Introduction to R

Road-map

- Data management
- Descriptive statistics
- Tests of association
- Linear regression and ANOVA
- Logistic and Cox proportional hazards regression

Overview of R

- Free general-purpose statistical software

- Command line user interface

- Broad range of statistical functionality

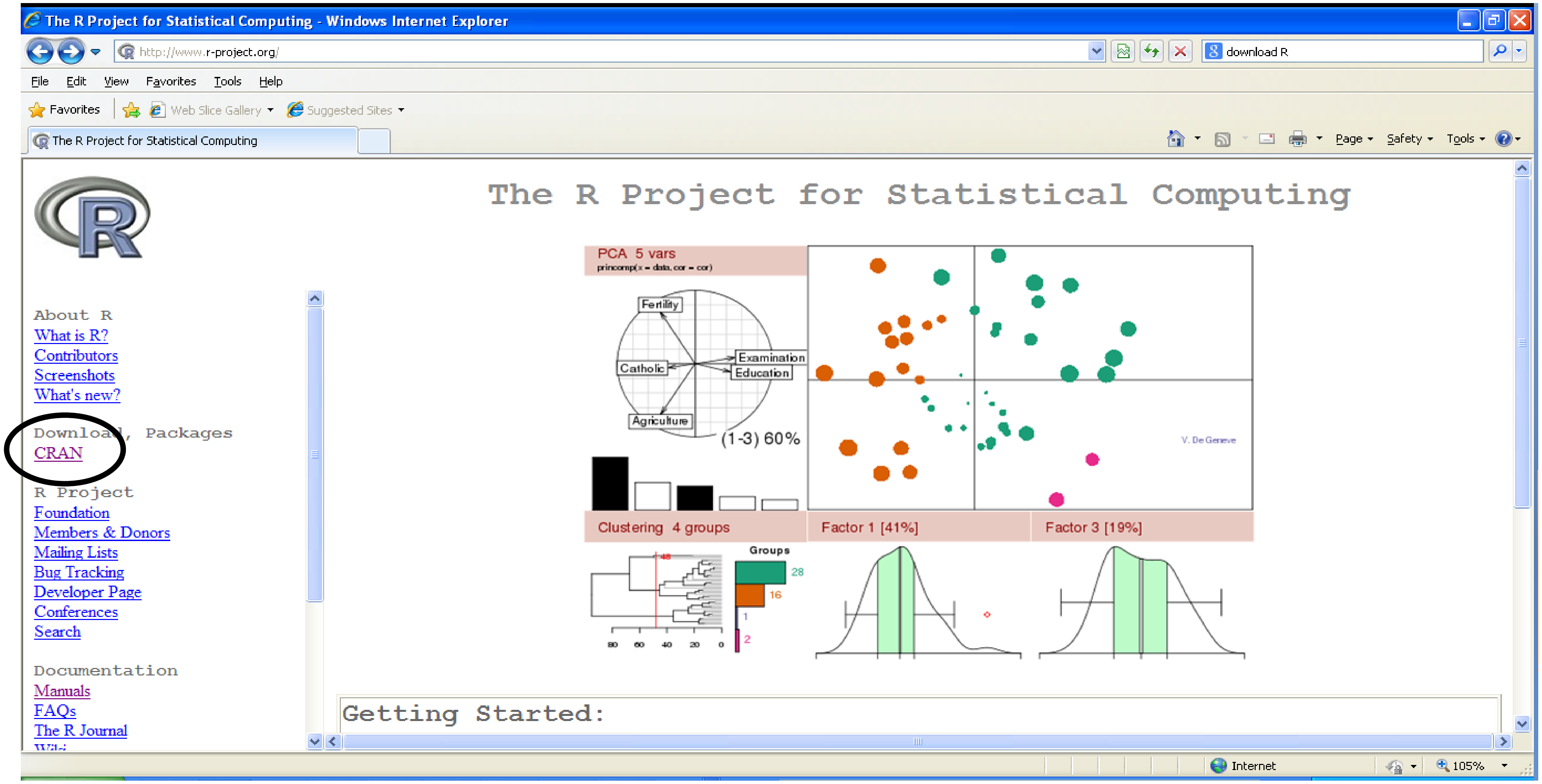
- Excellent graphics generation capabilities

- *Extensive* additional functionality available through free downloadable packages

- User can write their own functions and scripts to further enhance and customize functionality

R download

- R is free and versions for Windows or Mac (or Linux) can be downloaded from http://www.r-project.org/ (choose your favorite mirror)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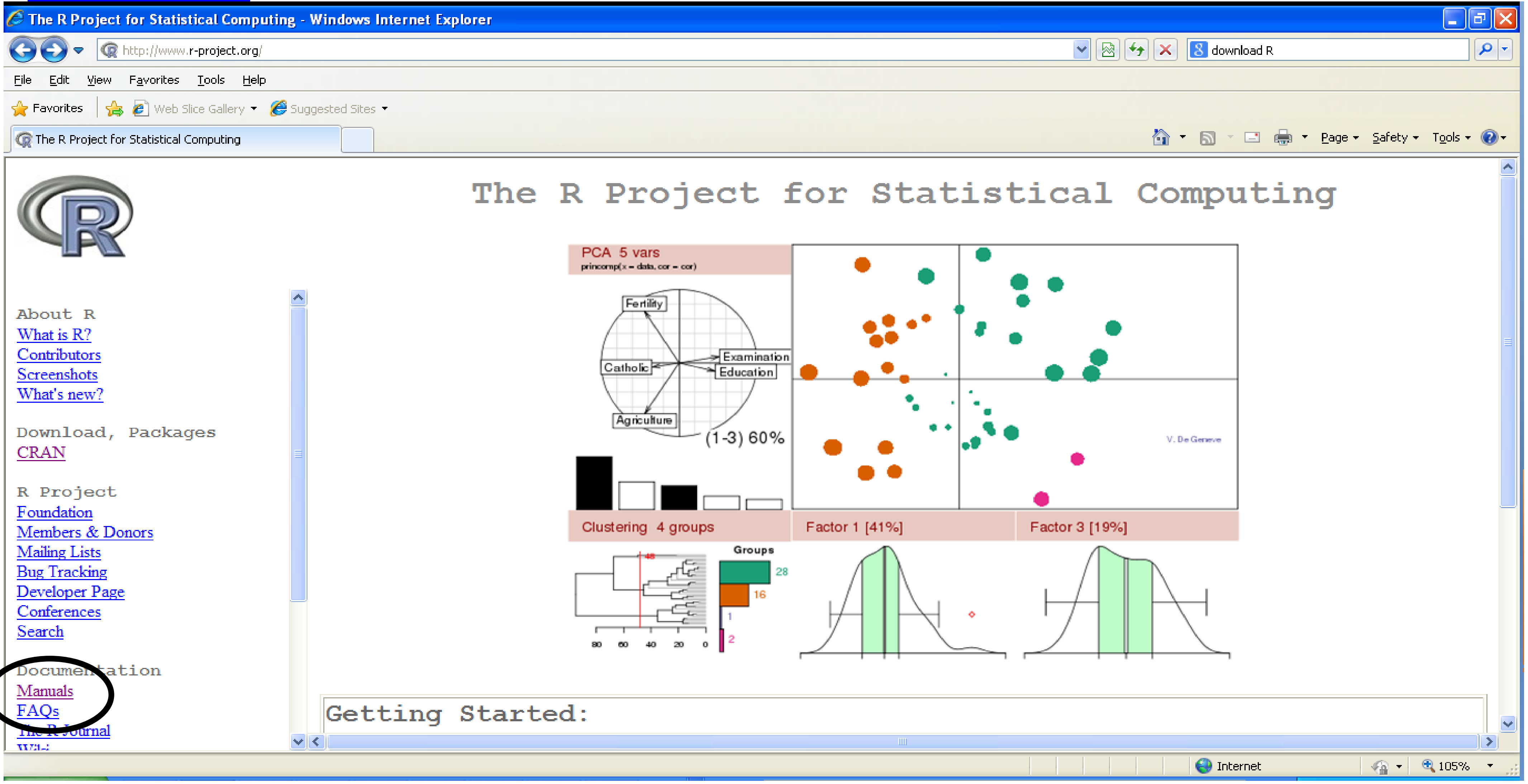
Getting Started:

A few R resources

- A few reference manuals at http://www.r-project.org/
- Short reference card available at http://cran.r-project.org/doc/contrib/Short-refcard.pdf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Getting Started:

R Reference Card

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Getting help

Most R functions have online documentation.

`help(topic)` documentation on `topic`
`?topic` id.
`help.search("topic")` search the help system
`apropos("topic")` the names of all objects in the search list matching the regular expression "topic"
`help.start()` start the HTML version of help
`str(a)` display the internal *str*ucture of an R object
`summary(a)` gives a "summary" of `a`, usually a statistical summary but it is *generic* meaning it has different operations for different classes of `a`
`ls()` show objects in the search path; specify `pat="pat"` to search on a pattern
`ls.str()` str() for each variable in the search path
`dir()` show files in the current directory
`methods(a)` shows S3 methods of `a`
`methods(class=class(a))` lists all the methods to handle objects of class a

Input and output

`load()` load the datasets written with `save`
`data(x)` loads specified data sets
`library(x)` load add-on packages
`read.table(file)` reads a file in table format and creates a data frame from it; the default separator `sep=""` is any whitespace; use `header=TRUE` to read the first line as a header of column names; use `as.is=TRUE` to prevent character vectors from being converted to factors; use `comment.char=""` to prevent `"#"` from being interpreted as a comment; use `skip=n` to skip `n` lines before reading data; see the help for options on row naming, NA treatment, and others
`read.csv("filename",header=TRUE)` id. but with defaults set for reading comma-delimited files
`read.delim("filename",header=TRUE)` id. but with defaults set for reading tab-delimited files
`read.fwf(file,widths,header=FALSE,sep="\t",as.is=FALSE)` read a table of *f*ixed *w*idth *f*ormatted data into a 'data.frame'; `widths` is an integer vector, giving the widths of the fixed-width fields
`save(file,...)` saves the specified objects (...) in the XDR platform-independent binary format
`save.image(file)` saves all objects
`cat(..., file="", sep=" ")` prints the arguments after coercing to character; `sep` is the character separator between arguments
`print(a, ...)` prints its arguments; generic, meaning it can have different methods for different objects
`format(x,...)` format an R object for pretty printing
`write.table(x,file="",row.names=TRUE,col.names=TRUE, sep=" ")` prints `x` after converting to a data frame; if `quote` is `TRUE`, character or factor columns are surrounded by quotes (`"`); `sep` is the field separator; `eol` is the end-of-line separator; `na` is the string for missing values; use `col.names=NA` to add a blank column header to get the column headers aligned correctly for spreadsheet input
`sink(file)` output to `file`, until `sink()`

Most of the I/O functions have a `file` argument. This can often be a character string naming a file or a connection. `file=""` means the standard input or output. Connections can include files, pipes, zipped files, and R variables.

