A briefly Introduction to R language

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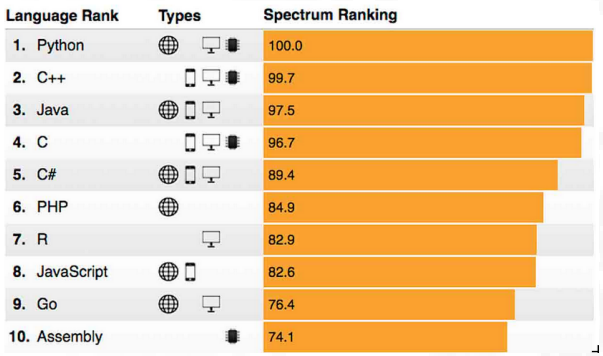
The R Project

- Environment for statistical computing and graphics:
- Free software and Open-source;
- A simple programming language:
  - it is an open-source implementation of S language;
  - it is among the Top 10 Programming Languages in 2018 for *IEEE Spectrum Journal*;



Language Rank	Types	Spectrum Ranking
1. Python		100.0
2. C++		99.7
3. Java		97.5
4. C		96.7
5. C#		89.4
6. PHP		84.9
7. R		82.9
8. JavaScript		82.6
9. Go		76.4
10. Assembly		74.1

- software and packages can be downloaded from:

www.cran.r-project.org

- Versions of R exist of Windows, MacOS, Linux and various other Unix-like OS.

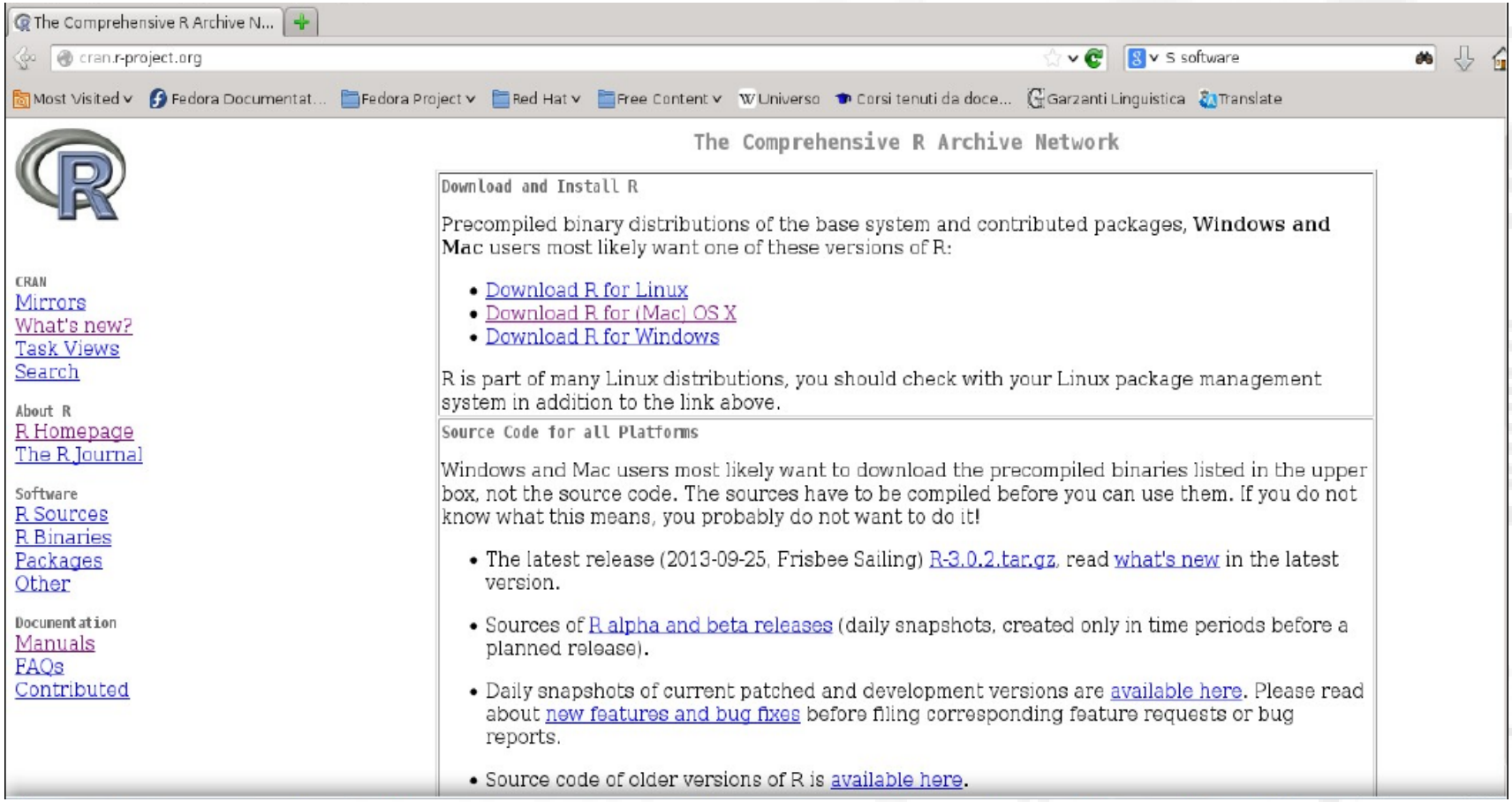
Why to use R language

- Implement many common statistical and bioinformatics procedures;
- Provide excellent graphics functionality;
- A convenient starting point for many data analysis projects
- Libraries (namely packages) can be automatically downloaded from:

  www.cran.r-project.org
  https://www.bioconductor.org/

- It is standard for data mining and statistical analysis;
- Efficient data structures make programming easier.

