# Introduction to R

# Road-map

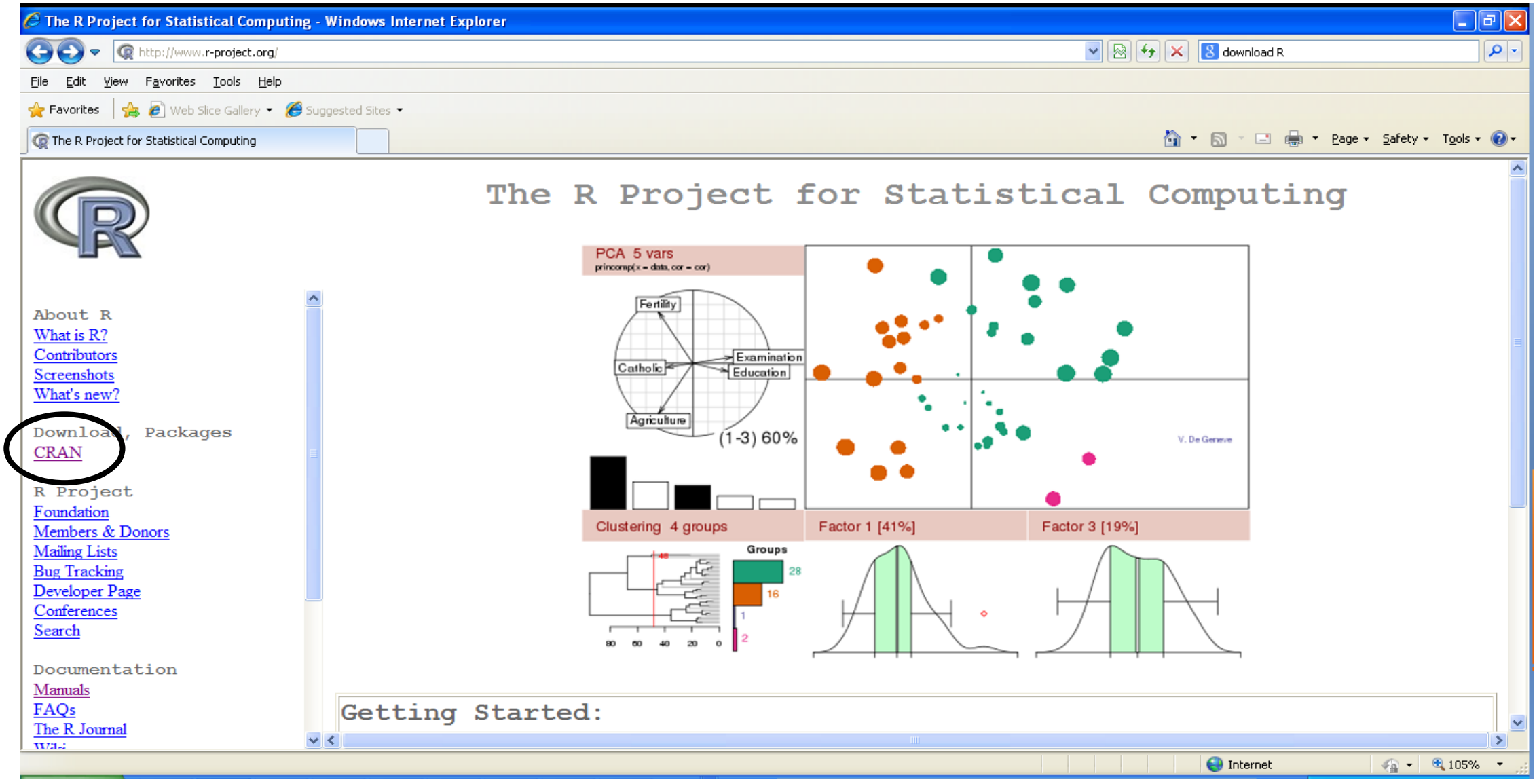
- Data management
- Descriptive statistics
- Tests of association
- Linear regression and ANOVA
- Logistic and Cox proportional hazards regression