On windows, the file connection can also be used with `description = "clipboard"`. To read a table copied from Excel, use
`x <- read.delim("clipboard")`
To write a table to the clipboard for Excel, use
`write.table(x,"clipboard",sep="\t",col.names=NA)`
For database interaction, see packages `RODBC`, `DBI`, `RMySQL`, `RPgSQL`, and `ROracle`. See packages `XML`, `hdf5`, `netCDF` for reading other file formats.

Data creation

`c(...)` generic function to combine arguments with the default forming a vector; with `recursive=TRUE` descends through lists combining all elements into one vector
`from:to` generates a sequence; ":" has operator priority; 1:4 + 1 is "2,3,4,5"
`seq(from,to)` generates a sequence `by=` specifies increment; `length=` specifies desired length
`seq(along=x)` generates `1, 2, ..., length(along)`; useful for `for` loops
`rep(x,times)` replicate `x` `times`; use `each=` to repeat "each" element of `x` `each` times; `rep(c(1,2,3),2)` is 1 2 3 1 2 3; `rep(c(1,2,3),each=2)` is 1 1 2 2 3 3
`data.frame(...)` create a data frame of the named or unnamed arguments; `data.frame(v=1:4,ch=c("a","B","c","d"),n=10)`; shorter vectors are recycled to the length of the longest
`list(...)` create a list of the named or unnamed arguments; `list(a=c(1,2),b="hi",c=3i)`;
`array(x,dim=)` array with data `x`; specify dimensions like `dim=c(3,4,2)`; elements of `x` recycle if `x` is not long enough
`matrix(x,nrow=,ncol=)` matrix; elements of `x` recycle
`factor(x,levels=)` encodes a vector `x` as a factor
`gl(n,k,length=n*k,labels=1:n)` generate levels (factors) by specifying the pattern of their levels; `k` is the number of levels, and `n` is the number of replications
`expand.grid()` a data frame from all combinations of the supplied vectors or factors
`rbind(...)` combine arguments by rows for matrices, data frames, and others
`cbind(...)` id. by columns

Slicing and extracting data

Indexing vectors

`x[n]`	nth element
`x[-n]`	all *but* the nth element
`x[1:n]`	first `n` elements
`x[-(1:n)]`	elements from `n+1` to the end
`x[c(1,4,2)]`	specific elements
`x["name"]`	element named `"name"`
`x[x > 3]`	all elements greater than 3
`x[x > 3 & x < 5]`	all elements between 3 and 5
`x[x %in% c("a","and","the")]`	elements in the given set

Indexing lists

`x[n]`	list with elements `n`
`x[[n]]`	nth element of the list
`x[["name"]]`	element of the list named `"name"`
`x$name`	id.

Indexing matrices

`x[i,j]`	element at row `i`, column `j`
`x[i,]`	row `i`
`x[,j]`	column `j`
`x[,c(1,3)]`	columns 1 and 3
`x["name",]`	row named `"name"`

Indexing data frames (matrix indexing plus the following)

`x[["name"]]`	column named `"name"`
`x$name`	id.

Variable conversion

`as.array(x), as.data.frame(x), as.numeric(x), as.logical(x), as.complex(x), as.character(x), ...` convert type; for a complete list, use `methods(as)`

Variable information

`is.na(x), is.null(x), is.array(x), is.data.frame(x), is.numeric(x), is.complex(x), is.character(x), ...` test for type; for a complete list, use `methods(is)`
`length(x)` number of elements in `x`
`dim(x)` Retrieve or set the dimension of an object; `dim(x) <- c(3,2)`
`dimnames(x)` Retrieve or set the dimension names of an object
`nrow(x)` number of rows; `NROW(x)` is the same but treats a vector as a one-row matrix
`ncol(x)` and **`NCOL(x)`** id. for columns
`class(x)` get or set the class of `x`; `class(x) <- "myclass"`
`unclass(x)` remove the class attribute of `x`
`attr(x,which)` get or set the attribute `which` of `x`
`attributes(obj)` get or set the list of attributes of `obj`

Data selection and manipulation

`which.max(x)` returns the index of the greatest element of **`x`**
`which.min(x)` returns the index of the smallest element of **`x`**
`rev(x)` reverses the elements of `x`
`sort(x)` sorts the elements of `x` in increasing order; to sort in decreasing order: `rev(sort(x))`
`cut(x,breaks)` divides `x` into intervals (factors); `breaks` is the number of cut intervals or a vector of cut points
`match(x, y)` returns a vector of the same length than `x` with the elements of `x` which are in `y` (`NA` otherwise)
`which(x == a)` returns a vector of the indices of `x` if the comparison operation is true (`TRUE`), in this example the values of `i` for which `x[i] == a` (the argument of this function must be a variable of mode logical)
`choose(n, k)` computes the combinations of k events among n repetitions $= n!/[(n-k)!k!]$
`na.omit(x)` suppresses the observations with missing data (`NA`) (suppresses the corresponding line if `x` is a matrix or a data frame)
`na.fail(x)` returns an error message if `x` contains at least one `NA`

`unique(x)` if `x` is a vector or a data frame, returns a similar object but with the duplicate elements suppressed

`table(x)` returns a table with the numbers of the differents values of `x` (typically for integers or factors)

`subset(x, ...)` returns a selection of `x` with respect to criteria (`...`, typically comparisons: `x$V1 < 10`); if `x` is a data frame, the option `select` gives the variables to be kept or dropped using a minus sign

`sample(x, size)` resample randomly and without replacement `size` elements in the vector `x`, the option `replace = TRUE` allows to resample with replacement

`prop.table(x,margin=)` table entries as fraction of marginal table

Math

`sin,cos,tan,asin,acos,atan,atan2,log,log10,exp`

`max(x)` maximum of the elements of `x`

`min(x)` minimum of the elements of `x`

`range(x)` id. then `c(min(x), max(x))`

`sum(x)` sum of the elements of `x`

`diff(x)` lagged and iterated differences of vector `x`

`prod(x)` product of the elements of `x`

`mean(x)` mean of the elements of `x`

`median(x)` median of the elements of `x`

`quantile(x,probs=)` sample quantiles corresponding to the given probabilities (defaults to 0,.25,.5,.75,1)

`weighted.mean(x, w)` mean of `x` with weights `w`

`rank(x)` ranks of the elements of `x`

`var(x)` or `cov(x)` variance of the elements of `x` (calculated on $n-1$); if `x` is a matrix or a data frame, the variance-covariance matrix is calculated

`sd(x)` standard deviation of `x`

`cor(x)` correlation matrix of `x` if it is a matrix or a data frame (1 if `x` is a vector)

`var(x, y)` or `cov(x, y)` covariance between `x` and `y`, or between the columns of `x` and those of `y` if they are matrices or data frames

`cor(x, y)` linear correlation between `x` and `y`, or correlation matrix if they are matrices or data frames

`round(x, n)` rounds the elements of `x` to `n` decimals

`log(x, base)` computes the logarithm of `x` with base `base`

`scale(x)` if `x` is a matrix, centers and reduces the data; to center only use the option `center=FALSE`, to reduce only `scale=FALSE` (by default `center=TRUE, scale=TRUE`)

`pmin(x,y,...)` a vector which *i*th element is the minimum of `x[i]`, `y[i]`, ...

`pmax(x,y,...)` id. for the maximum

`cumsum(x)` a vector which *i*th element is the sum from `x[1]` to `x[i]`

`cumprod(x)` id. for the product

`cummin(x)` id. for the minimum

`cummax(x)` id. for the maximum

`union(x,y)`, `intersect(x,y)`, `setdiff(x,y)`, `setequal(x,y)`, `is.element(el,set)` "set" functions

`Re(x)` real part of a complex number

`Im(x)` imaginary part

`Mod(x)` modulus; `abs(x)` is the same

`Arg(x)` angle in radians of the complex number

`Conj(x)` complex conjugate

`convolve(x,y)` compute the several kinds of convolutions of two sequences

`fft(x)` Fast Fourier Transform of an array

`mvfft(x)` FFT of each column of a matrix

`filter(x,filter)` applies linear filtering to a univariate time series or to each series separately of a multivariate time series

Many math functions have a logical parameter `na.rm=FALSE` to specify missing data (NA) removal.

Matrices

`t(x)` transpose

`diag(x)` diagonal

`%*%` matrix multiplication

`solve(a,b)` solves `a %*% x = b` for `x`

`solve(a)` matrix inverse of `a`

`rowsum(x)` sum of rows for a matrix-like object; **`rowSums(x)`** is a faster version

`colsum(x)`, `colSums(x)` id. for columns

`rowMeans(x)` fast version of row means

`colMeans(x)` id. for columns

Advanced data processing

`apply(X,INDEX,FUN=)` a vector or array or list of values obtained by applying a function `FUN` to margins (`INDEX`) of `X`

`lapply(X,FUN)` apply `FUN` to each element of the list `X`

`tapply(X,INDEX,FUN=)` apply `FUN` to each cell of a ragged array given by `X` with indexes `INDEX`

`by(data,INDEX,FUN)` apply `FUN` to data frame `data` subsetted by `INDEX`

`merge(a,b)` merge two data frames by common columns or row names

`xtabs(a b,data=x)` a contingency table from cross-classifying factors

`aggregate(x,by,FUN)` splits the data frame `x` into subsets, computes summary statistics for each, and returns the result in a convenient form; `by` is a list of grouping elements, each as long as the variables in `x`

`stack(x, ...)` transform data available as separate columns in a data frame or list into a single column

`unstack(x, ...)` inverse of `stack()`

`reshape(x, ...)` reshapes a data frame between 'wide' format with repeated measurements in separate columns of the same record and 'long' format with the repeated measurements in separate records; use `(direction="wide")` or `(direction="long")`

Strings

`paste(...)` concatenate vectors after converting to character; `sep=` is the string to separate terms (a single space is the default); `collapse=` is an optional string to separate "collapsed" results

`substr(x,start,stop)` substrings in a character vector; can also assign, as `substr(x, start, stop) <- value`

`strsplit(x,split)` split `x` according to the substring `split`

`grep(pattern,x)` searches for matches to `pattern` within `x`; see `?regex`

`gsub(pattern,replacement,x)` replacement of matches determined by regular expression matching `sub()` is the same but only replaces the first occurrence.