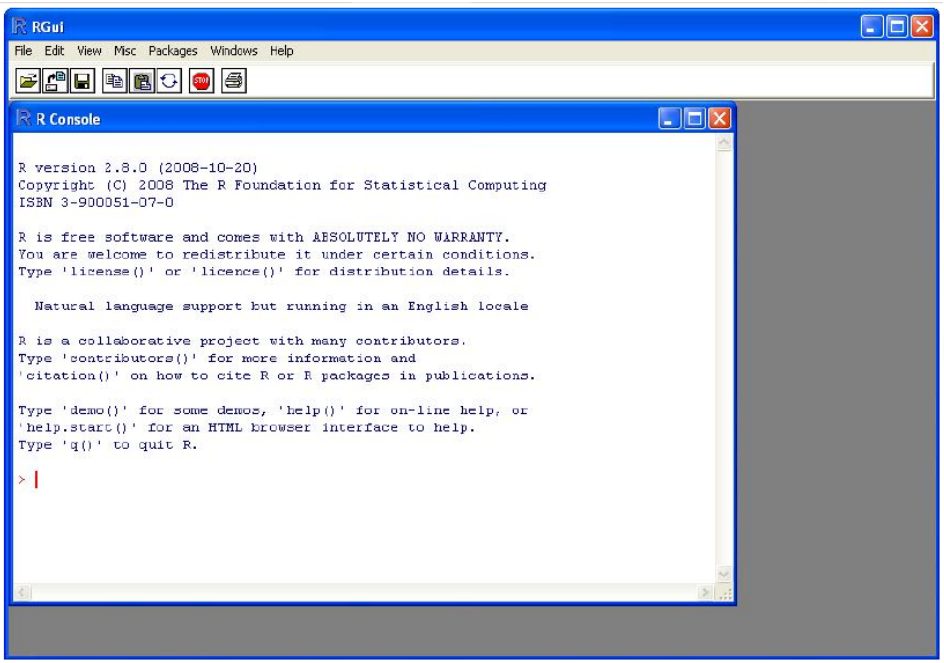
Download and Install R language



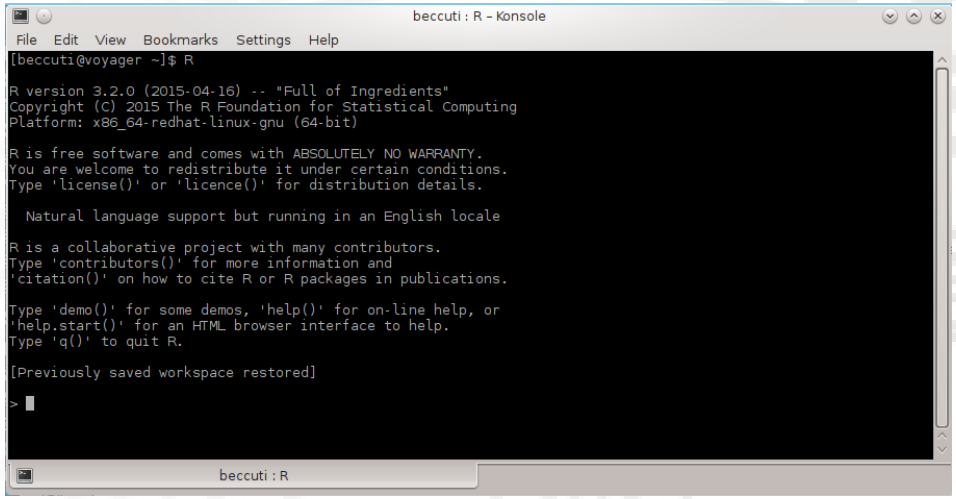
http://cran.mirror.garr.it/mirrors/CRAN/

Download the appropriate version (w.r.t. your OS) and follow the instructions to install the program.

