



MAX PLANCK INSTITUTE FOR **BIOLOGY OF AGEING**



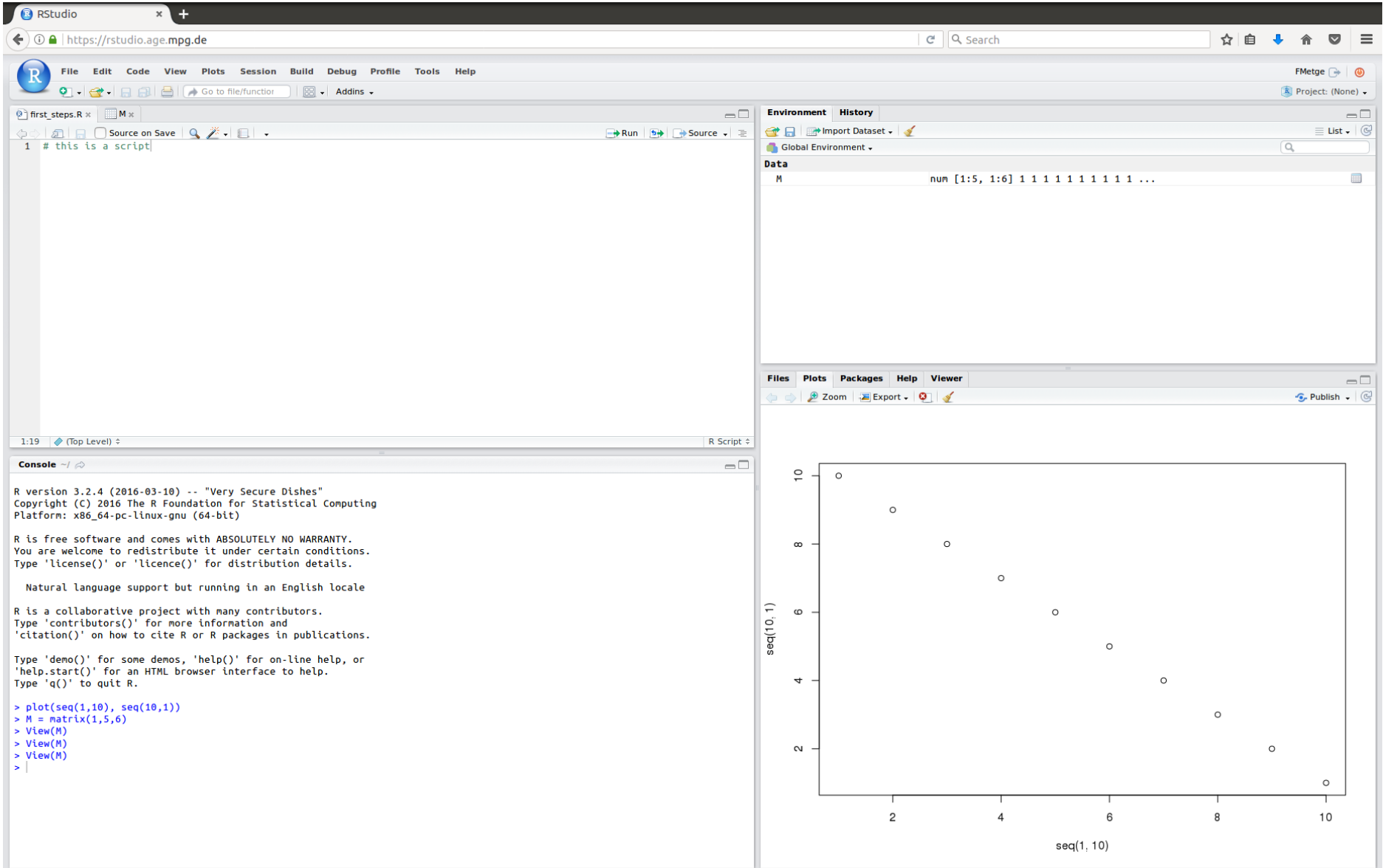
Introduction to R

bioinformatics@age.mpg.de

Outline

- 1) Introduction to R Studio
- 2) Overview over basic data types
- 3) Overview over basic functions
- 4) How to get help
- 5) Read in data
- 6) Basic table functions
- 7) Basic table manipulation
- 8) Loops and if queries

END OF DAY 1



Reinforce what you have learned in the online tutorial

Basic calculations:

- Add 5 and 7

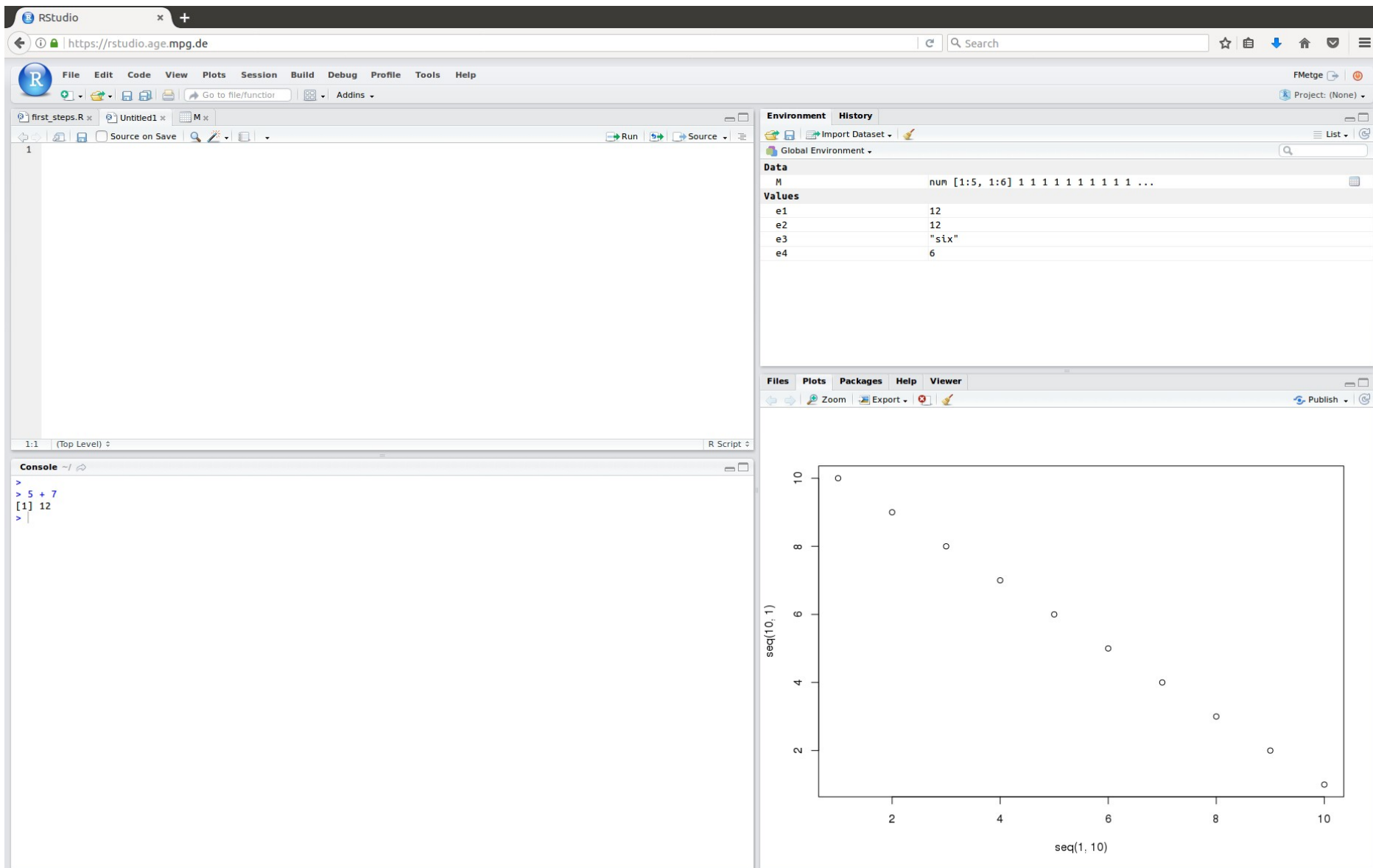
- Divide the results by 2

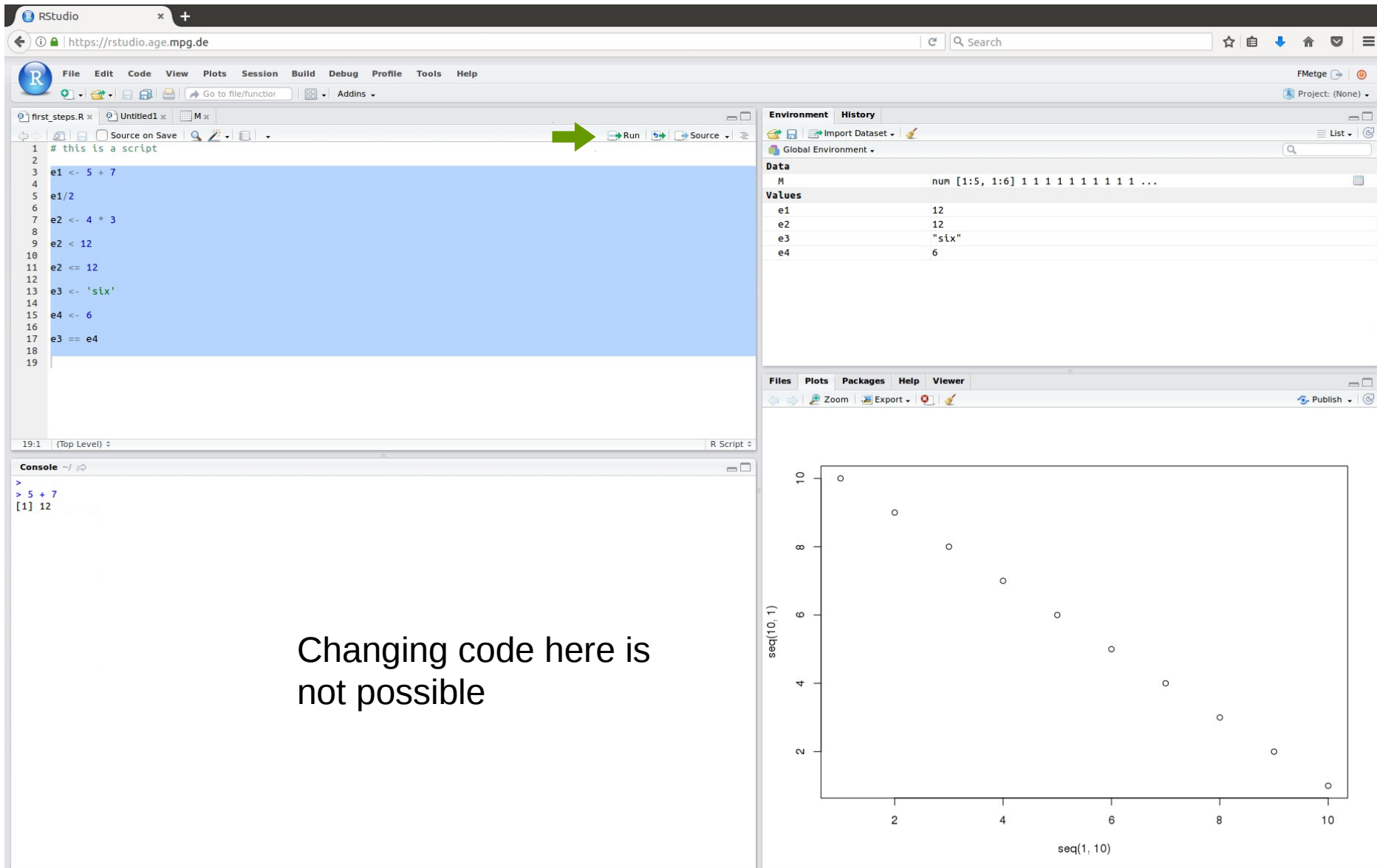
- Multiply 4 and 3

- Test if the result is smaller than 12

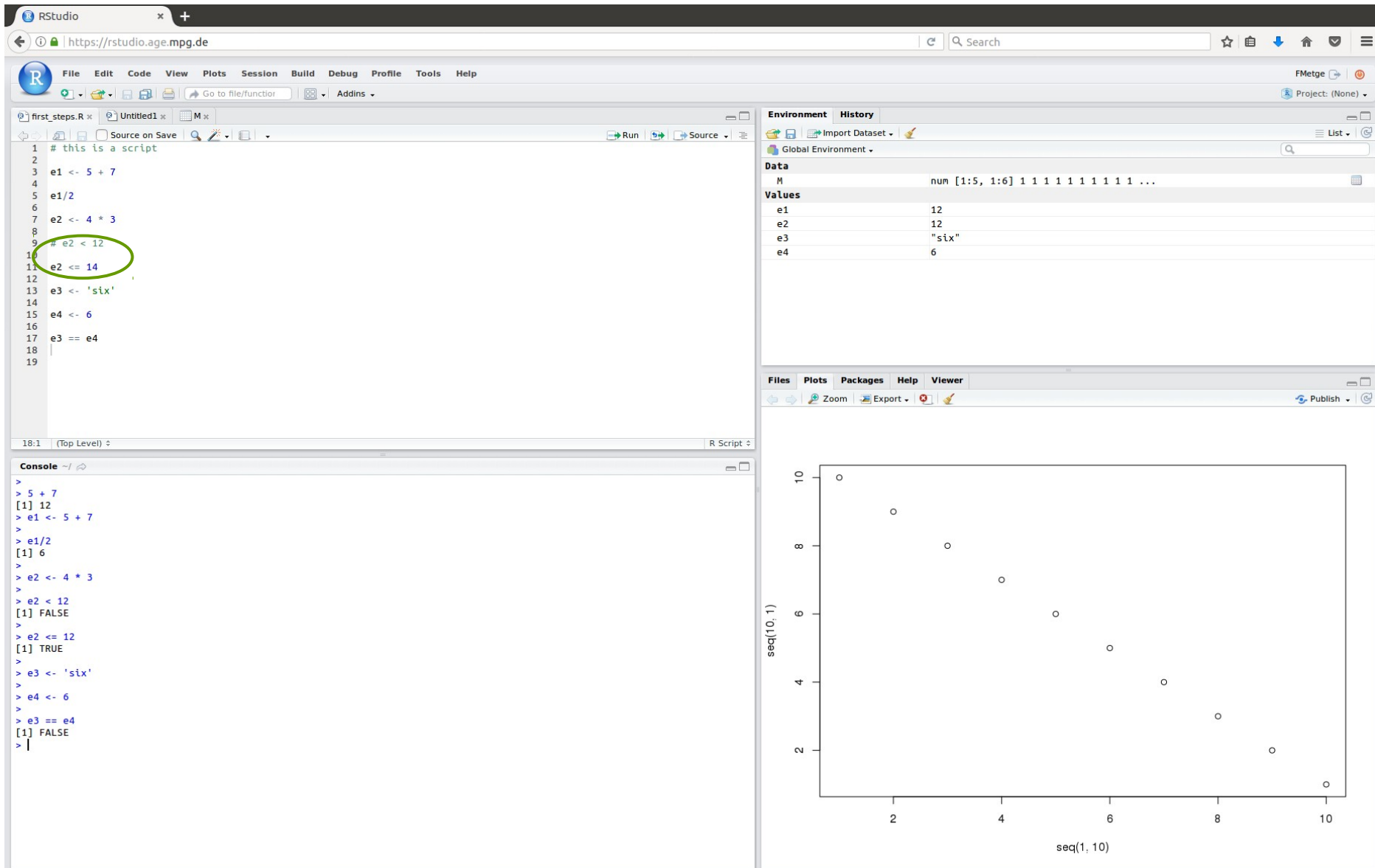
Create one variable with six as character and one with 6 as number

Compare if both variables are the same





Changing code here is
not possible



RStudio interface showing a script, environment, console, and a plot.

Script Editor: The script contains the following R code:

```
1 # this is a script
2
3 e1 <- 5 + 7
4
5 e1/2
6
7 e2 <- 4 * 3
8
9 # e2 < 12
10
11 e2 <= 14
12
13 e3 <- 'six'
14
15 e4 <- 6
16
17 e3 == e4
18
19
```

Environment: The environment shows the following values:

Variable	Value
e1	12
e2	12
e3	"six"
e4	6

Console: The console shows the execution of the script:

```
> e2 < 12
[1] FALSE
> e2 <= 12
[1] TRUE
> e3 <- 'six'
> e4 <- 6
> e3 == e4
[1] FALSE
```

Plot: A scatter plot titled 'seq(10, 1)' showing the relationship between 'seq(1, 10)' on the x-axis and 'seq(10, 1)' on the y-axis. The plot displays a decreasing trend, with points approximately at (1, 10), (2, 9), (3, 8), (4, 7), (5, 6), (6, 5), (7, 4), (8, 3), (9, 2), and (10, 1).

In the future, code will displayed this way

```
# this is code  
> 3+7  
[10]
```

Basic data types

- Numeric

```
> x <- 10.5 # or x <- 10
```

- Integer

```