`tolower(x)` convert to lowercase

`toupper(x)` convert to uppercase

`match(x,table)` a vector of the positions of first matches for the elements of `x` among `table`

`x %in% table` id. but returns a logical vector

`pmatch(x,table)` partial matches for the elements of `x` among `table`

`nchar(x)` number of characters

Dates and Times

The class `Date` has dates without times. `POSIXct` has dates and times, including time zones. Comparisons (e.g. >), `seq()`, and `difftime()` are useful. `Date` also allows + and −. `?DateTimeClasses` gives more information. See also package `chron`.

`as.Date(s)` and **`as.POSIXct(s)`** convert to the respective class; `format(dt)` converts to a string representation. The default string format is "2001-02-21". These accept a second argument to specify a format for conversion. Some common formats are:

`%a`, `%A` Abbreviated and full weekday name.
`%b`, `%B` Abbreviated and full month name.
`%d` Day of the month (01–31).
`%H` Hours (00–23).
`%I` Hours (01–12).
`%j` Day of year (001–366).
`%m` Month (01–12).
`%M` Minute (00–59).
`%p` AM/PM indicator.
`%S` Second as decimal number (00–61).
`%U` Week (00–53); the first Sunday as day 1 of week 1.
`%w` Weekday (0–6, Sunday is 0).
`%W` Week (00–53); the first Monday as day 1 of week 1.
`%y` Year without century (00–99). Don't use.
`%Y` Year with century.
`%z` (output only.) Offset from Greenwich; `-0800` is 8 hours west of.
`%Z` (output only.) Time zone as a character string (empty if not available).

Where leading zeros are shown they will be used on output but are optional on input. See `?strftime`.

Plotting

`plot(x)` plot of the values of `x` (on the *y*-axis) ordered on the *x*-axis

`plot(x, y)` bivariate plot of `x` (on the *x*-axis) and `y` (on the *y*-axis)

`hist(x)` histogram of the frequencies of `x`

`barplot(x)` histogram of the values of `x`; use `horiz=FALSE` for horizontal bars

`dotchart(x)` if `x` is a data frame, plots a Cleveland dot plot (stacked plots line-by-line and column-by-column)

`pie(x)` circular pie-chart

`boxplot(x)` "box-and-whiskers" plot

`sunflowerplot(x, y)` id. than `plot()` but the points with similar coordinates are drawn as flowers which petal number represents the number of points

`stripplot(x)` plot of the values of `x` on a line (an alternative to `boxplot()` for small sample sizes)

`coplot(x~y | z)` bivariate plot of `x` and `y` for each value or interval of values of `z`

`interaction.plot (f1, f2, y)` if `f1` and `f2` are factors, plots the means of `y` (on the *y*-axis) with respect to the values of `f1` (on the *x*-axis) and of `f2` (different curves); the option `fun` allows to choose the summary statistic of `y` (by default `fun=mean`)

matplot(x,y) bivariate plot of the first column of x *vs.* the first one of y, the second one of x *vs.* the second one of y, etc.
fourfoldplot(x) visualizes, with quarters of circles, the association between two dichotomous variables for different populations (x must be an array with dim=c(2, 2, k), or a matrix with dim=c(2, 2) if $k = 1$)
assocplot(x) Cohen–Friendly graph showing the deviations from independence of rows and columns in a two dimensional contingency table
mosaicplot(x) 'mosaic' graph of the residuals from a log-linear regression of a contingency table
pairs(x) if x is a matrix or a data frame, draws all possible bivariate plots between the columns of x
plot.ts(x) if x is an object of class "ts", plot of x with respect to time, x may be multivariate but the series must have the same frequency and dates
ts.plot(x) id. but if x is multivariate the series may have different dates and must have the same frequency
qqnorm(x) quantiles of x with respect to the values expected under a normal law
qqplot(x, y) quantiles of y with respect to the quantiles of x
contour(x, y, z) contour plot (data are interpolated to draw the curves), x and y must be vectors and z must be a matrix so that dim(z)=c(length(x), length(y)) (x and y may be omitted)
filled.contour(x, y, z) id. but the areas between the contours are coloured, and a legend of the colours is drawn as well
image(x, y, z) id. but with colours (actual data are plotted)
persp(x, y, z) id. but in perspective (actual data are plotted)
stars(x) if x is a matrix or a data frame, draws a graph with segments or a star where each row of x is represented by a star and the columns are the lengths of the segments
symbols(x, y, ...) draws, at the coordinates given by x and y, symbols (circles, squares, rectangles, stars, thermometres or "boxplots") which sizes, colours ... are specified by supplementary arguments
termplot(mod.obj) plot of the (partial) effects of a regression model (mod.obj)

The following parameters are common to many plotting functions:
add=FALSE if TRUE superposes the plot on the previous one (if it exists)
axes=TRUE if FALSE does not draw the axes and the box
type="p" specifies the type of plot, "p": points, "l": lines, "b": points connected by lines, "o": id. but the lines are over the points, "h": vertical lines, "s": steps, the data are represented by the top of the vertical lines, "S": id. but the data are represented by the bottom of the vertical lines
xlim=, ylim= specifies the lower and upper limits of the axes, for example with xlim=c(1, 10) or xlim=range(x)
xlab=, ylab= annotates the axes, must be variables of mode character
main= main title, must be a variable of mode character
sub= sub-title (written in a smaller font)

Low-level plotting commands

points(x, y) adds points (the option type= can be used)
lines(x, y) id. but with lines
text(x, y, labels, ...) adds text given by labels at coordinates (x,y); a typical use is: plot(x, y, type="n"); text(x, y, names)
mtext(text, side=3, line=0, ...) adds text given by text in the margin specified by side (see axis() below); line specifies the line from the plotting area
segments(x0, y0, x1, y1) draws lines from points (x0,y0) to points (x1,y1)
arrows(x0, y0, x1, y1, angle= 30, code=2) id. with arrows at points (x0,y0) if code=2, at points (x1,y1) if code=1, or both if code=3; angle controls the angle from the shaft of the arrow to the edge of the arrow head
abline(a,b) draws a line of slope b and intercept a
abline(h=y) draws a horizontal line at ordinate y
abline(v=x) draws a vertical line at abcissa x
abline(lm.obj) draws the regression line given by lm.obj
rect(x1, y1, x2, y2) draws a rectangle which left, right, bottom, and top limits are x1, x2, y1, and y2, respectively
polygon(x, y) draws a polygon linking the points with coordinates given by x and y
legend(x, y, legend) adds the legend at the point (x,y) with the symbols given by legend
title() adds a title and optionally a sub-title
axis(side, vect) adds an axis at the bottom (side=1), on the left (2), at the top (3), or on the right (4); vect (optional) gives the abcissa (or ordinates) where tick-marks are drawn
rug(x) draws the data x on the *x*-axis as small vertical lines
locator(n, type="n", ...) returns the coordinates (*x*,*y*) after the user has clicked n times on the plot with the mouse; also draws symbols (type="p") or lines (type="l") with respect to optional graphic parameters (...); by default nothing is drawn (type="n")

Graphical parameters

These can be set globally with **par(...)**; many can be passed as parameters to plotting commands.
adj controls text justification (0 left-justified, 0.5 centred, 1 right-justified)
bg specifies the colour of the background (ex. : bg="red", bg="blue", ... the list of the 657 available colours is displayed with colors())
bty controls the type of box drawn around the plot, allowed values are: "o", "l", "7", "c", "u" ou "]" (the box looks like the corresponding character); if bty="n" the box is not drawn
cex a value controlling the size of texts and symbols with respect to the default; the following parameters have the same control for numbers on the axes, cex.axis, the axis labels, cex.lab, the title, cex.main, and the sub-title, cex.sub
col controls the color of symbols and lines; use color names: "red", "blue" see colors() or as "#RRGGBB"; see rgb(), hsv(), gray(), and rainbow(); as for cex there are: col.axis, col.lab, col.main, col.sub
font an integer which controls the style of text (1: normal, 2: italics, 3: bold, 4: bold italics); as for cex there are: font.axis, font.lab, font.main, font.sub
las an integer which controls the orientation of the axis labels (0: parallel to the axes, 1: horizontal, 2: perpendicular to the axes, 3: vertical)
lty controls the type of lines, can be an integer or string (1: "solid", 2: "dashed", 3: "dotted", 4: "dotdash", 5: "longdash", 6: "twodash", or a string of up to eight characters (between "0" and "9") which specifies alternatively the length, in points or pixels, of the drawn elements and the blanks, for example lty="44" will have the same effect than lty=2
lwd a numeric which controls the width of lines, default 1
mar a vector of 4 numeric values which control the space between the axes and the border of the graph of the form c(bottom, left, top, right), the default values are c(5.1, 4.1, 4.1, 2.1)
mfcol a vector of the form c(nr,nc) which partitions the graphic window as a matrix of nr lines and nc columns, the plots are then drawn in columns
mfrow id. but the plots are drawn by row
pch controls the type of symbol, either an integer between 1 and 25, or any single character within ""

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16 ● 17 ▲ 18 ◆ 19 ● 20 • 21 ○ 22 □ 23 ◇ 24 △ 25 ▽ " * . · X X a a ? ?

ps an integer which controls the size in points of texts and symbols
pty a character which specifies the type of the plotting region, "s": square, "m": maximal
tck a value which specifies the length of tick-marks on the axes as a fraction of the smallest of the width or height of the plot; if tck=1 a grid is drawn
tcl a value which specifies the length of tick-marks on the axes as a fraction of the height of a line of text (by default tcl=-0.5)
xaxt if xaxt="n" the *x*-axis is set but not drawn (useful in conjonction with axis(side=1, ...))
yaxt if yaxt="n" the *y*-axis is set but not drawn (useful in conjonction with axis(side=2, ...))