R under GUI



from Windows

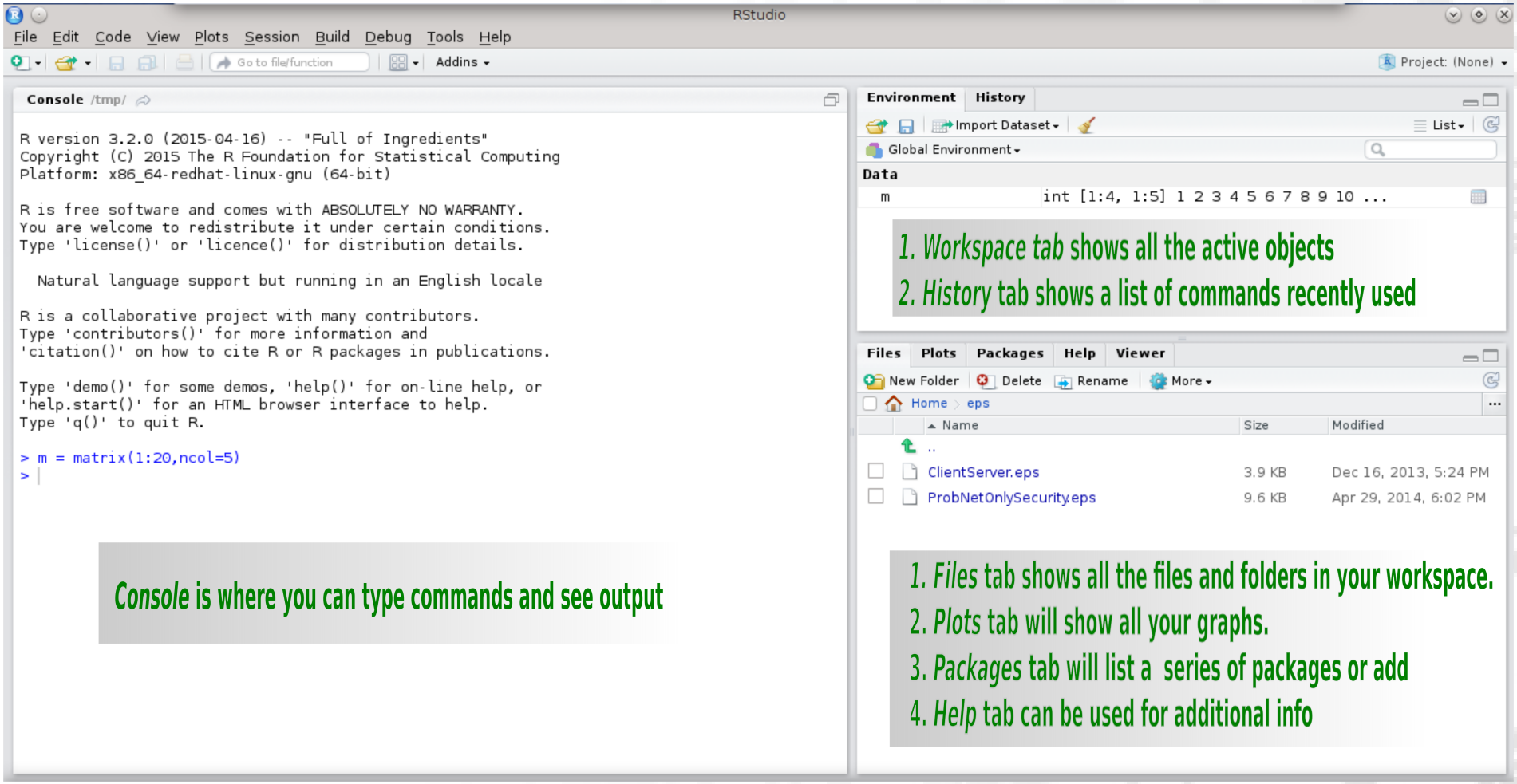


from Linux

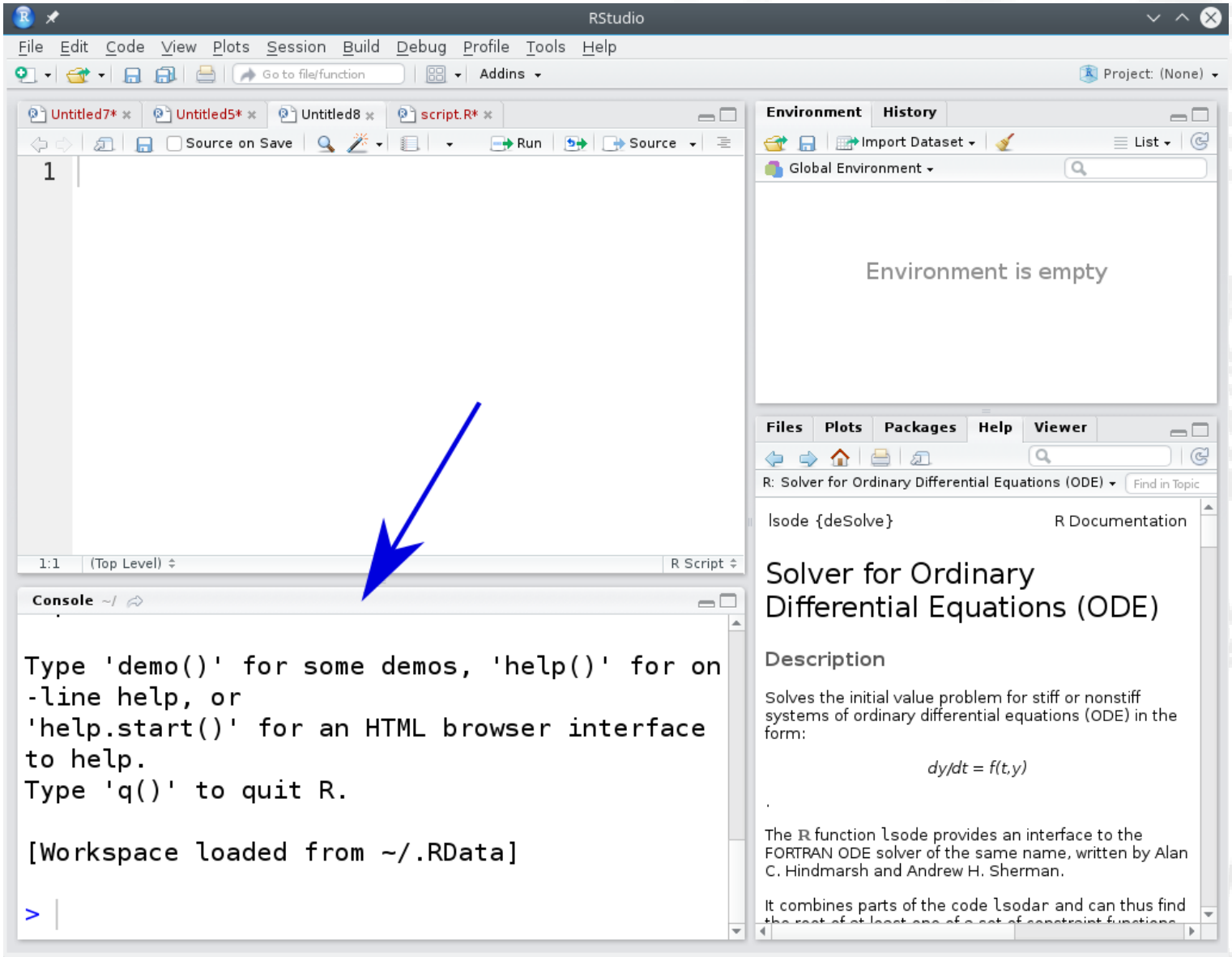
R under GUI using Rstudio

RStudio allows the user to run R in a more user friendly environment.