> x <- as.integer(2)
```

- Complex

```
> x <- 1 + 2i  
> sqrt(-1) # NaN  
> sqrt(as.complex(-1)) # 0+1i
```

- Logical

```
> x <- TRUE; FALSE; T; F
```

- Character

```
> apple <- "Apple"  
> x <- "6"
```

Useful functions

- Find out type of a variable

```
> class(x)
> typeof(x)
```

- Test if variable is of a certain type

```
> is.numeric(x)
> is.logical(x)
```

- Force a variable to be in a certain type

```
> as.numeric(x)
> as.character(x)
> as.integer(5.7)      # 5
> as.integer("apple")  # NA
> as.integer(TRUE)     # 1
```

More complex data structures (Vector)

A vector is a sequence of elements of the same basic type

```
> # numerical vector
> a <- c(2, 3, 4)

> # logical vector
> b <- c(TRUE, FALSE, TRUE)

> # character vector
> c <- c("apple", "six")

> # mixed vector?
> d <- c("six", a, 5)

> length(d)
```

More complex data structures (Matrix)

A matrix is a collection of elements of the same data type arranged in a two-dimensional rectangular layout.

```
> # 3 columns, fill matrix column wise (default)
> A <- matrix(c(2,3,4,5,6,7), ncol = 3)

> # 2 rows, fill matrix row wise
> A <- matrix(c(2,3,4,5,6,7), nrow = 2, byrow = T)

> # alternative matrix generation
> B <- matrix(1, 2, 3)
> C <- matrix(NA, 3, 2)

> # transpose a matrix
> t(A)

> # concatenate two matrices row or column wise
> D <- cbind(A, B) # rbind(A, B)
```