Lattice (Trellis) graphics

xyplot(y~x) bivariate plots (with many functionalities)
barchart(y~x) histogram of the values of y with respect to those of x
dotplot(y~x) Cleveland dot plot (stacked plots line-by-line and column-by-column)
densityplot(~x) density functions plot
histogram(~x) histogram of the frequencies of x
bwplot(y~x) "box-and-whiskers" plot
qqmath(~x) quantiles of x with respect to the values expected under a theoretical distribution
stripplot(y~x) single dimension plot, x must be numeric, y may be a factor
qq(y~x) quantiles to compare two distributions, x must be numeric, y may be numeric, character, or factor but must have two 'levels'
splom(~x) matrix of bivariate plots
parallel(~x) parallel coordinates plot
levelplot(z~x*y|g1*g2) coloured plot of the values of z at the coordinates given by x and y (x, y and z are all of the same length)
wireframe(z~x*y|g1*g2) 3d surface plot
cloud(z~x*y|g1*g2) 3d scatter plot

In the normal Lattice formula, `y x|g1*g2` has combinations of optional conditioning variables `g1` and `g2` plotted on separate panels. Lattice functions take many of the same arguments as base graphics plus also `data=` the data frame for the formula variables and `subset=` for subsetting. Use `panel=` to define a custom panel function (see `apropos("panel")` and `?llines`). Lattice functions return an object of class trellis and have to be `print`-ed to produce the graph. Use `print(xyplot(...))` inside functions where automatic printing doesn't work. Use `lattice.theme` and `lset` to change Lattice defaults.

Optimization and model fitting

`optim(par, fn, method = c("Nelder-Mead", "BFGS", "CG", "L-BFGS-B", "SANN")` general-purpose optimization; `par` is initial values, `fn` is function to optimize (normally minimize)
`nlm(f,p)` minimize function `f` using a Newton-type algorithm with starting values `p`
`lm(formula)` fit linear models; `formula` is typically of the form `response termA + termB + ...`; use `I(x*y) + I(x^2)` for terms made of nonlinear components
`glm(formula,family=)` fit generalized linear models, specified by giving a symbolic description of the linear predictor and a description of the error distribution; `family` is a description of the error distribution and link function to be used in the model; see `?family`
`nls(formula)` nonlinear least-squares estimates of the nonlinear model parameters
`approx(x,y=)` linearly interpolate given data points; `x` can be an xy plotting structure
`spline(x,y=)` cubic spline interpolation
`loess(formula)` fit a polynomial surface using local fitting
Many of the formula-based modeling functions have several common arguments: `data=` the data frame for the formula variables, `subset=` a subset of variables used in the fit, `na.action=` action for missing values: `"na.fail"`, `"na.omit"`, or a function. The following generics often apply to model fitting functions:
`predict(fit,...)` predictions from `fit` based on input data
`df.residual(fit)` returns the number of residual degrees of freedom
`coef(fit)` returns the estimated coefficients (sometimes with their standard-errors)
`residuals(fit)` returns the residuals
`deviance(fit)` returns the deviance
`fitted(fit)` returns the fitted values
`logLik(fit)` computes the logarithm of the likelihood and the number of parameters
`AIC(fit)` computes the Akaike information criterion or AIC

Statistics

`aov(formula)` analysis of variance model
`anova(fit,...)` analysis of variance (or deviance) tables for one or more fitted model objects
`density(x)` kernel density estimates of `x`
`binom.test()`, **`pairwise.t.test()`**, **`power.t.test()`**, **`prop.test()`**, **`t.test()`**, ... use `help.search("test")`

Distributions

`rnorm(n, mean=0, sd=1)` Gaussian (normal)
`rexp(n, rate=1)` exponential
`rgamma(n, shape, scale=1)` gamma
`rpois(n, lambda)` Poisson
`rweibull(n, shape, scale=1)` Weibull
`rcauchy(n, location=0, scale=1)` Cauchy
`rbeta(n, shape1, shape2)` beta
`rt(n, df)` 'Student' (t)
`rf(n, df1, df2)` Fisher–Snedecor (F) (χ^2)
`rchisq(n, df)` Pearson
`rbinom(n, size, prob)` binomial
`rgeom(n, prob)` geometric
`rhyper(nn, m, n, k)` hypergeometric
`rlogis(n, location=0, scale=1)` logistic
`rlnorm(n, meanlog=0, sdlog=1)` lognormal
`rnbinom(n, size, prob)` negative binomial
`runif(n, min=0, max=1)` uniform
`rwilcox(nn, m, n)`, `rsignrank(nn, n)` Wilcoxon's statistics
All these functions can be used by replacing the letter `r` with `d`, `p` or `q` to get, respectively, the probability density (`d`*`func`*`(x, ...)`), the cumulative probability density (`p`*`func`*`(x, ...)`), and the value of quantile (`q`*`func`*`(p, ...)`, with $0 < p < 1$).

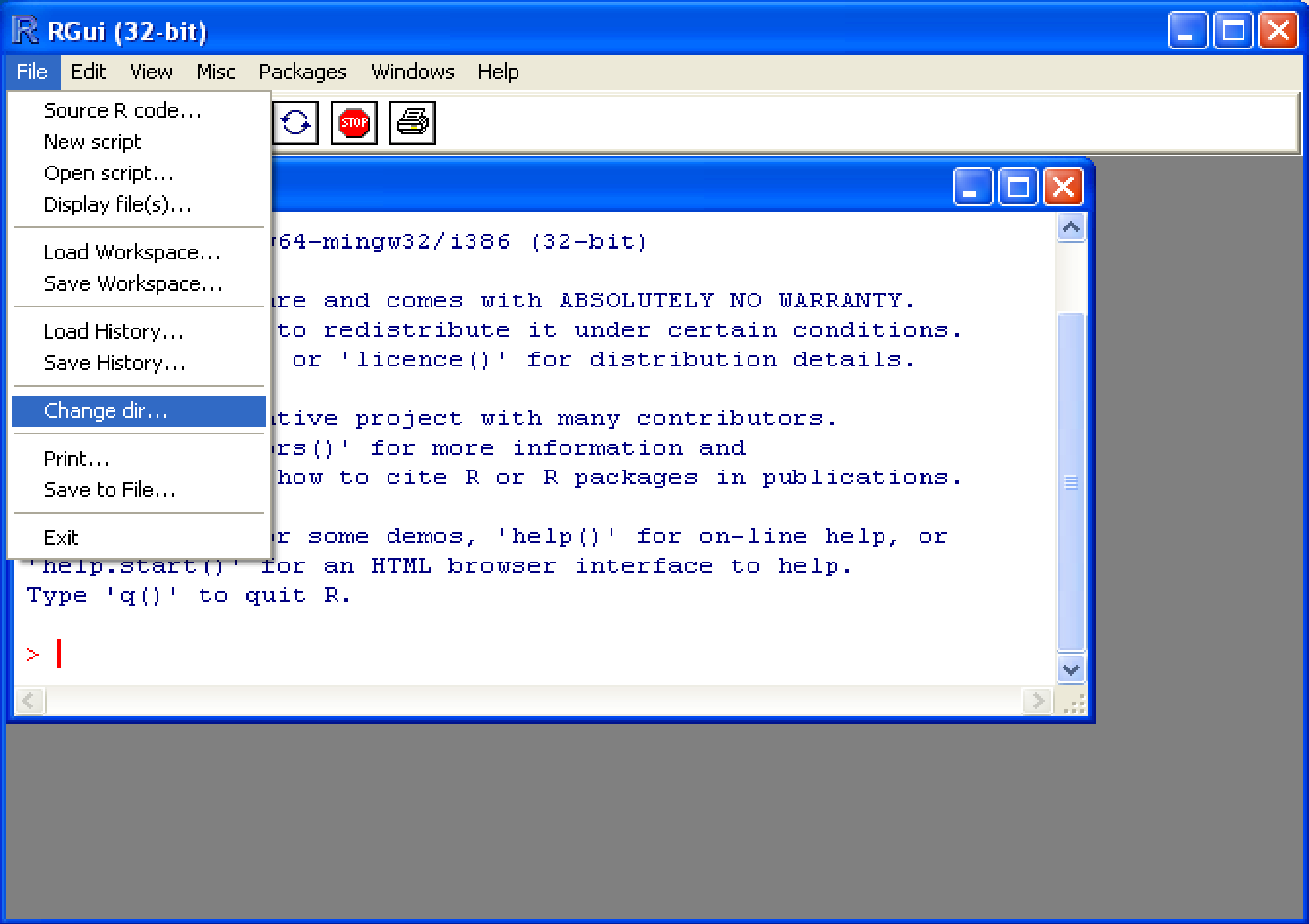
Programming

`function( arglist ) expr` function definition
`return(value)`
`if(cond) expr`
`if(cond) cons.expr else alt.expr`
`for(var in seq) expr`
`while(cond) expr`
`repeat expr`
`break`
`next`
Use braces {} around statements
`ifelse(test, yes, no)` a value with the same shape as `test` filled with elements from either `yes` or `no`
`do.call(funname, args)` executes a function call from the name of the function and a list of arguments to be passed to it