It is free-software and available at `http://www.rstudio.com/`

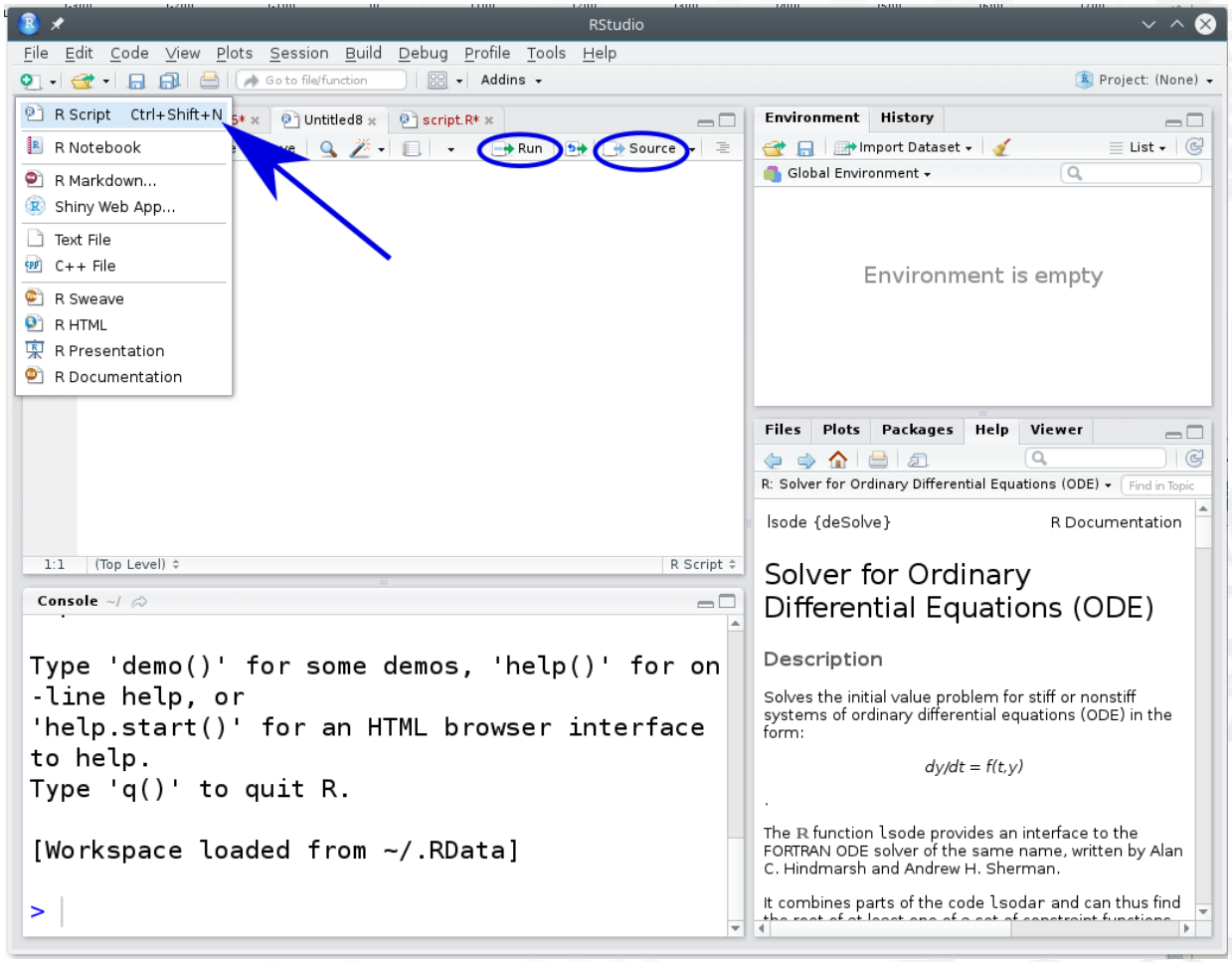


RStudio prompt and script



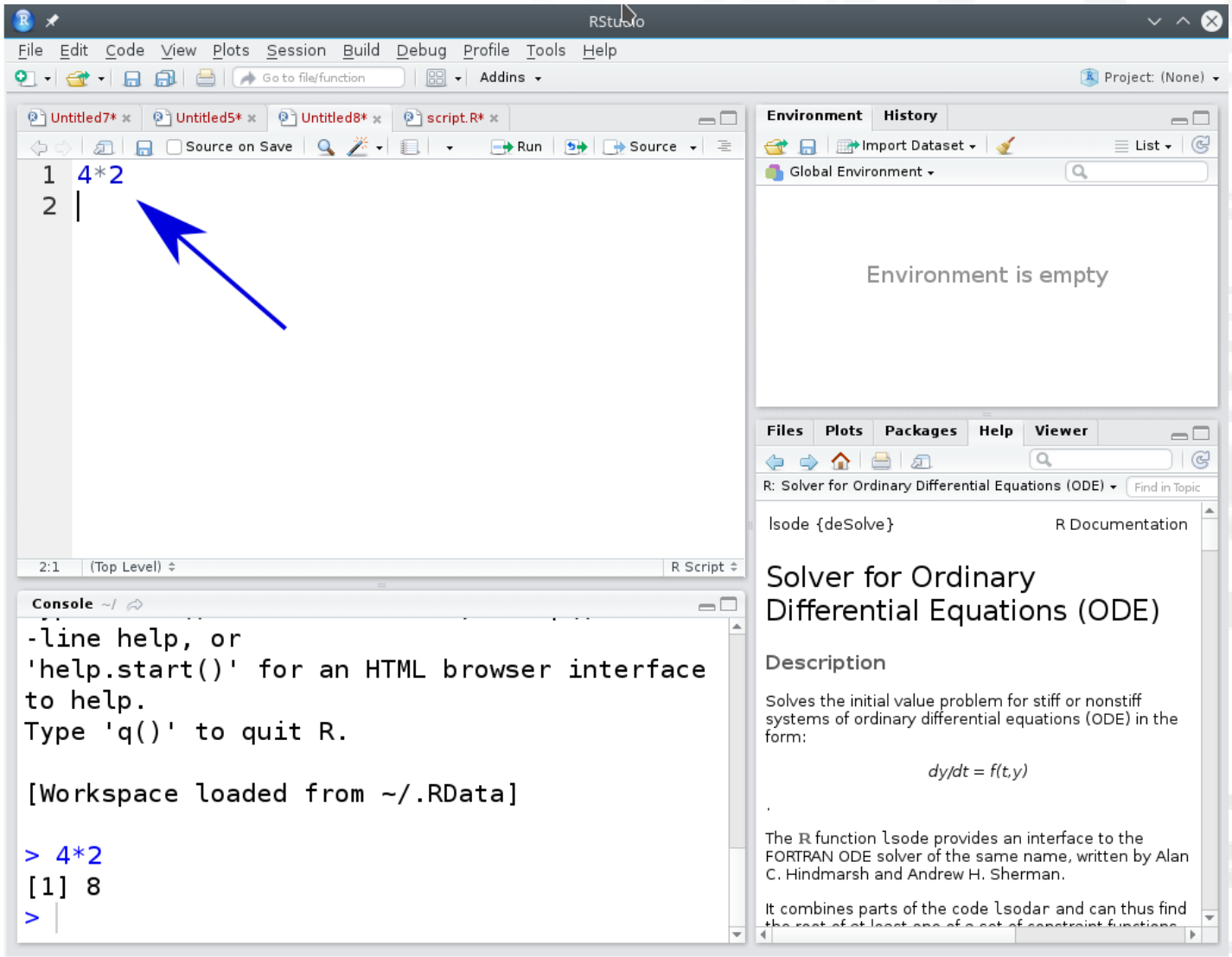
RStudio prompt and script

- R script can be used to save R commands into a file;
- Commands into R script can be executed line by line (clicking on Run) or globally (clicking on Source).



RStudio prompt and script

- Commands can be directly typed into the R script console.



Assignments in R

It is often required to store intermediate results so that they do not need to be re-typed over and over again. To assign a value of 324 to the variable X type:

$> X < -324$

or

$> X = 324$

Variable X can be used in next expressions:

Example

$> X$
[1]324

$> X + X$
[1]648

$> sqrt(X)$
[1]18

$> X = X + X; X$
[1]648

$> X/4$
[1]162

$> X \hat{} sqrt(X)$
[1]1.54814e + 45

Variable name in R

R is a case-sensitive language, hence x and X do not refer to the same variable.

Variable name:

- can be created using letters, digits and the . (dot) symbol;

  $> data1.address$
  $> d1_4.f$

- must not start with **a digit** or a . followed by a digit.

- some names are reserved by the system: *if, while, NULL, TRUE ...*

Variable type in R

Basic variable types are:

Numeric: integer, floating point values;

Boolean: values corresponding to **True** or **False**;

Strings: sequences of characters.

Type is determined automatically when variable is created with $<-$ or $=$ operator.

Data structures/Objects are:

R provides types of different object.

Vector: a collection of elements (numbers, logical values and character strings) with same type;

Array: a generalization of a vector;

List: collections of objects of any type;
e.g. list of vectors, list of matrices, etc.

Data Frame: an array in which the type of each element can be different;

Factor: takes on a limited number of values;

Getting help in R

R provides a built-in help facility.

- To get more information on any specific function, e.g. sqrt(), the command is:
  help(sqrt)
  or
  ?sqrt

- help on features specified by special characters must enclose in single or double quotes (e.g. "[[") *help("[[")*

- Help is also available in HTML format by running *help.start()*

- For more information use
  ?help

Argument Matching in R

How does R know to match arguments?

Argument matching is done in a few different ways:

- The arguments are matched by their positions. The first supplied argument is matched to the first formal argument and so on.

