

Introduction
to R

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- R is the actual programming language
- RStudio is an IDE (Integrated Development Environment) for R.
- R is **case sensitive**; e. g., **Mean** \neq **mean**
- R(Studio) may not work very well when files (or directory containing working files) have accented characters. If the locale language of your filesystem is not in English, then some errors may occur in those cases.

Basic calculations

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- R can be used as a calculator
- Mathematical constants:
 - $\pi = 3.142$
 - $\exp(1) = 2.718$
- Logarithms:
 - $\log(e) = 1$
 - $\log_{10}(100) = 2$
 - $\log(16, \text{base} = 4) = 2$
- Getting help: in the console, put a question mark before the function name; RStudio will display the documentation:
`?cos`

Installing packages

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One of the strengths of R is the increasing number of available packages (more than 14,000 of them): [CRAN Packages](#)

To install and use a package we have

- firstly to **install** it;
- then, to **load** it in the current session.

To install a package (e.g., `tseries`), we can use the `install.packages("tseries")` function.

To load it in the current session, use `library(tseries)`

To install a package, we can also use the **Tools** option in the RStudio window and follow **Install Packages...**

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Data types

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The data types used by R are

- numeric (double precision): 2.718, 1.4, ...
- integer: 1, -13, ...
- complex: $2 - 3i$, ...
- logical: TRUE, FALSE. Also NA is considered logical
- character: "one plus two", "Hello world!"

Data Structure

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- Vector: basic data structure in R. Its components have the same data type.
- Matrix: think of linear algebra.
 - A matrix as a collection of vectors.
- Dataframe: similar to a matrix, except that it is not necessarily homogeneous.
 - A collection of vectors (of possible different types) with the same length.
- List: generic data structure containing other **objects** (vectors, other lists), **not necessarily of the same length.**

Assignment operator

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In R, we assign a value, **value**, to an object **x** by means of **<-**:

```
x <- value
```

It is also possible to use **=**, but the equal sign has lower priority than **<-**.

Check the discussion at [StackExchange](#).

Vectors

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The easiest way to create a vector in R is to use the `c()` function:

```
v <- c(1, 3, 5, 7, 9)  
v
```

```
## [1] 1 3 5 7 9
```

Vectors: coercion

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If we define a vector with components of different data types, the result will be coerced to the same data type

```
w <- c(1.56, "Hello World", 4, TRUE)
```

```
typeof(w)
```

```
## [1] "character"
```

Notice that

```
u <- c(1.56, 4, TRUE)
```

```
typeof(u)
```

```
## [1] "double"
```

Vectors by sequences

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- Create a vector with the first 30 integer numbers:

```
(x <- 1:30)
```

```
## [1] 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15  
## [24] 24 25 26 27 28 29 30
```

- In reverse order:

```
(x <- 30:1)
```

```
## [1] 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16  
## [24] 7 6 5 4 3 2 1
```

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- Create a sequence of the first odd numbers, up to 11:

```
(y <- seq(1, 11, 2))
```

```
## [1] 1 3 5 7 9 11
```

- Repeat the character "Hello" 5 times:

```
(z <- rep("Hello", 5))
```

```
## [1] "Hello" "Hello" "Hello" "Hello" "Hello"
```

- Repeat the vector y, defined above, 2 times:

```
(rep(y,2))
```

```
## [1] 1 3 5 7 9 11 1 3 5 7 9 11
```

Length of a vector

The length of a vector (number of its components) is obtained with the function `length()`

```
x <- 1:30  
length(x)
```

```
## [1] 30
```

```
y <- seq(1, 11, 2)  
length(y)
```

```
## [1] 6
```

```
z <- rep("Hello", 5)  
length(z)
```

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

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Let `y <- seq(1,11,2)`: 1, 3, 5, 7, 9, 11.

- Select the third component: `y[3]` = 5
- Exclude the fourth component: `y[-4]`: 1, 3, 5, 9, 11.
- Select the first four components: `y[c(1:4)]`: 1, 3, 5, 7
- Select the first, fifth and last element:

```
y[c(1, 5, length(y))]
```

```
## [1] 1 9 11
```

or

```
y[c(1, length(y) - 1, length(y))]
```

```
## [1] 1 9 11
```

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- Remove the first four components: `y[-c(1:4)]`: 9, 11.
- Select the second, fifth and sixth components: `y[c(2, 5, 6)]`: 3, 9, 11.
- Select components by using a vector of logic type:

```
s <- c(TRUE, TRUE, FALSE, FALSE, TRUE, FALSE)
y[c(s)]
```

```
## [1] 1 3 9
```


Vectorization

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Consider the vector

```
x <- 1:100
```

Then,

- $x + 4 = 5, 6, 7, 8, 9, 10 \dots$
- $x^2 = 1, 4, 9, 16, 25, 36 \dots$
- $2*x+3 = 5, 7, 9, 11, 13, 15 \dots$
- $\text{sqrt}(x) = 1, 1.414, 1.732, 2, 2.236, 2.449 \dots$
- $\log(x) = 0, 0.693, 1.099, 1.386, 1.609, 1.792 \dots$

Vectorization

We can add up two vectors even when they have different lengths, provided that the length of one is an integer multiple of the other:

```
x <- seq(1,11,2)
y <- 1:12
x + y
```

```
## [1] 2 5 8 11 14 17 8 11 14 17 20 23
```

Check for identity

```
all(x + y == rep(x,2) + y)
```

```
## [1] TRUE
```

```
identical(x + y, rep(x,2) + y)
```

```
## [1] TRUE
```

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Logical operators

Each of the following operators returns either **TRUE** or **FALSE**.

- **==** (equality)
- **!=** (not equal to)
- **>** (greater than)
- **<** (less than)
- **>=** (greater than or equal to)
- **<=** (less than or equal to)
- **!x** (not **x**)
- **x | y** (**x** OR **y**)
- **x & y** (**x** AND **y**)

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Examples

Let `x <- c(1,2,3,4,5,6)`

- `x > 4`: FALSE, FALSE, FALSE, FALSE, TRUE, TRUE
- `x == 4`: FALSE, FALSE, FALSE, TRUE, FALSE, FALSE
- `x != 3`: TRUE, TRUE, FALSE, TRUE, TRUE, TRUE
- `x == 4 | x != 3`: TRUE, TRUE, FALSE, TRUE, TRUE, TRUE
- `x == 4 & x != 3`: FALSE, FALSE, FALSE, TRUE, FALSE, FALSE
- `as.numeric(x == 4 | x != 3)`: 1, 1, 0, 1, 1, 1
- `sum(as.numeric(x == 4 | x != 3))`: 5

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Logical operators and subsetting

Subsetting will extract the values of the components that satisfy the given logical condition.

Let `x <- c(1,2,3,4,5,6)`

- `x[x > 3]`: 4, 5, 6
- `x[x != 3]`: 1, 2, 4, 5, 6
- `x[x <= 0]`: `numeric(0)` (empty set)
- `x[x <= 0 | x > 3]`: 4, 5, 6
- `x[x <= 0 & x > 3]`: `numeric(0)` (empty set)
- `sum(x[x <= 0 & x>3])`: 0

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Selection

```
y <- c(1, -2, 4, 6, 9, 2, 1)
```

- `which(y <= 4)`: 1, 2, 3, 6, 7

It selects which entries satisfy the condition. Indexing of vectors starts from 1.

- `y[which(y <= 4)]`: 1, -2, 4, 2, 1

It returns the values of the entries satisfying the condition.

- `which(y == max(y))`: 5 <= **entry of the vector**
- `y[which(y == max(y))]`: 9 <= **maximum value**

Matrices

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A matrix A is specified by the number of its rows and columns, $m \times n$.

The **order** of rows and columns is **important**.

Matrix can be created by means of the `matrix()` function:

```
x <- 1:8  
A <- matrix(x, nrow = 4, ncol = 2)  
B <- matrix(x, nrow = 2, ncol = 4)  
dim(A) # rows = 4; columns = 2
```

```
## [1] 4 2
```

```
dim(B) # rows = 2; columns = 4
```

```
## [1] 2 4
```

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A

##		[,1]	[,2]
##	[1,]	1	5
##	[2,]	2	6
##	[3,]	3	7
##	[4,]	4	8

B

##		[,1]	[,2]	[,3]	[,4]
##	[1,]	1	3	5	7
##	[2,]	2	4	6	8

Matrices: Subsetting

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- Select the entry of the matrix A in the first row, second column:

```
A[1,2]
```

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

- Select the third column of the matrix B

```
B[,3]
```

```
## [1] 5 6
```

- Select the third row of the matrix A

```
A[3,]
```

```
## [1] 3 7
```

Matrices: Subsetting

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- Select the first and fourth column of the matrix B

```
B[, c(1,4)]
```

```
##           [,1] [,2]  
## [1,]         1    7  
## [2,]         2    8
```

Binding vectors: by columns

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```
u <- 1:4
v = rev(u)
w <- rep(1,4)
C <- cbind(u,v,w)
rownames(C) <- c("1st", "2nd", "3rd", "4th")
C
```