# 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

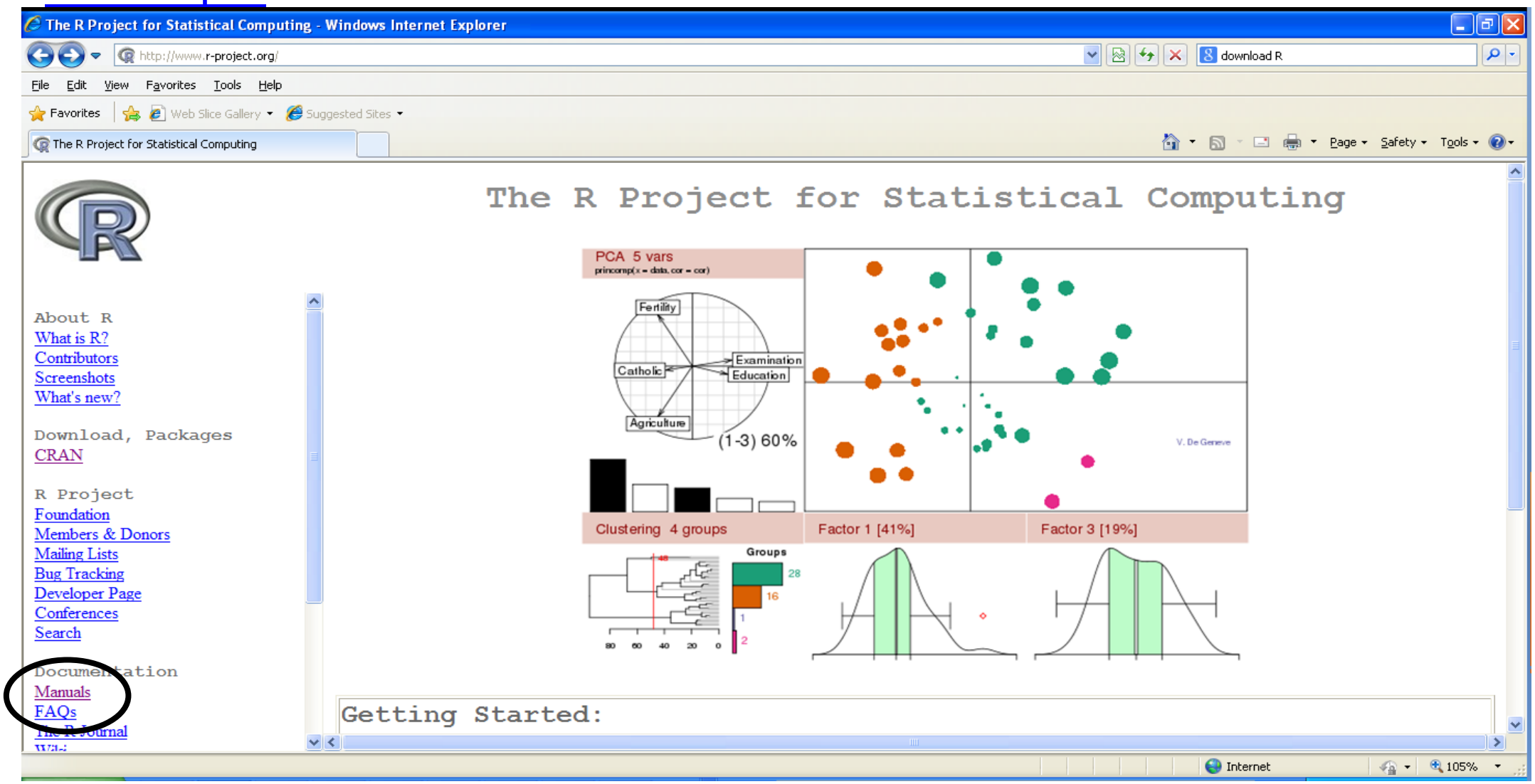
# R download

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



# 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



# 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="",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] | $n^{th}$ element |
| x[-n] | all *but* the $n^{th}$ 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]] | $n^{th}$ 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)

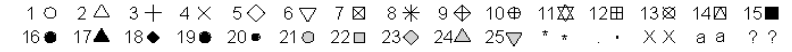
## Low-level plotting commands

**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 ""




**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 ($F$) ($\chi^2$)

**`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 (`dfunc(x, ...)`), the cumulative probability density (`pfunc(x, ...)`), and the value of quantile (`qfunc(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.

RGui (32-bit)

File Edit View Misc Packages Windows Help

Source R code...
New script
Open script...
Display file(s)...

Load Workspace...
Save Workspace...

Load History...
Save History...

Change dir...

Print...
Save to File...