More complex data structures (List)

A list is a generic vector containing objects of the same or different data types

```
> n = c(2, 3, 5)
> s = c("aa", "bb", "cc", "dd")
> b = c(TRUE, FALSE, TRUE)

> # list without names
> x = list(n, s, b)

> # same list with names
> xn = list(Numbers = n, Strings = s, Boolean = b)

> # access list elements
> x[2] # vs. x[[2]]
> xn$Strings # vs. xn["Strings"] or xn[["Strings"]]
```

More complex data structures (Data Frame)

A data frame is list of vectors of equal length organized in rows and columns

```
> n = c(2, 3, 5)
> s = c("aa", "bb", "cc")
> b = c(TRUE, FALSE, TRUE)

> # data frame without names
> df = data.frame(n, s, b)

> # data frame with column names
> names(df) <- c("Numbers", "Strings", "Boolean")
> dfn = data.frame(Numbers = n, Strings = s, Boolean = b)

> # access elements in a data frame
> dfn$Numbers # whole first column
> dfn[,1]     # whole first column
> dfn[2,3]    # second element of the third column
```

5min Break

Basic functions

- Sum

```
> M = matrix(c(5,6,7,8), 2)
> sum(M)          # 26
> rowSums(M)      # 12 14
> colSums(M)      # 11 15
```

- Mean

```
> mean(M)         # 6.5
> rowMeans(M)     # 6 7
> colMeans(M)     # 5.5 7.5
```

- Variation and standard deviation

```
> var(as.numeric(M)) # 1.67
> sd(M)              # 1.29
```

Basic functions

- Median

```
> mean(c(5,6,7,89))      # 26.75  
> median(c(5,6,7,89))    # 6.5
```

- Quantiles

```
> quantile(c(5,6,7,89), probs  
           = c(.25, .5, .75))  
#   25%   50%   75%  
# 5.75  6.50 27.50
```

Basic functions

- Sequence

```
> seq(from = 1, to = 10, by = 1)
[1] 1 2 3 4 5 6 7 8 9 10
```

- Repeat

```
> rep(x = NA, times = 3)
[1] NA NA NA
> rep(c(0,1), 5)
[1] 0 1 0 1 0 1 0 1 0 1
```

- Random Numbers

```
> rnorm(n = 5, mean = 5, sd = 1)
[1] 4.62 5.46 6.58 4.60 5.42
> runif(n = 5, min = 1, max = 5)
[1] 1.46 1.07 3.55 4.96 3.28
```

Distribution	R function
Normal	rnorm(n, mean, sd)
Uniform	runif(n, min, max)
Binomial	rbinom(n, size, prob)
Beta	rbeta(n, shape1, shape2, ncp)
Exponential	rexp(n, rate)
Poisson	rpois(n, lambda)
Chi^2	rchisq(n, df, ncp)
Student's t	rt(n, df, ncp)
...	

How to get help (inside R)

- If you have a rough idea what the function might be called

```
> ??rowmean
```

- If you know what the function is called

```
> ?seq
```

All R help functions are structured the same way:

Description	A short overview of what the function intends to do
Usage	How to call this function and which arguments may be supplied. The order of arguments is meaningful
Arguments	A detailed description of the arguments that are passed to the function
Details	A more or less detailed description of the function
Value	The value which is returned by the function
References/See Also	Citation and related functions
Examples	Different examples on how to use the function

How to get help (outside R)

The screenshot shows a Google search for "R column wise means". The search results include:

- colSums**
<https://stat.ethz.ch/R-manual/R-devel/library/.../colSums.html> ▾ Diese Seite übersetzen
integer: Which dimensions are regarded as 'rows' or 'columns' to sum over. For row*, the sum or mean is over dimensions dims+1, ... ; for col* it is over ...
- R: Form Row and Column Sums and Means**
<https://astrostatistics.psu.edu/su07/R/html/base/html/colSums.html> ▾ Diese Seite übersetzen
colSums(x, na.rm = FALSE, dims = 1) rowSums(x, na.rm = FALSE, dims = 1) colMeans(x, na.rm = FALSE, dims = 1) rowMeans(x, na.rm = FALSE, dims = 1) ...
- dataframe - calculate the mean for each column of a matrix in R - Stack ...**
<https://stackoverflow.com/.../calculate-the-mean-for-each-column...> ▾ Diese Seite übersetzen
16.02.2014 - You can use colMeans : ### Sample data set.seed(1) m <- data.frame(matrix(sample(100, 20, replace = TRUE), ncol = 4)) ### Your error ...
- r - Calculate row means on subset of columns - Stack Overflow**
<https://stackoverflow.com/.../calculate-row-means-on-subset-of-c...> ▾ Diese Seite übersetzen
08.06.2012 - Calculate row means on a subset of columns: Create a new data.frame which specifies the first column from DF as an column called ID and ...

At the bottom left, there is a small box with the text "R column v".

stackoverflow.com

5min Break

Read in data

Table

```
> D = read.table("mouse.tab", as.is = T, header = F )
```

CSV

```
> D = read.csv("mouse.csv", as.is = T, header = T)  
> # default separator ",", decimals as "."
```

EXCEL

- Not in the standard library, but various packages are available

```
> library(xlsx)  
> D = read.xlsx("mouse.xlsx", sheetName = "first")
```

script

```
> source("test_table_script.R")  
> ls()
```

RStudio

https://rstudio.age.mpg.de

140%

Search

☆

📁

⬇

🏠

📧

☰

File Edit Code View Plots Session Build Debug Profile Tools Help

FMetge

Project: (None)

first_steps.R * analyse_mouse_data.R * M * test_table_script.R * Experiment1 *

Filter

	mouseID	cage	sex	weight	lifespan	treatment
1	mouse_1	18	f	21.17279	78.32947	1
2	mouse_2	6	m	23.83484	82.03214	1
3	mouse_3	8	f	19.07602	83.61970	1
4	mouse_4	11	m	25.06987	82.75583	1
5	mouse_5	18	f	18.30442	80.61941	1
6	mouse_6	4	m	25.86508	69.15672	1
7	mouse_7	18	f	18.07888	80.33831	1
8	mouse_8	18	m	27.43817	72.95142	1
9	mouse_9	13	f	19.24896	79.79750	1
10	mouse_10	12	m	27.51745	70.83524	1
11	mouse_11	2	f	19.38122	74.30991	1
12	mouse_12	4	m	23.54157	73.26933	1
13	mouse_13	4	f	20.03807	75.57698	1