```
##      u v w
## 1st  1 4 1
## 2nd  2 3 1
## 3rd  3 2 1
## 4th  4 1 1
```

Binding vectors: by rows

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```
u <- 1:4
v = rev(u)
w <- rep(1,4)
D <- rbind(u,v,w)
colnames(D) <- c("1st", "2nd", "3rd", "4th")
D
```

##		1st	2nd	3rd	4th
##	u	1	2	3	4
##	v	4	3	2	1
##	w	1	1	1	1

Matrix operations

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- The sum of two compatible matrices is $A + B$
- The subtractino of two compatible matrices is $A - B$
- The product of two compatible matrices is $A \%*\% B$
- The transpose of a matrix A is $t(A)$
- The inverse of a square matrix, A , if it exists, is $solve(A)$

Inverse matrix

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```
x <- c(1,2,3,5, 4, 1, 2,2,1)
A <- matrix(x, nrow = 3, ncol = 3)
A1 <- solve(A)
A1 %*% A
```

```
##           [,1] [,2]      [,3]
## [1,] 1.00e+00  0 2.22e-16
## [2,] 8.88e-16  1 1.11e-15
## [3,] 0.00e+00  0 1.00e+00
```

The result is the identity matrix, up to round-off errors.

More matrices

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- We can use the function `all.equal()` to compare the results of `solve(A)` and `A1 %*% A` with the identity matrix:

```
all.equal(A1 %*% A, diag(3))
```

```
## [1] TRUE
```

- The function `diag()` can also be used to extract the diagonal elements of a matrix

```
diag(A)
```

```
## [1] 1 4 1
```

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```
diag((1:5)^(.5))
```

##		[,1]	[,2]	[,3]	[,4]	[,5]
##	[1,]	1	0.00	0.00	0	0.00
##	[2,]	0	1.41	0.00	0	0.00
##	[3,]	0	0.00	1.73	0	0.00
##	[4,]	0	0.00	0.00	2	0.00
##	[5,]	0	0.00	0.00	0	2.24

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```
diag(log(1):log(5))
```

```
##           [,1] [,2]  
## [1,]         0  0  
## [2,]         0  1
```

```
diag(log(1:5))
```

```
##           [,1] [,2] [,3] [,4] [,5]  
## [1,]         0 0.000  0.0  0.00 0.00  
## [2,]         0 0.693  0.0  0.00 0.00  
## [3,]         0 0.000  1.1  0.00 0.00  
## [4,]         0 0.000  0.0  1.39 0.00  
## [5,]         0 0.000  0.0  0.00 1.61
```

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R has some built-in functions to deal with matrices. Consider

A

```
##           [,1] [,2] [,3]
## [1,]         1     5     2
## [2,]         2     4     2
## [3,]         3     1     1
```

- `rowSums(A)` = 8, 8, 5
- `colSums(A)` = 6, 10, 5
- `rowMeans(A)` = 2.667, 2.667, 1.667
- `colMeans(A)` = 2, 3.333, 1.667

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The operator `%*%`

The operator `%*%` works differently on vectors and matrices.

- On vectors it computes the **dot product**
- On matrices, the matrix multiplication (matrix multiplication is a form of ordered, vectorized dot product)

```
a <- c(1,2,3)
```

```
b <- c(4,5,6)
```

```
a %*% b
```

```
##      [,1]
```

```
## [1,] 32
```

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Vector can be coerced to work as matrices; in this case, columns matrices:

```
as.matrix(a)
```

```
##           [,1]
```

```
## [1,]      1
```

```
## [2,]      2
```

```
## [3,]      3
```

```
t(as.matrix(b)) %*% as.matrix(a) # dot product
```

```
##           [,1]
```

```
## [1,]    32
```

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```
as.matrix(a) %*% t(as.matrix(b))
```

##		[,1]	[,2]	[,3]
##	[1,]	4	5	6
##	[2,]	8	10	12
##	[3,]	12	15	18

Dataframes

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- Statistical analysis is done using datasets. A dataset contains a certain number of variables and observations.
- It is a good practice to have each variable set as a column vector and each observation as a row vector.
- A dataframe, in R, is the data structure of an observed dataset.
- A dataframe can be thought of as a matrix in which different columns may have different data types.

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When loading a dataset for analysis, there are some aspects to consider.

- 1 Understand the data: what the dataset is about; what are its variables; how many observation the dataset contains.
- 2 Determine whether there are missing observations; some functions will not work properly otherwise.
- 3 Visualize some of its variables.

Import the dataset with RStudio

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Information about the dataset

- The dataset is taken from the [UCI, Machine Learning Repository](#) website.
- The dataset can be found [here](#).
 - Clicking the link will download the file; we will load the dataset more conveniently later on, with a different set of tools.
- The dataset will be called **cleve** hereinafter in the presentation.
- The dataset format is **csv** (comma separated variables).

Import the dataset with RStudio

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- Copy the link <https://archive.ics.uci.edu/ml/machine-learning-databases/heart-disease/processed.cleveland.data>
- Click on **Files** in RStudio window and follow **Import Dataset...** and select **From Text (readr)**
- The variables (columns) in the dataset have no names in the dataset.
 - When importing the dataset, **deselect** the option **First Row as Names**.

Working with the dataset

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- Set the names of the variables:

```
cleve.names <- c("age", "sex", "cp", "trestbps",  
                 "chol", "fbs", "restcg", "thalac",  
                 "exang", "oldpeak", "slope", "ca",  
                 "thal", "diagnostic")  
  
names(cleve) <- cleve.names
```

- The documentation of the dataset is found [here](#)
- To work with only one variable from the dataset, e.g., *age*, we can **extract** it by means of `$`.

```
age <- cleve$age
```

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The dataset is a dataframe

```
class(cleve)
```

```
## [1] "data.frame"
```

with

```
dim(cleve)
```

```
## [1] 303 14
```

$\text{nrow}(\text{cleve}) = 303$ observations and $\text{ncol}(\text{cleve}) = 14$ variables.

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The names of the variables can also be obtained by `colnames(cleve)`.

The first six observations can be displayed by

```
head(cleve)
```

(Output omitted because it does not fit the slide.)

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Display the first 3 observations of the first, third and seventh through ninth variables:

```
cleve[1:3,c(1,3,7:9)]
```

##		age	cp	restcg	thalac	exang
##	1	63	1	2	150	0
##	2	67	4	2	108	1
##	3	67	4	2	129	1

or with (omitted for space)

```
cleve[1:2, c("age", "cp", "restcg",  
             "thalac", "exang")]
```

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Examples

- 1 Compute the number of individuals whose age is greater than, or equal to, 50 years:

```
length(cleve$age[cleve$age >= 50])
```

```
## [1] 216
```

- 2 Compute the number of individuals without a diagnosis of heart disease:

```
length(cleve$sex[cleve$diagnostic == 0])
```

```
## [1] 164
```

Remark The variable `diagnostic` is strictly positive if there is indication of a heart condition.

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Examples

- ③ Compute the number of individuals with a diagnosis of heart disease **and** with fasting blood sugar > 120 mg/dl

```
length(cleve$sex[cleve$diagnostic > 0 &  
               cleve$fbs == 1])
```

```
## [1] 22
```

- ④ Compute the number of individuals with a diagnosis of heart disease **or** with fasting blood sugar > 120 mg/dl

```
length(cleve$sex[cleve$diagnostic > 0 |  
               cleve$fbs == 1])
```

```
## [1] 162
```

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Consider, e.g., the variable *age*. Compute:

- 1 the mean (average)

```
mean(cleve$age)
```

```
## [1] 54.4
```

- 2 the median

```
median(cleve$age)
```

```
## [1] 56
```

- 3 the interquartile range

```
IQR(cleve$age) # Q3 - Q1
```

```
## [1] 13
```

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- ④ the summary of the principal statistics

```
summary(cleve$age)
```

##	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
##	29.0	48.0	56.0	54.4	61.0	77.0

Remark The function `summary()` does not return neither the variance nor the standard deviation.

- ⑤ Quantile distribution

```
quantile(cleve$age, c(.1, .25, .40, .60, .80))
```

##	10%	25%	40%	60%	80%
##	42	48	53	58	62

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It is possible to apply the `summary()` function to a full dataset, or to several variables of it

```
summary(cleve[,c(1,5,8)])
```

##	age	chol	thalac
##	Min. :29.0	Min. :126	Min. : 71
##	1st Qu.:48.0	1st Qu.:211	1st Qu.:134
##	Median :56.0	Median :241	Median :153
##	Mean :54.4	Mean :247	Mean :150
##	3rd Qu.:61.0	3rd Qu.:275	3rd Qu.:166
##	Max. :77.0	Max. :564	Max. :202

(Only three variables are selected for space.)