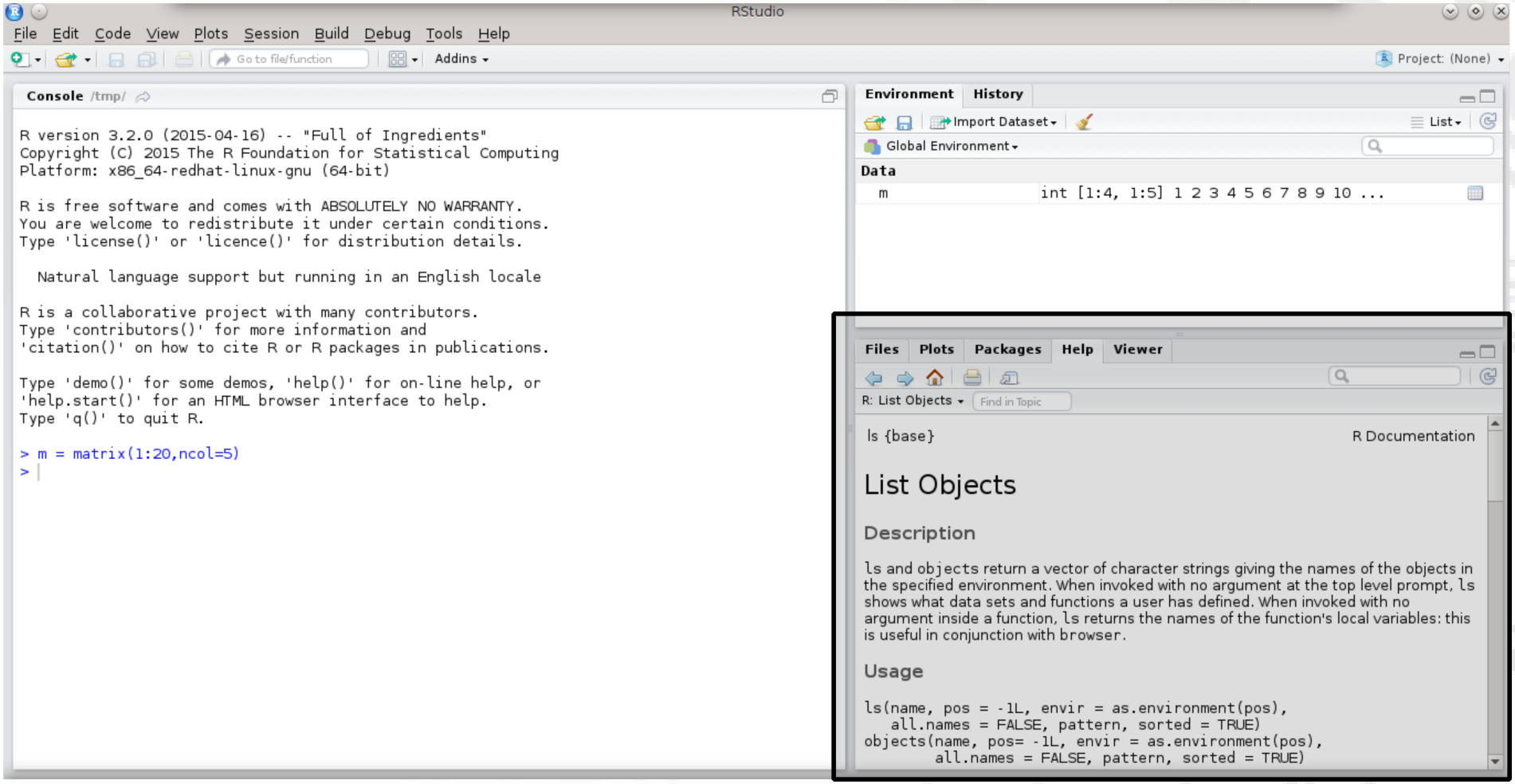
  $> myfun(3, 4, 7)$ **x=3, y=4 and p=7**

- The arguments are matched by name. A named argument is matched to the formal argument with the same name:

  $> myfun(y = 4, x = 3, p = 7)$ **x=3, y=4 and p=7**

- Name matching happens first, then positional matching is used for any unmatched arguments.

Getting help in Rstudio

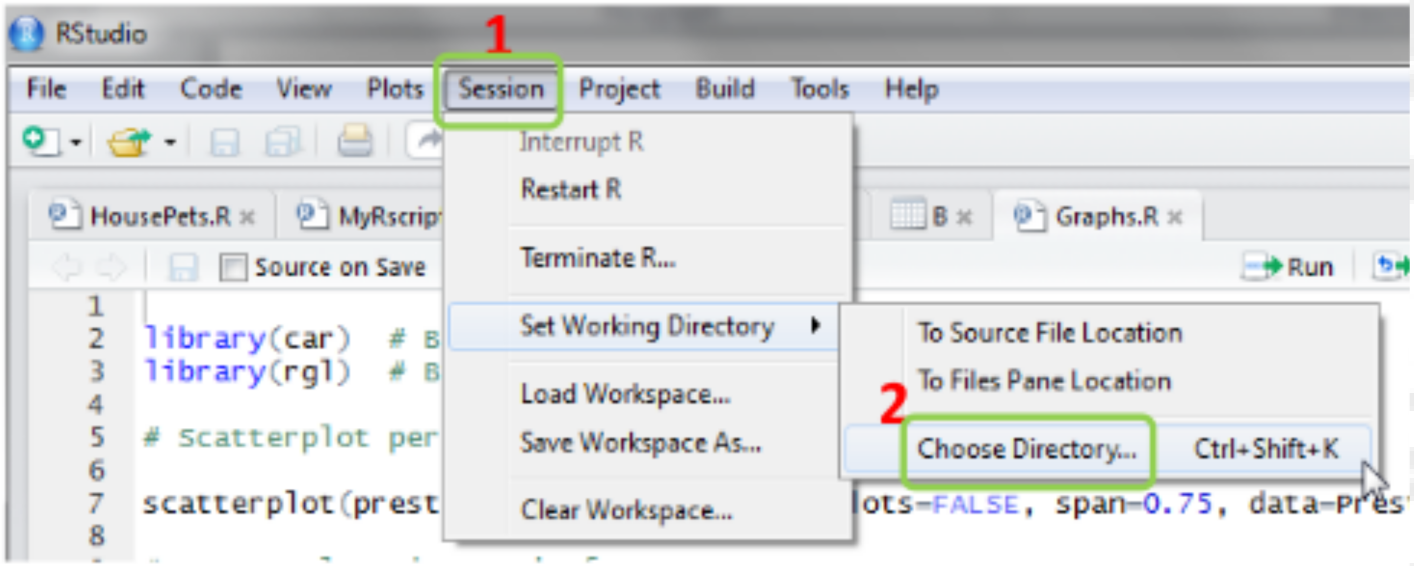


Working directory

Working directory in R:

- Working directory contains data and R scripts. It is a directory of the file-system;
- *getwd()* returns the current Working directory;
- *setwd("new_path")* sets Working directory;

Working directory in RStudio:



Packages in R

- R provides libraries of packages. Packages contain various functions and data sets for numerous purposes;
- Some packages are part of the basic installation. Others can be downloaded from CRAN:
  $> install.packages(\text{“}devtools\text{”})$
- To use functions and data sets of a package, it must be loaded into the workspace:
  $> library(devtools)$
- To check what packages are currently loaded into the workspace:
  $> search()$
- A loaded package can be removed:
  $> detach(\text{“}package:devtools\text{”})$

Observe:

if you terminated your session and start a new session with the saved workspace, you must load the packages again.

