

Statistics with R

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<http://web.abo.fi/fak/mnf/mate/kurser/statisticsr/>

References:

"A Practical Guide to Geostatistical Mapping of Environmental Variables", Tomislav Hengl, Joint Research Centre, Institute for Environment and Sustainability pp. 56, 80

The R Core Team, "What is R?", R News, Volume 1/1, January 2001

http://cran.r-project.org/doc/html/interface98-paper/paper_2.html

http://en.wikipedia.org/wiki/R_%28programming_language%29

Believe nothing merely because you have been told it.
Do not believe what your teacher tells you merely out of respect for the teacher.
But whatever, after due examination and analysis, you find to be kind, conducive to the good,
the benefit, the welfare of all beings - that doctrine believe and cling to, and take it as your
guide.

However many holy words you read, however many you speak, what good will they do you if
you do not act on upon them?

There are only two mistakes one can make along the road to truth; not going all the way, and
not starting.

What we think, we become.

Buddha, spiritual teacher from India



I hear and I forget. I see and I remember. I do and I understand.

Confucius

Chinese philosopher & reformer
(551 BC - 479 BC)



How the classes will be organized

Revision of R/statistical concepts

Examples of reviewed R/statistical concepts

R commands to work on these concepts

Questions, to be solved with R, by the students

Answers and explanations before moving on

Course structure

The course will be 14 lessons of 2 hours each.

The class starts 10 minutes after the scheduled hour.

The grade is pass/fail.

To pass, a student must attend 11 lessons and answer correctly 10 questions from the questionnaire.

Alternatively, a student must answer correctly 15 questions from the questionnaire.

The reading assignments are optional but recommended, in particular for students who will not attend the class.

The online material is enough to learn the basics and answer the questionnaire.

The classes will cover more details and have from 5 to 10 times more examples than the online material. This can be exhausting, but you must ask if you want something explained differently or if you need a break.

The classes will also be more friendly to students not from Computer Science, unlike the online material.

Course structure

R has many strong points, two of which are its great help system and available packages.

However, many students complaint that, after an introductory course on R, they are not comfortable with using the help or packages.

Usually it doesn't matter because they will never use R again or use it only for a few histograms or boxplots, once in a blue moon.

Students from Statistics, Bioinformatics and Environmental Sciences will have to work with many packages and find help on any topic without assistance.

That is why the initial lessons will be long and boring, but necessary to get solid foundations on R.

The R Project for Statistical Computing

“R is a free software environment for statistical computing and graphics. It compiles and runs on a wide variety of UNIX platforms, Windows and MacOS.”

“R is an integrated suite of software facilities for data manipulation, calculation and graphical display. It includes an effective data handling and storage facility, a suite of operators for calculations on arrays, in particular matrices, a large, coherent, integrated collection of intermediate tools for data analysis, graphical facilities for data analysis and display either on-screen or on hardcopy, and a well-developed, simple and effective programming language which includes conditionals, loops, user-defined recursive functions and input and output facilities. ”

<http://www.r-project.org/>

What is R

R is a software environment and programming language for statistical computing and graphics. R is the open source equivalent to the programming language S. S is very popular on statistical methodology research and was developed by John Chambers and, previously, by Rick Becker and Allan Wilks of Bell Laboratories. The name "R" comes from the fact that "R" precedes "S" and both authors' names start with "R", Ross Ihaka and Robert Gentleman.

The R basic distribution comes with plenty of statistical procedures such as: linear and generalized linear models, nonlinear regression models, time series analysis, classical parametric and nonparametric tests, clustering and smoothing. There are many graphical procedures such as: plot, scatterplot, boxplot, distribution-comparison plot, histogram, dotchart, contour lines, 3D surface, etc... R is extensible with a multitude of packages, some of them for very specialized areas or highly optimized for intensive computations. R is a programming language, allowing object-oriented programming (OOP) and with lexical (static) scoping semantics similar to Scheme (dialect of Lisp).

C, C++, and Fortran code can be linked and called at run time, adding more power and flexibility.

The history of R

R was developed by Ross Ihaka and Robert Gentleman at the University of Auckland, New Zealand.

Ross Ihaka read the book "The Structure and Interpretation of Computer Programs" about the Scheme programming language. Later, he tried to use lexical scope, to obtain own variables, in S, which didn't work because of the differences in the scoping rules of S and Scheme. Years passed, and Robert Gentleman and Ross Ihaka were at the University of Auckland, both working on statistical computing. They decided to create a small Scheme-like interpreter, to be used as a software environment. It was similar to S in syntax because Scheme and S are similar and both authors were familiar with S.

There was a first release in August of 1993. In June of 1995, the source code was distributed under the terms of the Free Software Foundation's GNU general license (GPL).

The interest kept growing and a small mailing list to exchange ideas had to grow to a larger automated mailing list, then to newsgroups and the distribution of code, documentation and binaries expanded to more mirror sites. Finally, the core group of developers had to grow, as well.

In 2001, Robert Gentleman started the project Bioconductor that uses statistical computing, with R, in Computational Biology.

Portable R

R is "perfectly relocatable", that is, after being installed in one machine, the directory can be copied, for example, to a memory stick and it will run from there.

Notes:

Installing packages - download the package from CRAN, use Packages -> Install Package(s) from local zip file(s)

workspace and history can be relocated by copying .Rhistory and .RData

<http://my.opera.com/semin/blog/2007/04/02/portable-r>

Portable GIS

Runs from a memory stick.

Contents:

- Desktop GIS packages GRASS (windows native version 6.3: does not need cygwin), QGIS (version 0.10 with GRASS plugin) and gvSIG (version 1.1),
- FWTools (GDAL and OGR toolkit, version 2.10)
- XAMPPlite (Apache2/MySQL5/Php5),
- PostgreSQL (version 8.2)/Postgis (version 1.1),
- Mapserver, OpenLayers, Tilecache, Featureserver, and Geoserver web applications.

<http://www.archaeogeek.com/blog/portable-gis/>

Portable GIMP

The GIMP (GNU Image Manipulation Program), Open Source image editor in a portable version:

http://portableapps.com/apps/graphics_pictures/gimp_portable

OpenOffice.org Portable

OpenOffice.org Portable is a complete OpenOffice.org office suite, compatible with Microsoft Office, Word Perfect, Lotus and other office applications.

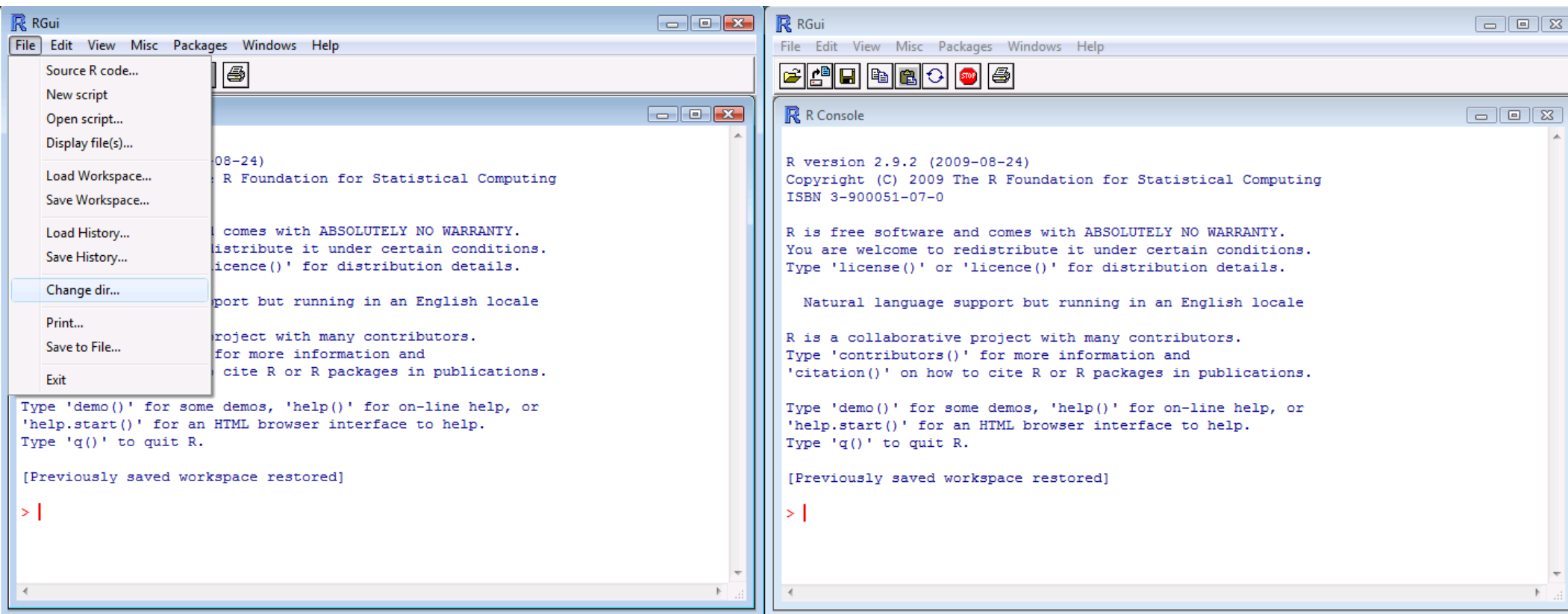
Includes:

- Word processor
- Spreadsheet
- Presentation tool
- Drawing package
- Database

http://portableapps.com/apps/office/openoffice_portable

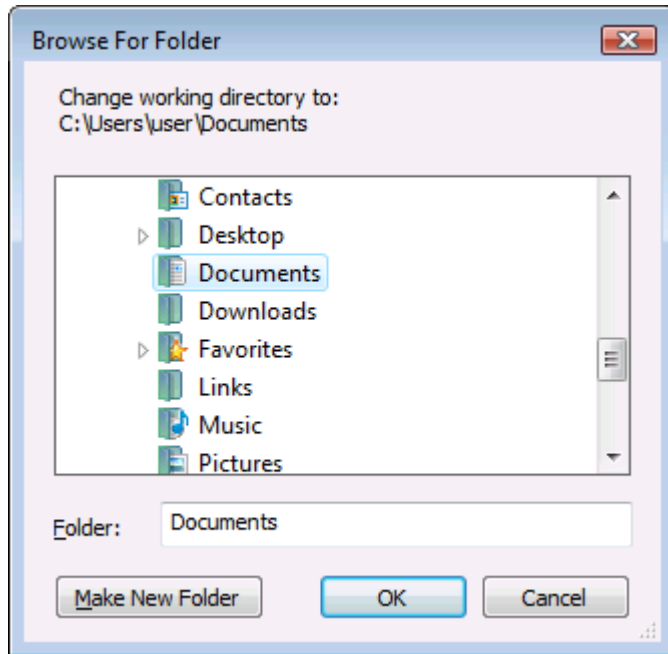
Two students sharing one computer

Open two R windows and change the working directory on both:

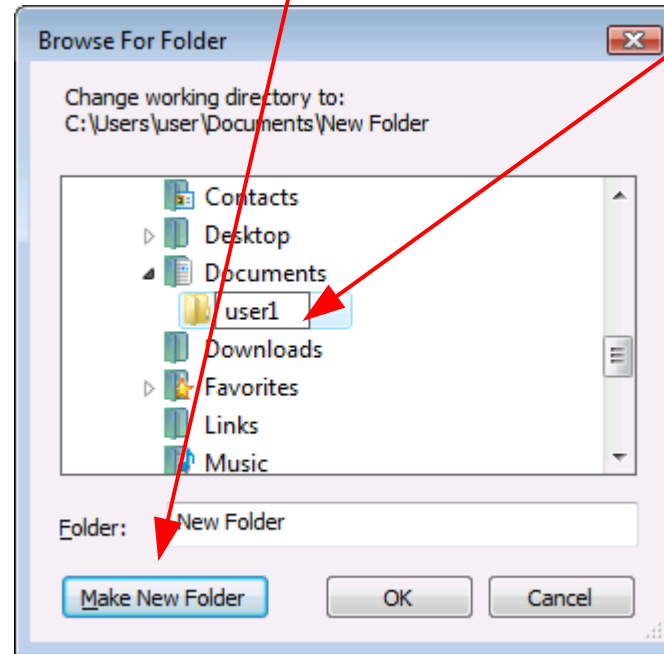


Two students sharing one computer

If the default is user\Documents



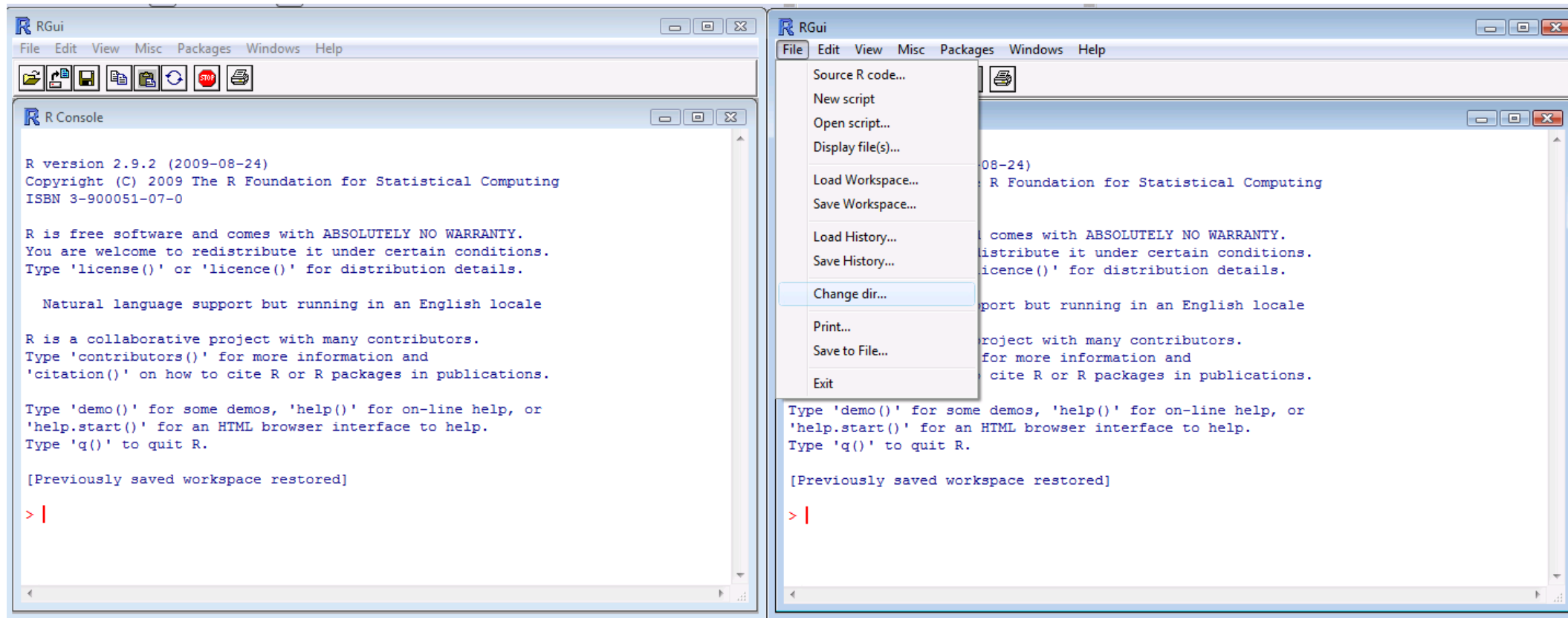
Click Make New Folder and name it user1



Do the same for the other R window but creating a directory user2

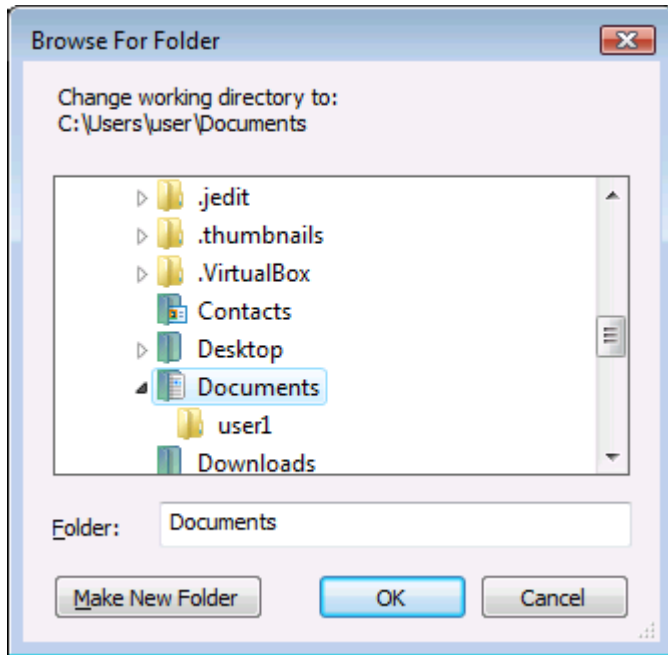
Two students sharing one computer

Change the working directory on the other R window:

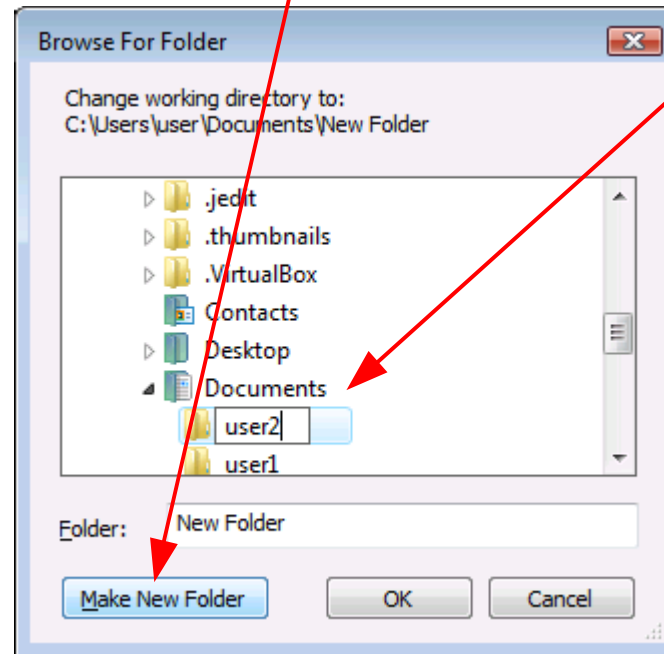


Two students sharing one computer

If the default is user\Documents

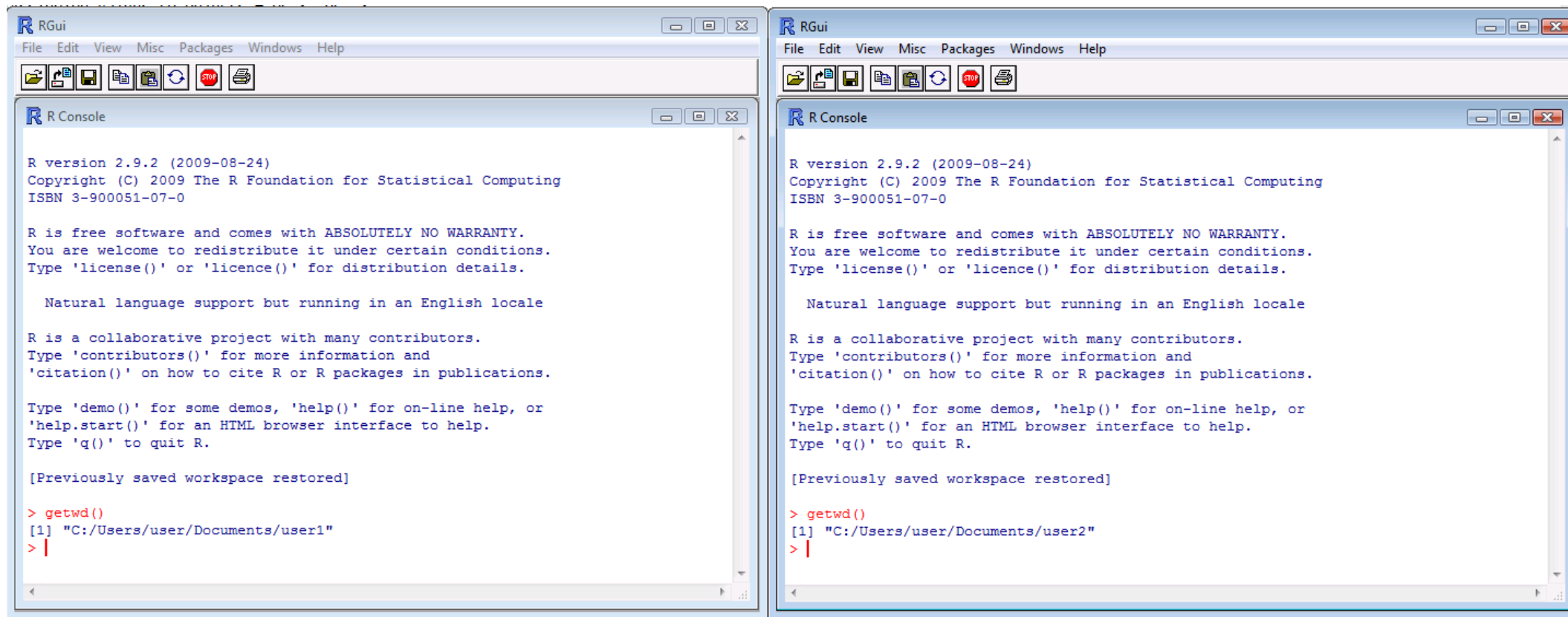


Click Make New Folder and name it user2



Two students sharing one computer

Use `getwd()` to check the current working directory:

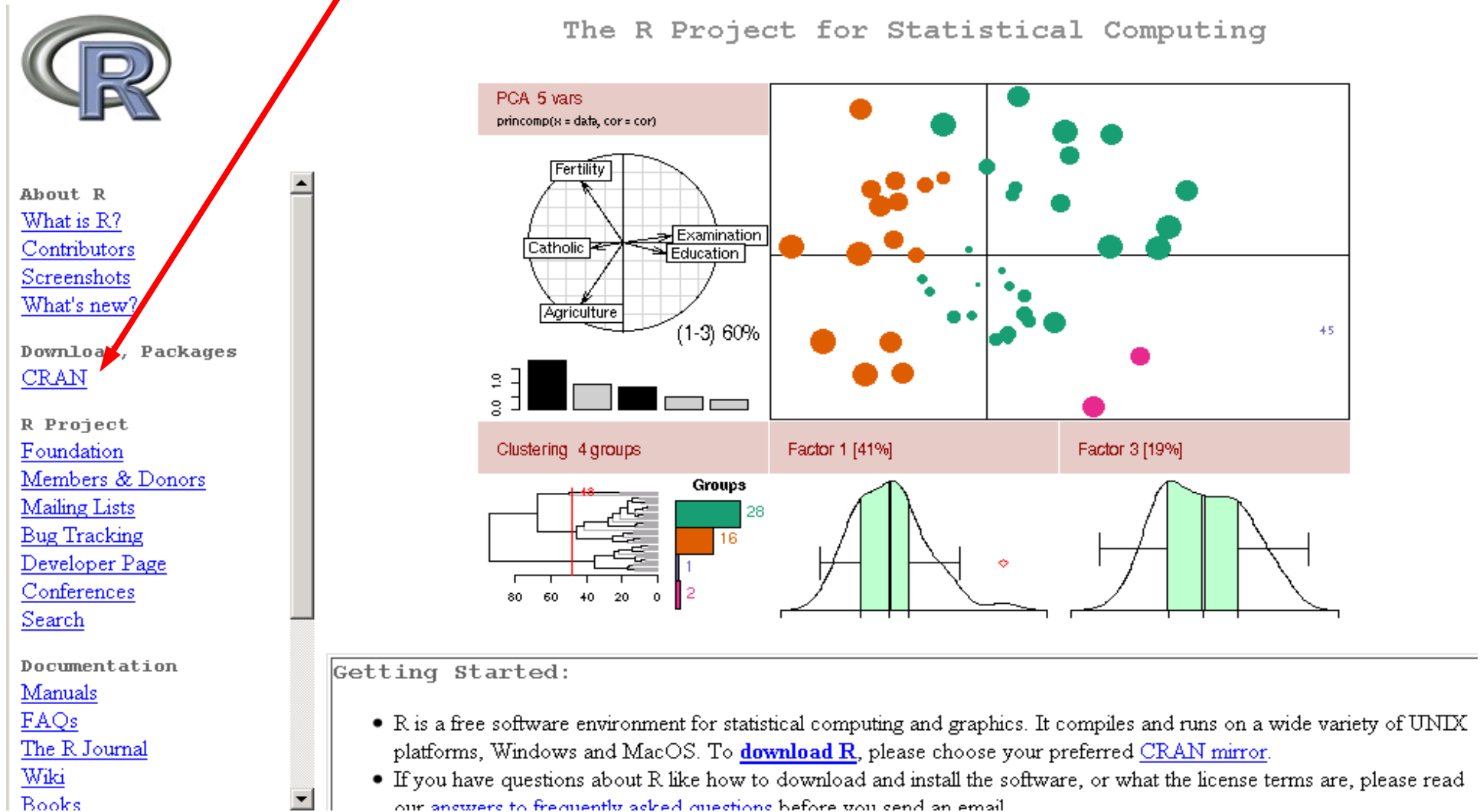


Both students can take turns on the computer, using their own R window and saving their work to separate workspaces.

Downloading and Installing R

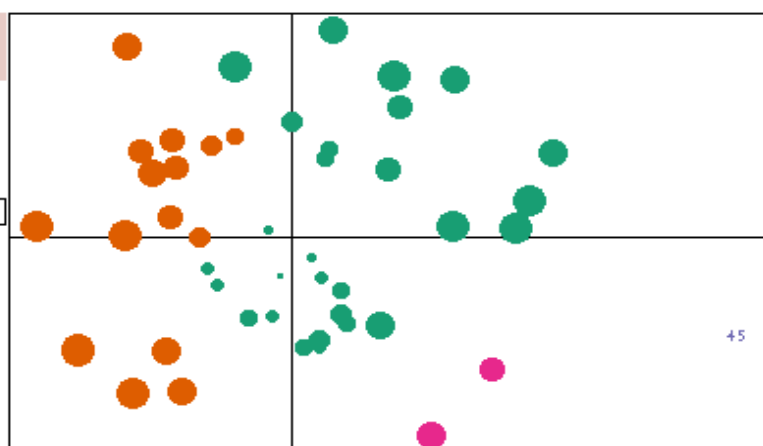
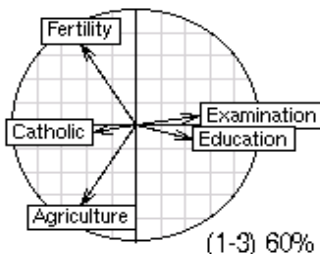
The R Project for Statistical Computing Homepage:
<http://www.r-project.org/>

That page has a link to another page with the CRAN mirrors

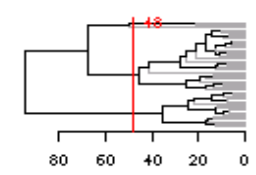


The R Project for Statistical Computing

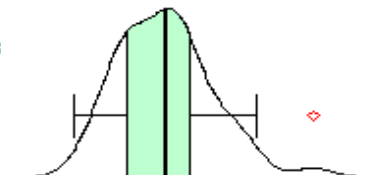
PCA 5 vars
`princomp(x = data, cor = cor)`



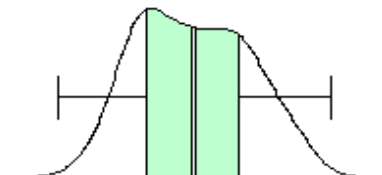
Clustering 4 groups



Factor 1 [41%]



Factor 3 [19%]



Getting Started:

- R is a free software environment for statistical computing and graphics. It compiles and runs on a wide variety of UNIX platforms, Windows and MacOS. To [download R](#), please choose your preferred [CRAN mirror](#).
- If you have questions about R like how to download and install the software, or what the license terms are, please read our [answers to frequently asked questions](#) before you send an email

Scrolling down the list, there are links to Sweden, UK and the US, among many others

CRAN Mirrors

The Comprehensive R Archive Network is available at the following URLs, please choose a location close to you. Some statistics on the status of the mirrors can be found [here](#).