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Variance and standard deviation

- The variance (resp., standard deviation) is computed by `var()` (resp., `sd()`).
- If the variable has `NA` (missing values), then `var()`, `sd()` return `NA`:

```
var(cleve$thal)
```

```
## [1] NA
```

```
sd(cleve$thal)
```

```
## [1] NA
```

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Variance

We can apply the function `var()` to a single variable or several of them; in the latter case, we obtain the variance-covariance matrix of the selected variables:

```
var(cleve[, c(1, 3, 5, 6)])
```

##		age	cp	chol	fbs
##	age	81.697	0.9037	97.787	0.3816
##	cp	0.904	0.9218	3.595	-0.0137
##	chol	97.787	3.5951	2680.849	0.1815
##	fbs	0.382	-0.0137	0.181	0.1269

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Standard deviation

The standard deviation `sd()`, on the other hand, can only be applied to a single variable:

```
sd(cleve$age)
```

```
## [1] 9.04
```

```
sd(cleve$chol)
```

```
## [1] 51.8
```

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Standard deviation of a set of variables

We have to vectorize the function `sd()` by means of `apply()`:

```
apply(cleve[,11:13], 2, sd)
```

- The value `2` in the second parameter of the function `apply()` computes the standard deviation, `sd`, of each variable (column).
- The value `1` would compute the standard deviation of each row (observation).

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Standard deviation of a set of variables

```
apply(cleve[,11:13], 2, sd)
```

```
## slope      ca    thal
```

```
## 0.616      NA     NA
```

There are missing values in the dataset.

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Count and remove NA's

Let's count them:

```
sum(is.na(cleve))
```

```
## [1] 6
```

We can eliminate them (less than 2% of the observed values)

```
cleve <- na.omit(cleve)
```

```
sum(is.na(cleve))
```

```
## [1] 0
```

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Standard deviation of a set of variables

```
apply(cleve[,11:13], 2, sd)
```

```
## slope      ca    thal
```

```
## 0.618 0.939 1.939
```

The variable **slope** has a slightly larger standard deviation now.

Contingency Tables

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Write a contingency table of gender and diagnosis of heart disease:

```
table(cleve$sex, cleve$diagnostic)
```

```
##  
##      0  1  2  3  4  
##  0 71  9  7  7  2  
##  1 89 45 28 28 11
```

Using the `with()` function:

```
with(cleve, table(age, diagnostic))
```

(Same result; output omitted for space.)

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Alternative to `table`

Using the `xtabs()` function:

```
xtabs(~ cleve$sex + cleve$diagnostic)
```

```
##           cleve$diagnostic
## cleve$sex  0  1  2  3  4
##           0 71  9  7  7  2
##           1 89 45 28 28 11
```

Estimated Frequencies

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Redefine the variable **diagnostic** as dummy, with value 1 if some heart problem is observed:

```
cleve$diagnostic[cleve$diagnostic >0] <- 1
```

Table of estimated frequencies:

```
table(cleve$sex, cleve$diagnostic)/nrow(cleve)
```

##			
##		0	1
##	0	0.2391	0.0842
##	1	0.2997	0.3771

Visualization: Barplot

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```
barplot(table(cleve$diagnostic),  
         main = "Diagnostic (observed)")
```

Visualization: Barplot

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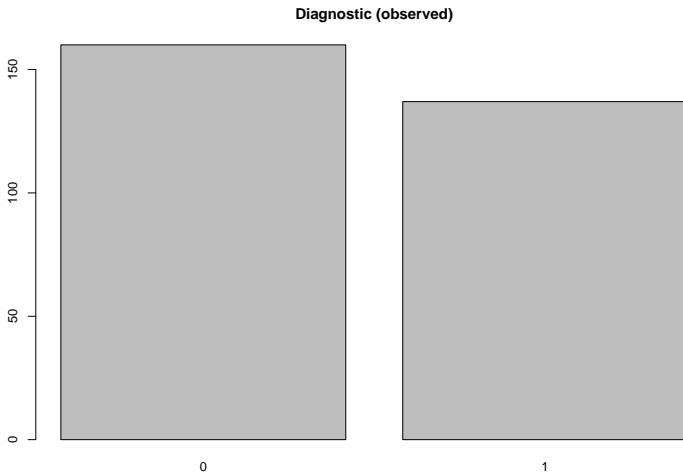
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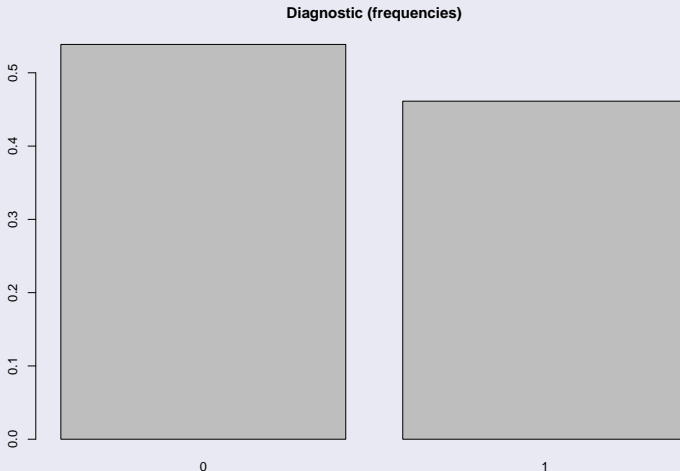
Time series

Barplot with observed frequencies

```
barplot(table(cleve$diagnostic)/nrow(cleve),  
        main = "Diagnostic (frequencies)")
```

Visualization: Barplot

Barplot with observed frequencies



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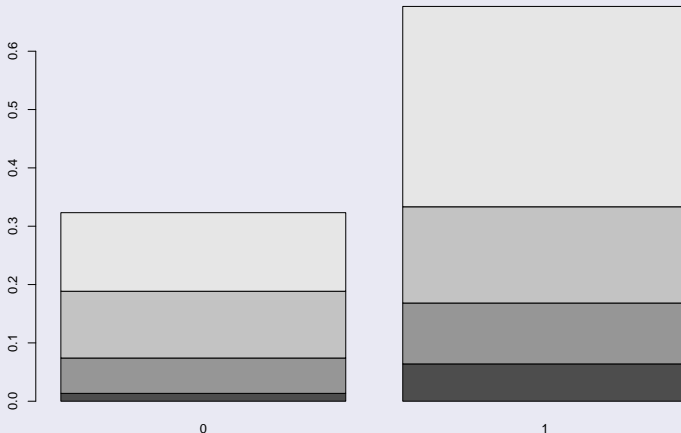
Barplot with a contingency table

```
barplot(table(cleve$cp,  
              cleve$sex)/nrow(cleve),  
        main = "Chest pain by gender")
```

Visualization: Barplot

Barplot with a contingency table

Chest pain by gender



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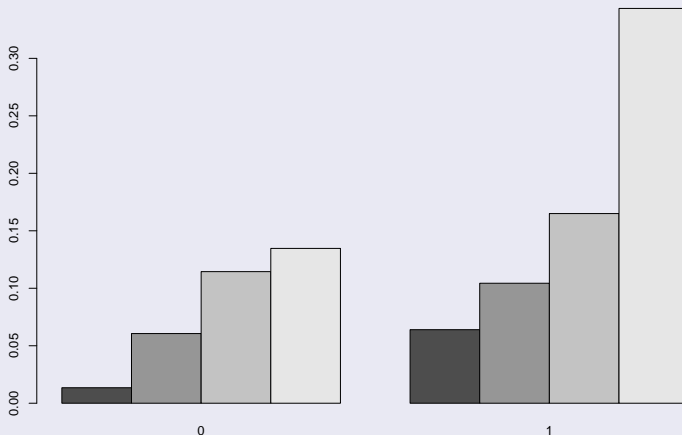
Grouped barplots

```
barplot(table(cleve$cp,  
              cleve$sex)/nrow(cleve),  
        main = "Diagnostic (frequencies)",  
        beside = TRUE)
```

Visualization: Barplot

Grouped barplots

Chest pain by gender



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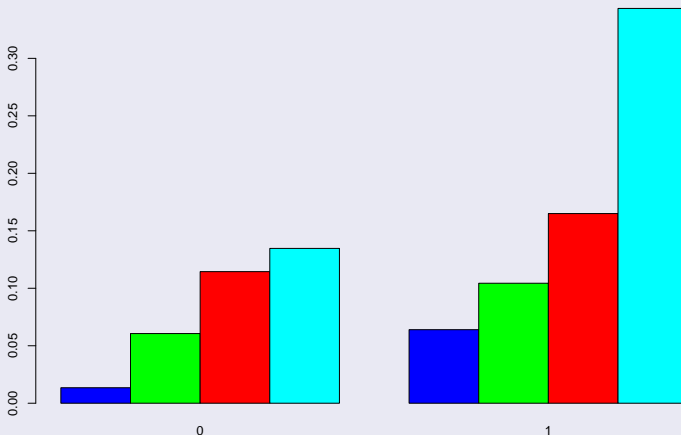
Grouped barplots with colors

```
barplot(table(cleve$cp,  
              cleve$sex)/nrow(cleve),  
        main = "Chest pain by gender",  
        beside = TRUE,  
        col = c("blue", "green", "red", "cyan"))
```

Visualization: Barplot

Grouped barplots with colors

Chest pain by gender



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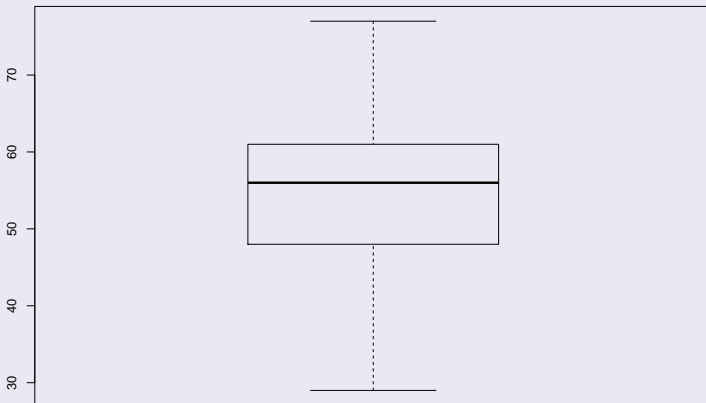
Time series

Variable “age”