Vector in R

Vectors in R

- an ordered list of homogeneous elements;
- Vectors are the simplest type of object in R;
  There are 3 main types of vectors:
  - Numeric vectors;
  - Character vectors;
  - Logical vectors.
- To create a numeric vector x consisting of 6 numbers, 1.4, 6, 23.1, 65.43, 2.7, 55 use:

  $> x = c(1.4, 6, 23.1, 65.43, 2.7, 55)$

  or

  $> assign("x", c(1.4, 6, 23.1, 65.43, 2.7, 55))$

Numeric vectors in R

- To print the contents of x:

  $> x$
  [1]1.4 6 23.1 65.43 2.7 55

  symbol [1] in front of the result is the index of the first element in the vector x.

- To access a particular element of x:

  $> x[1]$
  [1]1.4

  $> x[6]$
  [1]55

  $> x[c(1,6)]$
  [1]1.4 55

  $> x[-c(1,5)]$ **Operator - means: select all the elements except those ....**
  [1]6 23.1 65.43 55

Numeric vectors in R

- To modify a particular vector element:

  $> x[2] = 5$ **to modify the 2nd element of x in 5**
  [1]1.4 5 23.1 65.43 2.7 55

  $> x[4] = 5$
  [1]1.4 5 23.1 5 2.7 55

- To modify more than one vector elements:

  $> x[c(2,4)] = c(6, 65.43)$
  [1]1.4 6 23.1 65.43 2.7 55

  $> y = x$
  $> y[y < 3] = 1$
  $> y$
  [1]1 6 23.1 65.43 1 55

Numeric vectors in R

- A vector can be used to do further assignments:

  $> y = c(x, 2, 3, x[c(1, 3)])$

  vector y with 10 entries is created:

  $> y$
  [1]1.4 6 23.1 65.43 2.7 55 2 3 1.4 23.1

- Operation are performed on each single element:

  $> x/10$
  [1]0.14 0.6 2.31 6.543 0.27 5.5

- Short vectors are "recycled" to match long ones (if it is possible):

  $> v = x[c(1, 2)] + y$ $x[c(1, 2)]$ **is repeated 5 times**
  $> v$
  [1]2.8 12 24.5 71.43 4.1 61 3.4 9 2.829.1

How to generate sequences in R

- In R it is possible to generate sequences of numbers
  - using operator ":"
    $> 1 : 5$
    [1]1 2 3 4 5
  - using function seq()
    $> seq(1, 5)$
    [1]1 2 3 4 5
    $> seq(from = 1, to = 5)$
    [1]1 2 3 4 5
    We can also specify a step size (using by=value) or a length (using length.out=value) for the sequence.
    $> seq(1, 5, by = 0.5)$
    [1]1 1.5 2 2.5 3 3.5 4 4.5 5
    $> seq(from = 1, to = 5, length.out[= 9)$
    [1]1 1.5 2 2.5 3 3.5 4 4.5 5
  - using function rep()
    $> rep(x, 3)$
    [1]1.40 6.00 23.10 65.43 2.70 55.00 1.40 6.00 23.10 65.43 2.70 55.00
    [13]1.40 6.00 23.10 65.43 2.70 55.00

Character vector in R

- A string is identify by " "
- A string vector is defined as well as number vector by c() operator
  $> y = c(\text{“}ROMA\text{”}, \text{“}MILANO\text{”}, \text{“}TORINO\text{”})$
- several functions in R to manipulate character vectors.
  paste, as.character, is.character, strsplit, substr. . .

  $> paste(\text{“}HOME\text{”}, \text{“}WHILE\text{”}, \text{“}DOG\text{”}, sep = \text{“ : ”})$
  [1]“$HOME : WHILE : DOG$” **Concatenate char vectors**

  $> x = c(1, 3, 45, 7)$
  $> is.character(x)$ **test if an object is of type character**
  [1]$FALSE$

  $> is.character(as.character(x))$
  [1]$TRUE$

Data Frame in R

Data Frame in R

- It is used to storage data table in R;
- It can be considered as a matrix in which columns can contain different types;
- We can create data frames from pre-existing variables:

```
> name = c("GENE1","GENE2","GENE3")
> seq = c("ATCCT..","CCTTT..","CCAACT..")
> count = c(100,20,4)
> d = data.frame(name,seq,count)
> d
```

	name	seq	count
1	GENE1	ATCCT..	100
2	GENE2	CCTTT..	20
3	GENE3	CCACT..	4

Data Frame in R

Main operations:

- attributes(d) returns the data frame attributes:

  $> attributes(d)$
  $\$names$
  [1]"name" "seq" "count"
  $\$row.names$
  [1]1 2 3
  $\$class$ [1]"data.frame"

- colnames(d) returns the names of data frame columns:

  $> colnames(d)$
  [1]"name" "seq" "count"

  $> colnames(d) = c(\text{“}c1\text{”}, \text{“}c2\text{”}, \text{“}c3\text{”}, \text{“}c4\text{”})$ **change column names.**

- rownames(d) returns the names of data frame rows:

  $> rownames(d)$
  [1]1 2 3

Indexing Data Frame in R

- it is possible to use the same method of matrices to access values of a data frame.

$> d$

	name	*seq*	*count*
1	*GENE*1	*ATCCT*..	100
2	*GENE*2	*CCTTT*..	20
3	*GENE*3	*CCACT*..	4

$> d[2,2]$ **gives the value in the 2nd row and 2nd column of d.**
[1]*CCTTT*..