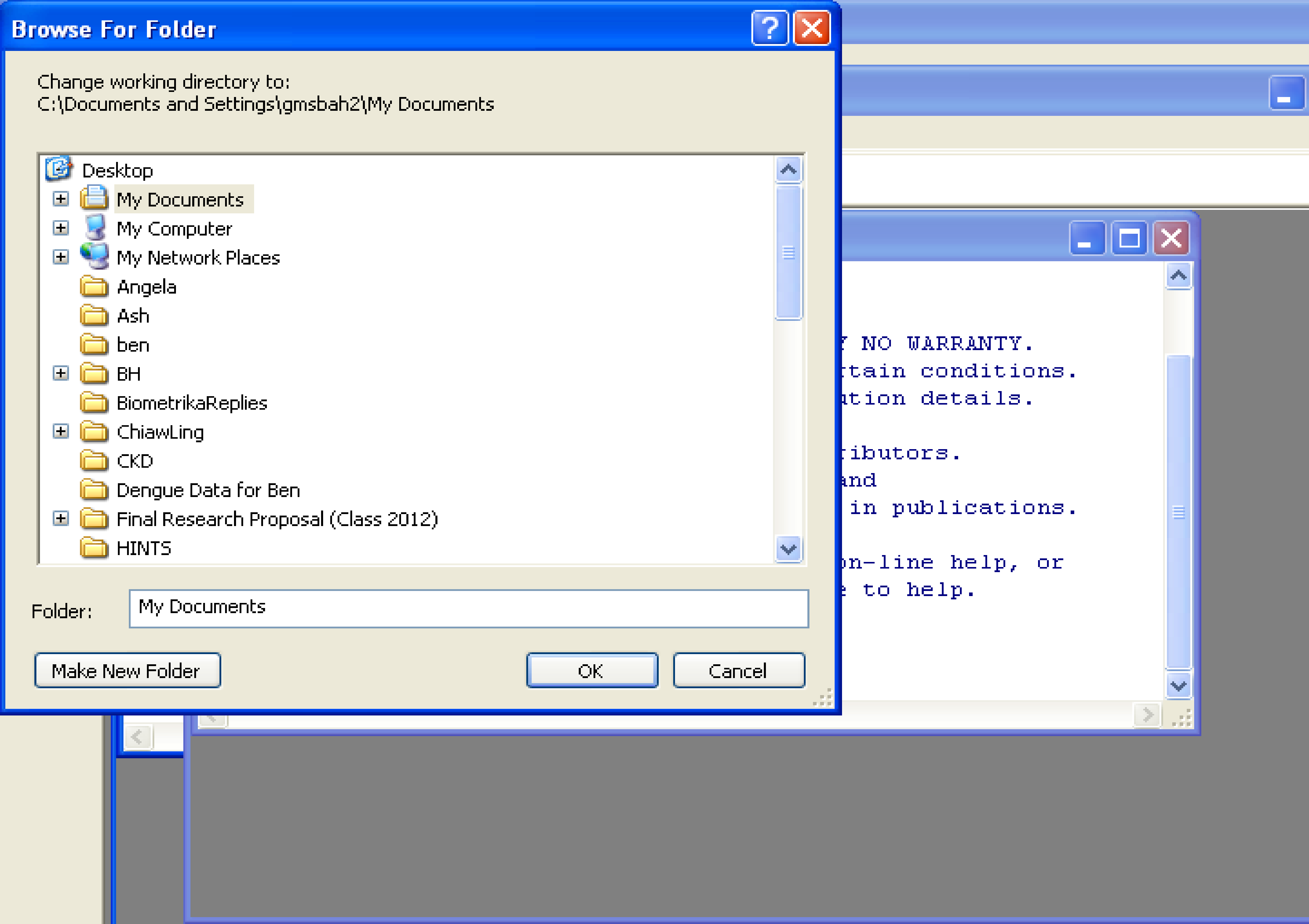
Changing the working directory in R

- Open R

- Change working directory
  - When loading data into R, the software will look in the working directory (unless directed otherwise)
  - Change to <relevant directory>.
  - “File”, “Change dir…” Then, browse to directory.



```
                   r64-mingw32/i386 (32-bit)

                   re and comes with ABSOLUTELY NO WARRANTY.
                    to redistribute it under certain conditions.
                     or 'licence()' for distribution details.

                   tive project with many contributors.
                   rs()' for more information and
                    how to cite R or R packages in publications.

                   r some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> 
```



Browse For Folder

Change working directory to:
C:\Documents and Settings\gmsbah2\My Documents

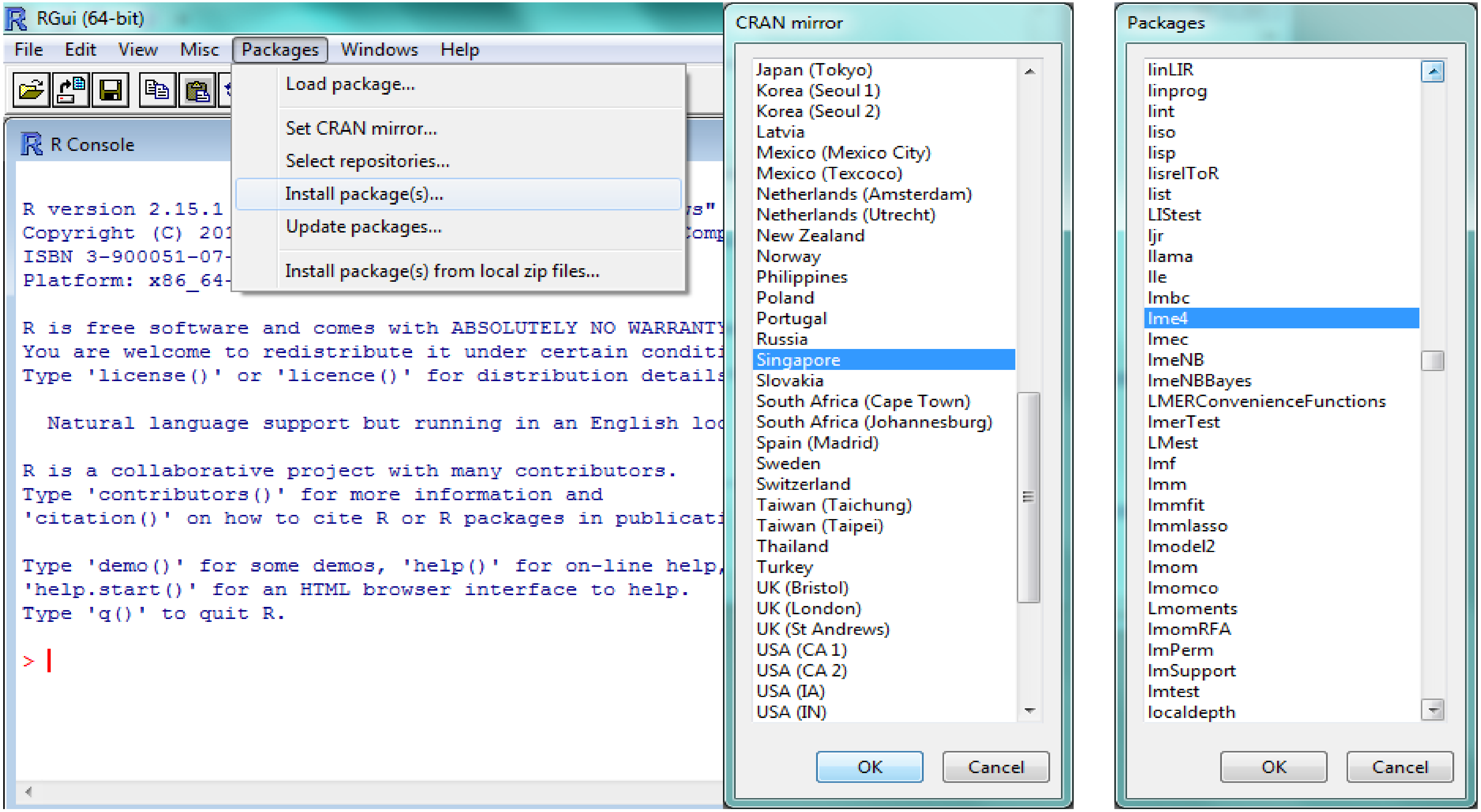
Folder: My Documents

```
Y NO WARRANTY.
rtain conditions.
ation details.

ributors.
and
 in publications.

on-line help, or
e to help.
```

Installing packages in R

- Install packages
  - Particular types of functionality in R require the user to install packages
  - Install packages lme4 (generalized linear mixed models), geepack (generalized estimating equations models), and survival (survival analyses)
  - “Packages”, “Install package(s)…” Then, select mirror, and select package (packages have already been installed on these computers).

Installing packages in R



```
R version 2.15.1                                                   s"
Copyright (C) 201                                                 Comp
ISBN 3-900051-07-
Platform: x86_64-

R is free software and comes with ABSOLUTELY NO WARRANTY
You are welcome to redistribute it under certain conditi
Type 'license()' or 'licence()' for distribution details

  Natural language support but running in an English loc

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publicati

Type 'demo()' for some demos, 'help()' for on-line help,
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> |
```

CRAN mirror:

Japan (Tokyo)
Korea (Seoul 1)
Korea (Seoul 2)
Latvia
Mexico (Mexico City)
Mexico (Texcoco)
Netherlands (Amsterdam)
Netherlands (Utrecht)
New Zealand
Norway
Philippines
Poland
Portugal
Russia
[✓ Singapore]
Slovakia
South Africa (Cape Town)
South Africa (Johannesburg)
Spain (Madrid)
Sweden
Switzerland
Taiwan (Taichung)
Taiwan (Taipei)
Thailand
Turkey
UK (Bristol)
UK (London)
UK (St Andrews)
USA (CA 1)
USA (CA 2)
USA (IA)
USA (IN)

