Epidemiologic data analysis using R

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Contents

- Basic properties of R
- Script files
- Data structures and objects
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What is R

- Statistical software or ''package" — and a lot more
- R is a **language**and **environment**for statistical computing and graphics (`www.r-project.org/`)
- Developed by volunteers, coordinated by the **R Development Core Team**.
- Available for Windows, Linux, Mac, Unix, ...
- Is expanding rapidly: new version every 6 months.
- No licence fee(!) & source code open.

For further information and download:
{`http://www.r-project.org/`}

Properties of R

- Large repertory of basic and advanced methods.
- Versatile graphics of high quality.
- R Reads datasets from Stata, SAS, SPSS, Epi-Info – even Excel
- Deals simultaneously with different objects or data structures newline – not just a single data matrix.
- Results of analysis saved as **objects**, readily available for further processing.
- Parsimonious output listing!
- For advanced users! Easy to expand and tailor to specific needs using the **object-oriented**programming tools.

To learn more about R

- Hills, M., Plummer, M., Carstensen, B.
  A Short Introduction to R for Epidemiology, 2011.
  `http://bendixcarstensen.com/Epi/R-intro.pdf`

- Dalgaard, P. *Introductory Statistics with R, 2nd Ed.*
  Springer, New York, 2008.

- *Statistical Practice in Epidemiology Using R*. An international course, IARC, Tarto, 2020.
  `http://bendixcarstensen.com/SPE/`

- R blog

- Masses of books, articles, websites, etc ...

What does R offer for epidemiologists?

- Descriptive tools
  - Versatile tabulation
  - High-quality graphics
- Analytic methods
  - Basic epidemiologic statistics
  - Generalized linear models and their extensions
  - Survival analysis methods
  - Other ...

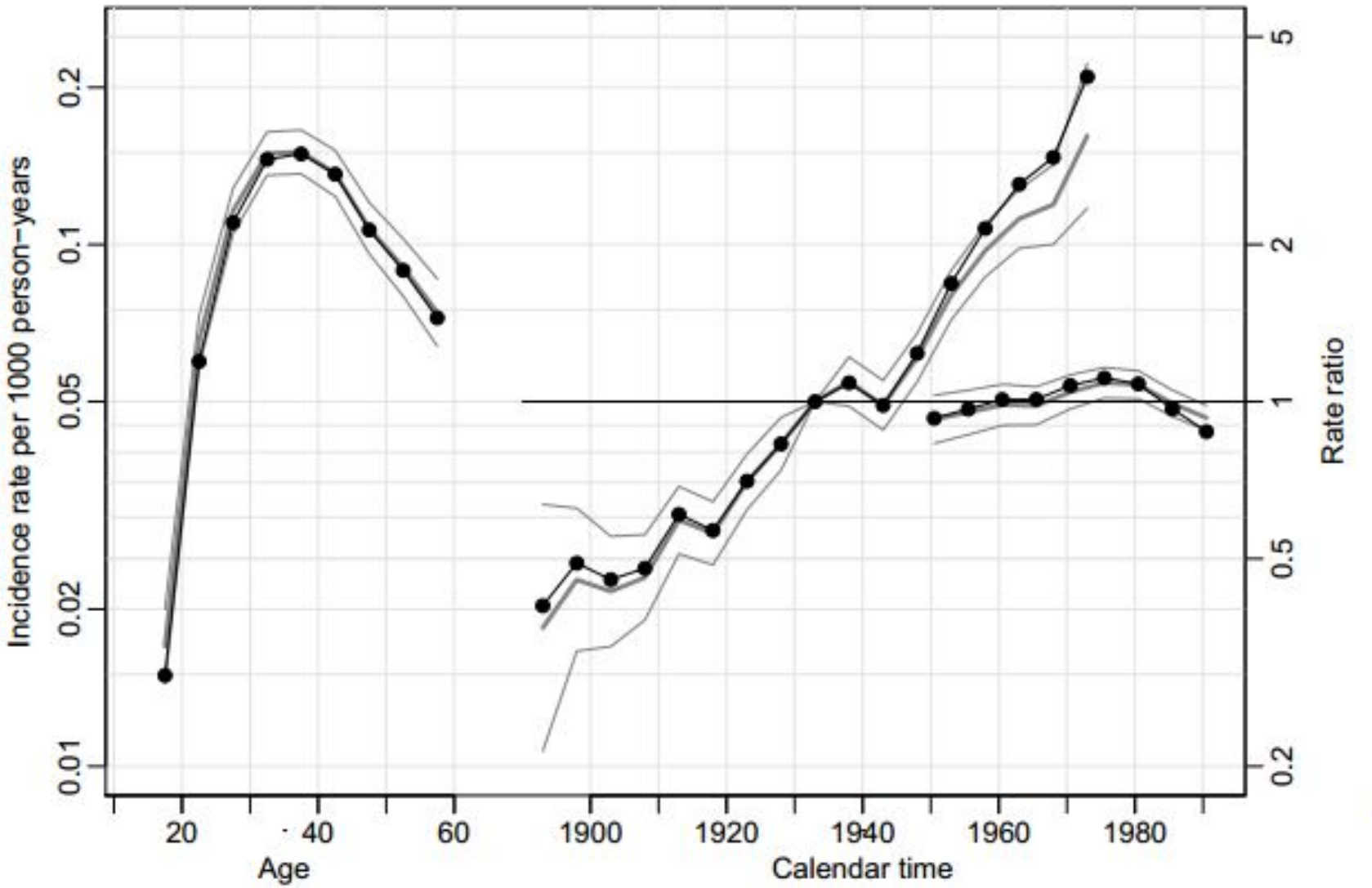
These are provided by SAS and Stata, too, so why R ...?