```
boxplot(cleve$age)
```

Visualization: Boxplot

Variable “age”



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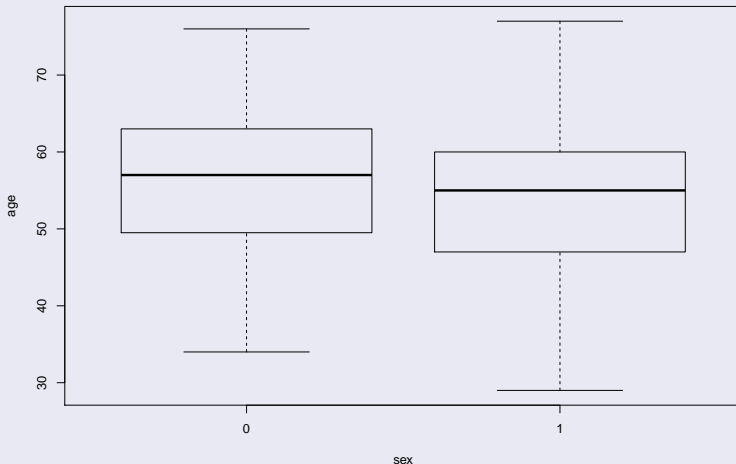
Time series

Age as a function of gender

```
boxplot(age ~ sex, data = cleve)
```

Visualization: Boxplot

Age as a function of gender



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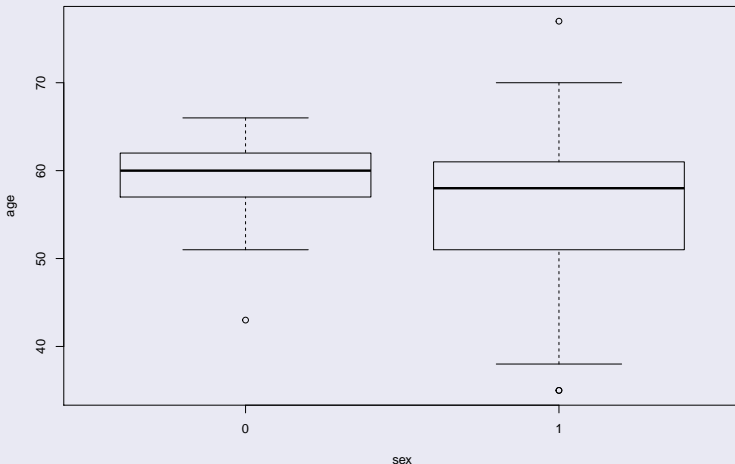
Time series

Age as a function of gender, with positive diagnosis

```
boxplot(age ~ sex, data = cleve,  
        subset = diagnostic == 1)
```

Visualization: Boxplot

Age as a function of gender, with positive diagnosis



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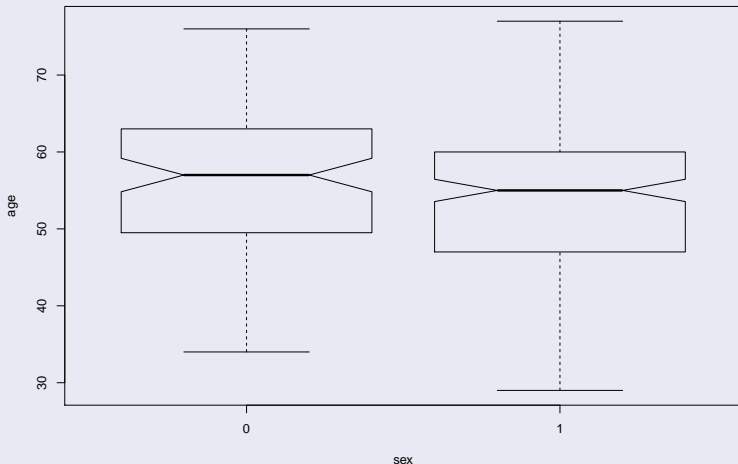
```
boxplot(age ~ sex, data = cleve,  
        notch = TRUE)
```

Justification

See, e.g., John M. Chalmers, William S. Cleveland, Beat Kleiner, Paul A. Tukey, "Graphical Methods for Data Analysis", Wadsworth International Group, Duxbury Press, 1983, pp. 60-63.

Visualization: Boxplot with notch

Age as a function of gender



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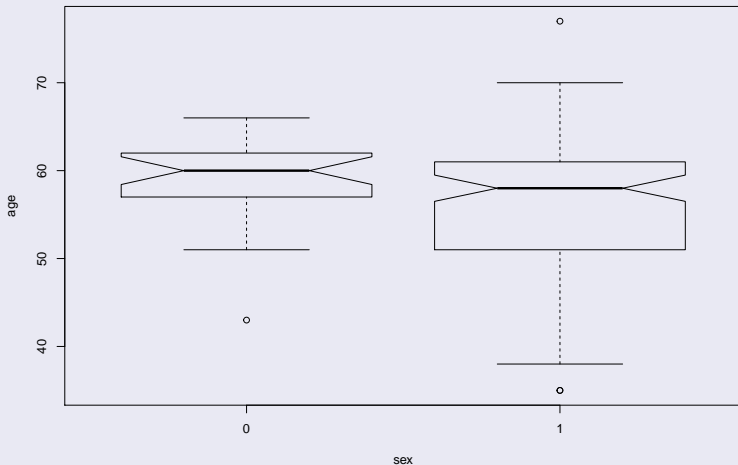
Time series

Age as a function of gender with positive diagnosis

```
boxplot(age ~ sex, data = cleve,  
        notch = TRUE,  
        subset = diagnostic == 1)
```

Visualization: Boxplot with notch

Age as a function of gender with positive diagnosis



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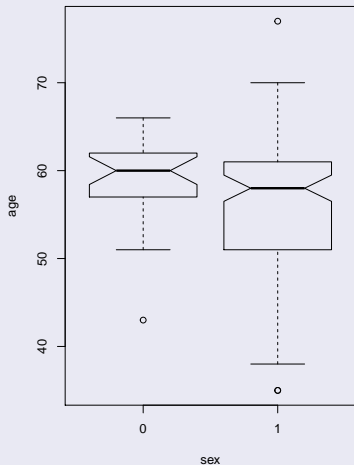
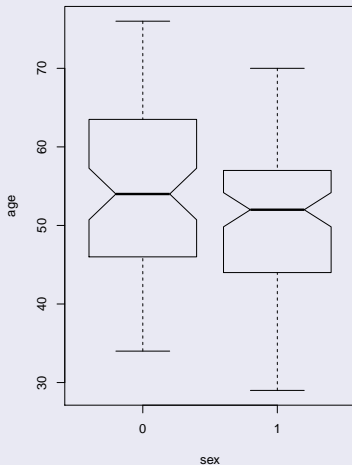
Time series

Two graphs side by side

```
par(mfrow=c(1,2))  
boxplot(age ~ sex, data = cleve,  
        notch = TRUE,  
        subset = diagnostic == 0)  
boxplot(age ~ sex, data = cleve,  
        notch = TRUE,  
        subset = diagnostic == 1)  
par(mfrow = c(1,1))
```

Visualization: Boxplot

Two graphs side by side



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```
mosaicplot(cleve$sex ~ cleve$diagnostic,  
            shade=F, color=T,  
            main = "Diagnosis by gender", xlab="Gender",  
            ylab = "Diagnostic")
```

Visualization: Mosaicplot

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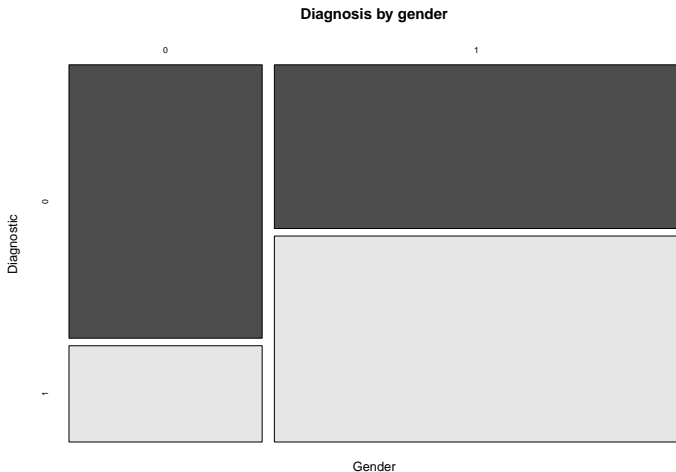
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```
mosaicplot(cleve$cp ~ cleve$diagnostic,  
            shade=F, color=T,  
            xlab = "Chest pain", ylab = "Diagnostic",  
            main = "Diagnostic by Chest Pain")
```

The variable **cp** has four levels.

Visualization: Mosaicplot

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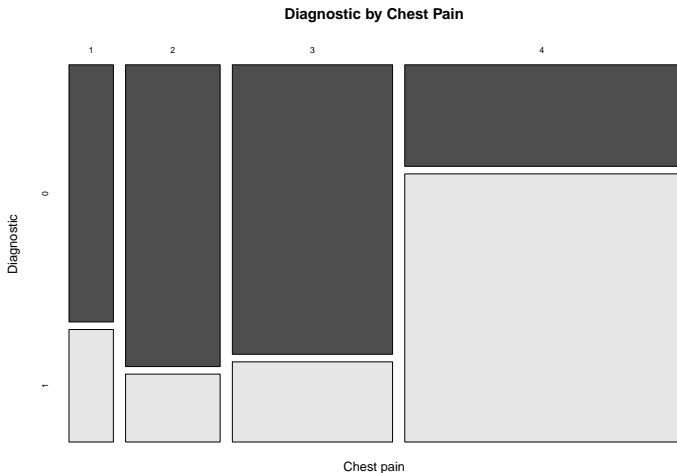
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```
mosaicplot(cleve$exang ~ cleve$diagnostic,  
            shade=F, color=T,  
            xlab = "Exercise-induced angina",  
            ylab = "Diagnostic",  
            main = "Diagnostic by Angina")
```