Exit

```
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

- Desktop
  - My Documents
  - My Computer
  - My Network Places
  - Angela
  - Ash
  - ben
  - BH
  - BiometrikaReplies
  - ChiawLing
  - CKD
  - Dengue Data for Ben
  - Final Research Proposal (Class 2012)
  - HINTS

Folder: My Documents

Make New Folder | OK | Cancel

```
 NO WARRANTY.
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and
 in publications.

n-line help, or
 to help.
```
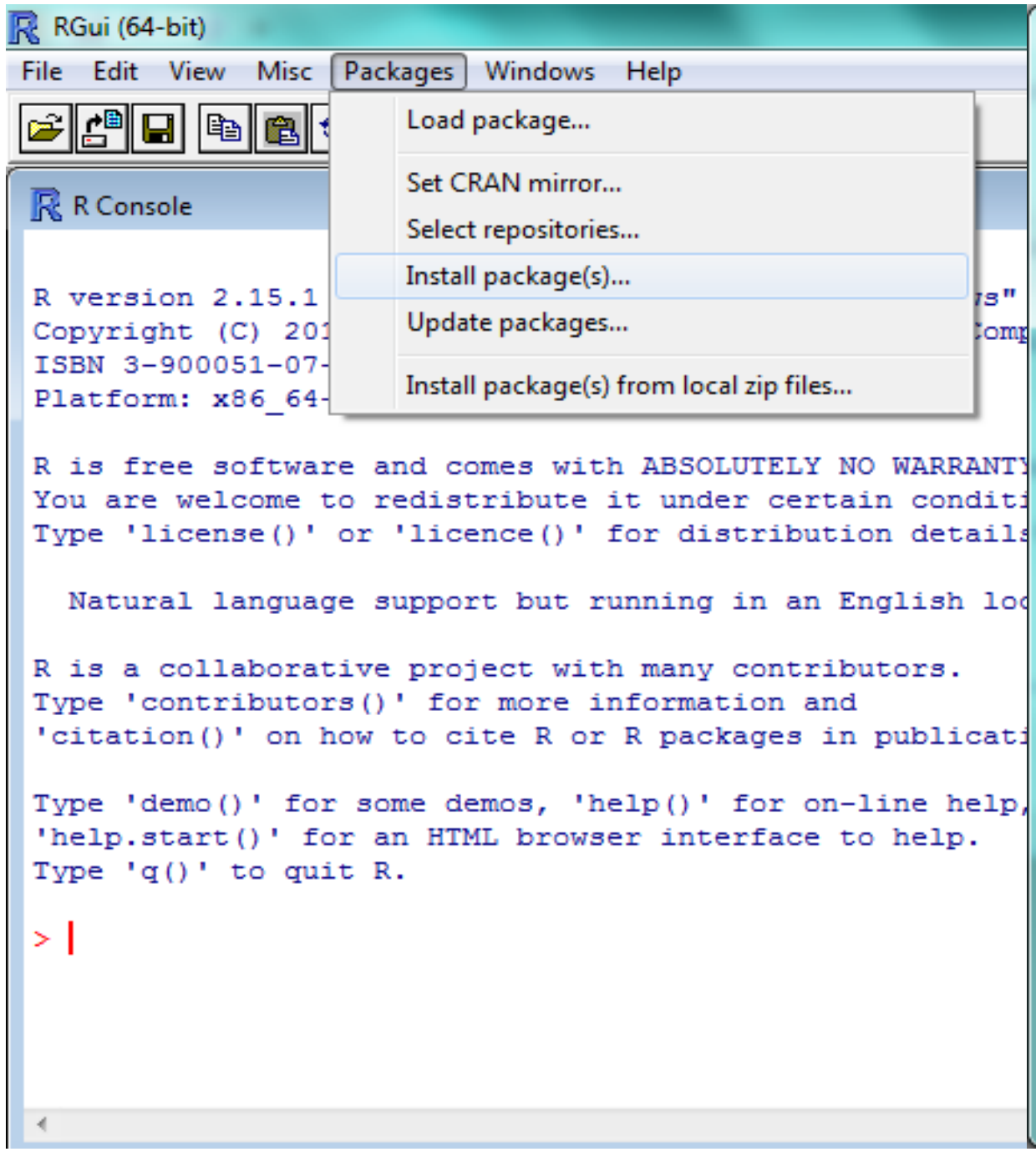
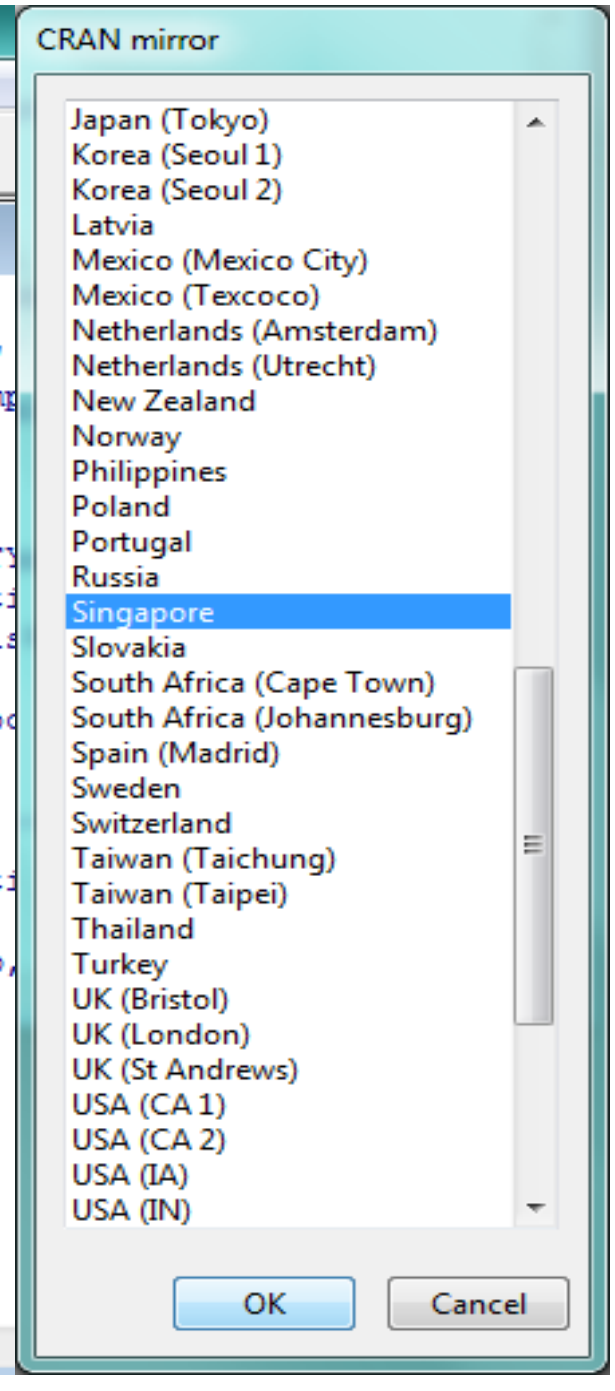