Many features of R are more appealing in the long run.

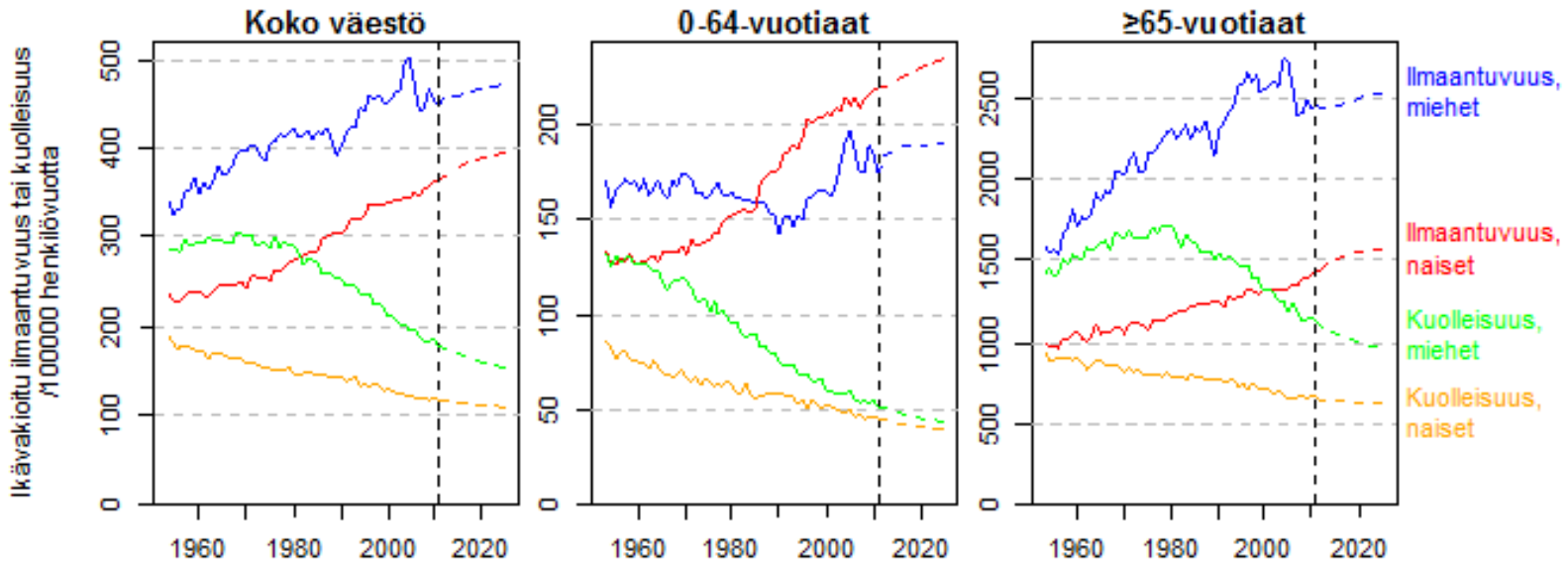
Graphics in R

- Versatile, flexible, high quality, . . .
- Easy to add items (points, lines, text, legends . . .) to an existing graph.
- Fine tuning of symbols, lines, axes, colours, etc. by *graphical parameters* ($>$ 67 of them!)
- Interactive tools using the mouse
  - Put new things on a graph
  - Identify points
- Modern lattice or *Trellis* graphics.
- Saving formats: Metafile, .pdf, .png, .bmp, .jpg, . . .