The variable **exang** (exercise induced angina): 1 = yes; 0 = no

Visualization: Mosaicplot

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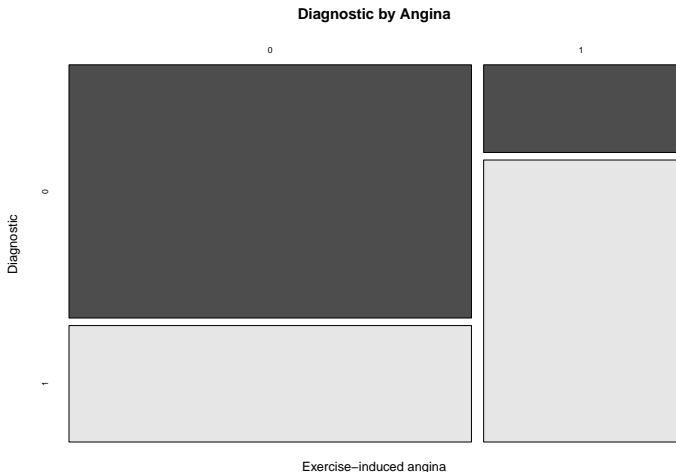
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Consider the variable *age*.

```
plot(cleve$age)
```

gives the scatterplot of the variable.

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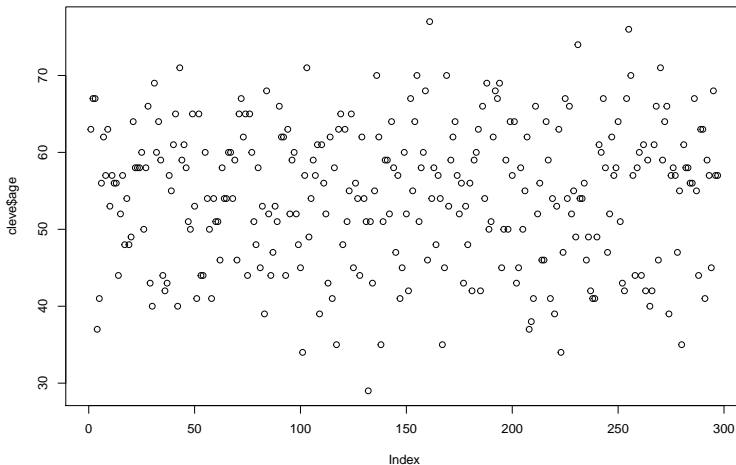
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```
plot(cleve$age, cleve$chol)
```

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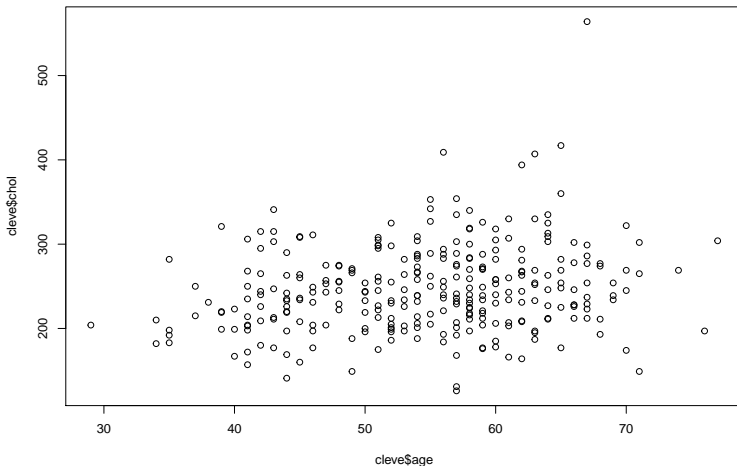
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With regression line:

```
plot(cleve$age, cleve$chol)
abline(lm(chol ~ age, data = cleve), col = "red")
```

Visualization of continuous variables

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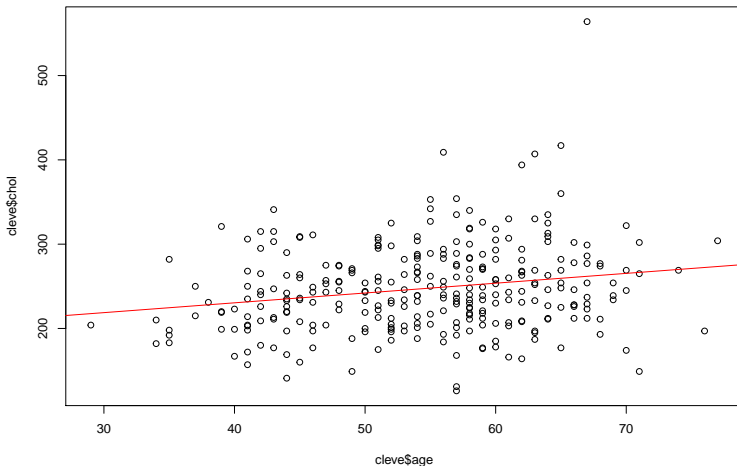
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More Visualization

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See the script `visualization.R`

Classification by K-means clustering

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See the script `classification.R`

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We want to determine whether there is a difference in age between individuals with no heart condition and those with an indication of a heart condition.

```
age.pos <- cleve$age[cleve$diagnostic == 1]  
age.neg <- cleve$age[cleve$diagnostic == 0]
```

Formally

$$H_0 : \text{age.pos} = \text{age.neg}$$

$$H_1 : \text{age.pos} \neq \text{age.neg}$$

(significance level: $\alpha = .05$)

Hypothesis testing

95% Confidence interval

```
t.test(age.pos, age.neg, mu = 0)
```

```
##
```

```
## Welch Two Sample t-test
```

```
##
```

```
## data: age.pos and age.neg
```

```
## t = 4, df = 295, p-value = 6e-05
```

```
## alternative hypothesis: true difference in means is not equal to 0
```

```
## 95 percent confidence interval:
```

```
## 2.12 6.11
```

```
## sample estimates:
```

```
## mean of x mean of y
```

```
## 56.8 52.6
```

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99% Confidence interval

```
t.test(age.pos, age.neg, mu = 0, conf.level = .99)

##
##  Welch Two Sample t-test
##
## data:  age.pos and age.neg
## t = 4, df = 295, p-value = 6e-05
## alternative hypothesis: true difference in means is not equal to 0
## 99 percent confidence interval:
##  1.49 6.74
## sample estimates:
## mean of x mean of y
##      56.8      52.6
```

Hypothesis testing

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- The function `t.test()` uses by default the Welch *t*.test, with Welch-Satterthwaite correction for degrees of freedom.
- When the variances are equal, we can use

```
t.test(age.pos, age.neg, mu = 0,  
       var.equal = TRUE)
```

- The test for equal variances is

```
var.test(age.pos, age.neg, mu = 0, ratio = 1)
```

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Power calculation

Having rejected the null hypothesis, we compute the power of the test under the alternative

$$H_1 : \text{age.pos} - \text{age.neg} = 2.5$$

A power calculation needs four parameters, α , sd , n (sample size), δ (true difference in mean). It must also specify whether the test is one sided or two sided.

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Power calculation

```
power.t.test(n = nrow(cleve), sd =  
  sqrt(var(age.pos)+var(age.neg)),  
  sig.level = .05, delta = 2.5,  
  alternative = "two.sided"  
)
```

Hypothesis testing

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Power calculation

```
##  
##      Two-sample t test power calculation  
##  
##              n = 297  
##            delta = 2.5  
##             sd = 12.4  
##    sig.level = 0.05  
##         power = 0.689  
## alternative = two.sided  
##  
## NOTE: n is number in *each* group
```

Hypothesis testing

Power calculation

Compute the sample size needed so that the power of the test is .90, when $\delta = 2.5$; $sd = 12.395$, with $\alpha = .05$ in a two sided alternative:

```
##  
##           Two-sample t test power calculation  
##  
##               n = 518  
##             delta = 2.5  
##             sd = 12.4  
##       sig.level = 0.05  
##             power = 0.9  
##       alternative = two.sided  
##  
## NOTE: n is number in *each* group
```

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Power curve

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```
curve(power.t.test(n=50,delta = x,  
  sd = sqrt(var(age.pos)+var(age.neg)),  
  type="two.sample",  
  alternative="two.sided")$power,  
  from=.1, to=10, xlab="delta",  
  ylab="power")
```

Power curve

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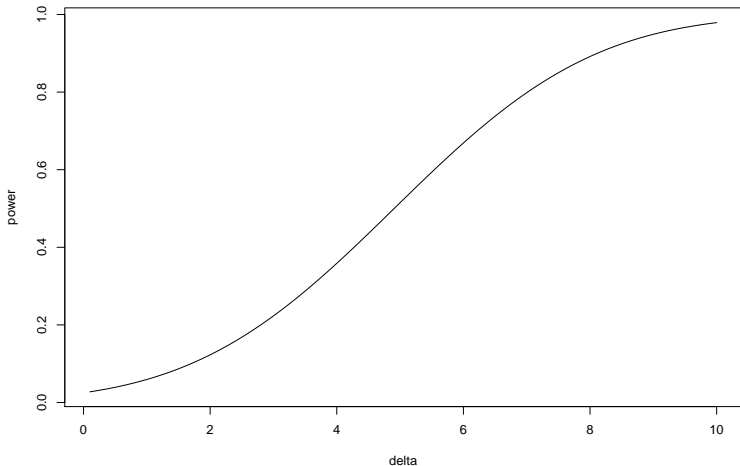
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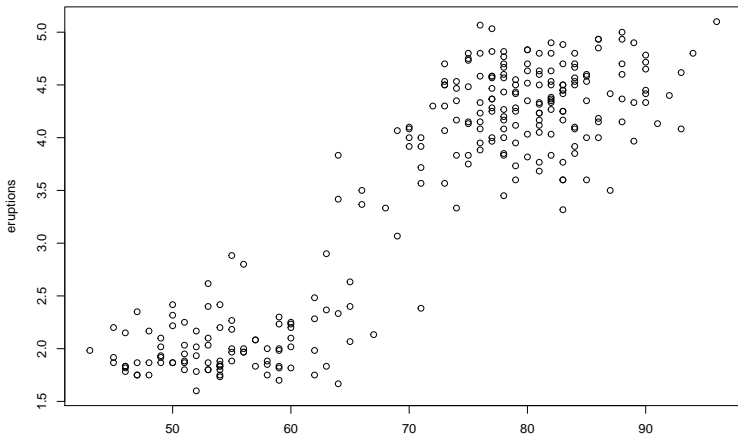
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Linear regression models

Simple linear regression model

```
attach(faithful)
plot(waiting, eruptions)
```



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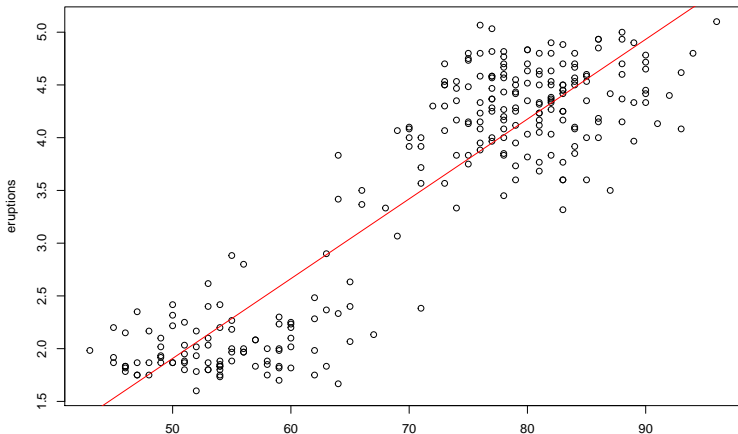
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Simple linear regression model

```
plot(waiting, eruptions)
abline(lm(eruptions ~ waiting), col = "red")
```



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Let us consider the model

$$eruptions = \beta_0 + \beta_1 waiting + u$$

```
slrm <- lm(eruptions ~ waiting, data = faithful)
```

Simple linear regression model

```
summary(slmr)
```

```
##  
## Call:  
## lm(formula = eruptions ~ waiting, data = faithful)  
##  
## Residuals:  
##      Min       1Q   Median       3Q      Max   
## -1.2992 -0.3769  0.0351  0.3491  1.1933   
##  
## Coefficients:  
##              Estimate Std. Error t value Pr(>|t|)      
## (Intercept) -1.87402     0.16014   -11.7   <2e-16 *      
## waiting      0.07563     0.00222    34.1   <2e-16 *      
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##
```

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Estimation

Estimate *eruptions*, when *waiting* = 90.

```
eruptions.fit.coef <- coefficients(slrn)
```

```
c <- c(1,90)
```

```
eruptions.fit.coef %*% c
```

```
##      [,1]
```

```
## [1,] 4.93
```

Simple linear regression model

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Confidence interval

Find a 99% confidence interval for *eruptions*, when *waiting* = 90.

```
predict.lm(slm, data.frame(waiting = 90),  
           interval = "confidence",  
           level = .99)
```

```
##      fit lwr  upr  
## 1 4.93 4.8 5.07
```

Simple linear regression model

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Prediction interval

Find a 99% confidence interval for a prediction of *eruptions*, when *waiting* = 90.

```
predict.lm(slm, data.frame(waiting = 90),  
           interval = "prediction",  
           level = .99)
```

```
##      fit  lwr  upr  
## 1 4.93 3.64 6.23
```

Multiple linear regression

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Consider the data **hsb2.csv**, which is in the Documentation of the workshop.

The description of the variables can be found [here](#).

Estimate the standardized math score by race:

$$math = \beta_0 + \beta_1 race + u.$$

The variable *race* is **categorical**.

Multiple linear regression

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```
hsb2 <- read.csv("hsb2.csv")
m1 <- lm(math ~ factor(race), data = hsb2)
summary.m1 <- summary(m1)
typeof(summary.m1)

## [1] "list"
```

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```
summary.m1$coefficients
```

##	Estimate	Std. Error	t value	Pr(> t)
## (Intercept)	47.417	1.82	26.018	1.72e-65
## factor(race)2	9.856	3.25	3.032	2.76e-03
## factor(race)3	-0.667	2.70	-0.247	8.05e-01
## factor(race)4	6.556	1.97	3.332	1.03e-03

Multiple linear regression

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Vectorization

```
summary.m1$coefficients[2,]
```

##	Estimate	Std. Error	t value	Pr(> t)
##	9.85606	3.25084	3.03185	0.00276

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Factor interaction

Estimate the standardized math score for gender, race.

R code

```
m2 <- lm(math ~ female*factor(race), data = hsb2)
summary.m2 <- summary(m2)
```

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Factor interaction

Standardized math score for gender, race.

Result

```
summary(m2)$coefficients
```

##	Estimate	Std. Error	t value	P
## (Intercept)	49.23	2.49	19.760	3
## female	-3.96	3.68	-1.076	2
## factor(race)2	9.44	5.75	1.640	1
## factor(race)3	-3.95	4.21	-0.937	3
## factor(race)4	4.96	2.72	1.824	6
## female:factor(race)2	2.04	7.11	0.287	7
## female:factor(race)3	6.21	5.59	1.111	2
## female:factor(race)4	3.55	3.97	0.893	3

In-sample and out-of-sample validation

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We randomly split the data and use one set to estimate the model and the rest to estimate the goodness of fit. To ensure reproducibility, we set the RNG seed to `set.seed(13)`.

```
set.seed(13)
TrainRows <- sample(1:nrow(hsb2),
                    .8*nrow(hsb2), replace = FALSE)
Train <- hsb2[TrainRows,]
Valid <- hsb2[-TrainRows, ]
linmodel.Train <-
  lm(math ~ female*factor(race), data = Train)
mathPredic <-
  predict(linmodel.Train, Valid)
actual.predic <-
  data.frame(cbind(actual = Valid$math,
                    predicted = mathPredic))
```

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Correlation matrix

```
corr.accuracy <- cor(actual.predic)
corr.accuracy
```

##	actual	predicted
## actual	1.000	0.278
## predicted	0.278	1.000

In-sample and out-of-sample validation

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Accuracy: Min-Max

The Min-Max method compute the mean of the minimum over the mean of the maximum.

Values very close to 1 (Min-Max > .90) denotes excellent accuracy.

R code

```
min.max.accuracy <-  
  mean(apply(actual.predic,  
              1, min)/apply(actual.predic, 1, max))  
min.max.accuracy  
## [1] 0.863
```

In-sample and out-of-sample validation

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Accuracy: Mean Absolute Error (MAE)

If A_i are the actual (observed) values of the response and F_i are the forecast ones, then

$$MAE = \frac{1}{n} \sum_{i=1}^T |A_i - F_i|;$$

T is the sample size.