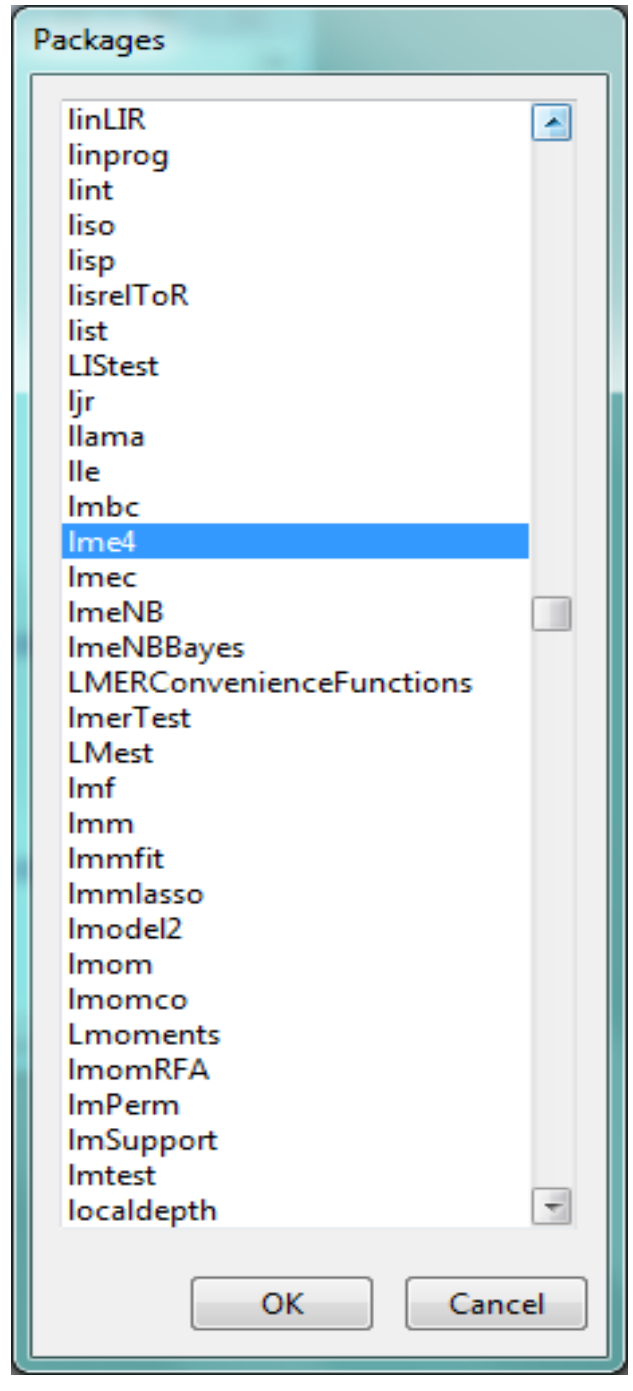

# Installing packages in R

- 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



# Starting a new R script

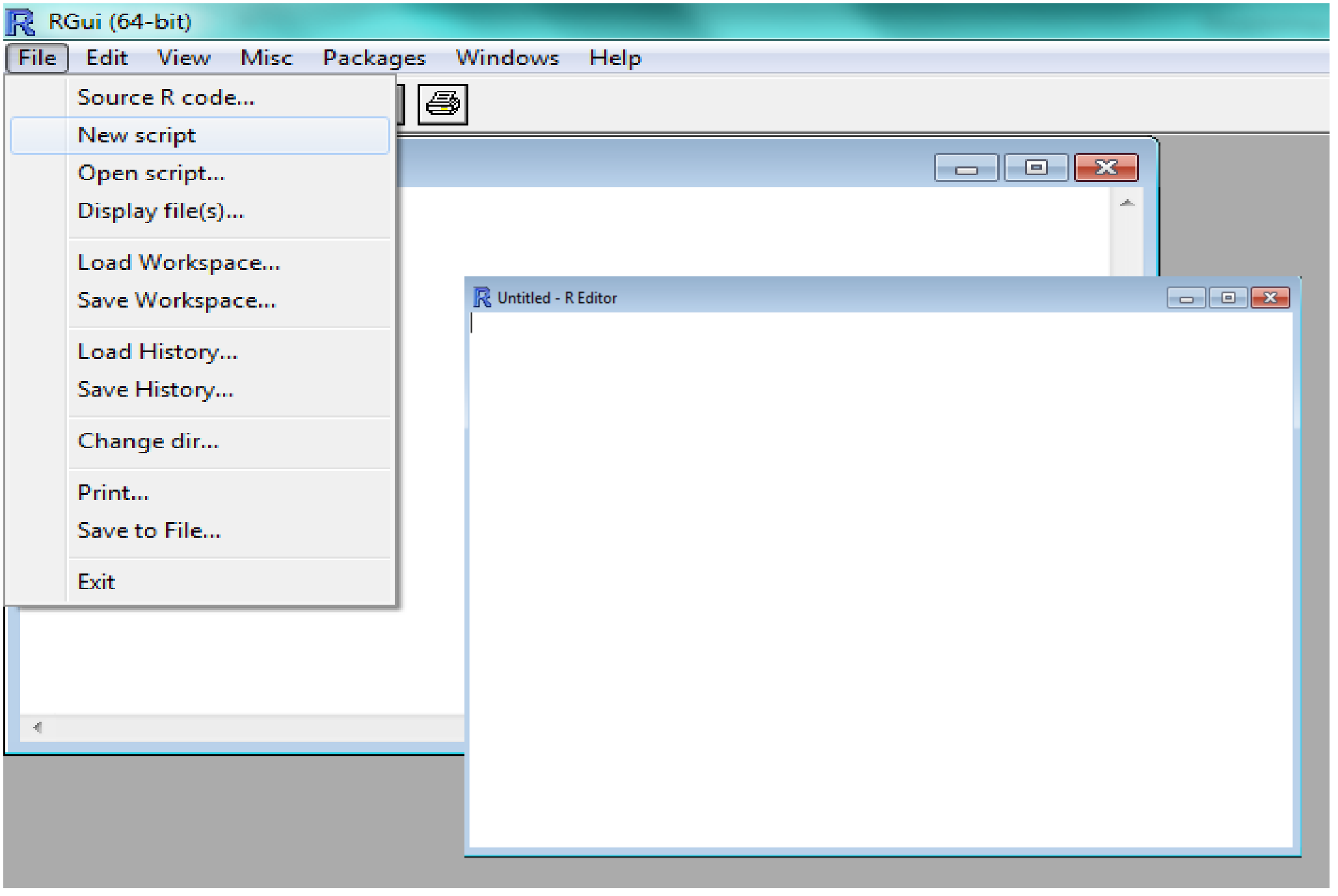
- Typically, R commands are stored in a script which can be executed at the user's leisure or at a later date