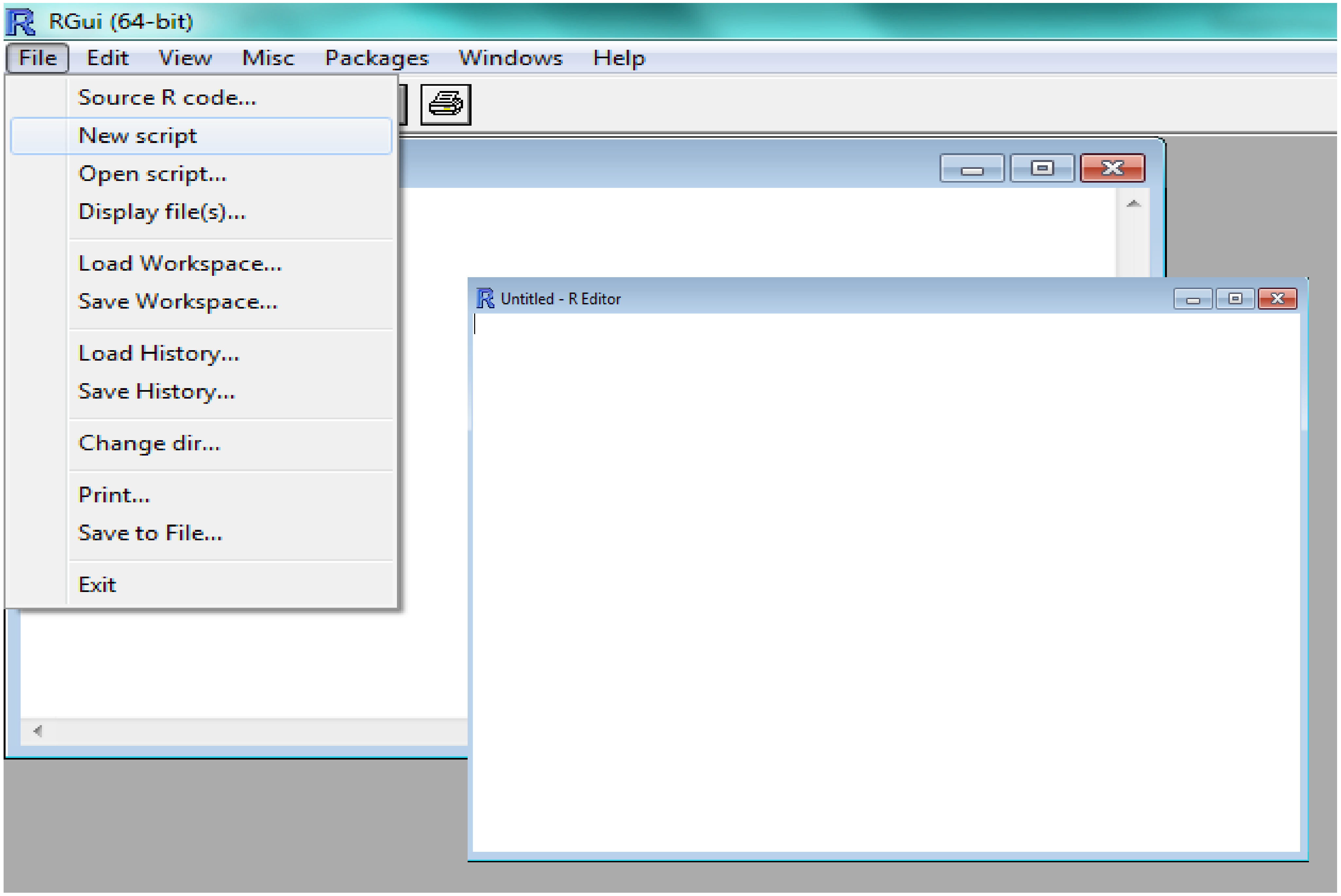
Packages:

linLIR
linprog
lint
liso
lisp
lisrelToR
list
LIStest
ljr
llama
lle
lmbc
[✓ lme4]
lmec
lmeNB
lmeNBBayes
LMERConvenienceFunctions
lmerTest
LMest
lmf
lmm
lmmfit
lmmlasso
lmodel2
lmom
lmomco
Lmoments
lmomRFA
lmPerm
lmSupport
lmtest
localdepth

Starting a new R script

- Typically, R commands are stored in a script which can be executed at the user’s leisure or at a later date
- Open a new script in the R console. “File”, “New script”Then, browse to directory.
- Click “Save as…”, browse to selected location, and name the script.
- Don’t forget “.R” or “.txt” after the file name (e.g. RworkshopScript.txt)

Starting a new R script



Miscellaneous items before importing the data

- **Naming rules/tips**
  - R is case sensitive (i.e. mydata and myData are different)
  - Use upper & lower case e.g. myData
- **Comments/help**
  - ?seq help(seq)
  - ??"generalized estimating equations“
- **Logical tests (TRUE/FALSE)**

```
myNumbers=seq(0,18,3)
myNumbers==12
myNumbers<=5
myNumbers>10
```

Miscellaneous items before importing the data

- **Objects**
  - Scalars

```
myNumber=4
```

  - Vectors and matrices

```
myVector=c(1,2,3)
myMatrix=matrix(seq(0,15,3),byrow=TRUE,ncol=2)
```

  - Dataframes store row and column names as well as column types (numeric, factor, etc.)
  - Lists can store any type of R object
- **Indexing**
  - Scalars have only one element (no indices)
  - Individual entries in vectors, matrices, dataframes, and lists can be accessed using numeric indices or vectors of logicals (TRUE/FALSE)

```
myVector[2]
myMatrix[3,]
myMatrix[2,2]
```

Preparing data for R

- Data saved as .csv (comma delimited) is a good choice for loading into R.
- Other formats (e.g. SAS or SPSS) can *potentially* be loaded (foreign package)
- Open our datafiles “dataset.xls” and “data1.xls” Click “Save As”, select “CSV (Comma delimited)” from “Save as type:” box.
- Note that only selected sheet is saved
- Text fields with commas can cause problems

Loading and examining data in R

```
#### Read data into R ####

myData=read.csv("dataset.csv",header=TRUE)

#### Display myData ####

myData

#### or ####

fix(myData)

#### Show attributes of myData (or any other object in R) ####

attributes(myData)

#### Show variable names myData ####

attributes(myData)$names
```

Checking and assigning variable types in R

```
#### Examine the type of each variable ####

class(myData$patient_id)
class(myData$age)
class(myData$gender)
class(myData$diabetes)
class(myData$pain)
class(myData$health_status)
class(myData$mortality_12months)
class(myData$pain2)

#### Assign proper variable types to each variable ####

myData$patient_id=as.factor(myData$patient_id)
myData$age=as.numeric(myData$age)
myData$gender=as.factor(myData$gender)
myData$diabetes=as.factor(myData$diabetes)
myData$pain=as.numeric(myData$pain)
myData$health_status=as.factor(myData$health_status)
myData$mortality_12months=as.factor(myData$mortality_12months)
myData$pain2=as.numeric(myData$pain2)
```

Summarizing variables in R

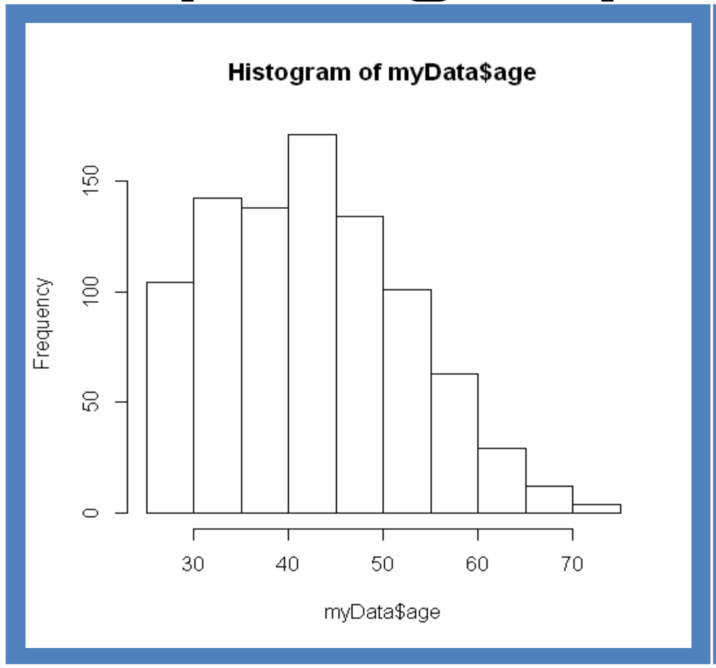
```
#### Summaries of variables ####

summary(myData$age)
summary(myData$gender)
summary(myData$diabetes)
summary(myData$pain)
summary(myData$health_status)
summary(myData$mortality_12months)
summary(myData$pain2)

mean(myData$age,na.rm=TRUE)
sd(myData$age,na.rm=TRUE)

median(myData$pain)
min(myData$pain)
max(myData$pain)
IQR(myData$pain)
```

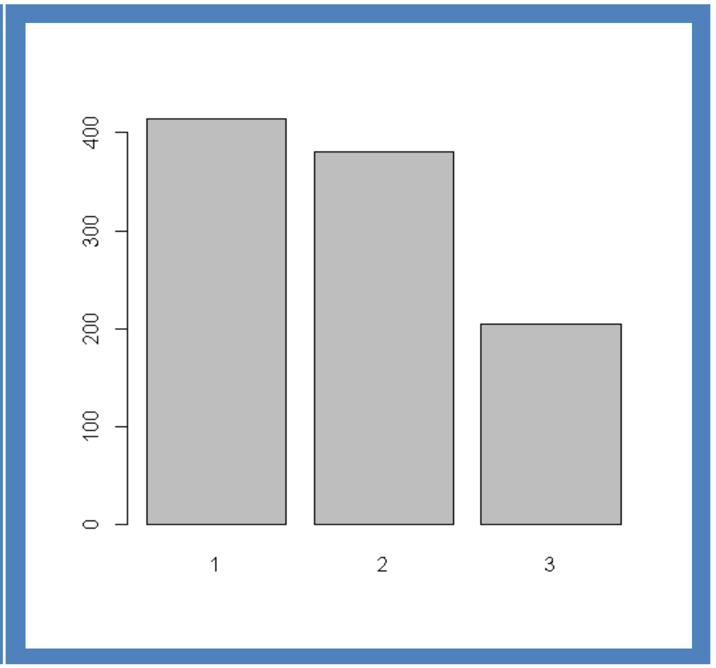
```
#### A few more detailed summaries ####

#### Summary of women's ages ####

summary(myData$age[myData$gender=="0"])

#### Cross-tabulation of gender and diabetes
    ####

table(myData$gender,myData$diabetes)
```