$> d[2,]$ **gives the values in the 2nd row of d.**
[1]*GENE*2 *CCTTT*.. 20

$> d[,3]$ **gives the values in the 3rd column of d.**
[1]100 20 4

Data Frame in R

Main operations(2):

- summary(d) returns a summary of data frame:

  $> summary(d)$

name	seq		count
GENE1 : 1	ATCCT.. : 1	Min. :	4.000
GENE2 : 1	CCTTT.. : 1	1stQu. :	12.00
GENE3 : 1	CCACT.. : 1	Median :	20.00
		Mean :	41.33
		3rdQu. :	60.00
		Max. :	100.00

- subset(d,cond) returns a subset of rows according to condition:

  $> subset(d, d[, 3] > 10)$

	name	seq	count
1	GENE1	ATCCT..	100
2	GENE2	CCTTT..	20

I/O in R language

Input from a file in R

- R provides a set of functions to read data from files:
  - read.table() is used to read data frames from formatted text files.
    A variable separator can be specified.
  - read.csv() is used to read data frames from comma separated variable files.
  - read.csv2() is used to read data frames from semicolon separated variable files.
  - load() is used to reload datasets written with the function save().
    Data are stored in binary format (more compact!!).

Input from a file in R

- read.table() reads a file in table format and creates a data frame from it,

read.table(file,header=FALSE, sep= " ", dec=".", stringAsFactors=TRUE ...)

file	: the name of the file in which the data are stored;
header	: a logical value indicating whether the file contains the names of the variables as its first line;
sep	: the field separator character;
dec	: the character used for decimal points;
stringAsFactors	: logical: should character vectors be converted to factors?;
row.names	: it can be a vector giving the actual row names, or a single number giving the column of the table which contains the row name;
...	: optional arguments;

$> d = read.table(\text{“./example.txt”}, header = TRUE, sep = \text{“!”})$

$> b = read.table(\text{“./example1.txt”}, header = FALSE, sep = \text{“ ”})$

Input from a file in R

- read.csv() reads a file in table format and creates a data frame from it,

  read.csv(file,header=FALSE, sep=",", dec=".",...)

  file : the name of the file in which the data are stored;
  header : a logical value indicating whether the file contains the names of the variables as its first line;
  sep : the field separator character;
  dec : the character used for decimal points;
  stringAsFactors : logical: should character vectors be converted to factors?;
  row.names : it can be a vector giving the actual row names, or a single number giving the column of the table which contains the row name
  ... : optional arguments;

  $> d = read.csv(\text{“./example.txt”}, header = TRUE)$

  $> b = read.csv(\text{“./example1.txt”}, header = FALSE)$

Input from a file in R

- read.csv2() reads a file in table format and creates a data frame from it,

  read.csv2(file,header=FALSE, sep=";", dec=".", ...)

  file : the name of the file in which the data are stored;
  header : a logical value indicating whether the file contains the names of the variables as its first line;
  sep : the field separator character;
  dec : the character used for decimal points;
  stringAsFactors : logical: should character vectors be converted to factors?;
  row.names : it can be a vector giving the actual row names, or a single number giving the column of the table which contains the row name
  ... : optional arguments;

  $> d = read.csv2(\text{“./example.txt”}, header = T)$

  $> b = read.csv2(\text{“./example1.txt”}, header = F)$

Input from a file in R

- load() reload datasets written with the function save().

  load(file, ...)

  File : the name of the file in which the data are stored;
  verbose = FALSE : if TRUE item names are printed;
  ... : optional arguments;

  > *load*("./*example.data*")

  > *load*("./*example.data*", *verbose* = *T*)
  Loading objects :
  m

Writing a file in R

- R provides a set of functions to write data into files:
  - write.table() is used to write data frames into formatted text files.
    A variable separator can be specified.
  - write.csv() is used to write data frames into comma separated variable files.
  - write.csv2() is used to write data frames into semicolon separated variable files.
  - save() is used to save datasets into a binary file.
    Data are stored in binary format (more compact!!).

Writing a file in R

- write.table() is used to write data frames into formatted text files ,

write.table(x,file,col.names=TRUE,row.names=TRUE, sep=" ", dec=".", ...)

x	:	the object to be written;
file	:	the name of the file in which the data are stored;
col.names	:	if TRUE column names are stored;
row.names	:	if TRUE row names are stored;;
sep	:	the field separator character;
dec	:	the character used for decimal points;
...	:	optional arguments;

$> write.table(b, \text{“./example.txt”}, col.names = TRUE, row.names = TRUE, sep = \text{“!”})$

$> write.table(b, \text{“./example.txt”}, col.names = FALSE, row.names = FALSE, sep = \text{“,”})$

Writing a file in R

- write.csv() is used to write data frames into formatted text files ,

  write.csv(x,file,col.names=TRUE,row.names=TRUE, sep=",", dec=".", ...)

x	:	the object to be written;
file	:	the name of the file in which the data are stored;
col.names	:	if TRUE column names are stored;
row.names	:	if TRUE row names are stored;;
sep	:	the field separator character;
dec	:	the character used for decimal points;
...	:	optional arguments;

  $> write.csv(b, \text{“./example.txt”}, col.names = TRUE, row.names = TRUE)$

  $> write.csv(b, \text{“./example.txt”}, col.names = FALSE, row.names = FALSE)$

Writing a file in R

- write.csv2() is used to write data frames into formatted text files ,

  write.csv2(x,file,col.names=TRUE,row.names=TRUE, sep=";",dec=",", ...)

x	:	the object to be written;
file	:	the name of the file in which the data are stored;
col.names	:	if TRUE column names are stored;
row.names	:	if TRUE row names are stored;;
sep	:	the field separator character;
dec	:	the character used for decimal points;
...	:	optional arguments;

  $> write.csv2(b, \text{“./example.txt”}, col.names = TRUE, row.names = TRUE)$

  $> write.csv2(b, \text{“./example.txt”}, col.names = FALSE, row.names = FALSE)$

Writing a file in R

- save() writes an external representation of R objects to the specified file,

  save(...,file, ...)

  ... : a list of objects to be saved;
  file : the name of the file in which the data are stored;
  ... : optional arguments;

  $> save(b, c, file = \text{“./example.data”})$