Argentina

<http://cran.patan.com.ar/>

Patan.com.ar, Buenos Aires

<http://mirror.cricyt.edu.ar/r/>

CONICET, Mendoza

Australia

<http://cran.ms.unimelb.edu.au/>

University of Melbourne

Austria

<http://cran.at.r-project.org/>

Wirtschaftsuniversitaet Wien

Belgium

<http://www.freeststatistics.org/cran/>

K.U.Leuven Association

Brazil

<http://cran.br.r-project.org/>

Universidade Federal do Parana

<http://cran.fiocruz.br/>

Oswaldo Cruz Foundation, Rio de Janeiro

<http://www.vps.fmvz.usp.br/CRAN/>

University of Sao Paulo, Sao Paulo

<http://brieger.esalq.usp.br/CRAN/>

University of Sao Paulo, Piracicaba

Canada

<http://cran.stat.sfu.ca/>

Simon Fraser University, Burnaby

<http://probability.ca/cran/>

University of Toronto

<http://cran.parentinginformed.com/>

iWeb, Montreal

Scroll down to Sweden

Sweden

<http://ftp.sunet.se/pub/lang/CRAN/>

Swedish University Computer Network, Uppsala

Links to the different platforms

The Comprehensive R Archive Network

Frequently used pages

Download and Install R

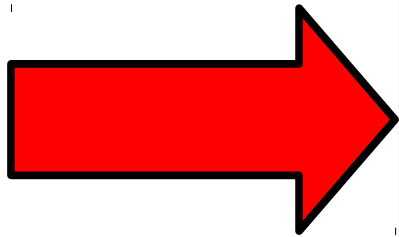
Precompiled binary distributions of the base system and contributed packages, **Windows and Mac** users most likely want one of these versions of R:

- [Linux](#)
- [MacOS X](#)
- [Windows](#)

Source Code for all Platforms

Windows and Mac users most likely want the precompiled binaries listed in the upper box, not the source code. The sources have to be compiled before you can use them. If you do not know what this means, you probably do not want to do it!

- **The latest release** (2009-08-24): [R-2.9.2.tar.gz](#) (read [what's new](#) in the latest version).
- Sources of [R alpha and beta releases](#) (daily snapshots, created only in time periods before a planned release).
- Daily snapshots of current patched and development versions are [available here](#). Please read about [new features and bug fixes](#) before filing corresponding feature requests or bug reports.
- Source code of older versions of R is [available here](#).
- Contributed extension [packages](#)



Let's download the Windows version (base)

base	Binaries for base distribution (managed by Duncan Murdoch)
contrib	Binaries of contributed packages (managed by Uwe Ligges)

R-2.9.2 for Windows



[Download R 2.9.2 for Windows](#) (34 megabytes)

[Installation and other instructions](#)

New features in this version: [Windows specific](#), [all platforms](#).

If you want to double-check that the package you have downloaded exactly matches the package distributed by R, you can compare the [md5sum](#) of the .exe to the [true fingerprint](#). You will need a version of md5sum for windows: both [graphical](#) and [command line versions](#) are available.

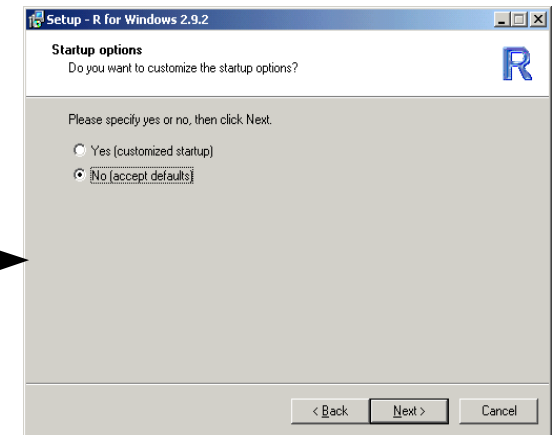
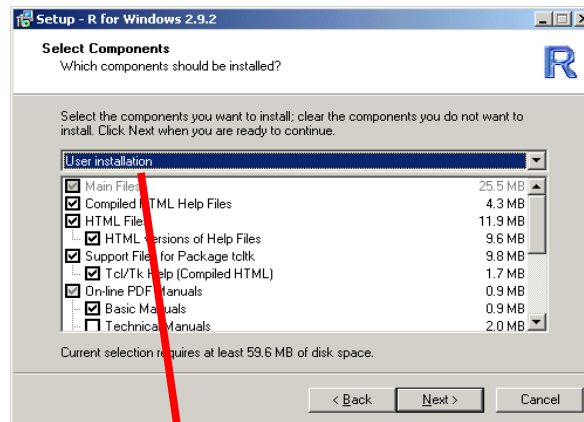
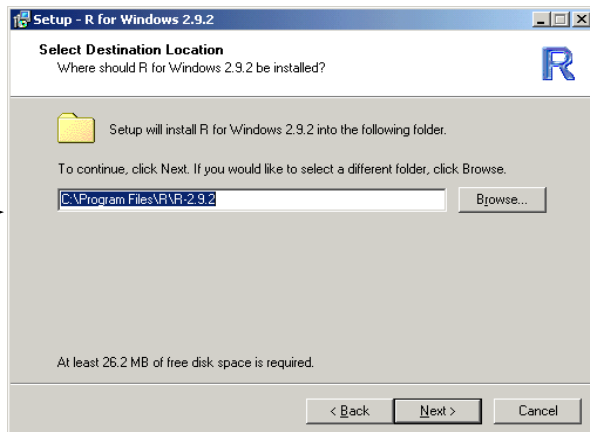
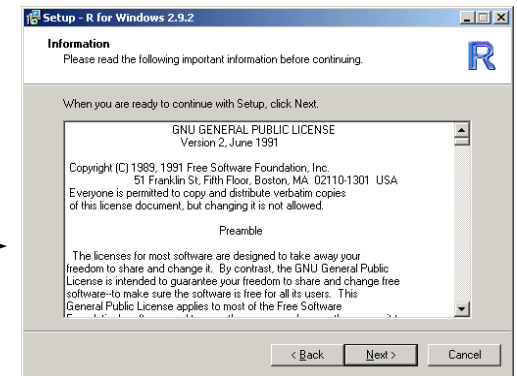
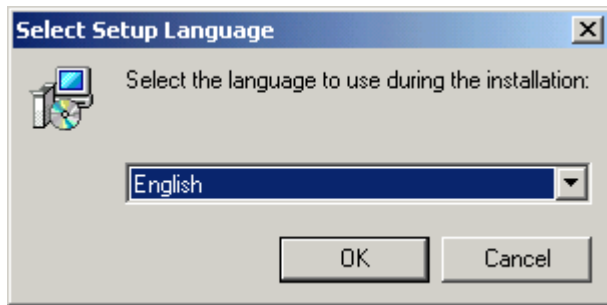
Frequently asked questions

- [How do I install R when using Windows Vista?](#)
- [How do I update packages in my previous version of R?](#)

Please see the [R FAQ](#) for general information about R and the [R Windows FAQ](#) for Windows-specific information.

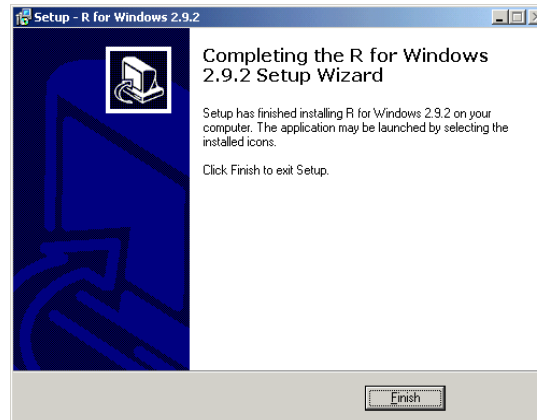
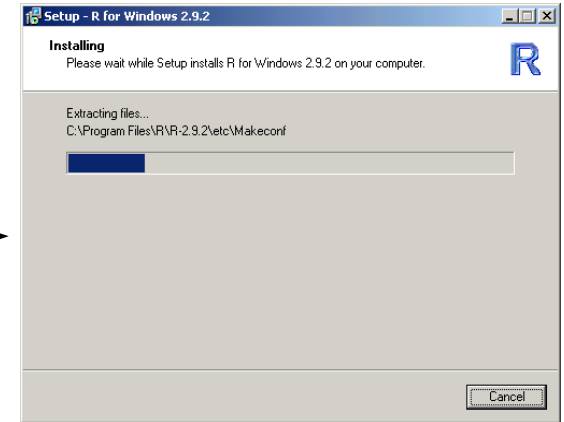
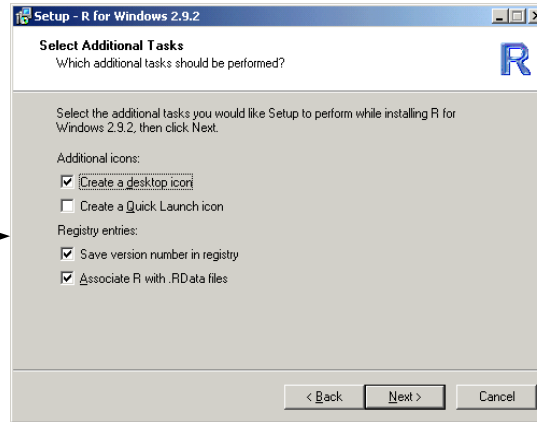
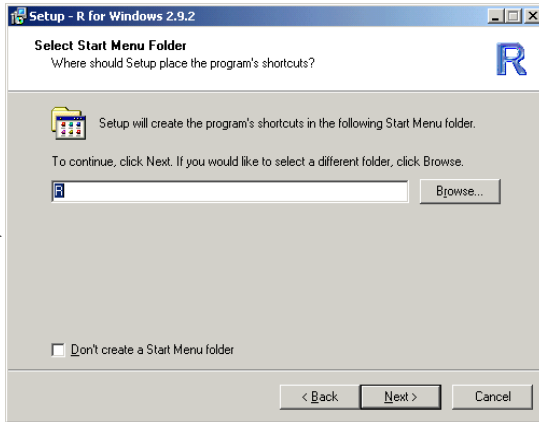
Installing the Windows version (base)

Download R-2.9.2-win32.exe (the 2.9.2 is the version number, it might be different) and execute it. There are several languages that can be used during the installation, which is very straightforward.



User installation
Minimal user installation
Full installation
Custom installation

Installing the Windows version (base)



Installing the Linux version

On Fedora 10, as root:
yum install R

On Fedora 8 or 9, as root:
yum install R R-devel



The screenshot shows a web directory listing for the path `/pub/lang/CRAN/bin/linux`. On the left is a navigation menu with links for Home, Search, News, About, Contact, and Feedback. The main content area displays a table of sub-directories for different Linux distributions. A red oval highlights the `redhat/` entry with the text "More info here".

Name	Last modified	Size
Parent Directory		-
debian/	17-Sep-2009 22:00	-
redhat/	31-Aug-2009 18:05	-
suse/	29-Jun-2009 09:17	-
ubuntu/	17-Sep-2009 16:57	-

This service is maintained by archive@ftp.sunet.se

Installing the Linux version

On Ubuntu:

```
gpg --keyserver subkeys.pgp.net --recv-key E2A11821  
gpg -a --export E2A11821 | sudo apt-key add -
```

```
sudo gedit /etc/apt/sources.list
```

Add this line to the bottom of the sources.list file:

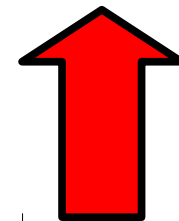
```
deb http://rh-mirror.linux.iastate.edu/CRAN/bin/linux/ubuntu hardy/
```

Use your own: feisty or jaunty, etc... instead of hardy

Save the file and go back to the Bash terminal.

```
sudo apt-get update
```

```
sudo apt-get install r-base r-base-dev
```



From: <https://stat.ethz.ch/pipermail/r-help/2009-February/187644.html>

Installing the MacOSX version

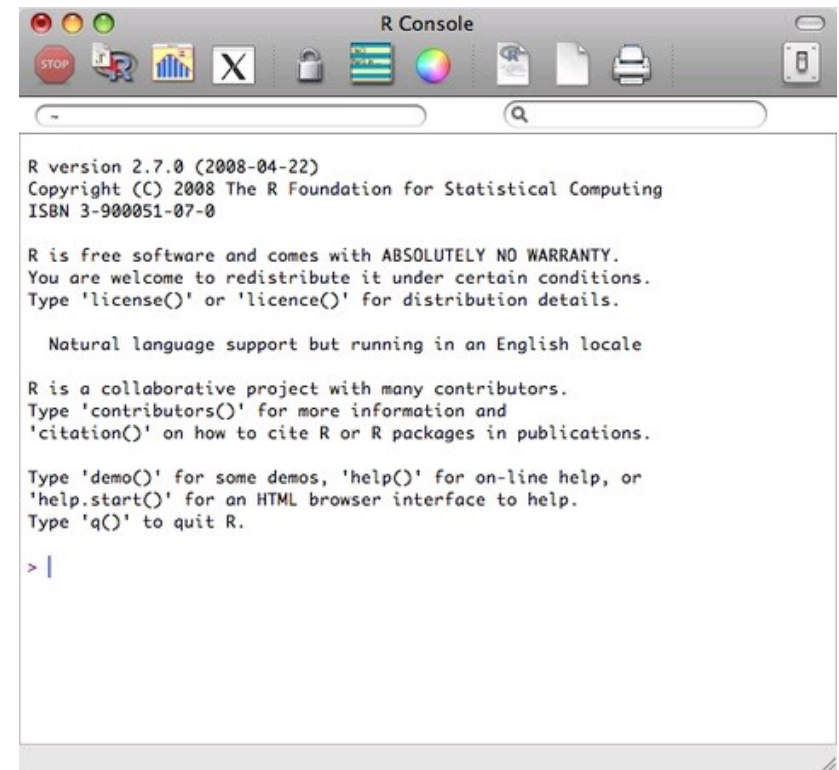
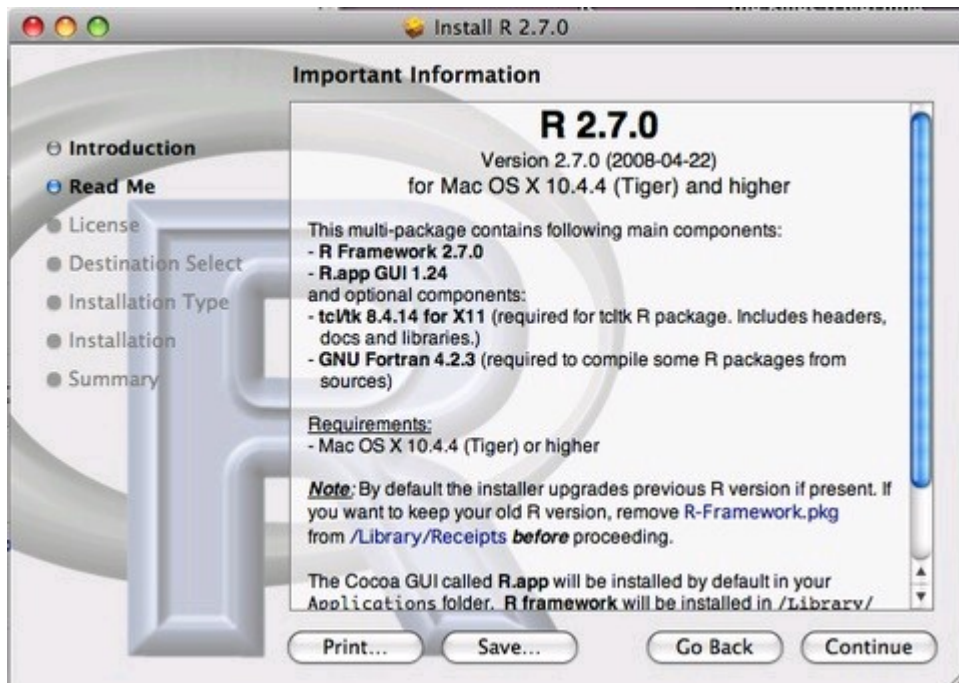
First, download "R-2.9.2.dmg" from the "bin/macosx" directory of a CRAN site