- 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)

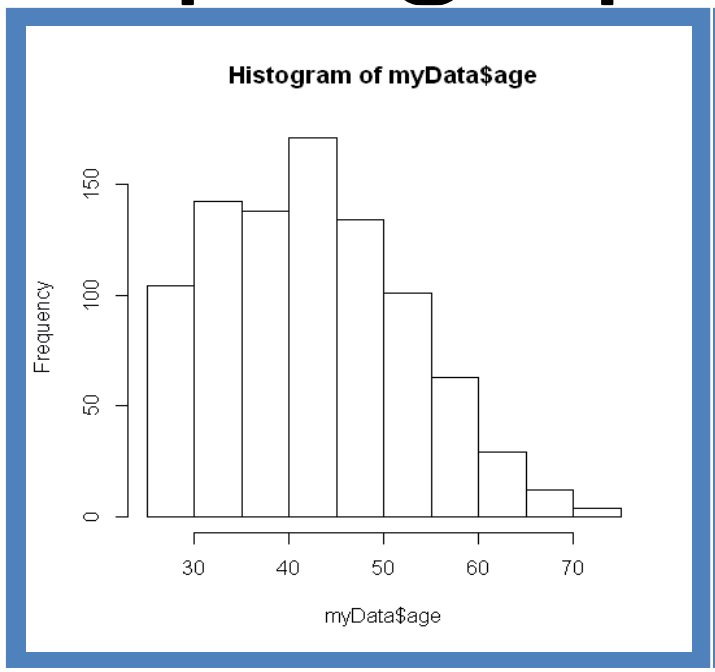
#### Scatterplot of pain by age ####

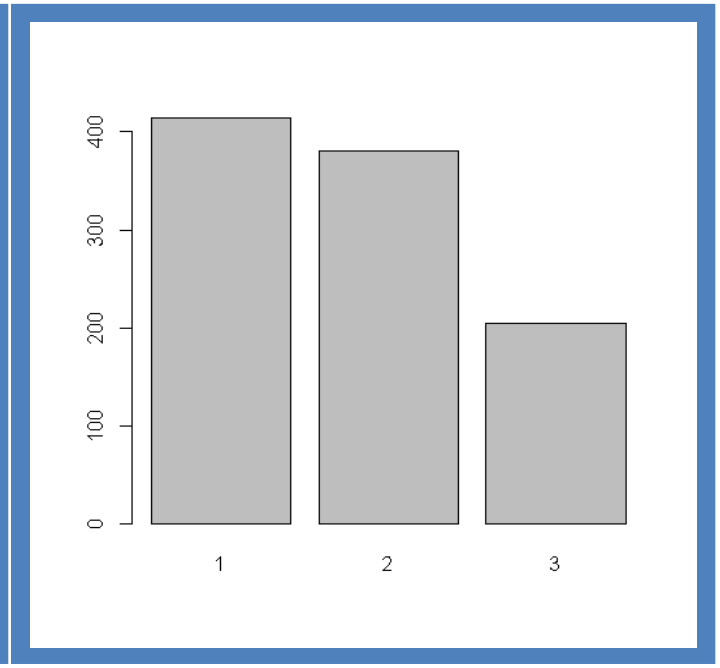
plot(myData$age,myData$pain)

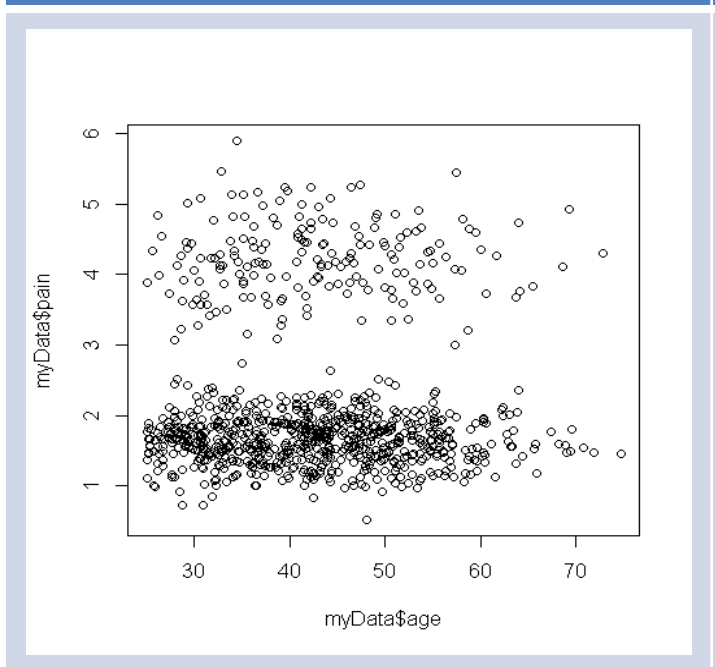