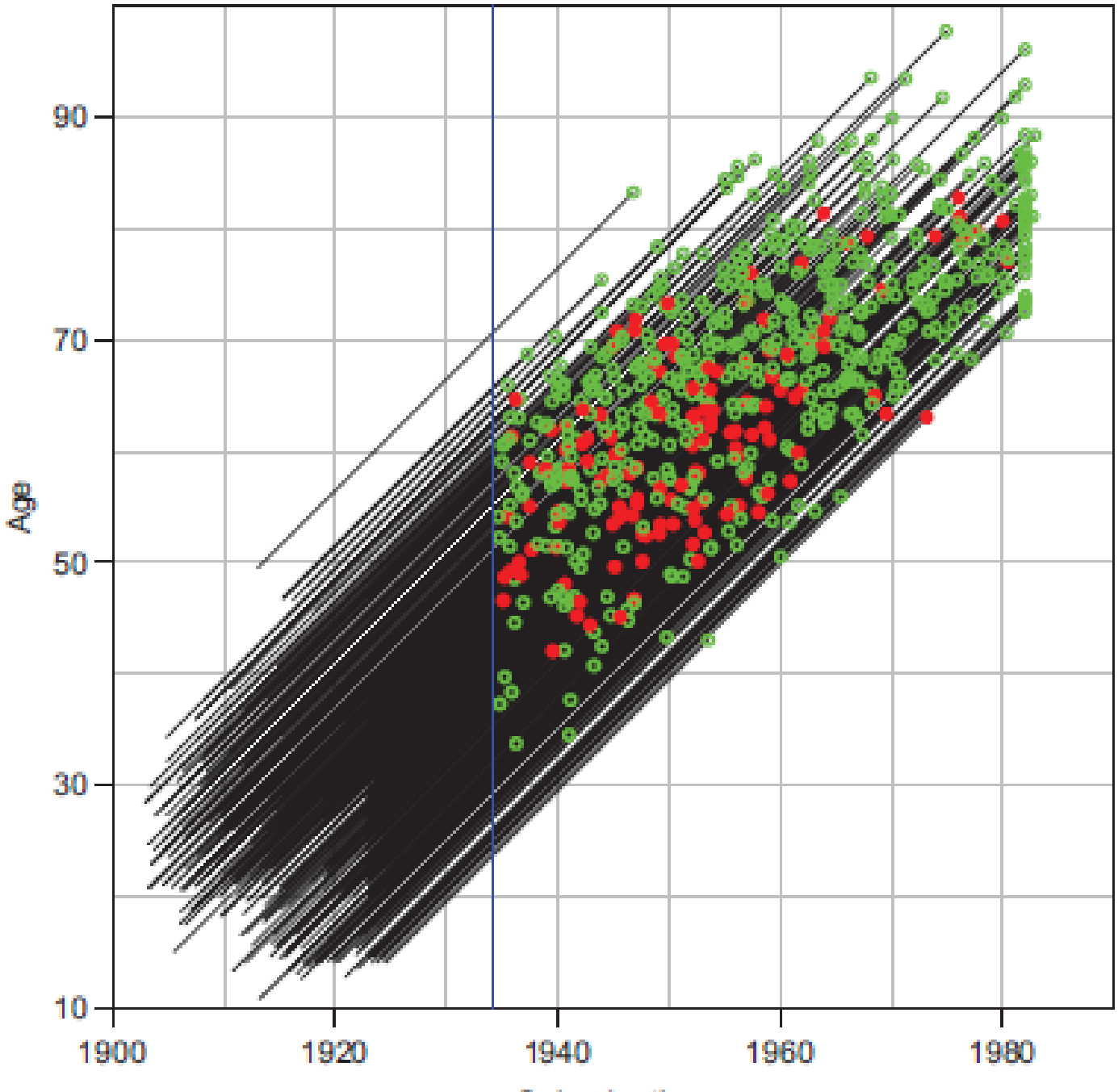
Age-period-cohort incidence in DK



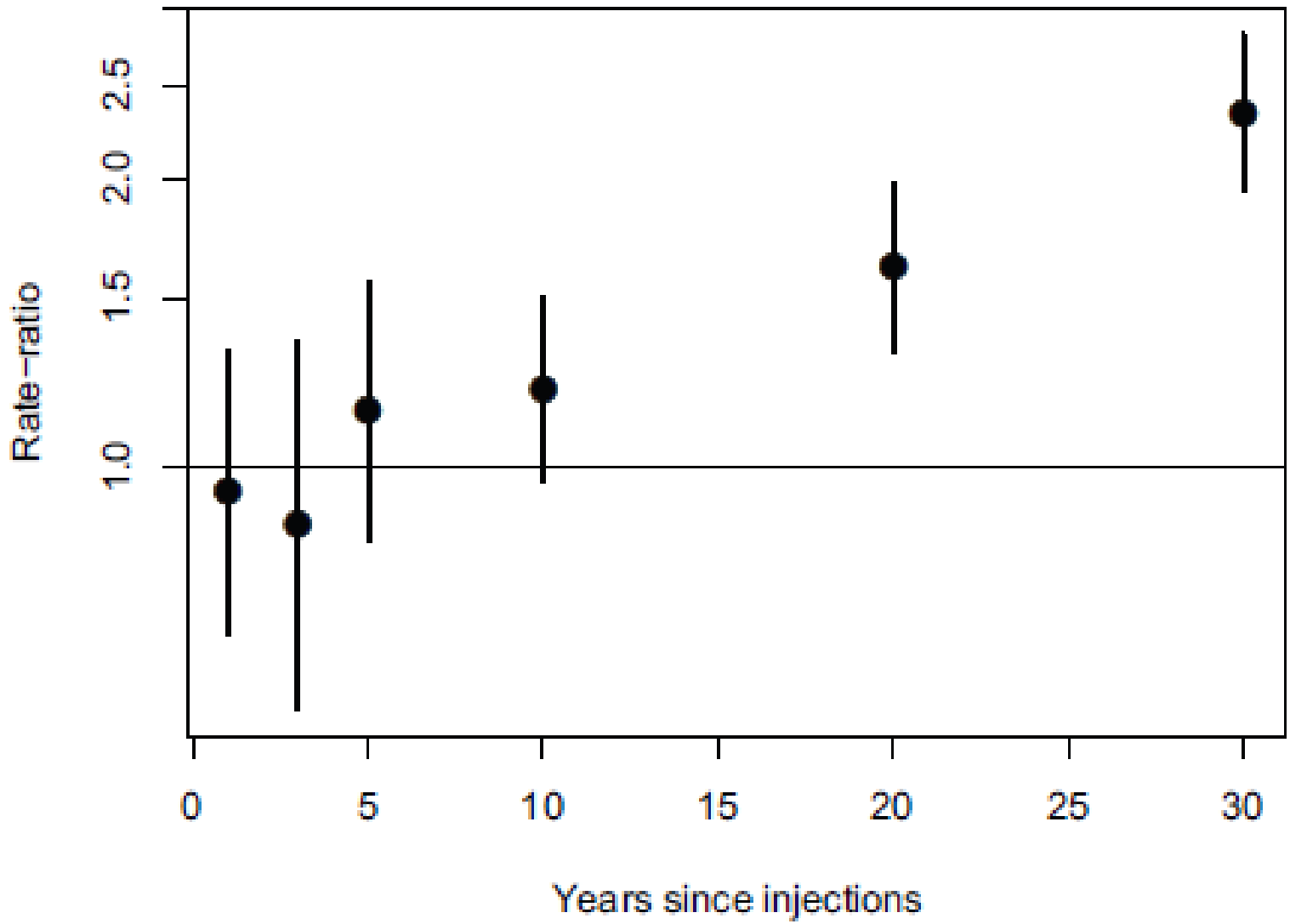
Cancer Predictions in Finland



Follow-up of Welsh nickel cohort in Lexis diagram



RRs & CIs by exposure in a cohort study



Package or library

- Collection of functions pertaining to some specialized application area, e.g. *survival*, *boot*
- Contributed by users of R.
- Available after loading:
  $>$ *library(survival)*
- Alternatively load from the menu bar:
  {*Packages - Load package... - Select one*}
- *New versions easily updated from Internet.*
  (https://www.rdocumentation.org/trends)