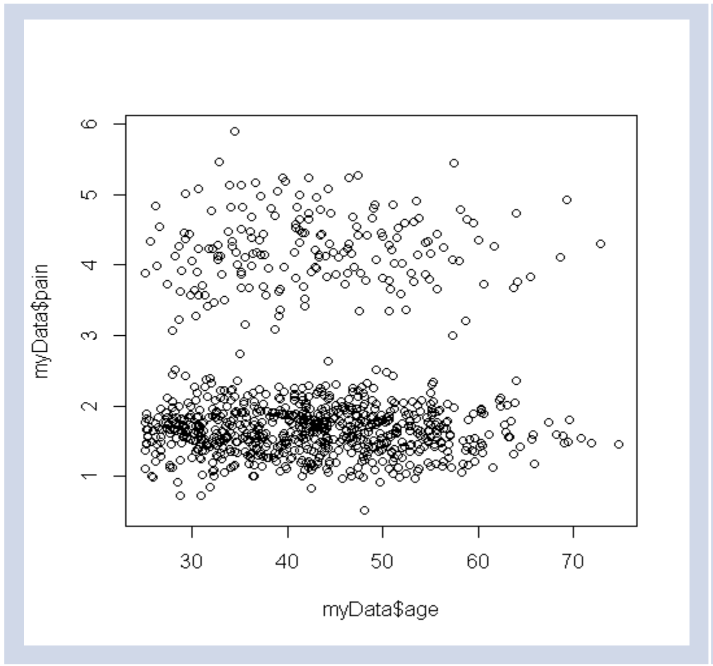
Generating simple graphs in R

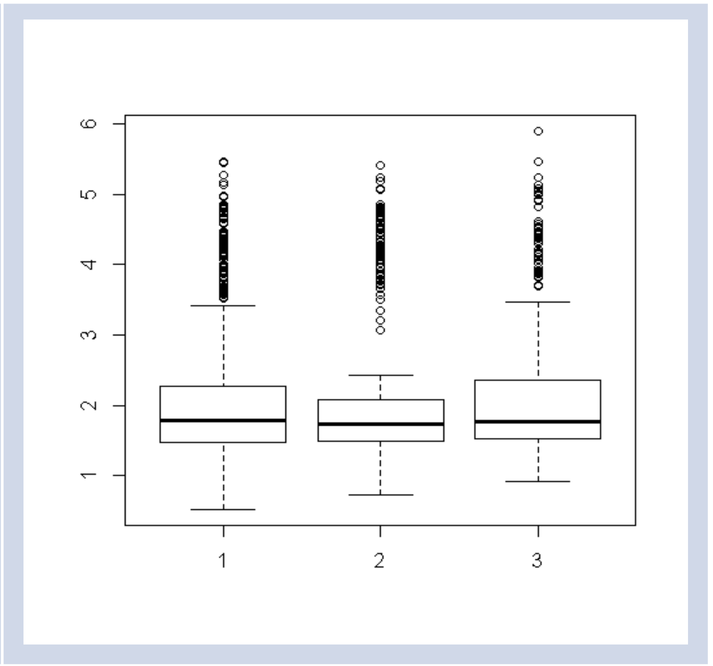
```
#### A few graphical summaries ####

#### Histogram of age ####

hist(myData$age)

#### Barchart of health status ####

plot(myData$health_status)

#### Scatterplot of pain by age ####

plot(myData$age,myData$pain)

#### Boxplots of pain by health status ####

plot(myData$health_status,myData$pain)
```

- To save, highlight plot window in R console, "File", "Save as", and select format.



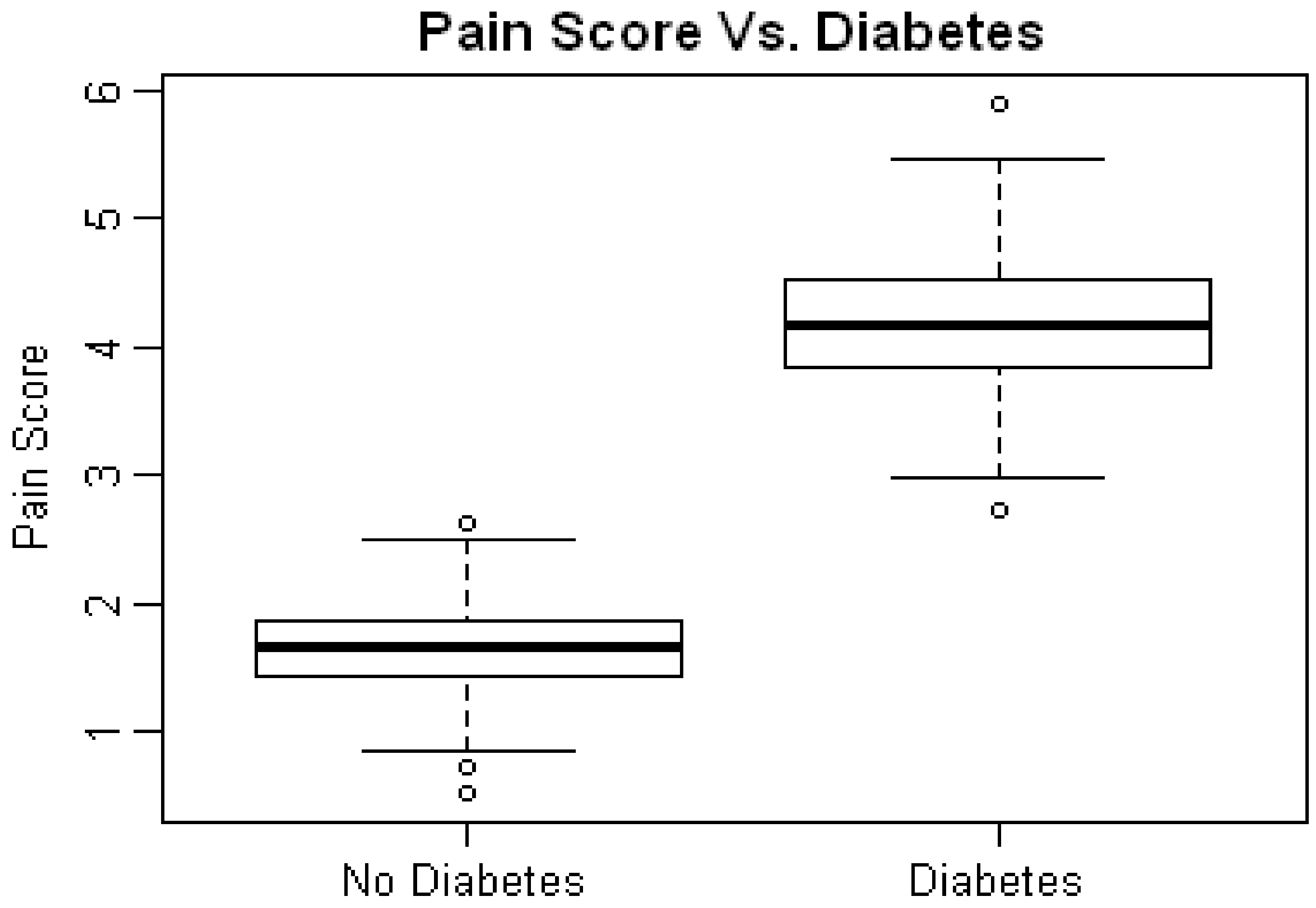






A more complete plot in R

```
#### A more complete plot ####

dev.new(height=3,width=4)

par(mai=c(0.3,0.5,0.3,0.05),cex=0.8)

plot(myData$diabetes,myData$pain,
    axes=FALSE,xlab="",ylab="",
    main="Pain Score Vs. Diabetes")

box()

axis(1,at=c(1,2),labels=c("No Diabetes","Diabetes"),
      padj=-0.5)

axis(2,padj=0.5)

title(ylab="Pain Score",line=2)

#### Check documentation for more options ####

?par
?plot
```



Creating new variables in R

- Suppose we want a log(pain) variable and to categorize age into <=35, 36-45, 46-55, >55 years

```
#### Create logPain variable ####

logPain=log(myData$pain)

#### Create categorized age variable ####

ageCats=sapply(myData$age,function(x){
  ifelse(x<=35,return("<=35"),
        ifelse(x<=45,return("36-45"),
              ifelse(x<=55,return("46-
    55"),return(">55"))))
})
```

```
#### alternatively ####

ageCatsV2=cut(myData$age,breaks=c(0,35,45,5
    5,Inf))

#### how do they look? ####

cbind(ageCats,ageCatsV2)

#### use as.character(),
#### so that factor labels are displayed
#### instead of factor numbers

cbind(ageCats,as.character(ageCatsV2))
```

Univariate tests of association for independent observations

- Comparing central tendency (e.g. means) in 2 or more independent groups (t-test, Wilcoxon rank sum test, ANOVA, Kruskal-Wallis)

- Comparing proportions in 2 or more groups (chi-squared test, Fisher’s exact test)

- Tests of correlation (Pearson, Spearman)

Comparing central tendency in 2 or more independent groups

- Consider comparing the mean ages of diabetics and non-diabetics

```
#### t-test of mean age by diabetes status
#### (two groups) ####

t.test(myData$age~myData$diabetes)

#### Wilcoxon rank sum test of whether ages
#### tend to be larger to smaller by
#### diabetes status
#### (two groups) ####

wilcox.test(myData$age~myData$diabetes)
```

- Consider comparing the mean pain scores across health status

```
#### ANOVA of pain by health status
#### (two or more groups) ####

summary(lm(myData$pain~myData$health_status))

#### Kruskal-Wallis test of whether pain
#### scores tend to be larger to smaller by
#### health status
#### (two or more groups) ####

kruskal.test(myData$pain~myData$health_status)
```

Comparing proportions in 2 or more independent groups

- Consider comparing the proportion of mortalities at 12 months among diabetics and non-diabetics

```
#### Chi-squared test of mortality by diabetes ####

chisq.test(myData$mortality_12month,myData$diabetes)

#### Fisher's exact test of mortality by diabetes ####

fisher.test(myData$mortality_12month,myData$diabetes)

#### alternatively ####

myTable=table(myData$mortality_12month,myData$diabetes)

chisq.test(myTable)

fisher.test(myTable)
```

Tests of correlation

- Consider testing for an association between age and pain score

```
#### test for correlation between age
#### and pain score ####

cor.test(myData$age,myData$pain)

#### if we think the relationship may be
#### non-linear ####

cor.test(myData$age,myData$pain,
            method="spearman")
```

```
#### alternatively, linear regression ####

#### Wald test p-values ####

summary(lm(myData$age~myData$pain))

#### or ####

summary(lm(myData$pain~myData$age))

#### or ####

summary(lm(logPain~myData$age))
```

Univariate tests of association for dependent observations

- Comparing central tendency (e.g. means) in 2 or more dependent groups (paired t-test, Wilcoxon signed rank test, linear mixed or GEE model)