#### Boxplots of pain by health status ####

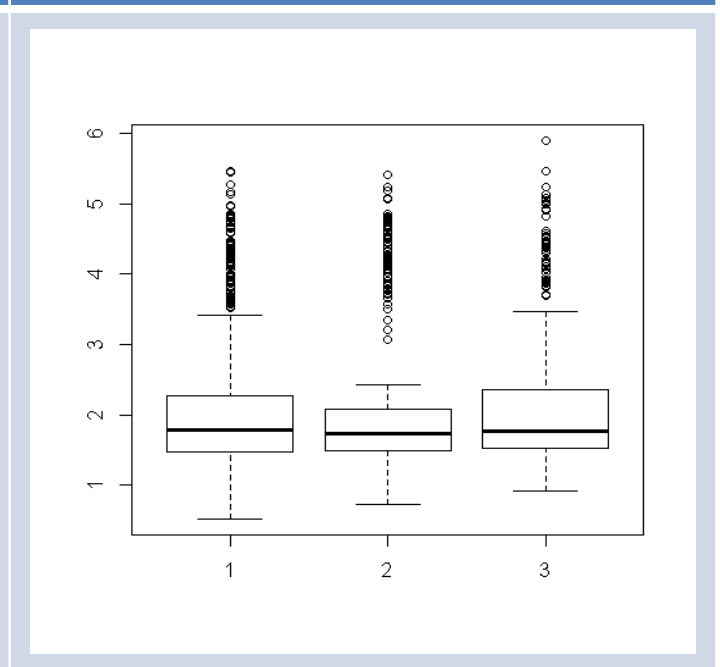
plot(myData$health_status,myData$pain)

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



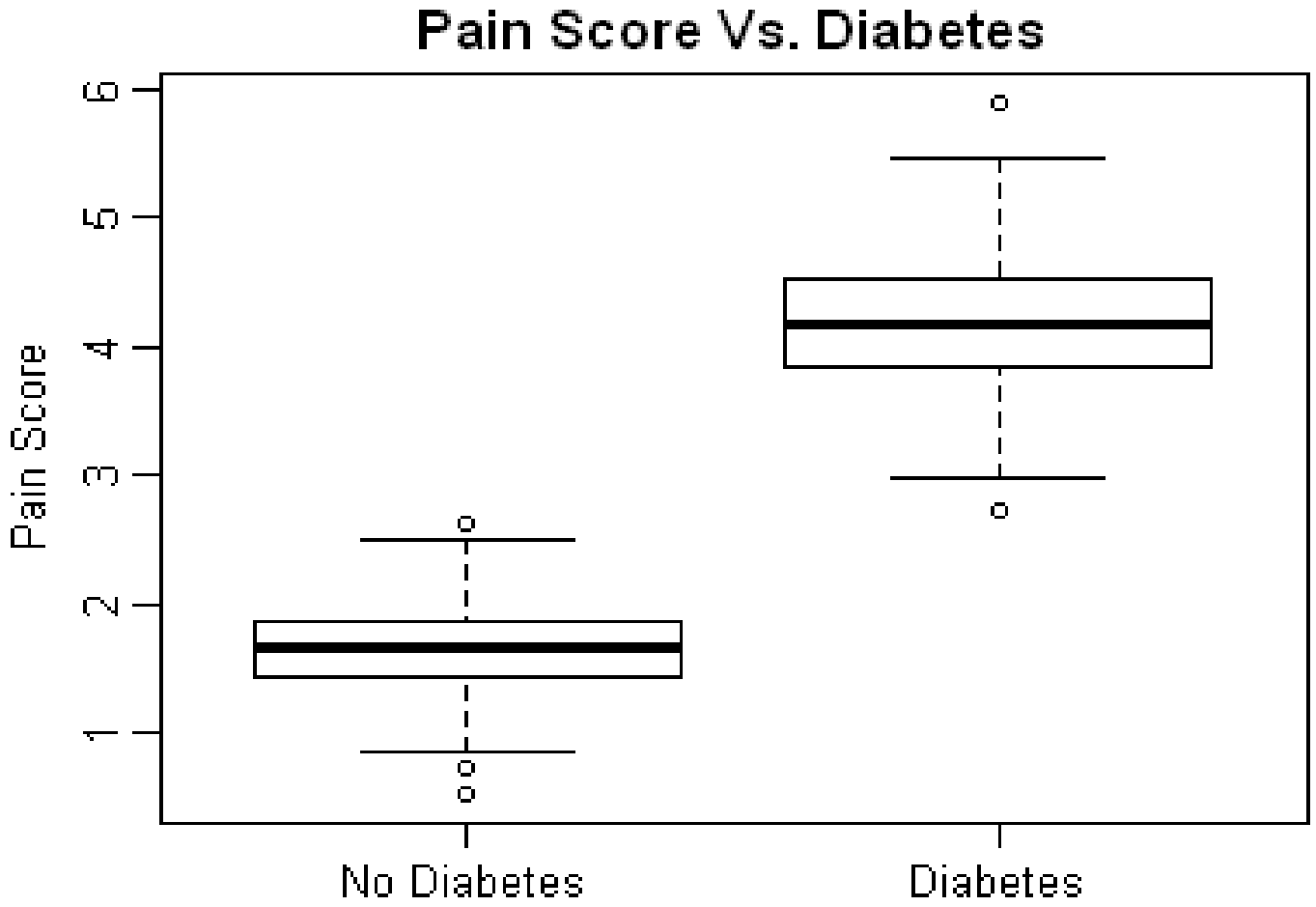



# A more complete plot in R

