 0, fill = "red", colour = NA, alpha=0.5) + geom_segment(data = ymax 
 df_d, x = -3, y = 0.41, x = -3, y = 0, x = -3, x = -3, y = 0, x = -3, x = 
 3, yend = 0.41) + geom_segment(data = df_d, x = -2, y = 0, xend = -2, yend = 0.41) +
geom\_segment(data = df\_d, x = -1, y = 0, xend = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, y = 0, xend = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, y = 0, xend = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, y = 0, xend = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, y = 0, xend = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, y = 0, xend = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, y = 0, xend = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, y = 0, xend = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, y = 0, xend = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = df\_d, x = -1, yend = 0.41) + geom\_segment(data = 
= 0, y = 0, xend = 0, yend = 0.41) + geom segment(data = df d, x = 1, y = 0, xend = 1, yend = 0
 0.41) + geom_segment(data = df_d, x = 2, y = 0, xend = 2, yend = 0.41) + geom_segment(data = 0.41)
 df d, x = 3, y = 0, xend = 3, yend = 0.41) + xlab("x") + ylab("y")
```

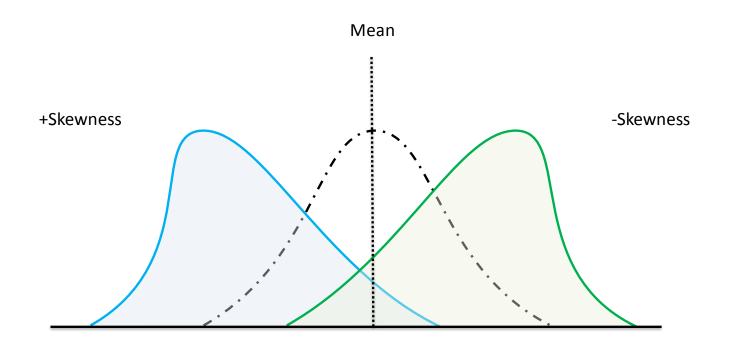
The **Skewness** is a measure of the **Asymmetry** of a distribution.

```
library(e1071)
skewness(n_data[ ,1])
```

If v < 0, then the distribution has a left tail (values below average - positive skewness).

If v = 0, then the distribution is approximately symmetrical.

If v > 0, then the distribution has a right tail (above average values - negative skewness).



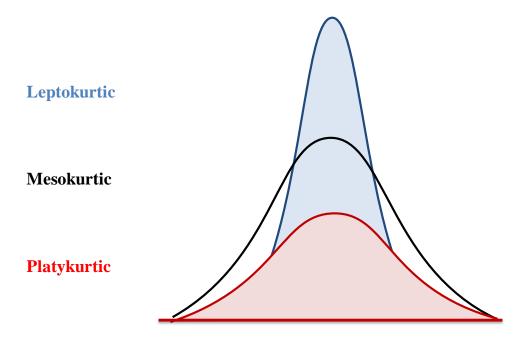
The **Kurtosis** is a measure of dispersion that characterizes the peak or flattening of the pdf curve.

```
library(e1071)
kurtosis(n_data[ ,1])
```

If k > 0, Leptokurtic: higher than the normal distribution.

If k = 0, **Mesokurtic**: same flattening the normal distribution.

If k < 0, Platykurtic: flatter than the normal distribution.

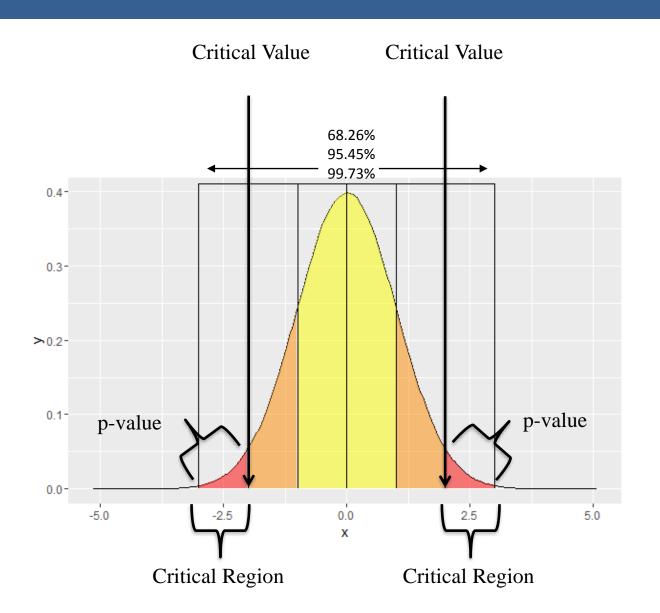


MVDA – Hypothesis Testing

A **hypothesis** in statistics is a statement about some property of a population and **hypothesis testing** is a method that accepts or rejects this claim through a sample of that population.

- Null hypothesis (H_0) : The statement that is being tested.
- Alternative Hypothesis (H_1) : What is believed to be true, when the null hypothesis is considered false.
- Critical Region: The region which the values cause the rejection of the null hypothesis.
- Critical Value: It's value that starts the critical region.
- Confidence Interval $(1 \alpha ; \alpha = \text{significance}; 0 \le \alpha \le 1)$: An estimated range of a parameter of interest of a population.
- **p value**: The area under the pdf curve that rejects the null hypothesis if its value is less than the significance level α ($0 \le \alpha \le 1$).
- Type I error (False Positive): It is the incorrect rejection of a true null hypothesis.
- Type II error (False Negative): It is the incorrect acceptance of a false null hypothesis.

MVDA – Hypothesis Testing



MVDA – Normality Test

The **Shapiro-Wilk test** (for samples ≤ 5000 observations) and the **Kolmogorov-Smirnov test** (for samples > 5000 observations) checks whether a sample came from a normally distributed population. With the following hypothesis:

 H_0 : The sample is normally distributed H_1 : The sample is not normally distributed

```
# R Shapiro-Wilk test supports up to 5000 observations shapiro.test()

# The KS test needs a reference distribution y. set.seed(101)
n_data <- as.data.frame(rnorm(900000, 0, 1))
r_data <- as.data.frame(runif(900000))
ks.test(x = m_data[, 1], y = n_data[, 1])
```

p-value < 2.2e-16 # rejects the null hypothesis, thus x is not normally distributed

MVDA

https://github.com/Valdecy/Multivariate_Data_Analysis

```
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```

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- # Course: Multivariate Data Analysis
- # Lesson: Descriptive Statistics with R

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repository: https://github.com/Valdecy/Multivariate_Data_Analysis

Bibliography

- CORRAR, L.J.; PAULO, E.; DIAS FILHO, J. M. **Análise Multivariada para Cursos de Administração,** Ciências Contábeis e Economia. ATLAS, 2009.
- FÁVERO, L. P.; BELFIORE, P.; SILVA, F. L.; CHAN, B. **Análise de Dados: Modelagem Multivariada** para **Tomada de Decisões**. CAMPUS, 2009.
- HAIR, J. F.; BLACK, W. C.; BABIN, B. J.; ANDERSON, R. E.; TATHAM, R. L. **Análise Multivariada de Dados**. BOOKMAN, 2009.
- LATTIN, J.; CARROLL, J. D.; GREEN, P. E. **Análise de Dados Multivariados**. CENGAGE Learning, 2011.
- LEVINE, D. M.; STEPHAN, D. F.; KREHBIEL, T. C.; BERENSON, M. L. **Estatística Teoria e Aplicações Usando Microsoft Excel**. LTC, 2012.