R code

```
mae <- mean(abs((actual.predic$predicted -  
                actual.predic$actual)))  
  
mae  
  
## [1] 7.94
```

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Accuracy: Mean Absolute Percentage Error (MAPE)

The mean absolute percentage error (MAPE) is defined as

$$MAPE = \frac{1}{n} \sum_{i=1}^T \left| \frac{A_i - F_i}{A_i} \right|.$$

- Mape can be interpreted as the average percentage error.
- Sometimes, MAPE can be very large, enve though the forecast is reasonably good. If, e.g., $A_i \approx 10^{-3}$ and $|F_i - A_i| \approx 10^{-1}$, entonces

$$\left| \frac{A_i - F_i}{A_i} \right| \approx 10^2$$

- If the forecast is exact, then $MAPE = 0$.

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MAPE: R code

```
mape <- mean(  
  abs((actual.predic$predicted -  
        actual.predic$actual))/actual.predic$actual)  
mape
```

```
## [1] 0.159
```

On the average, the error is of about 16%.

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The library `lmtest` permits to run tests to determine

- heteroskedasticity;
- serial autocorrelation;
- normality of errors, and
- correct specification of the model (RESET)

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Heteroskedasticity

The underlying hypothesis test is

H_0 : the model is homoskedastic

H_1 : the model is heteroskedastic

Function `bptest()`

Apply the function `bptest()` to the fitted model.

```
library(lmtest)
```

```
bptest(m2)
```

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Heteroskedasticity

```
bptest(m2)
```

```
##
```

```
## studentized Breusch-Pagan test
```

```
##
```

```
## data: m2
```

```
## BP = 12, df = 7, p-value = 0.1
```

```
There is no evidence of heteroskedasticity.
```

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Serial autocorrelation

The purpose of the test is to determine whether there is any linear dependence among terms of the innovations.

We can apply the Durbin-Watson test, `dwtest()`, and the Breusch-Godfrey test, `bgtest()`.

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Serial autocorrelation

```
dwtest(m2)
```

```
##
```

```
## Durbin-Watson test
```

```
##
```

```
## data: m2
```

```
## DW = 2, p-value = 0.5
```

```
## alternative hypothesis: true autocorrelation is gr
```

Result

There is no evidence that $\text{corr}(u_t, u_{t-1}) \neq 0$.

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Serial autocorrelation

```
bgtest(m2, order = 10)
```

```
##
```

```
## Breusch-Godfrey test for serial correlation of order
```

```
##
```

```
## data: m2
```

```
## LM test = 15, df = 10, p-value = 0.1
```

Result

There is no evidence of linear dependence among the first 10 terms of the innovations.

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Normality

There are several normality test available.

- The Shapiro-Wilk test is available in the **base** library (loaded by default), but it cannot be applied to vectors with more than 5,000 observations.
- The Jarque-Bera test is available in the library **tseries**:

```
library(tseries)
```

- The normality of errors is less of a concern when the sample size is sufficiently large.

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Normality: Shapiro-Wilk test

```
shapiro.test(m2$residuals)
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: m2$residuals
```

```
## W = 1, p-value = 0.06
```

Conclusion

There is no evidence of non-normality of errors.

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Jarque-Bera test

```
jarque.bera.test(m2$residuals)
```

```
##
```

```
## Jarque Bera Test
```

```
##
```

```
## data: m2$residuals
```

```
## X-squared = 3, df = 2, p-value = 0.3
```

Conclusion

There is no evidence of non-normality of errors.

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RESET

In this case the test is not very important, as there are only factors as regressors.

R code

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```
resettest(m2, type = "fitted", power = 2:3)
```

```
##
```

```
## RESET test
```

```
##
```

```
## data: m2
```

```
## RESET = 0, df1 = 2, df2 = 190, p-value = 1
```

```
resettest(m2, type = "regressor", power = 2:3)
```

```
##
```

```
## RESET test
```

```
##
```

```
## data: m2
```

```
## RESET = 0, df1 = 2, df2 = 190, p-value = 1
```

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Plots

We can also apply `plot()` to a `lm()` object to obtain these tests.

It is an interactive plot and it is convenient to do it in the console.

```
plot(m2)
```

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```
modelo.logit <- glm(diagnostic ~ chol + age,  
                    data = cleve,  
                    family = "binomial")  
  
# summary(modelo.logit)  
probs.predicted <- predict(modelo.logit,  
                             type = "response")
```

Logit model

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```
mu <- mean(cleve$diagnostic)
probs.predicted2 <-
  ifelse(probs.predicted > mu, 1, 0)
table(cleve$diagnostic,
      probs.predicted2)/nrow(cleve)
```

```
##      probs.predicted2
##           0         1
##  0 0.323 0.215
##  1 0.148 0.313
```


Logit model

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```
probs.predicted3 <-  
  ifelse(probs.predicted > .5, 1, 0)  
table(cleve$diagnostic,  
      probs.predicted3)/nrow(cleve)
```

```
##      probs.predicted3  
##           0         1  
##  0 0.374 0.165  
##  1 0.226 0.236
```

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Libraries

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Needed libraries are `forecast`, `tseries`.

Download them,

```
install.packages("forecast", "tseries")
```

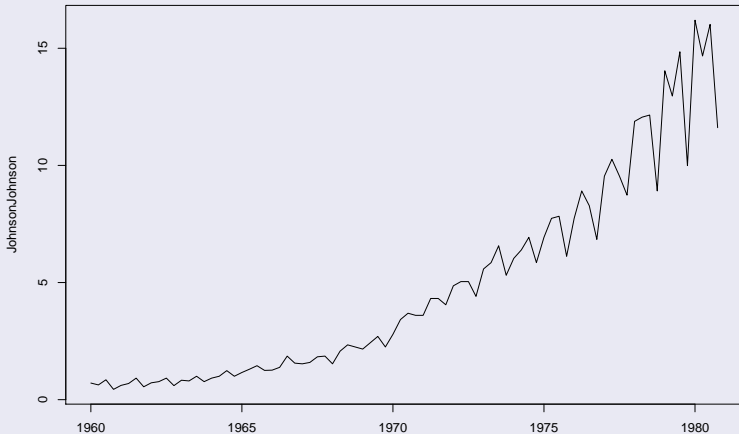
and then load them in your session

```
library(forecast)  
library(tseries)
```

Time series

Plots (Multiplicative model)

```
plot.ts(JohnsonJohnson)
```



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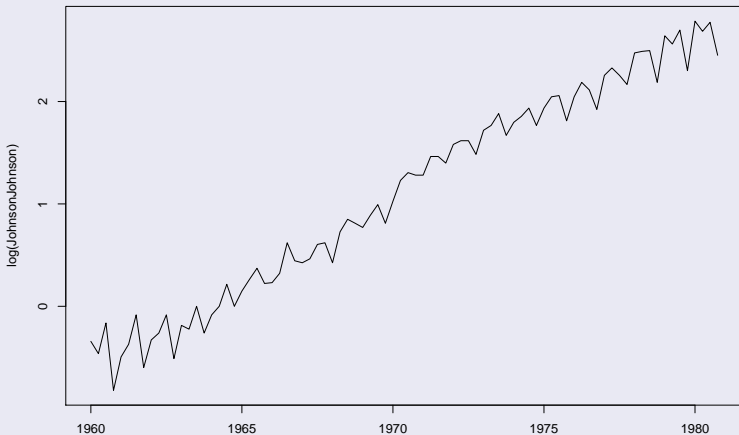
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Plots (Additive model)

```
plot.ts(log(JohnsonJohnson))
```



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Let y_t be a stochastic process.

The idea of exponential smoothing is to compute the *one-step ahead forecast*, $\hat{y}_{T+1|T}$, as a weighted mean of the previous observed terms:

$$\begin{aligned}\hat{y}_{T+1|T} &= \alpha y_T + \alpha(1 - \alpha)y_{T-1} + \cdots \\ &= \alpha y_T + (1 - \alpha)\hat{y}_{T|T-1}, \quad 0 \leq \alpha < 1;\end{aligned}$$

rearranging terms,

$$\hat{y}_{t+1|t} = \alpha y_t + (1 - \alpha)\hat{y}_{t|t-1},$$

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which gives

$$\begin{aligned}\hat{y}_{t+1|t} &= \alpha y_t + (1 - \alpha)\hat{y}_{t|t-1} = \hat{y}_{t|t-1} + \alpha(y_t - \hat{y}_{t|t-1}) \\ &= \hat{y}_{t|t-1} + \alpha e_t,\end{aligned}$$

where $e_t = y_t - \hat{y}_{t|t-1}$ is the forecast error.

The value α is estimated optimizing the errors squared.

The work by Holt & Winters allowed the inclusion of seasonal, s_t , and trending, b_t , terms, beside the level term, ℓ_t .

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Holt-Winters Modeling (Additive model)

$$y_{t+h|t} = \ell_t + hb_t + s_{t-m+h_m^+}$$

$$\ell_t = \alpha(y_t - s_{t-m}) + (1 - \alpha)(\ell_{t-1} - b_{t-1})$$

$$b_t = \beta^*(\ell_t - \ell_{t-1}) + (1 - \beta^*)b_{t-1}$$

$$s_t = \gamma(y_t - \ell_{t-1} - b_{t-1}) + (1 - \gamma)s_{t-m}$$

where m denotes the seasonality period (per year)

The symbol

$$h_m^+ = \lfloor (h - 1) \bmod(m) \rfloor + 1$$

makes sure that the estimation of the seasonality is the last year of the sample.