Showing 1 to 14 of 200 entries

Console /beegfs/group_bit/data/projects/departments/Bioinformatics/bit_R_workshop/scripts.FMetge/

> source("test_table_script.R")
>

Environment History

Import Dataset

Global Environment

Data

Experiment1 200 obs. of 6 variables

Values

cage num [1:200] 18 6 8 11 18 4 18 18 13 12 ...

lifespan num [1:200] 78.3 82 83.6 82.8 80.6 ...

mouseID chr [1:200] "mouse_1" "mouse_2" "mouse_3" "mouse_4" "mo...

sex chr [1:200] "f" "m" "f" "m" "f" "m" "f" "m" "f" "m" "f"...

treatment Factor w/ 2 levels "1","2": 1 1 1 1 1 1 1 1 1 1 ...

weight num [1:200] 21.2 23.8 19.1 25.1 18.3 ...

Files Plots Packages Help Viewer

R: Search Results Find in Topic

Search Results

No results found

Basic table functions

Summary

```
> summary(Experiment1)
```

	mouseID		cage	sex	weight	lifespan	treatment	
mouse_1	: 1	Min.	: 1.00	f:100	Min.	:17.48	Min. :60.46	1:100
mouse_10	: 1	1st Qu.	: 6.00	m:100	1st Qu.	:21.41	1st Qu.:71.59	2:100
mouse_100	: 1	Median	:10.00		Median	:24.50	Median :76.17	
mouse_101	: 1	Mean	:10.36		Mean	:24.53	Mean :75.38	
mouse_102	: 1	3rd Qu.	:15.00		3rd Qu.	:27.06	3rd Qu.:79.40	
mouse_103	: 1	Max.	:19.00		Max.	:34.01	Max. :93.09	
(Other)	:194							

Table

```
> table(Experiment1$cage)
```

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
4	11	7	11	10	8	13	14	10	16	8	11	13	13	13	8	11	13	6

Basic table functions

Correlation

```
> cor(Experiment1$cage, Experiment1$weight,  
      method = 'spearman')  
[1] 0.01028674  
> cor(Experiment1$lifespan, Experiment1$weight)  
[1] -0.6827497
```

Wilcoxon Test

```
> wilcox.test(Experiment1$lifespan ~ Experiment1$treatment)  
  
Wilcoxon rank sum test with continuity correction  
  
data: Experiment1$lifespan by Experiment1$treatment  
W = 7296, p-value = 2.037e-08  
alternative hypothesis: true location shift is not equal to 0
```

Basic table functions

Because both groups are normally distributed we can use a t-test

```
> t.test(Experiment1$lifespan ~ Experiment1$treatment)
```

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

```
data: Experiment1$lifespan by Experiment1$treatment
```

```
t = 6.0342, df = 193.78, p-value = 7.972e-09
```

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

```
95 percent confidence interval:
```

```
2.968538 5.851315
```

```
sample estimates:
```

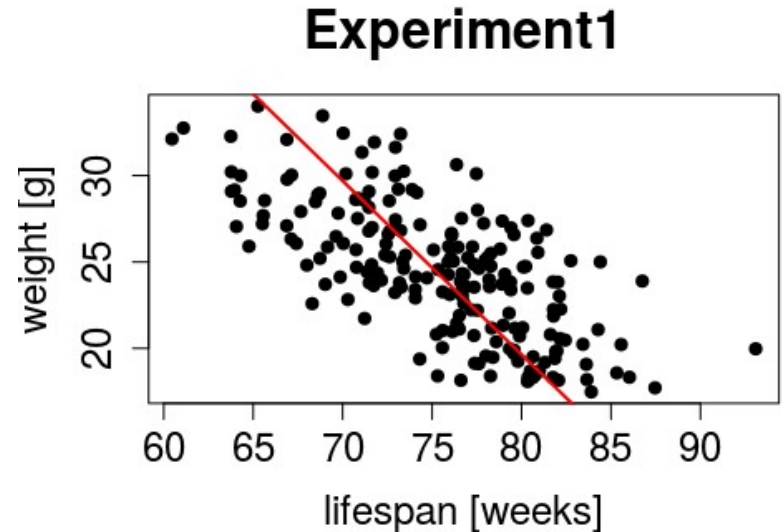
```
mean in group 1 mean in group 2
```

```
77.58123
```

```
73.17130
```

Basic Table functions

```
> plot(Experiment1$lifespan,  
       Experiment1$weight)  
  
> L = lm(Experiment1$lifespan  
       ~ Experiment1$weight)  
  
> L  
  
Call:  
lm(formula = Experiment1$lifespan  
    ~ Experiment1$weight)  
  
Coefficients:  
      (Intercept)  Experiment1$weight  
          100.028             -1.005  
  
> abline(L)
```



Basic table manipulations

You have a second treatment you want to add to the bottom of the existing data frame (rbind)

```
> Experiment <- rbind(Experiment1, Treatment3)
```

You have the body size of each mouse and you want to add it to the left of the existing data frame (cbind)

```
> Experiments <- cbind(Experiment, size)
```

Basic table manipulations

Merge

```
> ExperimentP <- merge(ExperimentS, Exp2,  
  by.x = 'mouseID', by.y = 'mouseID_pupps', all = T)
```

Subset

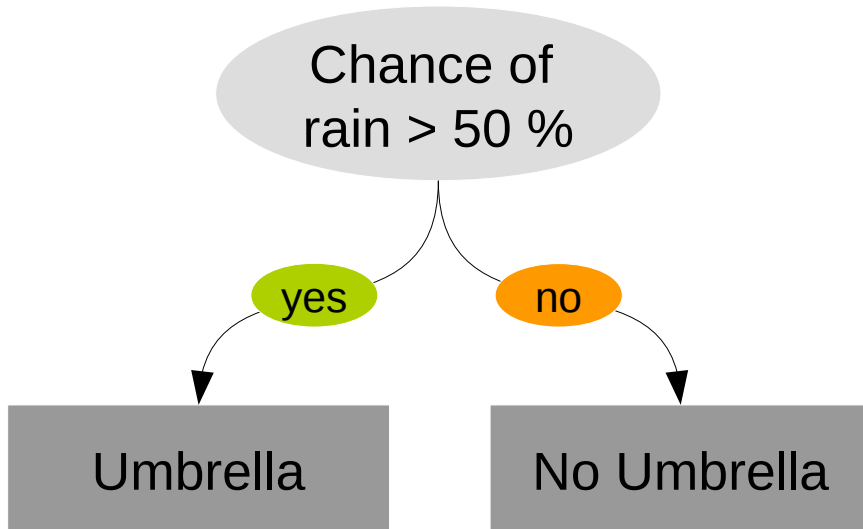
```
> Exp_cage10 <- subset(ExperimentP, cage == 10)  
> Exp_cage10_11 <- subset(ExperimentP,  
  cage %in% c(10, 11))[,1:8]
```