- Comparing proportions in 2 or more dependent groups (McNemar’s test, logistic mixed or GEE model)

Comparing 2 or more dependent groups

- Consider a cross-over study where each subject receives both treatment and placebo (in a random order), a subject’s response is considered successful if it exceeds 1

```
#### Generate some fake data!!!! ####

mySampleSize=100

personIndicator=rep(seq(1,mySampleSize,1),rep(2,mySampleSize))

personEffect=rnorm(n=mySampleSize,mean=0,sd=1)
personEffect=rep(personEffect,rep(2,mySampleSize))

treatmentIndicator=c(0,1)
treatmentIndicator=rep(treatmentIndicator,mySampleSize)

treatmentEffect=1.234*treatmentIndicator

myResponse=treatmentEffect+personEffect+rnorm(2*mySampleSize)

mySuccess=(myResponse>=1)

cbind(personIndicator,treatmentIndicator,myResponse,mySuccess)
```

Comparing central tendency in 2 or more dependent groups

- Consider comparing the response in the treatment and placebo groups (need to account for fact that observations on the same subject are dependent)

```
#### paired t.test for treatment effect ####

t.test(myResponse[treatmentIndicator=="1"],
    myResponse[treatmentIndicator=="0"],
    paired=TRUE)

#### signed rank test for treatment effect ####

wilcox.test(myResponse[treatmentIndicator=="1"],
    myResponse[treatmentIndicator=="0"],
    paired=TRUE)
```

```
#### alternatively ####

library(geepack)
library(lme4)

#### linear GEE model ####

summary(geeglm(myResponse~treatmentIndicator,
        id=personIndicator))

#### linear mixed effects model ####

summary(lmer(myResponse~treatmentIndicator+
            (1|personIndicator)))
```

Comparing proportions in 2 or more dependent groups

- Consider comparing success probability in treatment and placebo groups using McNemar’s test

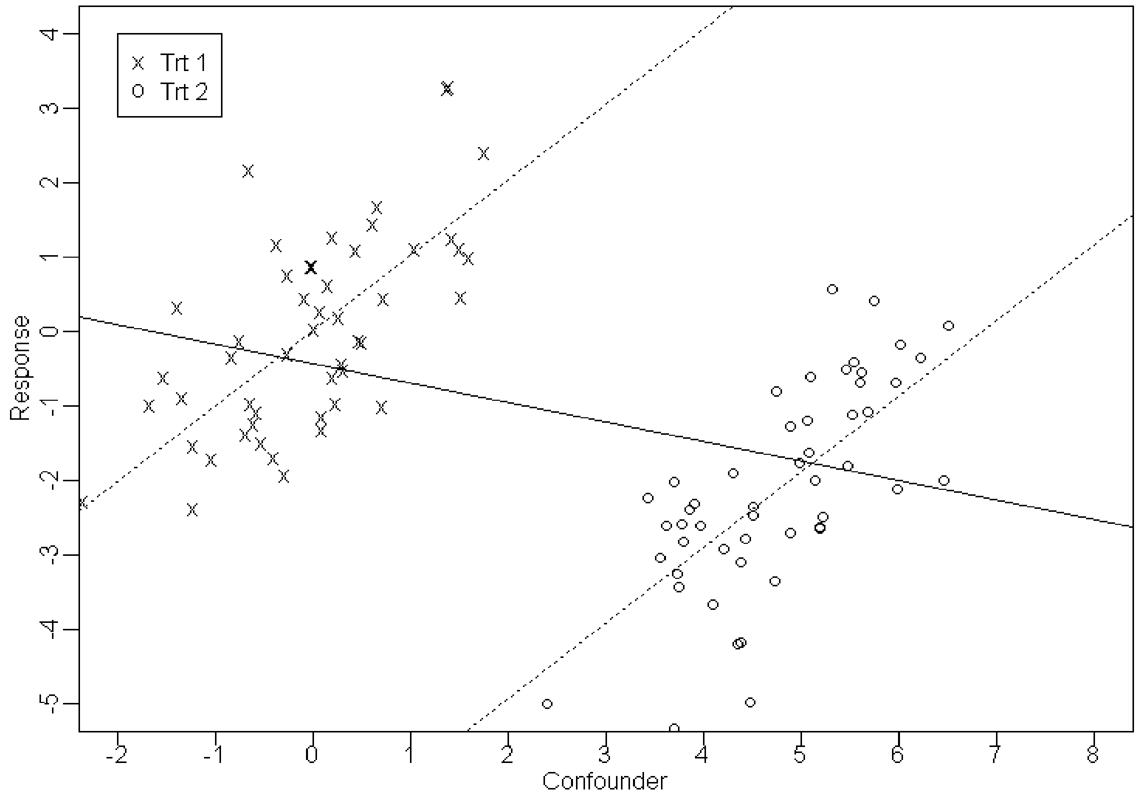
```
#### McNemar's test for comparing probability of success
#### in treatment and control groups ####

table(mySuccess[treatmentIndicator=="0"],
    mySuccess[treatmentIndicator=="1"])

mcnemar.test(mySuccess[treatmentIndicator=="0"],
        mySuccess[treatmentIndicator=="1"],correct=FALSE)

#### alternatively ####

discordant=c(table(mySuccess[treatmentIndicator=="0"],
            mySuccess[treatmentIndicator=="1"])[1,2],
        table(mySuccess[treatmentIndicator=="0"],
            mySuccess[treatmentIndicator=="1"])[2,1])

chisq.test(discordant,correct=FALSE)

#### or ####

2*(1-pbinom(discordant[1],sum(discordant),1/2))

#### alternatively ####

#### logistic GEE model ####

summary(geeglm(mySuccess~treatmentIndicator,
        id=personIndicator,
        family="binomial"))

#### logistic mixed effects model ####

summary(lmer(mySuccess~treatmentIndicator+
            (1|personIndicator),
            family="binomial"))
```

Multivariate Analyses

```
#### First, some fake data! ####

myTreatment=rep(c("Trt 1","Trt 2"),c(50,50))

myConfounder=c(rnorm(50),rnorm(50)+5)

myResponse=c(myConfounder[1:50]-rnorm(50),
        myConfounder[51:100]-rnorm(50)-7)

myFailure=(myResponse<0)

#### Examine relationship between
#### myResponse and myTreatment ####

summary(lm(myResponse~myTreatment))

#### Is the relationship modified
#### when we adjust by myConfounder? ####

summary(lm(myResponse~myConfounder+myTreatment))

#### Examine relationship between
#### myFailure and myTreatment ####

#### Logistic Regression ####

summary(glm(myFailure~myTreatment,
        family="binomial"))

#### Is the relationship modified
#### when we adjust by myConfounder? ####

summary(glm(myFailure~myConfounder+myTreatment,
        family="binomial"))
```

Multivariate Analyses (continued)

```
#### And make a plot ####

dev.new(height=6,width=8)
par(mai=c(0.5,0.5,0.05,0.05))

plot(x=NULL,y=NULL,xlim=c(-2,8),ylim=c(-5,4),axes=FALSE)
box()

points(x=myConfounder[myTreatment=="Trt 1"],
     y=myResponse[myTreatment=="Trt 1"],
     pch="x")
points(x=myConfounder[myTreatment=="Trt 2"],
     y=myResponse[myTreatment=="Trt 2"],
     pch=21)

abline(lm(myResponse~myConfounder)$coef)

myCoefs=lm(myResponse~myTreatment+myConfounder)$coef
abline(myCoefs[1],myCoefs[3],lty="dotted")
abline(myCoefs[1]+myCoefs[2],myCoefs[3],lty="dotted")

title(xlab="Confounder",line=1.25)
title(ylab="Response",line=1.5)
legend(-2,4,legend=c("Trt 1","Trt 2"),pch=c("x","o"))

axis(1,at=seq(-2,8,1),padj=-1)
```



Enrichment Work

1. Load the dataset “data1.csv” into R using the read.csv() command (don’t forget the header=TRUE option).

The dataset contains group indicators, log white blood cell counts, remission time subject to censoring by loss-to-follow up, and an event indicator.

2. Ensure that variables are of the appropriate type using the as.factor() and as.numeric() commands.

The event indicator should be numeric for our purposes.

Enrichment Work (continued)

3. Make a box-plot of logWBC vs. group using the plot() command. Adjust the margins and label the axes by replacing the ???s in the below code.

```
par(mai=c(???,???,???,???),cex=???)
plot(group,logWBC,axes=FALSE)
box()
axis(1,padj=-0.5)
axis(2,padj=0.5)
title(xlab=???,line=1.5)
title(ylab=???,line=1.75)
```

Enrichment Work (continued)

4. Load the survival library using the command library(survival).

5. Create a survival response (subject to non-informative right censoring) using the Surv() command.

The ingredients for this will be remission time and event indicator.

Enrichment Work (continued)

6. Plot Kaplan-Meier survival function estimates for each group by replacing the ???s in the below code.

```
par(mai=c(0.5,0.5,0.05,0.05),cex=0.8)
plot(survfit(???~???),lty=c("solid","dotted"),axes=FALSE)
box()
axis(1,padj=???)
axis(2,padj=???)
title(xlab="Remission Time",line=???)
title(ylab="Survival Probability",line=???)
legend(x="topright",
       legend=c("Group 0","Group 1"),
       lty=c("solid","dotted"))
```

The survival response should go to the left of the "~" and the group indicator should go to the right of the "~".

7. Annotate the plot with the p-value from the log-rank test by replacing the ???s in the below code.

```
summary(coxph(mySurv~group))
text(x=35,y=0,labels="Log-Rank p ???",pos=2)
```

Enrichment Work (continued)

8. Compare a Cox proportional hazards model adjusting for log WBC in addition to group to a model with group alone by updating the code below.

```
 fit1=coxph(???~???)
fit2=coxph(???~???+???)
anova(fit1,fit2)
```

The dependent variable goes on the left side of the "~" sign and predictors go on the right hand side of the "~", separated by "+" if there are multiple predictors.

Enrichment Work (continued)

9. Extract hazard ratio estimates and 95% confidence intervals from fit2 using the summary() command.

10. How should these hazard ratio estimates and confidence intervals be interpreted?