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Estimation

```
logJJ.forecast <- HoltWinters(  
  log(JohnsonJohnson), beta = TRUE, gamma = TRUE)  
logJJ.forecast
```

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Estimation

```
logJJ.forecast$coefficients[1]
```

```
##      a
```

```
## 2.61
```

```
logJJ.forecast$SSE # measure of estimate error
```

```
## [1] 0.661
```

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Plots

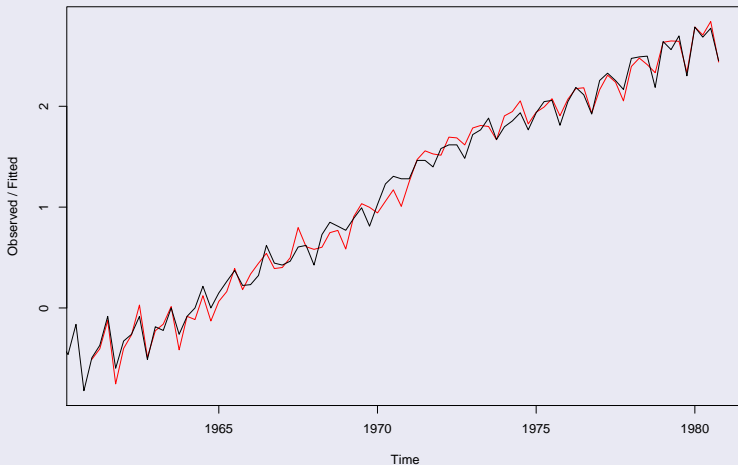
```
plot(logJJ.forecast)
```

The original series is plotted in black and the forecast is in red.

Exponential smoothing

Plots

Holt-Winters filtering



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Estimate with an initial value

```
logJJ.forecast2 <- HoltWinters(  
  log(JohnsonJohnson), beta = TRUE, gamma =  
    TRUE, l.start = .91) # arbitrary initial value  
logJJ.forecast2
```

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Estimate with an initial value

```
logJJ.forecast2$coefficients[1]
```

```
##      a
```

```
## 2.68
```

```
logJJ.forecast$coefficients[1]
```

```
##      a
```

```
## 2.61
```

```
logJJ.forecast$SSE # measure of estimate error
```

```
## [1] 0.661
```

```
logJJ.forecast2$SSE
```

```
## [1] 6.01
```

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Comparing plots

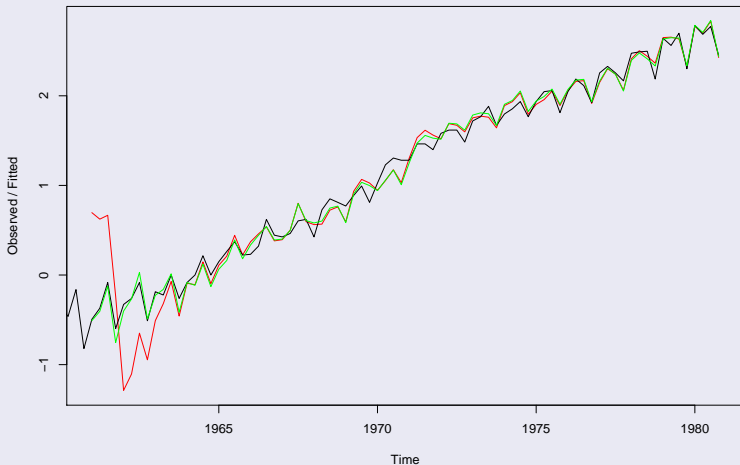
```
plot(logJJ.forecast2)  
lines(logJJ.forecast$fitted[,1], col = "green")
```

The object is a matrix whose columns are, respectively, the fitted time series; its level part; its trend part and the seasonality. We select above the fitted part.

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Comparing plots

Holt-Winters filtering



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Forecast

Forecast can be performed using the library **forecast**

```
library(forecast)
```

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Forecast

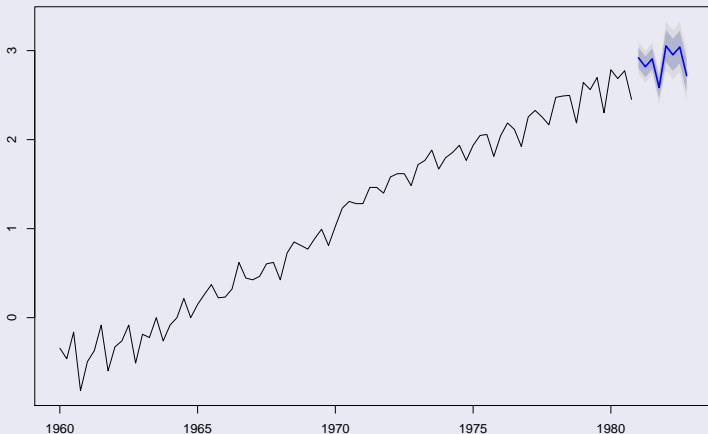
```
logJJ.forecast8095 <- forecast.HoltWinters(logJJ.fore
```

- We use the first estimate, `logJJ.forecast`, as it is proven to be the better.
- The parameter `h=8` will forecast the estimate **eight** periods in the future (two years).
- The forecast also plots a confidence interval (80%; 95% is the default).

Exponential smoothing

Forecast: Plot

Forecasts from HoltWinters



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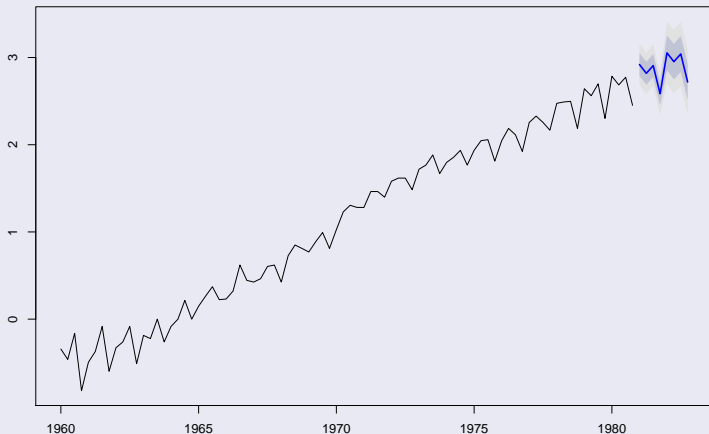
Forecast: Plot

```
logJJ.forecast8599 <- forecast(  
  logJJ.forecast, h=8, level = c(85,99))  
plot(logJJ.forecast8599)
```

Exponential smoothing

Forecast: Plot

Forecasts from HoltWinters



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Diagnostics

```
library(tseries)
ts8095.fitted <- as.ts(logJJ.forecast8095$fitted)
ts8095.fitted <- na.omit(ts8095.fitted)
ts8095.residuals <- as.ts(logJJ.forecast8095$residuals)
ts8095.residuals <- na.omit(as.ts(logJJ.forecast8095$residuals))
```

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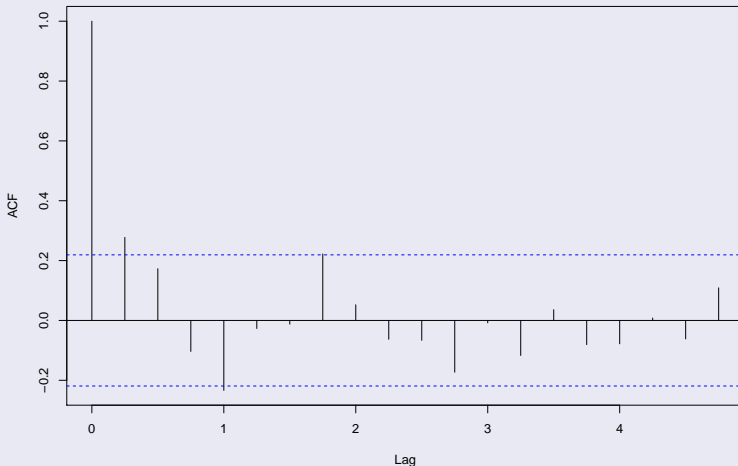
Diagnostics: ACF

```
acf(ts8095.residuals)
```

Exponential smoothing

Diagnostics: ACF

Series ts8095.residuals



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Exponential smoothing

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to R

Lino AA
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Introduction
to R(Studio)

Data Types
and Data
Structure

Working with
a Dataframe

Preliminary
analysis

Statistical
Inference

Linear
regression
models

Logit models

Time series

Diagnostics: Ljung-Box Test

```
Box.test(ts8095.residuals, lag = 20)

##
##   Box-Pierce test
##
## data:  ts8095.residuals
## X-squared = 25, df = 20, p-value = 0.2
```

Conclusion

We do not reject the null hypothesis of no autocorrelation (for the first 20 lags).

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Diagnostics: Augmented Dickey-Fuller Test

```
adf.test(ts8095.fitted)

##
##   Augmented Dickey-Fuller Test
##
## data:   ts8095.fitted
## Dickey-Fuller = -1, Lag order = 4, p-value = 0.8
## alternative hypothesis: stationary
```

Conclusion

There is evidence that the errors are not white noise.

Box-Jenkins approach

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See the script `BoxJenkins.R`