Names

```
> names(Exp_cage10_11)  
[1] "mouseID" "cage" "sex.x" "weight" "lifespan" "treatment" "size" "num_pupps"  
  
> names(Exp_cage10_11)[c(3, 9)] <- "sex"
```

5min Break

Conditional procedures



```
if( condition = True ){  
    – do something  
} else {  
    – do something different  
}
```

```
> chance_of_rain = 0.3  
  
> if(chance_of_rain > 0.5){  
    print("take umbrella")  
} else {  
    print("you don't need an  
        umbrella")  
}  
  
[1] "you don't need an  
    umbrella"
```


if / else if / else

```
> x = 5
> y = NA
> z = 'six'

if(x == 5){
  print("x is equal to 5")
}

if(x < 5){
  print('x is smaller than 5')
}else{
  print('x is equal or larger than 5')
}
```

if / else if / else

```
> x = 5
> y = NA
> z = 'six'

> if(x < 5){
+   print("x is smaller than 5")
+ }else if(x == 5){
+   print("x is equal to 5")
+ }else{
+   print("x is larger than 5")
+ }
```

if / else if / else

```
> x = 5
> y = NA
> z = 'six'

> if(is.na(y)){
+   print("y is not available")
+ }

> if(!is.character(z)){
+   print("z is not a character")
+ } else {
+   print("z is a character")
+ }
```

if / else if / else

```
> a = c(1,2,3)
> b = c(1,2,3)
> c = c(1,3)

> if(a == b){
+   print(paste("a and b agree on", sum(a == b),
+   "elements", sep = ' '))
+ }
[1] "a and b agree on 3 elements" # (warning)

> if(a == c){
+   print(paste("a and c agree on", sum(a == c),
+   "elements", sep = ' '))
+ }
[1] ERROR
```

if / else if / else

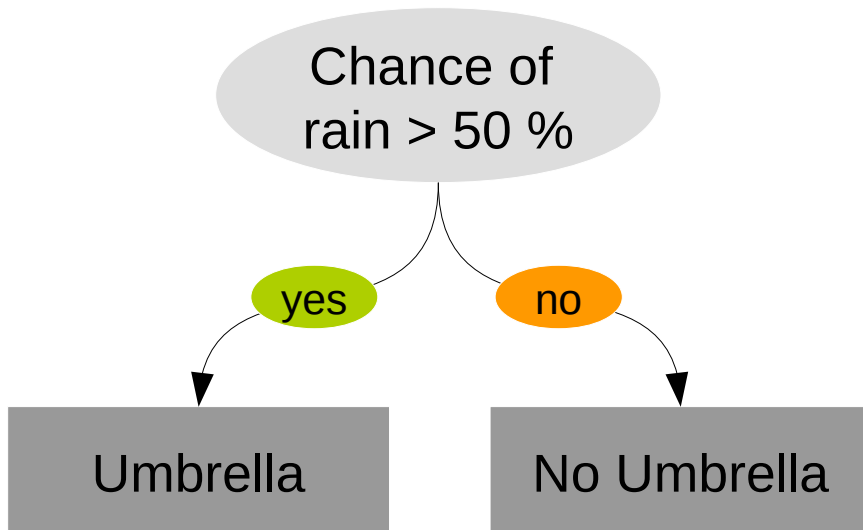
```
> a = c(1,2,3)
> b = c(1,2,3)
> c = c(1,3)

> if(length(a) == length(c) & a == c){
+   print(paste("a and c agree on", sum(a == c),
+     "elements", sep = ' '))
+} else {
+   print("a and c cannot be compared, they differ in length")
+}

> if(length(a) == length(c) && a == c){
+   print(paste("a and c agree on", sum(a == c),
+     "elements", sep = ' '))
+ } else {
+   print("a and c cannot be compared, they differ in length")
+}
```

5min Break

Loops



Köln

Mittwoch, 15:00

Überwiegend sonnig

 28 °C | °F

Niederschlag: 0%

Luftfeuchte: 39%

Wind: 16 km/h

Temperatur

Niederschlag

Wind



Loops

Loops are useful if you want to repeat the same command over and over again

Different type of loops

While loop

- Repeat while condition is true

For loop

- Iterate over index
- No conditional statement

Most procedures can be written as for or while loops. For loops are almost always the safer choice