Download and Install R

Precompiled binary distributions of the base system and contributed packages, **Windows and Mac** users most likely want one of these versions of R:

- [Linux](#)
- [MacOS X](#)
- [Windows](#)

Double-click on the icon to mount the disk image file



Installing R

References/to learn more:

The R book

Michael J. Crawley pp 1
2007 John Wiley & Sons Ltd

Basic statistics using R pp. 8

Jarno Tuimala (CSC) and Dario Greco (HY)
<http://www.csc.fi/english/csc/courses/archive/R2008s>

Statistics with R

Vincent Zoonekynd, pp 3
http://zoonek2.free.fr/UNIX/48_R/all.html

Aprendizaje del software estadístico R: un entorno para simulación y computación estadística

Prof. Alberto Muñoz García
Departamento de Estadística
Universidad Carlos III de Madrid
<http://ocw.uc3m.es/estadistica/aprendizaje-del-software-estadistico-r-un-entorno-para-simulacion-y-computacion-estadistica/introduccion-al-analisis-de-datos-y-al-lenguaje-s>

Geographic Data Analysis

Pat Bartlein
<http://geography.uoregon.edu/bartlein/courses/geog417/exercises/ex1.htm>

Software Tools, Part 1: introduction to R software

Petri Koistinen
<http://www.rni.helsinki.fi/~pek/s-tools/RGetToKnow.html>

Chem 351 Archives Page

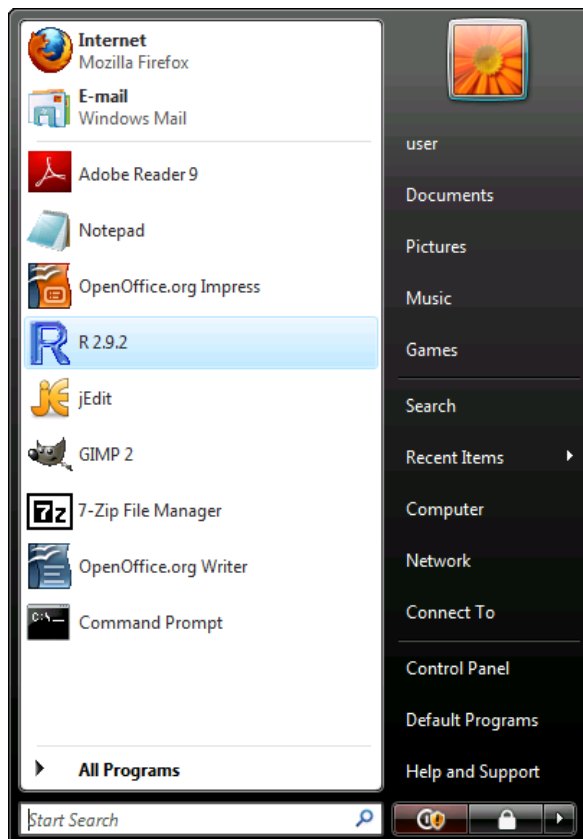
David Harvey
<http://fs6.depauw.edu:50080/~harvey/Chem%20351/PDF%20Files/Handouts/RDocs/Obtaining%20and%20Installing%20R.pdf>

Starting R

On Windows, if there is a shortcut on the desktop:

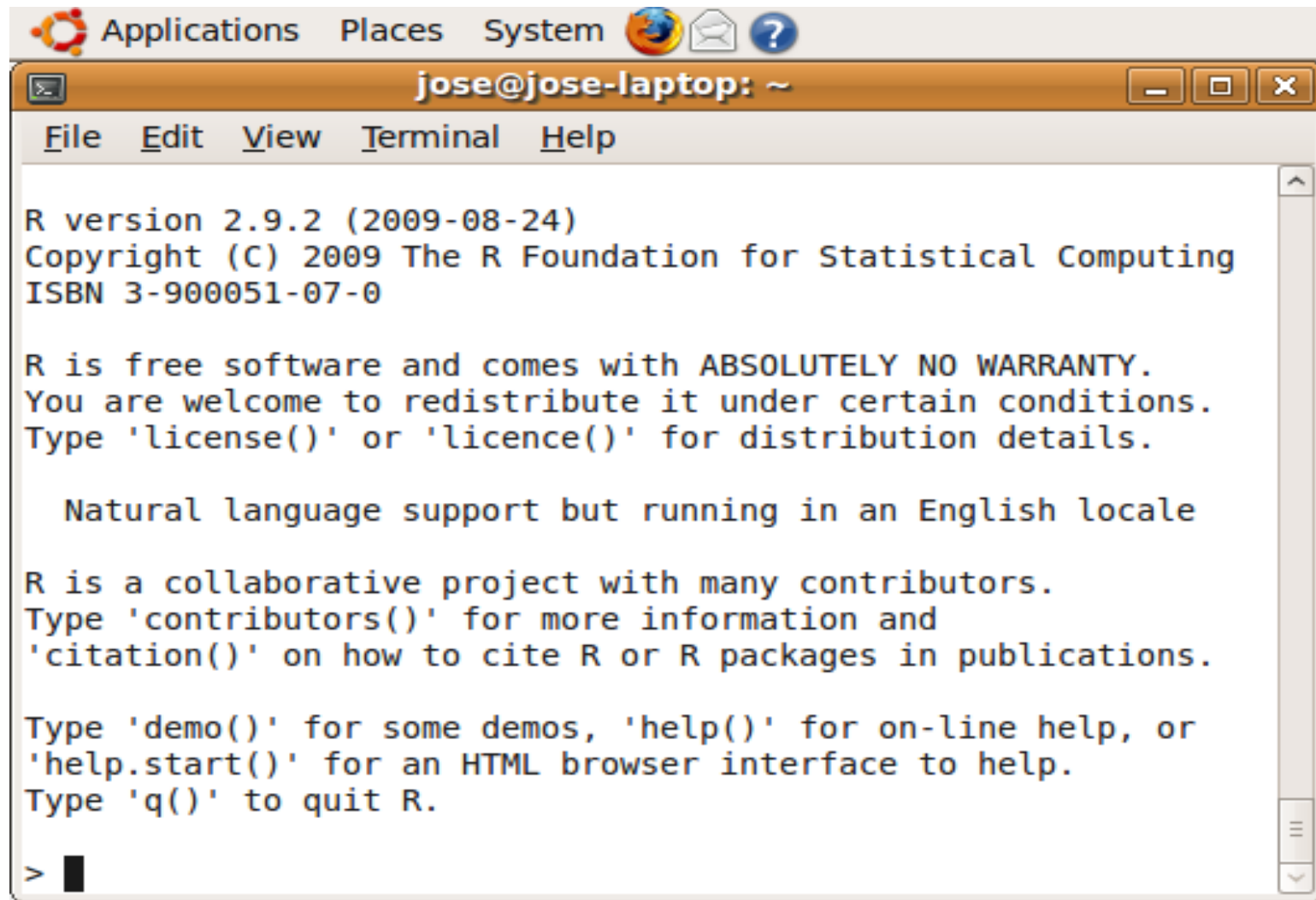





Or on the Start menu:



Starting R

On Ubuntu, type R at the prompt

A screenshot of a terminal window on an Ubuntu system. The window title is "jose@jose-laptop: ~". The terminal displays the R version 2.9.2 splash screen, which includes the R logo, version information, copyright notice, and a list of commands for help and quitting. The prompt ">" is visible at the bottom left of the terminal area.

```
Applications Places System   
jose@jose-laptop: ~
File Edit View Terminal Help
R version 2.9.2 (2009-08-24)
Copyright (C) 2009 The R Foundation for Statistical Computing
ISBN 3-900051-07-0

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

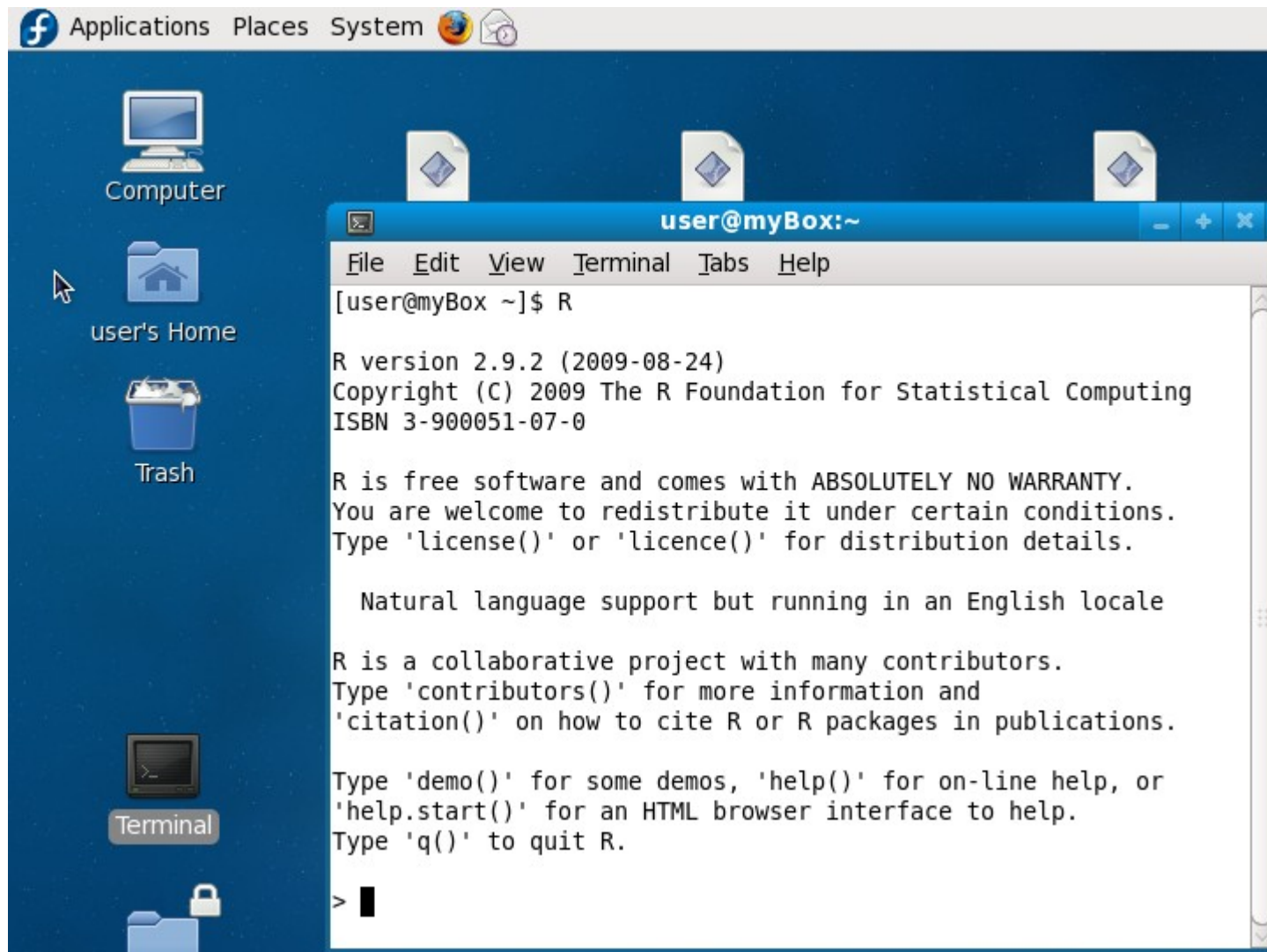
Natural language support but running in an English locale

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

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

Starting R

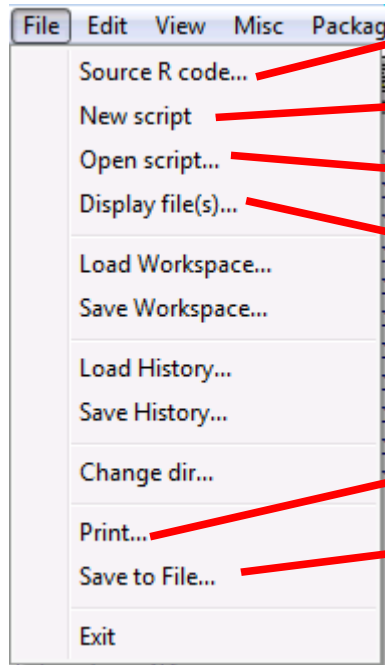
On Fedora, type R at the prompt



The screenshot shows a Fedora desktop environment with a blue background. The top panel includes the Fedora logo, 'Applications', 'Places', and 'System' menus, along with icons for the globe and mail. The desktop has icons for 'Computer', 'user's Home', 'Trash', and 'Terminal'. A terminal window titled 'user@myBox:~' is open, displaying the output of the 'R' command. The terminal output shows the R version (2.9.2), copyright information (© 2009 The R Foundation for Statistical Computing), and a disclaimer: 'R is free software and comes with ABSOLUTELY NO WARRANTY. You are welcome to redistribute it under certain conditions. Type 'license()' or 'licence()' for distribution details.' It also mentions 'Natural language support but running in an English locale' and provides instructions on how to get help and quit R.

