Biostatistics I: Introduction to R

Basics

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In this Section

- ▶ Using R
- ► Examples with Data
- ► Getting Familiar with R
- Importing data and saving your work
- ► A lot of practice

- ► R is a command-based procedural language
 - write and execute commands
 - use and define functions
- You may write the commands in the R console (Windows) or in a shell (Linux)

You will become more familiar with the syntax as you use it

- Strongly advisable to use a suitable text editor Some available options:
 - RWinEdt (for Windows; you also need WinEdt installed)
 - ► Tinn-R (for Windows; http://sciviews.org/Tinn-R/)
 - Rkward (for Linux)
 - Emacs (w. ESS, all platforms)
 - Visual Studio (for Windows)
 - Rstudio (all major platforms; http://www.rstudio.org/)
 - ▶ for more check https://r-dir.com/blog/2013/01/list-of-r-editors.html

- ► For this course: Rstudio (http://www.rstudio.org/)
 - ► free
 - works fine in Windows, MacOS and Linux
 - ► helpful with errors
 - alternative output options

► Can I use R without Rstudio?

► Can I use Rstudio without R?

► Package survival - pbc data set

id	time	status	trt	age	sex	bili	chol
1	400	2	1	58.76523	f	14.5	261
2	4500	0	1	56.44627	f	1.1	302
3	1012	2	1	70.07255	m	1.4	176
4	1925	2	1	54.74059	f	1.8	244
5	1504	1	2	38.10541	f	3.4	279

- ▶ id: case number
- ▶ time: number of days between registration and the earlier of death, transplantation, or study analysis in July, 1986
- ▶ status: status at endpoint, 0/1/2 for censored, transplant, dead
- ▶ trt: 1/2/NA for D-penicillamine, placebo, not randomised
- **age**: in years
- ► sex: m/f
- bili: serum bilirunbin (mg/dl)
- ► chol: serum cholesterol (mg/dl)

More details:

https://stat.ethz.ch/R-manual/R-devel/library/survival/html/pbc.html

id	time	status	trt	age	sex	bili	chol	dt
1	400	2	1	58.76523	f	14.5	261	1
2	4500	Ο	1	56.44627	f	1.1	302	2
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- Common questions
 - What is the average age?
 - What is the average serum bilirubin?
 - ▶ What is the average serum cholesterol?
 - ▶ What is the percentage of females?
 - ▶ How many missing values do we have for serum cholesterol?

All these questions can be answered using R!

- ► Elementary commands: **expressions** and **assignments**
- ► An expression given as command is evaluated printed and discarded
- ► An **assignment** evaluates an expression and passes the value to a variable the result is not automatically printed

Expression is given as a command,

103473

[1] 103473

▶ However, it cannot be viewed again unless the command is rerun.

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In order to store information, the expression should assign the command

[1] 103473

You can use R as a calculator!

► Basic arithmetics

```
+, -, *, /, ^
```

```
y <- 103473 + 100000
y
```

[1] 203473

► Complicated arithmetics

Tips:

- ► R is case sensitive, e.g.,
 - "sex" is different than "Sex"
- ► Commands are separated by a semi-colon or by a newline
- ► Comments can be put anywhere, starting with a hashmark #: everything to the end of the line is a comment
- Assign a value to an object by <- or =</p>
- Working directory: get with getwd() and set with setwd()

- Missing values
 - are coded as NA (i.e., not available) is.na()
- ► Infinity
 - is coded as Inf (plus infinity) or -Inf (minus infinity) is.finite()
- ► The Null objects
 - are coded as NULL (undefined) is.null()
- Not a number
 - ▶ is coded as NaN (Not a Number). Example:

0/0

[1] NaN

Importing Data

- ▶ function: read.table(), read.csv() and its variants
 - note: use forward slashes or double backward slashes in the file names, e.g.,

```
"C:/Documents and Settings/User/Data/file.txt" Or "C:\\Documents and Settings\\User\\Data\\file.txt"
```

- Specialized functions for importing data from other programs
 - package: foreign, function: read.spss(), read.dta()
 - package: Hmisc, function: sas.get()
 - package: openxlsx, function: read.xlsx()
 - package: readxl, function: read_excel()
 - package: haven, function: read_spss()
 - etc

Exporting Data

- Specialized functions for exporting data to other programs
 - ► function: write.table(), write.csv()
 - package: foreign, function: write.spss(), write.dta()
 - package: openxlsx, function: write.xlsx()
 - ► etc

Saving and Loading your Work

Multiple objects:

- You can save your R objects using save()
 - be careful about overwriting
- You can load your saved R objects using load()

Single object:

- Using saveRDS() you can save a single R object
- ▶ Using readRDS() you can load a single R object
 - we will need an assignment statement to store the results

Save your code by using the tab File in Rstudio!

Saving and Loading your Work

Tips:

- Short names are preferred over longer names
- Try to avoid using names that contain symbols
- Avoid spaces in names
- ► Remove any comments in your data set
- Make sure that any missing values in your data set are indicated with the same value (or no value)

Summary

Basic functions

- getwd(), setwd(),
- is.na(),
 is.finite(),
 is.null()

Import/Export

- read.csv(), write.csv()
- read.xlsx(), write.xlsx()
- read.table(), write.table()

Save/Load

- ► save(), saveRDS()
- ▶ load(), readRDS()