```
#### 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)

# 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

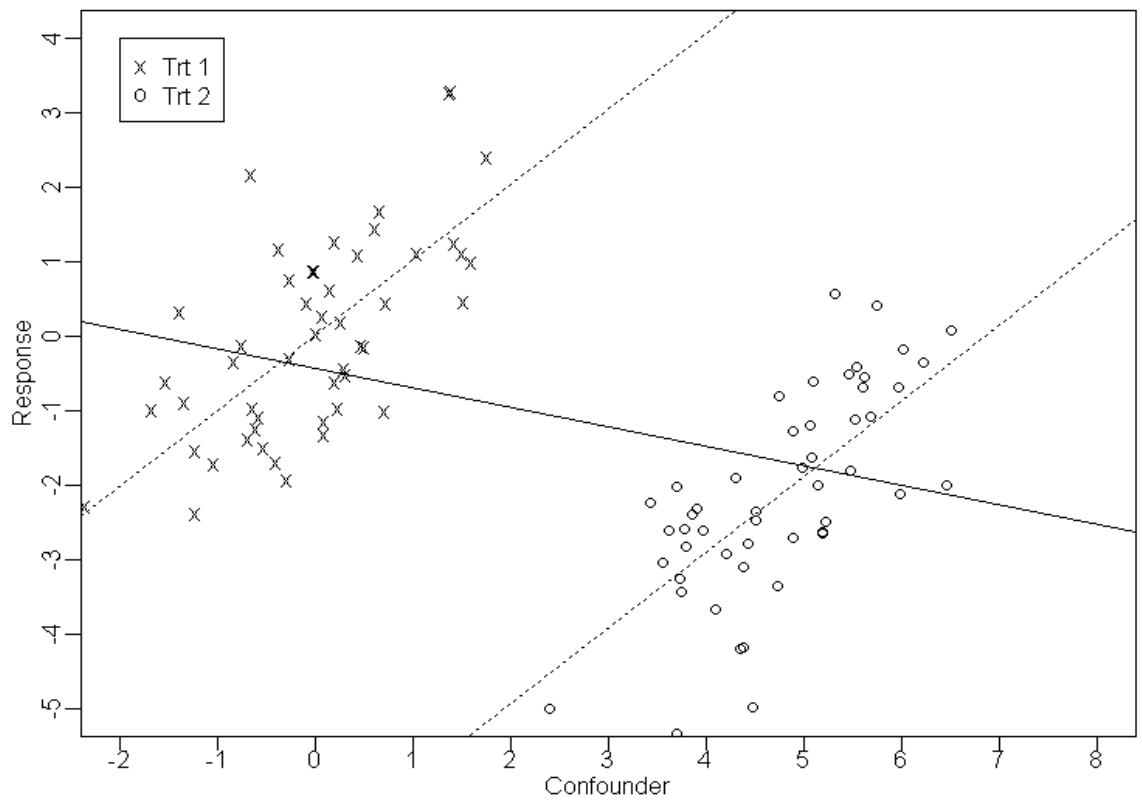
```
#### First, some fake data! ####

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?