R script – R Studio – commands in a file

\ **R script file** is an ASCII file containing a sequence of R commands to be executed.

gskip The **script editor} – use R-Studio R

- In {`R-Studio`} `open the script editor window:` {*New file - R script}, or when editing an existing {script file}: {File - Recent Files},
- *Save the {script file}: {Save} e.g. or {Save As } {*`.R`}
- `Excecute a line` {*Ctrl-Enter}

R script (cont'd)}

- Paint the lines to be excecuted and {*Ctrl -Enter*} *will execute lines.*

- *To run a whole script file, write in console window:* \ {> `source("c:/.../mycmds.R", echo=TRUE)}`

- `The script can also be written and edited by any external editor programs (like Notepad).`

Data objects of different kinds

- {vector}: ordered set of similar elements \ *e.g.* real numbers or character sequences,
- {factor}: categorical variable with levels \ *e.g.* {gender}, levels: {c(1,2)} or {c('male', 'female')};
- {matrix, array}: 2- and k-dimensional tables,
- {data.frame}: "data matrix" (more of this soon!),
- {ts}: time series object,
- {list}: sequence of different types of objects. % - {function, expression}, ...

##Attributes of data objects \ Functions that extract some key properties of objects:

- {length( )}: number of elements,
- {mode( )}: basic type of elements,

Data frame – data matrix

- [Data frame] = a **list** of column vectors
- Rows correspond to observational units, and \ columns (same length) refer to variables.
- Column vectors can be \ {`numeric, character`} or {`logical`}
- `Columns are` **`subobjects`** `of the data frame. Their \ names are not directly accessible. Two possibilities:`
  - `Use "surname$firstname", e.g. {mydata$var1},`
  - `Place the data frame in the search path at position 2: {attach(mydata)}; then use just "firstname": {var1}`

Data frame import from external files

- Common ASCII files, for example:
  read.table("C:/owndir/rfiles/mydata.txt", ...);
  read.table("http://cc.oulu.fi/~tilel/esan.txt",...)
- Files with fixed-width format: {`read.fwf()`};
- `Files created in SPSS, SAS, Stata` *`etc.`*`:`
  `functions \ {read.spss(), read.ssd(),`
  `read.dta()},` *`etc.`* `\ in package {foreign},`
- `Excel-files: either {read.table("clipboard",`
  `...)}, or\ (1) save the Excel-file in {.csv}`
  `or {.txt} format, \ (2) in R: {read.csv2( )}`
  `or {read.table( )} % - Files from an`
  `Internet-address: function {url( )}.`
- `Relational DBMSs: several R packages available.`

Data frame import from external files with R

Choose {*Import Datasets*}

- *[1.] {from text (base)} for **text** files*
- *[2.] {from text (readr)} for **csv** files*
- *[3.] {from excel} for **excel** files*
- *[4.] {from SPSS} for **spss** files*
- *[5.] {from SAS} for **sas** files*
- *[6.] {from STATA} for **stata** files*

Dealing with output

- The console contents, *i.e.* the flow of input commands and output results from the console window, can be \ $ - $ printed on paper: *{File - Print...}* \ *$ - $ saved to an ASCII file: {File - Save to file...}*
- *Selected parts can be copied from the console and pasted to an external file.*
- *Function* `{sink("results.txt")} diverts all subsequent output to an external text file. Back to console: {sink()}.`
- `Choose {it New File - R Markdown} output to MS-Word`
- `Graphs saved in desired format:` *{File - Save...}*

R is a functional language

Most computations in R involve the {invocation} or {call} of functions. They are called by name with a set of arguments separated by commas, *e.g.* `fun(x, y, z)` ; **Function**

- [=] sequence of rules on how to produce desired output:
- [□] **value** of the function, from given input, {*i.e.*}
- *[□] **arguments} of the function.*

Example: Function {`sqrt()`} computes square roots:

```
{> x <- c(0,1,2,3,4) #} argument vector defined\ {>
sqrt(x)    #} call with argument {x}; value printed:\
{[1] 0.000 1.000 1.414 1.732 2.000}
```

Defining a new function (1)

\ {*Example*}. *Function* {CIapp} to calculate an approximate confidence interval from point estimate ({estim}) and std error ({SE}) by formula {estim} $\pm$ $z_{\gamma/2}$ $\times$ {SE}.