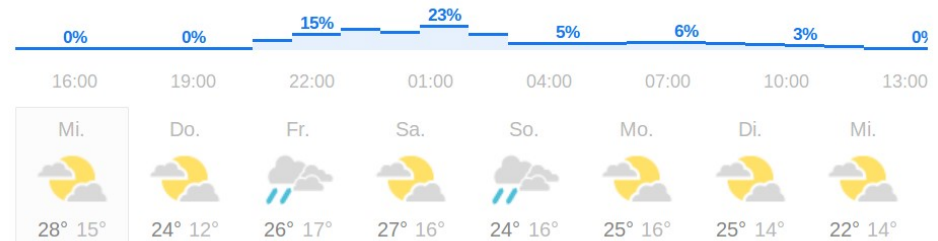
Köln

Mittwoch, 15:00
Überwiegend sonnig

 28 °C | °F

Niederschlag: 0%
Luftfeuchte: 39%
Wind: 16 km/h

Temperatur Niederschlag Wind



Day	1	2	3	4	5	6	7	8
Chance of rain [%]	0	0	15	23	5	6	3	0

For-loop

```
> for(i in something){  
+ do something  
+ }
```

Use if you have a fixed number of iterations

Will almost always finish

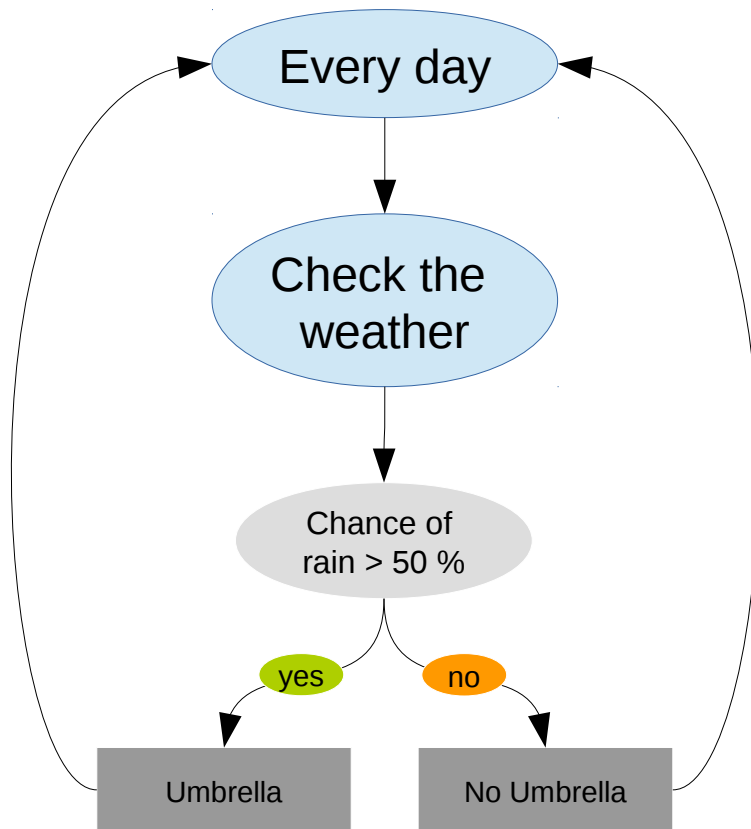
While-loop

```
> while(condition = TRUE){  
+ do something  
+ }
```

Use if you do not know how often you need to repeat something

Could run infinitely

While - loops



day	1	2	3	4	5	6	7	8
check_weather	0	0	15	23	5	6	3	0

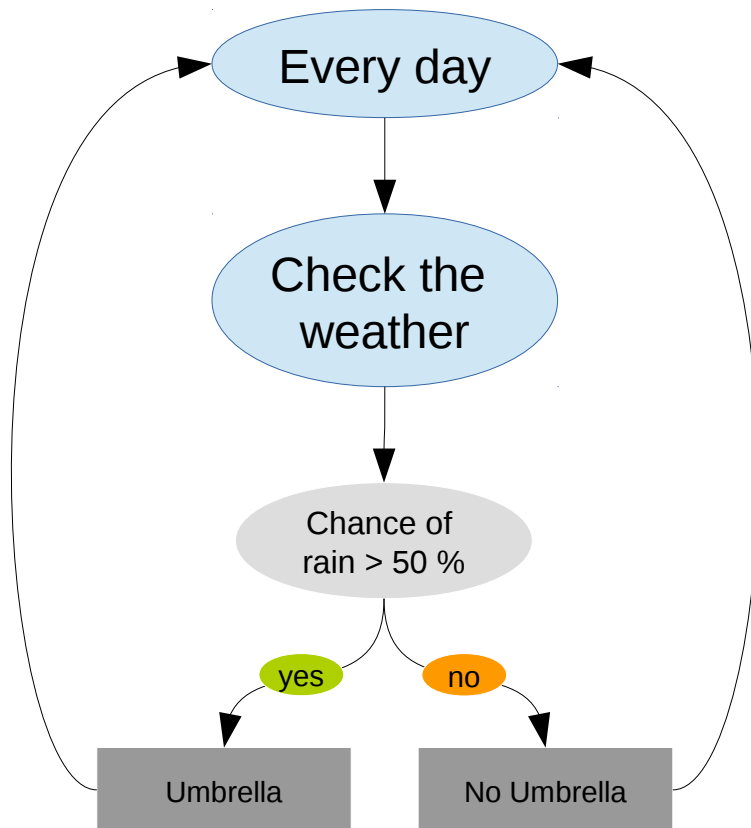
```
> day = 1
> while(day < 9){
+   chance_of_rain =
+       check_weather(day)
+
+   if(chance_of_rain > 10){
+     print("take umbrella")
+   } else {
+     print("you don't need an
+         umbrella")
+   }
+   day = day + 1
+ }
```

```
[1] "you don't need an
    umbrella"
```

```
...
```

```
[8] "you don't need an
    umbrella"
```

For - loops



day	1	2	3	4	5	6	7	8
check_weather	0	0	15	23	5	6	3	0

```
>  
> for(day in 1:8){  
+   chance_of_rain =  
+       check_weather(day)  
+  
+   if(chance_of_rain > 10){  
+       print("take umbrella")  
+   } else {  
+       print("you don't need an  
+         umbrella")  
+   }  
+ }  
+ }
```

```
[1] "you don't need an  
     umbrella"
```

```
...
```

```
[8] "you don't need an  
     umbrella"
```

More examples

for

```
> for(x in 2:4){  
+ print(c(x, x * x))  
+ }  
  
[1] 2 4  
[1] 3 9  
[1] 4 16
```

while

```
> x = 1  
> while(x < 4){  
+ x <- x + 1  
+ print(c(x, x * x))  
+ }  
  
[1] 2 4  
[1] 3 9  
[1] 4 16  
  
> x = 1  
> while(x < 4){  
+ print(c(x, x * x))  
+ x <- x + 1  
+ }
```

Exit a loop

```
> for(x in 2:4){  
+   if(x == 3){  
+     break  
+   } else {  
+     print(x)  
+   }  
+ }  
  
[1] 2
```

```
> x = 1  
> while(x < 5){  
+   x = x + 1  
+   if(x == 3){  
+     break  
+   } else {  
+     print(x)  
+   }  
+ }  
  
[1] 2
```

Skip one iteration in a loop

```
> for(x in 2:4){  
+   if(x == 3){  
+       next  
+   } else {  
+       print(x)  
+   }  
+ }
```

```
[1] 2  
[1] 4  
[1] 5
```

```
> x = 1  
> while(x < 5){  
+   x = x + 1  
+   if(x == 3){  
+       next  
+   } else {  
+       print(x)  
+   }  
+ }
```

```
[1] 2  
[1] 4  
[1] 5
```