```
user@myBox:~  
File Edit View Terminal Tabs Help  
[user@myBox ~]$ R  
R version 2.9.2 (2009-08-24)  
Copyright (C) 2009 The R Foundation for Statistical Computing  
ISBN 3-900051-07-0  
  
R is free software and comes with ABSOLUTELY NO WARRANTY.  
You are welcome to redistribute it under certain conditions.  
Type 'license()' or 'licence()' for distribution details.  
  
Natural language support but running in an English locale  
  
R is a collaborative project with many contributors.  
Type 'contributors()' for more information and  
'citation()' on how to cite R or R packages in publications.  
  
Type 'demo()' for some demos, 'help()' for on-line help, or  
'help.start()' for an HTML browser interface to help.  
Type 'q()' to quit R.  
> █
```

Rgui



Load R functions

Open the R editor

Open a file on the R editor

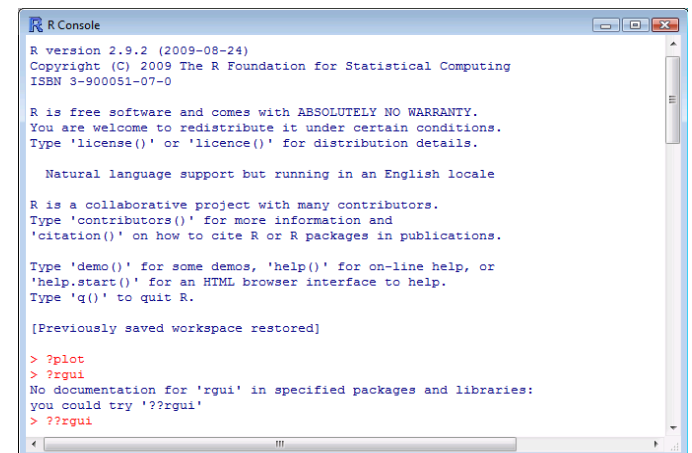
Display text file(s)

Print the History

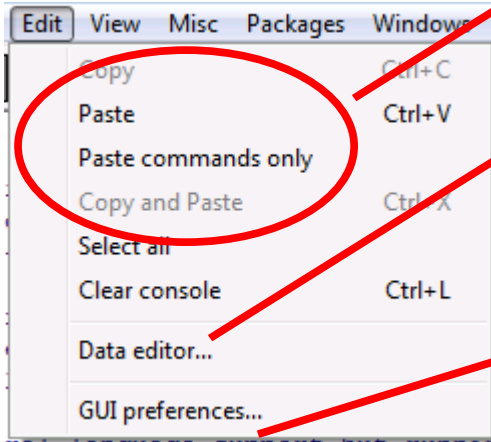
Save the History as text



History is the text on the console:



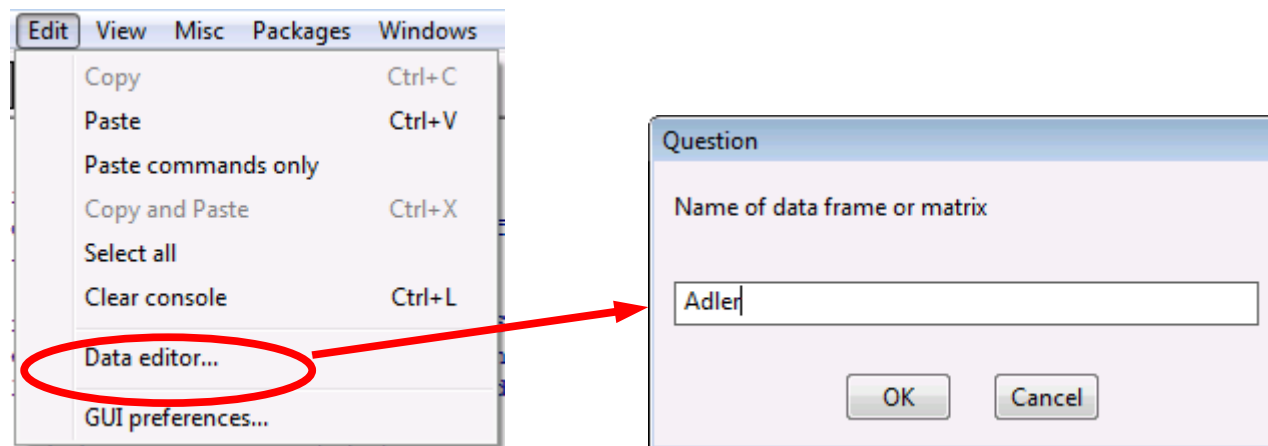
Rgui



For editing a matrix or dataframe from the current session

For customizing the GUI

Rgui



The image shows the R GUI interface with the R Console and Data Editor windows. The R Console window shows the following commands:

```
> library(car)
> attach(Adler)
> fix(Adler)
```

The Data Editor window shows a table with the following data:

	row.names	instruction	expectation	rating	var5	var6	var7
1	1	GOOD	HIGH	25			
2	2	GOOD	HIGH	0			
3	3	GOOD	HIGH	-16			
4	4	GOOD	HIGH	5			
5	5	GOOD	HIGH	11			
6	6	GOOD	HIGH	-6			
7	7	GOOD	HIGH	42			
8	8	GOOD	HIGH	-2			
9	9	GOOD	HIGH	-13			
10	10	GOOD	HIGH	14			
11	11	GOOD	HIGH	4			
12	12	GOOD	HIGH	-22			
13	13	GOOD	HIGH	19			
14	14	GOOD	HIGH	6			
15	18	GOOD	HIGH	-6			
16	19	GOOD	LOW	-25			
17	20	GOOD	LOW	-23			
18	21	GOOD	LOW	-28			
19	22	GOOD	LOW	-22			

Data Editor

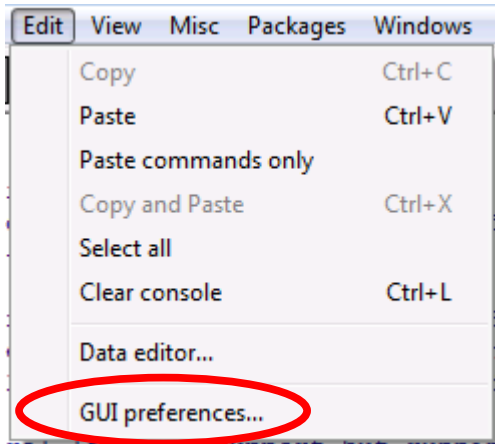
For editing a matrix or dataframe from the current session

Same as the fix function

The cells are editable, like a spreadsheet

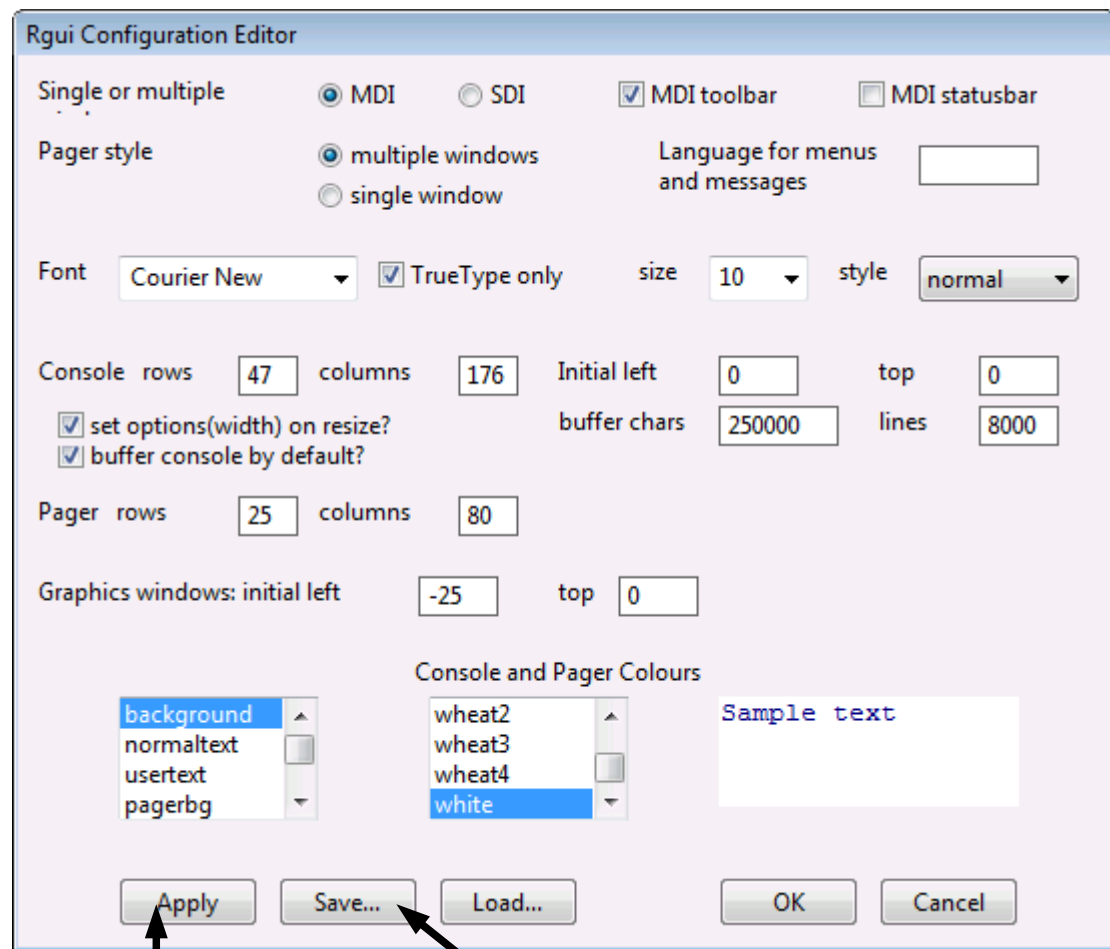
Rgui

Customizing the GUI



Some editors will only work with MDI

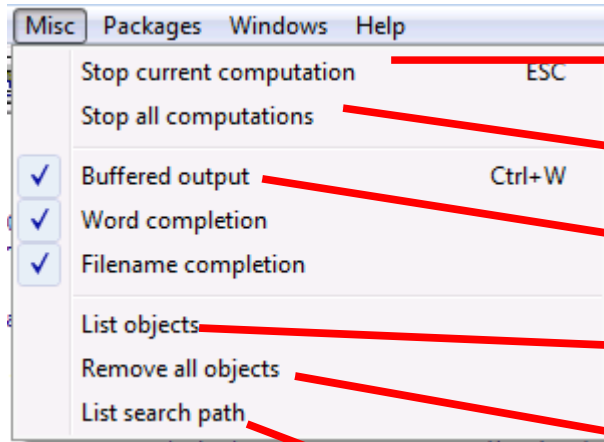
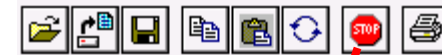
Buffer chars and Lines can be increased if it is necessary to work with a long History and there is an error because there is no space for it



This will apply the changes to the current session

To make changes permanent, that is, for every session, they must be saved. The default file Rconsole is loaded when a session starts

Rgui



Stop computation on the current window

Stop computation on all the windows

Uncheck to get output immediately on the console*

Lists the names of the objects on the workspace

Deletes all the objects on the workspace

Lists attached packages and R objects

ls()

rm(list=ls(all=TRUE))

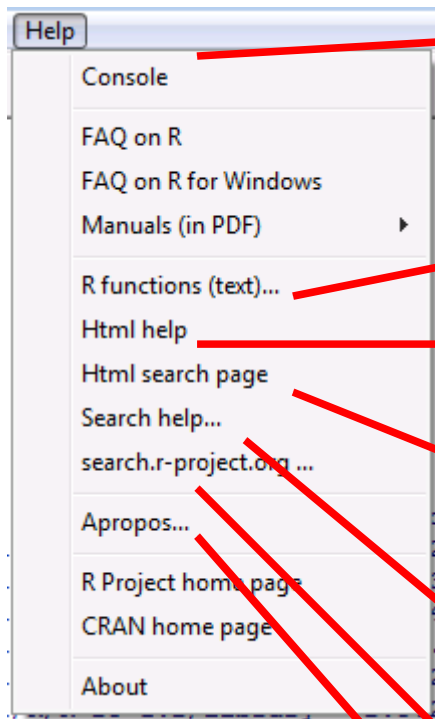
search()

* for example, to call some code and see its progress on the screen

???

R help

From the console:



Help about the console controls

Help about a known function name

`help("plot")`
`?plot`

R HTML manuals and references

`help.start()`

R HTML search engine for keywords, function and data names and text in help page titles

Search a reference from the manual

`help.search("test")`
`??test`

Use the online R Site Search

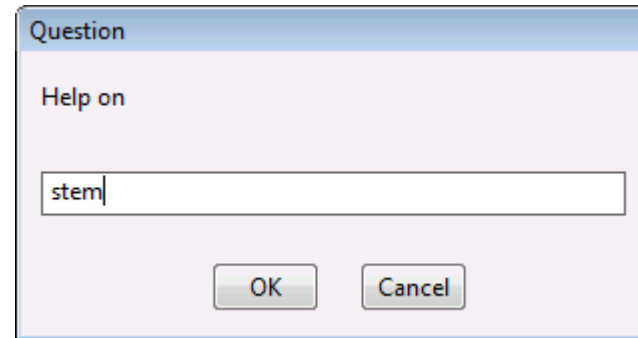
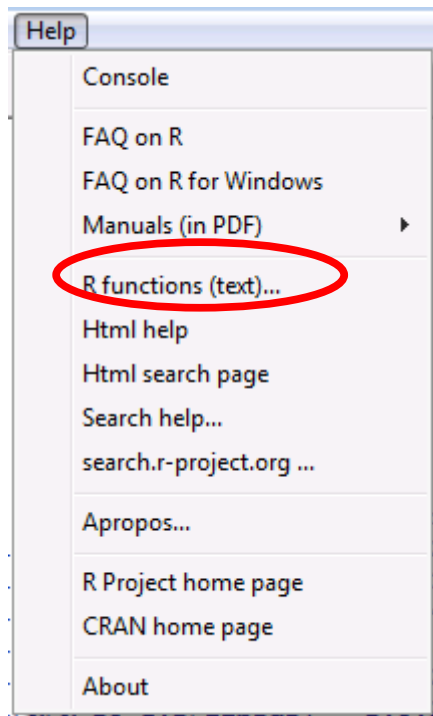
`RSiteSearch("test")`

Look for a function name, partially known

`apropos("test")`

R help

Search for function “stem”



On the console:

```
help("stem")
```

Which could be called directly..

A help file will open on a new window.

R help

Function stem was found

Description of what the function does

Function call with arguments

Description of arguments, sometimes with links to related objects

References to literature

How to use the function, the two examples provided will run automatically:

`example("stem")`

The screenshot shows the R Help window for the 'graphics' package. The window title is 'R Help for package graphics'. The top navigation bar includes 'Hide', 'Back', 'Print', and 'Options'. Below this is a tabbed interface with 'Contents', 'Index', and 'Search' tabs. The 'Index' tab is active, displaying a list of functions with question mark icons. The function 'stem(graphics)' is highlighted in the list. The main content area shows the documentation for 'stem(graphics)', which is titled 'Stem-and-Leaf Plots'. The documentation is organized into sections: 'Description', 'Usage', 'Arguments', 'References', and 'Examples'. Red arrows point from the text on the left to specific parts of the documentation: from 'Function stem was found' to the function name in the index; from 'Description of what the function does' to the 'Description' section; from 'Function call with arguments' to the 'Usage' section; from 'Description of arguments, sometimes with links to related objects' to the 'Arguments' section; from 'References to literature' to the 'References' section; and from 'How to use the function, the two examples provided will run automatically:' to the 'Examples' section. The 'Examples' section contains two lines of code: `stem(islands)` and `stem(log10(islands))`. At the bottom of the page, it says '[Package graphics version 2.9.2 [Index](#)]'. The window also shows 'R Documentation' in the top right corner.

R Help for package graphics

Hide Back Print Options

Contents Index Search

stem(graphics) R Documentation

Stem-and-Leaf Plots

Description

stem produces a stem-and-leaf plot of the values in x. The parameter `scale` can be used to expand the scale of the plot. A value of `scale=2` will cause the plot to be roughly twice as long as the default.

Usage

```
stem(x, scale = 1, width = 80, atom = 1e-05)
```

Arguments

`x` a numeric vector.
`scale` This controls the plot length.
`width` The desired width of plot.
`atom` a tolerance.

References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

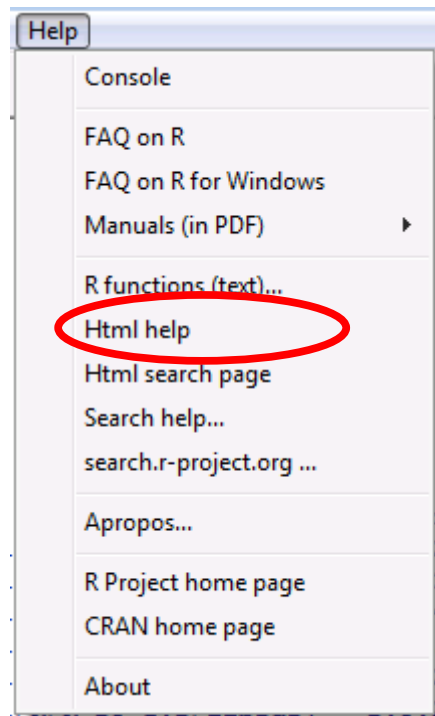
Examples

```
stem(islands)
stem(log10(islands))
```

[Package graphics version 2.9.2 [Index](#)]

R help

R HTML manuals and references



It doesn't show on the console but the equivalent command is:

`help.start()`

A new tab will open on the browser with the HTML help page.

R help

Manuals in HTML format

Statistical Data Analysis



Manuals

[An Introduction to R](#)

[The R Language Definition](#)

[Writing R Extensions](#)

[R Installation and Administration](#)

[R Data Import/Export](#)

[R Internals](#)

Reference

[Packages](#)

[Search Engine & Keywords](#)

Miscellaneous Material

[About R](#)

[Authors](#)

[Resources](#)

[License](#)

[Frequently Asked Questions](#)

[Thanks](#)

[FAQ for Windows port](#)

Very complete introduction to R

Installing and customizing R

R help

List of installed packages:

Statistical Data Analysis



Manuals

[An Introduction to R](#)

[Writing R Extensions](#)

[R Data Import/Export](#)

[The R Language Definition](#)

[R Installation and Administration](#)

[R Internals](#)

Reference

[Search Engine & Keywords](#)

Miscellaneous Material

[About R](#)

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[Authors](#)

[Frequently Asked Questions](#)

[FAQ for Windows port](#)

[Resources](#)

[Thanks](#)

[Packages](#)

R help

Click on MASS

List of installed packages:

KernSmooth	Functions for kernel smoothing for Wand & Jones (1995)
MASS	Main Package of Venables and Ripley's MASS
Matrix	Sparse and Dense Matrix Classes and Methods
base	The R Base Package
boot	Bootstrap R (S-Plus) Functions (Canty)
class	Functions for Classification
cluster	Cluster Analysis Extended Rousseeuw et al.
codetools	Code Analysis Tools for R
datasets	The R Datasets Package
foreign	Read Data Stored by Minitab, S, SAS, SPSS, Stata, Systat, dBase, ...
grDevices	The R Graphics Devices and Support for Colours and Fonts
graphics	The R Graphics Package
grid	The Grid Graphics Package
lattice	Lattice Graphics
methods	Formal Methods and Classes
mgcv	GAMs with GCV/AIC/REML smoothness estimation and GAMMs by PQL
nlme	Linear and Nonlinear Mixed Effects Models
nnet	Feed-forward Neural Networks and Multinomial Log-Linear Models
rpart	Recursive Partitioning
spatial	Functions for Kriging and Point Pattern Analysis
splines	Regression Spline Functions and Classes
stats	The R Stats Package
stats4	Statistical Functions using S4 Classes
survival	Survival analysis, including penalised likelihood.
tcltk	Tcl/Tk Interface
tools	Tools for Package Development
utils	The R Utils Package

Alternatively:

```
> installed.packages()  
Package  
base      "base"  
boot      "boot"  
class     "class"  
cluster   "cluster"  
codetools "codetools"  
datasets  "datasets"  
foreign   "foreign"  
graphics  "graphics"  
grDevices "grDevices"  
grid      "grid"  
KernSmooth "KernSmooth"  
lattice   "lattice"  
MASS      "MASS"  
Matrix    "Matrix"  
methods   "methods"  
mgcv      "mgcv"  
nlme      "nlme"  
nnet      "nnet"  
rpart     "rpart"  
spatial   "spatial"  
splines   "splines"  
stats     "stats"  
stats4    "stats4"  
survival  "survival"  
tcltk     "tcltk"  
tools     "tools"  
utils     "utils"  
Imports
```

This is a faster way to list the packages but without links to help

R help

Package MASS

Links to function names by their first character

Function names and a simple description

Main Package of Venables and Ripley's
MASS 

Documentation for package 'MASS' version 7.2-48
Help Pages

[A](#) [B](#) [C](#) [D](#) [E](#) [F](#) [G](#) [H](#) [I](#) [K](#) [L](#) [M](#) [N](#) [O](#) [P](#) [Q](#) [R](#) [S](#) [T](#) [U](#) [V](#) [W](#) [misc](#)

--- --

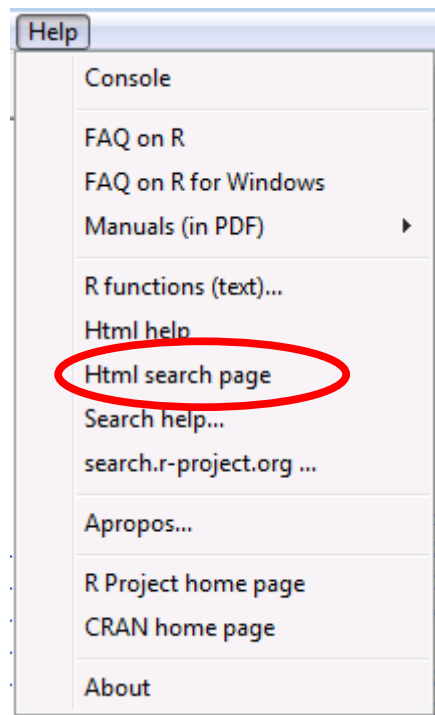
[.rat](#) Rational Approximation

--- A ---

[abbey](#) Determinations of Nickel Content
[accdeaths](#) Accidental Deaths in the US 1973-1978
[addterm](#) Try All One-Term Additions to a Model
[addterm.default](#) Try All One-Term Additions to a Model
[addterm.glm](#) Try All One-Term Additions to a Model
[addterm.lm](#) Try All One-Term Additions to a Model
[Aids2](#) Australian AIDS Survival Data
[Animals](#) Brain and Body Weights for 28 Species
[anorexia](#) Anorexia Data on Weight Change
[anova.negbin](#) Likelihood Ratio Tests for Negative Binomial GLMs
[area](#) Adaptive Numerical Integration
[as.character.fractions](#) Rational Approximation
[as.fractions](#) Rational Approximation

R help

R HTML search engine



It doesn't show on the console but the equivalent command would be:

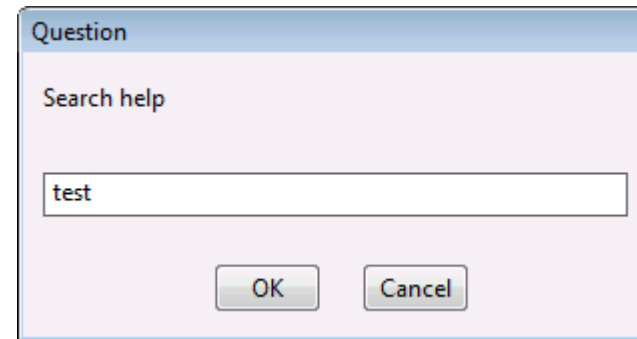
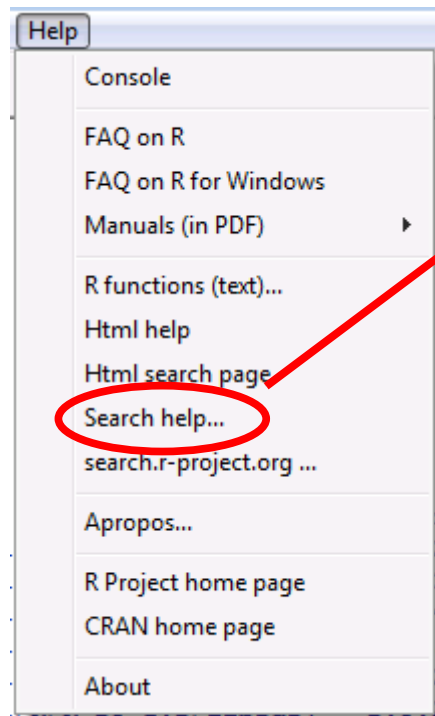
`help.start()`

Followed by clicking the link

[Search Engine & Keywords](#)

R help

Search for a reference from the manual on the keyword “test”



From the prompt:

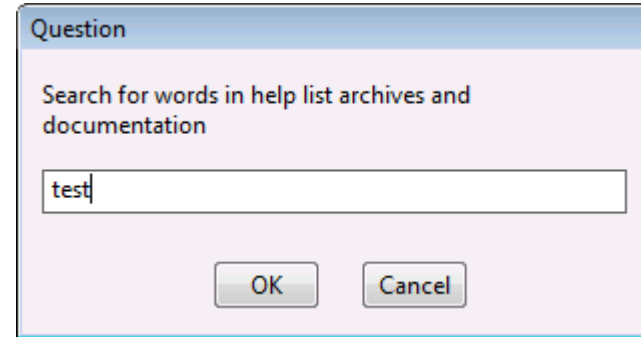
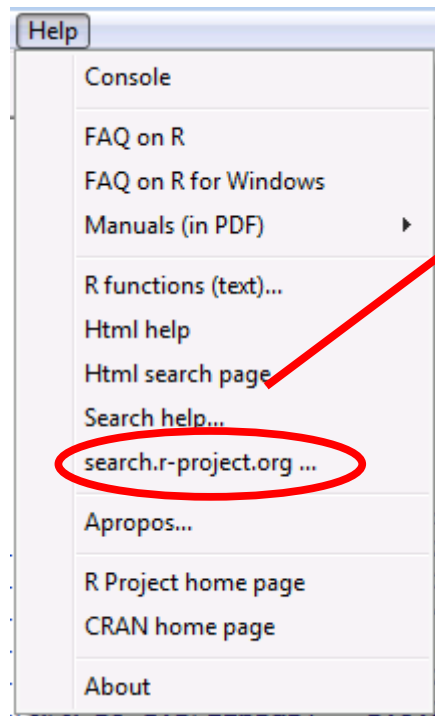
`help.search("test")`

or

`??test`

R help

Use the online R Site Search

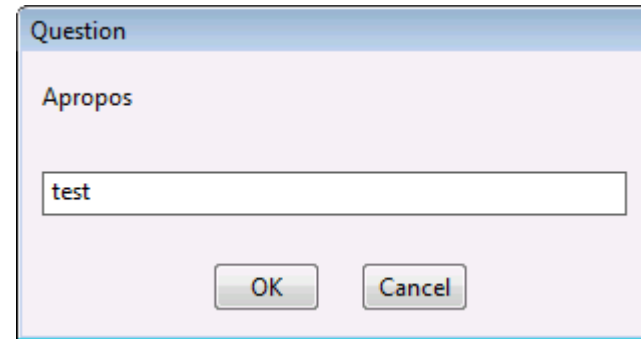
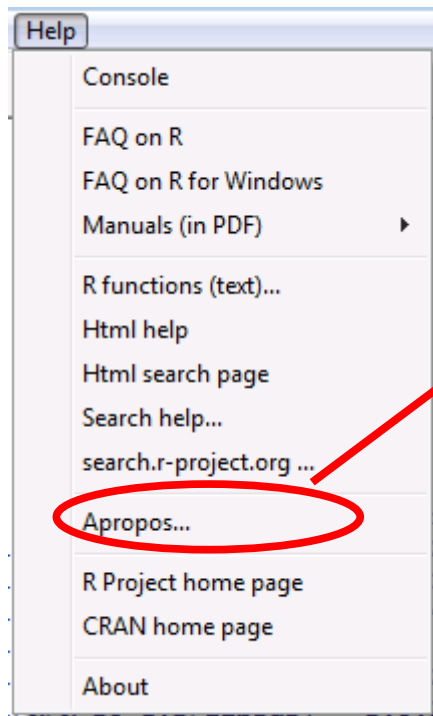


From the prompt:

```
RsiteSearch("test")
```

R help

Look for a function name,
partially known



From the prompt:

`apropos("test")`

Try this:

`apropos("test")`

`apropos(".test")`

`apropos("[\\.]test")`

`apropos("[^\\.]test")`

`apropos("^test")`

`apropos("([^\\.]test)|(^test)")`

R help

```
apropos("test")
apropos(".test")
apropos("[\\.]test")
apropos("[^\\.]test")
apropos("^test")
apropos("([^\\.]test)|(^test)")
```

1. "test" is anywhere within the function name
2. find "test" preceded by any character
3. find ".test"
4. find "test" preceded by any character, other than "."
5. find "test", only if at the end of the name
6. both 4. and 5.

Remember:
Apropos uses regular expressions for searches

```
> apropos("test")
[1] ".valueClassTest"      "ansari.test"      "bartlett.test"    "binom.test"      "Box.test"      "chisq.test"
[7] "cor.test"            "file_test"       "fisher.test"     "fligner.test"   "friedman.test" "kruskal.test"
[13] "ks.test"            "mantelhaen.test" "mauchly.test"    "mauchly.test"   "mcnemar.test"  "mood.test"
[19] "oneway.test"       "pairwise.prop.test" "pairwise.t.test" "pairwise.wilcox.test" "poisson.test"  "power.anova.test"
[25] "power.prop.test"    "power.t.test"    "PP.test"        "prop.test"      "prop.trend.test" "quade.test"
[31] "shapiro.test"     "t.test"         "testInheritedMethods" "testPlatformEquivalence" "testVirtual"   "var.test"
[37] "wilcox.test"

> apropos(".test")
[1] ".valueClassTest"      "ansari.test"      "bartlett.test"    "binom.test"      "Box.test"      "chisq.test"
[8] "file_test"          "fisher.test"     "fligner.test"    "friedman.test"   "kruskal.test"  "ks.test"
[15] "mauchly.test"       "mauchly.test"    "mcnemar.test"    "mood.test"       "oneway.test"   "pairwise.prop.test"
[22] "pairwise.wilcox.test" "poisson.test"    "power.anova.test" "power.prop.test" "power.t.test"  "PP.test"
[29] "prop.trend.test"    "quade.test"     "shapiro.test"    "t.test"         "var.test"      "wilcox.test"

> apropos("[^\\.]test")
[1] "ansari.test"         "bartlett.test"    "binom.test"      "Box.test"      "chisq.test"    "cor.test"
[8] "fligner.test"       "friedman.test"    "kruskal.test"    "ks.test"       "mantelhaen.test" "mauchly.test"
[15] "mcnemar.test"       "mood.test"        "oneway.test"     "pairwise.prop.test" "pairwise.t.test" "pairwise.wilcox.test"
[22] "power.anova.test"   "power.prop.test"  "power.t.test"    "PP.test"       "prop.test"      "prop.trend.test"
[29] "shapiro.test"     "t.test"         "var.test"       "wilcox.test"

> apropos("^test")
[1] ".valueClassTest" "file_test"

> apropos("^test")
[1] "testInheritedMethods" "testPlatformEquivalence" "testVirtual"

> apropos("([^\\.]test)|(^test)")
[1] ".valueClassTest"      "file_test"       "testInheritedMethods" "testPlatformEquivalence" "testVirtual"
```


R help

How to use help

To show the documentation

`help()` or `?help`

To find the documentation about the function "plot"

`?plot`

`help("plot")`

To find the documentation about reserved words or non-alphanumeric commands

`?"for"`

`?"["`

`?"<-.data.frame"`



To find all the installed help files (packages) that have an alias, concept or title named "plot"

`??plot`

`help.search("plot")`

Package "graphics" has a function "plot", let's examine it:

`?graphics::plot`

Package "lattice" has a function "xyplot", let's examine it:

`?lattice::xyplot`

To get a short description of a package:

`library(help = graphics)`

R help

How to use help

When not sure about the function name (on the search path), but it contains "plot"
`apropos("plot")`

To search R the web site and the R-help mailing list (<http://search.r-project.org>)
`RSiteSearch("plot")`

To run the examples from a help topic
`example(topic)`

To find where there are some demos for the loaded packages
`demo()`

To find where there are some demos for all the packages
`demo(package = .packages(all.available = TRUE))`

To show the demo "graphics" from package "graphics", pausing between pages
`demo(graphics, package="graphics", ask=TRUE)`

To show the demo "graphics" from package "graphics", without pausing between pages
`demo(graphics, package="graphics", ask=FALSE)`

R help

Other sources of help

R Project search engine

<http://www.r-seek.org>

mailing lists which are used by R users and developers. See

<http://www.R-project.org/mail.html>

Bug-tracking system

R has a bug-tracking system (or perhaps a bug-filing system is a more precise description) available on the net at

<http://bugs.R-project.org/>

The R Journal

<http://journal.r-project.org/>

Journal of Statistics Education

<http://www.amstat.org/PUBLICATIONS/JSE/>

Technology Innovations in Statistics Education

<http://repositories.cdlib.org/uclastat/cts/tise/>

Journal of Statistical Software

<http://www.jstatsoft.org>

R help

Exercise

How to get random numbers in R?

Use only the help tools discussed today

R help

?random # no results...

??random

base::RNG	Random Number Generation
base::sample	Random Samples and Permutations
datasets::randu	Random Numbers from Congruential Generator RANDU

?base::RNG # Random Number Generation

?base::sample # Random Samples and Permutations

?datasets::randu # Random Numbers from Congruential Generator RANDU ("widely considered to be one of the most ill-conceived random number generators designed", Wikipedia)

The command-line editor

Recall and correction of previous commands

R keeps a command history, a list of the commands executed at the prompt.

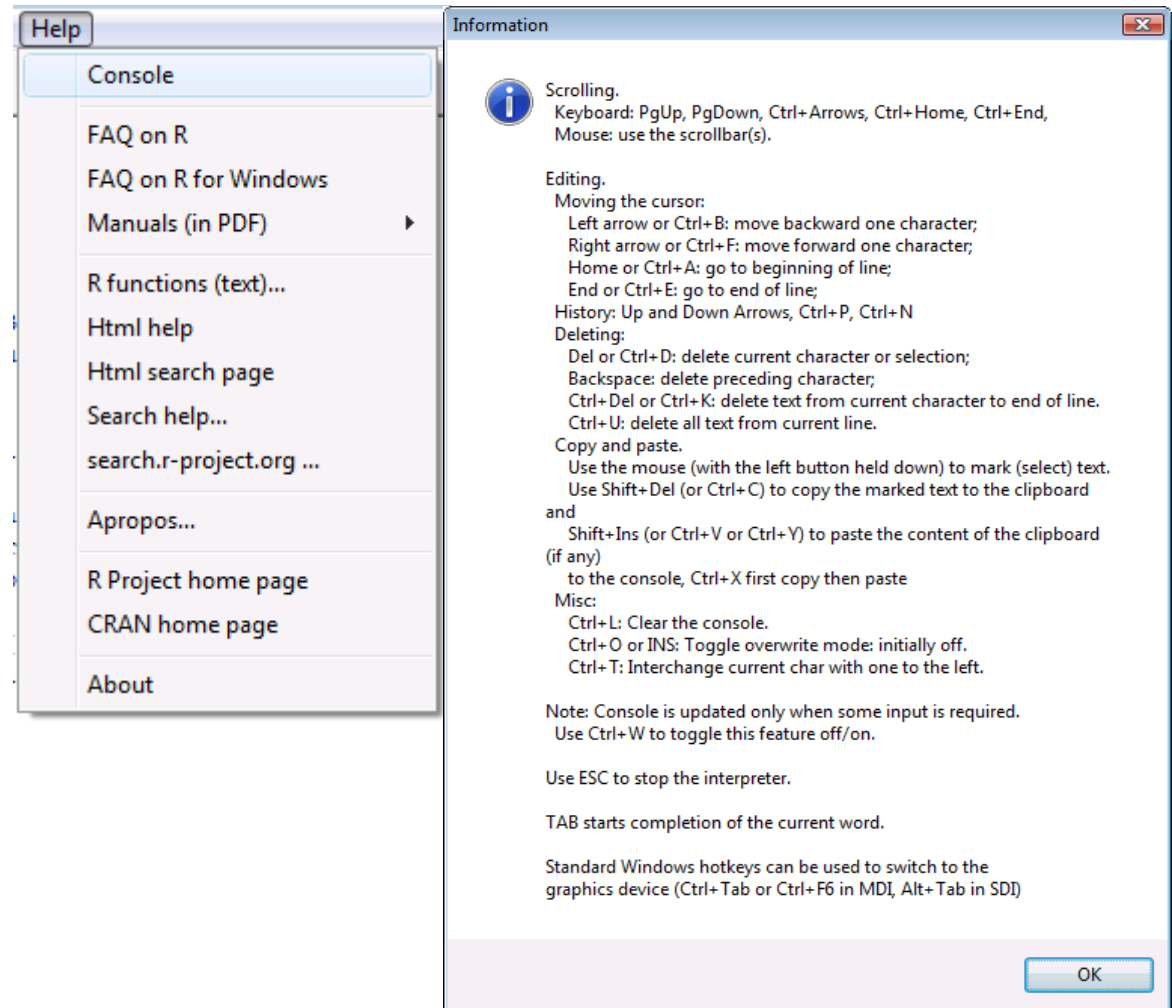
Enter will execute the current line of text, at the prompt.

Cursor keys:

Arrow up - show previous command

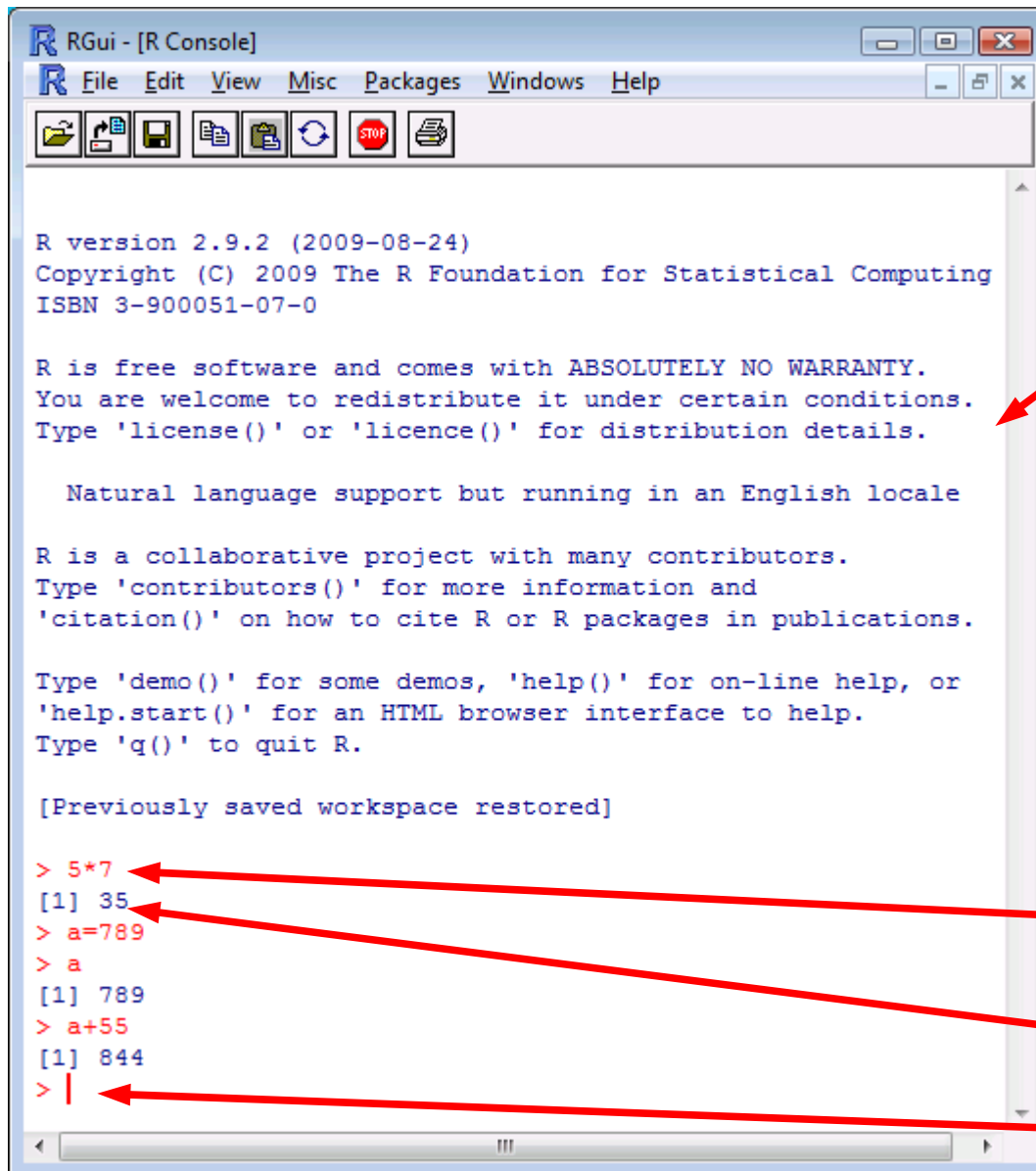
Arrow down - show next command

Arrows left and right - move around the current line of text, at the prompt.



Editor comands:

The command-line editor



```
RGui - [R Console]
File Edit View Misc Packages Windows Help

R version 2.9.2 (2009-08-24)
Copyright (C) 2009 The R Foundation for Statistical Computing
ISBN 3-900051-07-0

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

Natural language support but running in an English locale

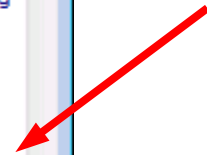
R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

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

[Previously saved workspace restored]

> 5*7
[1] 35
> a=789
> a
[1] 789
> a+55
[1] 844
> |
```

R startup message



User expression



Result



Prompt, this is the input area



The command-line editor

Incomplete expressions will result on an annoying + that will disappear once the expression is completed.