Defining code (without prompts): \ \ {CIapp <- function(estim, SE, level = 0.95) { \ z <- qnorm(1- (1-level)/2) # setting the quantile\ lower <- estim - z*SE ; upper <- estim + z*SE \ CIapp <- c(lower, upper) \ CIapp } }

- **Formal arguments}, here {estim, SE, level}

Calling the new function (1)

% \

- **Actual arguments}, used in function call:** \ {> `CIapp(3, 1, 0.9) #} 90% limits:` $3 \pm 1.645 \times 1$ \ {[1] `1.355 4.645 }\ NB!` Positional matching}: order of actual arguments.

- **Keyword matching}: the order of arguments in the call is irrelevant if the names of formal arguments are given \ {> `CIapp(SE=1.0, level=0.90, estim=3) }`

- `If a **default value} for an argument is given in the definition and is OK, it can be omitted in calling \ {> CIapp(3, 1) #} 95% limits:` $3 \pm 1.96 \times 1$ \ {[1] `1.040 4.960 }`

Function call & value object

- Simple call: Evaluates the value of the function with given arguments and prints value items (according to the print **method** specific to the **class** of the value object).

- Call of function and assignment of its value to an object.

To extract information & items from the value object, *e.g.*

- `{str()}: overall structure,`
- `{names()}: names of the components,`
- `{print()}: selective printing of value items,`
- `{summary()}: selective print (not available for all functions). % - {plot()}: certain graphical display, -"-`

Example, function {range()}

Returns the minimum and maximum values of a data vector.

```
{> y <- c(15.3, 10.8, 8.1, 19.5, 5.3) #} data vector
\ {> range(y)  #} simple call with argument {y}\ {[1]
5.3 19.5}\ {> ra <- range(y) #} call with assignment
of value\ {> ra     #} or {print(ra)}, equivalent to
simple call\ {[1] 5.3 19.5}\ {> str(ra)   #}
structure of the value object\ {num [1:2] 5.3 19.5}\
{> ra[1]   #} extracting an item from the value
object\ {[1] 5.3}
```

Different kinds of functions

- Mathematical, *e.g.* {sqrt(x); log(x); exp(x)}.\ Arguments and values typically numeric vectors.
- Data handling, *e.g.* \ {dafr <- data.frame(x, y); \ adata <- read.table("a.dat", header=T, ...); \ % redc1 <- subset(redc, group == "24 h");}\ Main argument(s): data object(s). Value: data object.
- Graphical, *e.g.* \ {plot(y ~ x); stripchart(y, xlim=c(0,3))} \ Main argument(s): data object(s). Value: graph. \ Ancillary arguments: *e.g.* graphical parameters.

Value of the function

- numeric object (*e.g.* vector, matrix) for many \ mathematical and statistical functions,
- data object (e.g. vector, data frame) for \ data handling functions,
- graph for graphical functions,
- table for tabulating functions,
- **list} = a sequence of objects of different kinds, for \ many statistical functions.

Statistical functions

- *{Main} argument(s): Typically data object(s). \ Often a {model formula} like* `{y ~ x} with \ {y} representing the` *response* `variable and \ expression {x} =` *explanatory* `variable(s) or factor(s).`

- *Ancillary* `arguments or` *parameters*`: additional specifications. Some default values usually offered for these.`

- *{Value}: Usually a {list} object consisting of several components of different types. %– Note however graphics functions.*

% Example (ks. vanha luentomoniste, t.test)

Function values as list objects

- **List** = object consisting of an ordered collection of component objects, maybe of different types.
- Provides a convenient way to return the \ results of statistical computation.
- A list with named components formed from existing objects: \ `${ } $ {Lista <- list(name=obj1,title=obj2,addr=obj3)} \ A single component identified: \ {Lista{$}name};`
- `Concatenation of several lists into one: \ {longlist <- c(list1, list2, ...)}.`

Ex: Function *t.test()*

\ Description of syntax in the {help()} page Default S3 method: t.test(x, y = NULL, alternative = c("two.sided", "less", "greater"), mu = 0, paired = FALSE, var.equal = FALSE, conf.level = 0.95, ...)

t.test(formula, data, subset, na.action, ...)
\begin{itemize} - Main argument(s): data vector(s) {x} (and {y}) or formula - Ancillary arguments, like {var.equal, conf.level}: \ Default values given. - **NB.} Dots '{...}'

Example. Red cell folate levels

The data describe red cell folate levels (variable `folate`, μg/l) in two groups
of cardiac bypass surgery patients given two different nitrous oxide ventilation (50% NO + 50% O_2) treatments (variable `group`):

- group 1 ($n_1 = 8$) continuously for 24 h (label `"24 h"`),
- group 2 ($n_2 = 9$) only during the operation (`"oper"`).