Example

You have several items you want to pack

Each Item has a weight

You are only allowed to pack 10kg
because you are flying Ryanair

Problem:

Add Items to your bag until you reached
the maximum weight



```
> items = c('shoes', 'shirt',  
+ 'pants', 'underwear',  
+ 'book', 'tooth brush',  
+ 'pillow', 'head phones',  
+ 'hair dryer')  
  
> sizes = c(2.4, 2, 3.1, 1.5,  
+ 1.1, 0.3, 0.8, 0.5, 1)  
  
> bag = 0
```

Example

```
> bag = 0
> things_packed = character(0)
> for(i in 1:length(items)){
+   if(bag + sizes[i] > 10){
+     break
+   }
+   bag = bag + sizes[i]
+   things_packed =
+   c(things_packed, items[i])
+   print(c(bag, things_packed))
+ }
```

```
[1] "2.4" "shoes"
[1] "4.4" "shoes" "shirt"
[1] "7.5" "shoes" "shirt" "pants"
[1] "9" "shoes" "shirt" "pants" "underwear"
```

```
> i = 1
> bag = 0
> things_packed = character(0)
> while( bag + sizes[i] < 10){
+   bag = bag + sizes[i]
+   things_packed =
+   c(things_packed, items[i])
+   i = i + 1
+   print(c(bag, things_packed))
+ }
```

```
[1] "2.4" "shoes"
[1] "4.4" "shoes" "shirt"
[1] "7.5" "shoes" "shirt" "pants"
[1] "9" "shoes" "shirt" "pants" "underwear"
```


Example improved

```
> bag = 0
> things_packed = character(0)
> for(i in 1:length(items)){
+   if(bag + sizes[i] > 10){
+     next
+   }
+   bag = bag + sizes[i]
+   things_packed =
+   c(things_packed, items[i])
+   print(c(bag, things_packed))
+ }
```

```
[1] "2.4" "shoes"
[1] "4.4" "shoes" "shirt"
[1] "7.5" "shoes" "shirt" "pants"
[1] "9" "shoes" "shirt" "pants" "underwear"
[1] "9.3" "shoes" "shirt" "pants" "underwear" "tooth brush"
[1] "9.8" "shoes" "shirt" "pants" "underwear" "tooth brush"
    "head phones"
```

```
> i = 1
> bag = 0
> things_packed = character(0)
> while( bag + sizes[i] < 10){
+   if(bag + sizes[i] > 10){
+     next
+   }
+   bag = bag + sizes[i]
+   things_packed =
+   c(things_packed, items[i])
+   i = i + 1
+   print(c(bag, things_packed))
+ }
```

```
[1] "2.4" "shoes"
[1] "4.4" "shoes" "shirt"
[1] "7.5" "shoes" "shirt" "pants"
[1] "9" "shoes" "shirt" "pants" "underwear"
```

```
# infinite - BAD !!!!!
```

Example while loop corrected

```
> i = 1
> bag = 0
> things_packed = character(0)
> while( bag + sizes[i] < 10){
+   if(bag + sizes[i] > 10){
+     i = i + 1
+     next
+   }
+   bag = bag + sizes[i]
+   things_packed =
+   c(things_packed, items[i])
+   i = i + 1
+   print(c(bag, things_packed))
+ }
```

```
[1] "2.4" "shoes"
[1] "4.4" "shoes" "shirt"
[1] "7.5" "shoes" "shirt" "pants"
[1] "9" "shoes" "shirt" "pants" "underwear"
[1] "9.3" "shoes" "shirt" "pants" "underwear" "tooth brush"
[1] "9.8" "shoes" "shirt" "pants" "underwear" "tooth brush"
    "head phones"
```

```
# exits on an ERROR (ran out of the array)
```

```
> i = 1
> bag = 0
> things_packed = character(0)
> while( bag < 10 &
+       i <= length(sizes)){
+   if(bag + sizes[i] > 10){
+     i = i + 1
+     next
+   }
+   bag = bag + sizes[i]
+   things_packed =
+   c(things_packed, items[i])
+   i = i + 1
+   print(c(bag, things_packed))
+ }
```

```
[1] "2.4" "shoes"
[1] "4.4" "shoes" "shirt"
[1] "7.5" "shoes" "shirt" "pants"
[1] "9" "shoes" "shirt" "pants" "underwear"
[1] "9.3" "shoes" "shirt" "pants" "underwear" "tooth brush"
[1] "9.8" "shoes" "shirt" "pants" "underwear" "tooth brush"
    "head phones"
```

Loops for real application

gene	R1	R2	R3	R4	R5	R6	Diff?
AA	10	10	6	9	7	11	
BB	11	12	11	11	13	9	
CC	10	12	9	11	9	10	
DD	11	6	12	28	20	17	
EE	12	5	9	10	10	11	

You want to know which genes are differentially expressed

Perform the T-test **for** each gene

```
> gene[1,9] = t.test(gene[1,2:4], gene[1,5:7])$p.value
> gene[2,9] = t.test(gene[2,2:4], gene[2,5:7])$p.value
> gene[3,9] = t.test(gene[3,2:4], gene[3,5:7])$p.value
> gene[4,9] = t.test(gene[4,2:4], gene[4,5:7])$p.value
...
> gene[8,9] = t.test(gene[8,2:4], gene[8,5:7])$p.value
> gene[9,9] = t.test(gene[9,2:4], gene[9,5:7])$p.value
```

Loops for real application

```
> gene<- read.csv("gene_exp1.csv")
> pvals = numeric(0)
> for(i in 1:9){
+   pvals[i] <- t.test(gene[i,2:4], gene[i,5:7])$p.value
+ }
> gene$Diff <- pvals < 0.05
> gene
```

	gene	R1	R2	R3	R4	R5	R6	Diff
1	AA	10	10	6	9	7	11	FALSE
2	BB	11	12	11	11	13	9	FALSE
3	CC	10	12	9	11	9	10	FALSE
4	DD	11	6	12	28	20	17	TRUE
5	EE	12	5	9	10	10	11	FALSE
6	FF	11	8	12	1	3	4	TRUE
7	GG	23	12	11	11	9	11	FALSE
8	HH	6	7	8	8	11	8	FALSE
9	II	11	8	13	21	18	20	TRUE

Exercise

Load the table generated in “create_gene_expression_table.R” using `source()`

Return all genes which are significant differentially expressed

Use the `t.test()`\$p.value and a for loop

END OF DAY 1