Observed folate levels in the two groups: $>$ folate[group==“24 h”] [1] 243 251 275 292 347 354 380 392 $>$ folate[group==“oper”] [1] 206 210 226 249 255 273 285 295 309

Ex: Call of {t.test()} by *formula* argument

t.test(folate ~ group, var.equal=TRUE, conf.level=0.9)

Output:

```
    Two Sample t-test
```

data: folate by group t = 2.5653, df = 15, p-value = 0.02153

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

90 percent confidence interval: 19.09502 101.51610

sample estimates: mean in group 24 h mean in group oper 316.7500 256.4444

Ex: Value returned by {t.test()} is a *list*}

\ Function value assigned to an object and examined: > tfol <- t.test(folate ~ group, var.equal=TRUE, + conf.level=0.9) > str(tfol) # The structure of the object

{List of 9 $ statistic : Named num 2.57 ..- attr(, *"names")= chr "t" $ parameter : Named num 15 ..- attr(*, "names")= chr "df" $ p.value : num 0.0215 $ conf.int : atomic [1:2] 19.1 101.5 ..- attr(, *"conf.level")= num 0.9 $ estimate : Named num [1:2] 317 256 ..- attr(*, "names")= chr [1:2] "mean in group 24 h" "mean in group oper" $ null.value : Named num 0 ..- attr(, *"names")= chr "difference in means" $ alternative: chr "two.sided" $ method : chr " Two Sample t-test" $ data.name : chr "folate by group" - attr(*, "class")= chr "htest"

names(tfol) [1] "statistic" "parameter" "p.value" "conf.int" "estimate" [6] "null.value" "alternative" "method" "data.name"

Ex: Value of {t.test()} utilized}

- Extracting items for further processing: > tfol$estimate # contents of the 'estimate' component mean in group 24 h mean in group oper 316.7500 256.4444

- Utilizing the component value in further calculations:

  mean.diff <- tfolestimate[1]$-$*tfolestimate[2] - Item names in the parent object "inherited". Can be renamed:*

  names(mean.diff) <- c("Mean difference") ; mean.diff
  Mean difference 60.30556

Defining a new function (2)}

We now create a new function {T.estimCI()}. It will return only the mean difference between the groups (which is not reported by {t.test()}!) and its confidence interval.

The function is defined as follows:

```
T.estimCI <- function(x, ... ) { tt <- t.test(x, ...) mean.diff <- ttestimate[1] − ttestimate[2]
names(mean.diff) <- c("Mean difference") T.estimCI <- list(Meandiff = mean.diff, Conflimits = tt$conf.int)
T.estimCI }
```

Calling the new function (2)

\ When {t.estimCI()} is called, a list with 2 named components is returned and printed: > T.estimCI(folate ~ group, var.equal=T, conf.level=0.9)

$Meandiff Mean difference 60.30556 $Conflimits [1] 19.09502 101.51610 attr(,"conf.level") [1] 0.90

Dealing with functions

- Defining code can (mostly) be viewed by typing the function name without parentheses and arguments.
- Functions can be saved into a separate script or source file, {*e.g.*} {`myfuns.R`}, `which may contain several functions.`
- `Source file accessible in an R run after \ {> source("C:/.../myfuns.R") }`
- `Alternatively from menu bar:` {*File – Source R code ...*}
- *Loading from Internet:*\ {> `source("http://.../myfuns.R")`}

Tabulation functions

- {table(c1, c2)}: simple contingency tables
- {xtabs( )}: more elaborate tabulation features
- {ftable(c1, c2, c3)}: "flat" contingency tables % - {apply( )} for e.g. calculating margins in a cont. table % - {sweep( )} for e.g. calculating percentages % in table cells
- {tapply(var,fac,fun)} tabulates values of function {fun()} (for example {mean()}) applied to values of variable {var} in categories of factor {fac},
- {stat.table(index = list(rvar, cvar)}, \ {contents = list(count(), percent(rvar))}, \ {...)} \ in package {Epi} for more informative tabulation.
- package plyr and ddply-funtion ...
- package data.table for BIG data ...
- missing variables...
- other ...