```
> a="ab
+
+ c"
>
> a
[1] "ab\n\nc"
```

A string must be within enclosing double quotes but, pressing enter, will cause a newline character to be part of the string.

```
> b=5*
+ 3
> b
[1] 15
```

An expression is incomplete if it ends with an operator. There are no side effects, once the expression is completed.

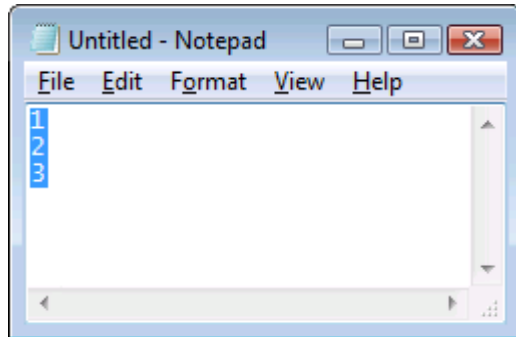
```
- -
> c=(3*(5+1)
+ )
> c
[1] 18
```

An expression with parenthesis will not work, until all the parenthesis are paired. There are no side effects, once the expression is completed.

The command-line editor

The console will accept multiple commands, if pasted, and execute one line at a time.

For example, copying from Notepad:

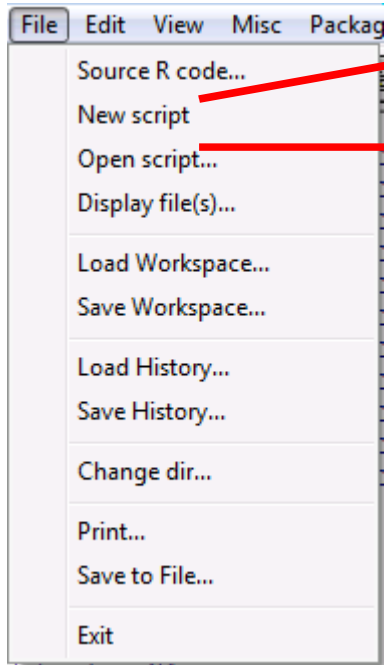


And pasting on R:

```
> 1  
[1] 1  
> 2  
[1] 2  
> 3  
[1] 3
```

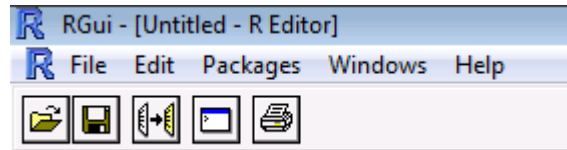
This is unnecessary because R has its own text editor, the R Editor

The R Editor



Open the R editor

Open a file on the R editor



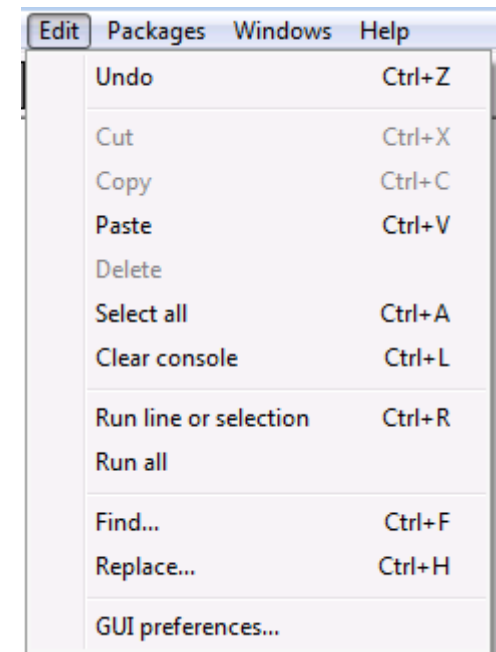
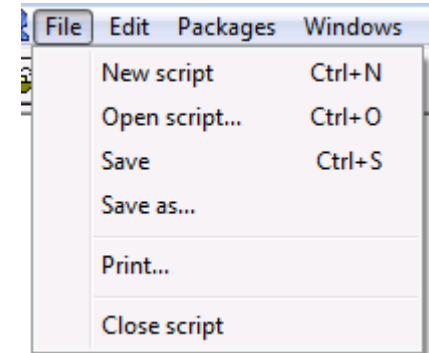
Open R file

Save R file

Run all the code

Run current line or selected code

Menu changes:



The R Editor

The R Editor has all the capabilities of a basic text editor, just like notepad or pico.

The R Editor can be an alternative to the console because it can execute code, one line at a time, a selection of lines or even a selected portion of code within a larger expression. The code can be saved and loaded as a text file with the extension .R.

On Rgui on the menu go to File/New script
Type this:

```
myvec <- seq(1,by=3, length.out=9)
mymatrix1 <- matrix(myvec,3,3)
mymatrix2 <- matrix(9:1,3,3)
# component-wise multiplication
mymatrix1 * mymatrix2
```

Edit/Run all

The R Editor

Position the cursor on any line and press ctrl-r, the line of code will execute on the R console and the cursor will move down to the next line. It is possible to follow the execution of code by pressing ctrl-r continuously.

```
myvec <- seq(1,by=3, length.out=9)
|mymatrix1 <- matrix(myvec,3,3)
mymatrix2 <- matrix(9:1,3,3)
# component-wise multiplication
mymatrix1 * mymatrix2
```

The cursor is on this line, ctrl-r will execute it

Position the cursor at the beginning of any line and use shift+cursor keys or keep the left-click button on the mouse pressed and move the cursor, to select a few lines of code and press ctrl-r, the line of code will execute on the R console.

```
myvec <- seq(1,by=3, length.out=9)
mymatrix1 <- matrix(myvec,3,3)
mymatrix2 <- matrix(9:1,3,3)
# component-wise multiplication
mymatrix1 * mymatrix2
```

The R Editor

Position the cursor at the beginning of an expression and use shift+cursor keys or keep the left-click button on the mouse pressed and move the cursor, to select a valid expression and press ctrl-r, the expression will execute on the R console.

```
myvec <- seq(1,by=3, length.out=9)
mymatrix1 <- matrix(myvec,3,3)
mymatrix2 <- matrix(9:1,3,3)
# component-wise multiplication
mymatrix1 * mymatrix2
```

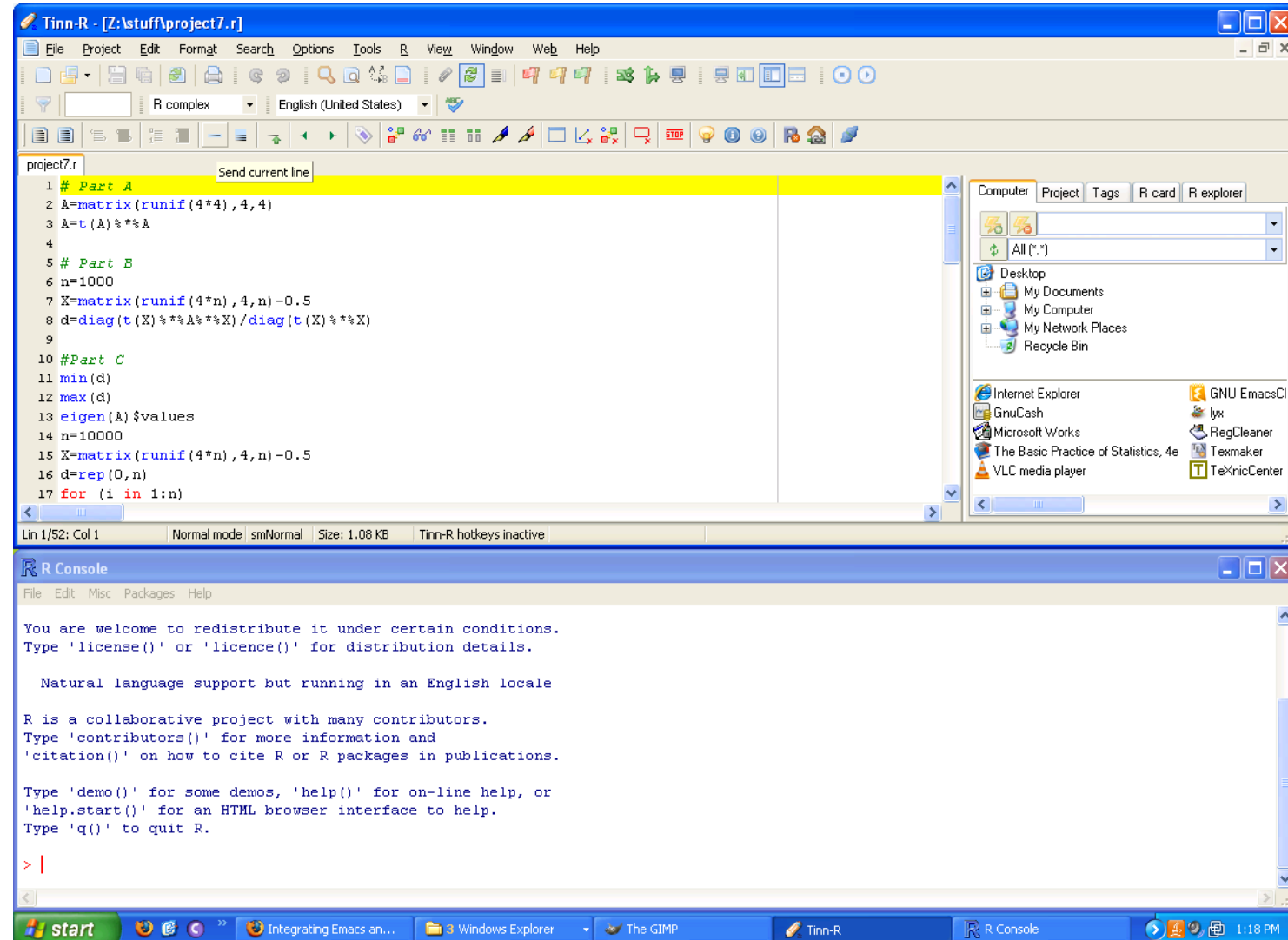
```
myvec <- seq(1,by=3, length.out=9)
mymatrix1 <- matrix(myvec,3,3)
mymatrix2 <- matrix(9:1,3,3)
# component-wise multiplication
mymatrix1 * mymatrix2
```

```
myvec <- seq(1,by=3, length.out=9)
mymatrix1 <- matrix(myvec,3,3)
mymatrix2 <- matrix(9:1,3,3)
# component-wise multiplication
mymatrix1 * mymatrix2
```

Tinn-R, an editor with more options

Features:

- R console window access from within Tinn-R.
- Incremental execution of R code.
- Integrated R help.
- R Object explorer.
- Line number for a source file.
- Search and Replace.
- Current line highlighting.
- Etc...



<http://jekyll.math.byuh.edu/other/howto/tinnr/using.shtml>

Getting information about R and the system

To get the R version	To get the license info	To learn how to cite R in publications	info about the platform under which R was built	system and user information
<code>R.version</code>	<code>license()</code>	<code>citation()</code>	<code>.Platform</code>	<code>Sys.info()</code>

```
> R.version
platform      _
1386-pc-mingw32
arch          1386
os            mingw32
system        1386, mingw32
status
major         2
minor         9.2
year          2009
month         08
day           24
svn rev       49384
language      R
version.string R version 2.9.2 (2009-08-24)
> # this might return a wrong value
> R.version$os
[1] "mingw32"
> # this is correct
> .Platform$OS.type
[1] "windows"
```

```
> Sys.info()[7]
      user
"Administrator"
> Sys.info()["user"]
      user
"Administrator"
```

Getting information about R and the system

To get a list of the installed packages	To get a list of new packages available	version information about R and attached or loaded packages	numerical characteristics of the machine	names of open graphics devices
<code>installed.packages()</code>	<code>old.packages()</code>	<code>sessionInfo()</code>	<code>.Machine</code>	<code>.Device</code>

command line+R Editor

References/to learn more:

The R book

Michael J. Crawley pp 9

2008 John Wiley & Sons Ltd

Basic statistics using R pp. 34

Jarno Tuimala (CSC) and Dario Greco (HY)

<http://www.csc.fi/english/csc/courses/archive/R2008s>

Software Tools, Part 1: introduction to R software

Petri Koistinen

<http://www.rni.helsinki.fi/~pek/s-tools/calculator.r>

Chem 351 Archives Page

David Harvey

<http://fs6.depauw.edu:50080/~harvey/Chem%20351/PDF%20Files/Handouts/RDocs/Some%20Basic%20R%20Commands.pdf>

Packages

The base distribution of R is the R programming language interpreter and some packages that are loaded by default. Packages, AKA extensions, are libraries that can be installed and used when needed and extend the functionality of R by adding new objects, for example new statistical functions, and their documentation and even data.

A package is a zip file, containing a file with the description of the package and subdirectories with the source code of the package and other information such as documentation, configuration, license, etc... This is described on the manual "Writing R Extensions".

Several projects distribute contributed packages, such as CRAN (The Comprehensive R Archive Network), Bioconductor (Analysis and comprehension of genomic data), OmegaHat (software for S, R and Xlisp-Stat), etc...

There are about 30 default packages, the base package has functions for the R programming language, other packages have functions for data input/output, graphics, utilities and statistical tools.

Packages are one of the strengths of R, with over 2000 packages available, therefore, there are many functions to handle packages.

Packages

How to get and use a package

Two steps for using a package



Get/download/**install** the package (get the file into the hard drive)

Use/access/**load** the package (get the file from the hard drive into memory, from R)

Packages

Installing a package

Select repository (repositories store packages distributed by the main projects), optional

Set CRAN mirror (there are CRAN mirrors in most countries, allowing fast downloads), optional

Install package (get the file into the hard drive)

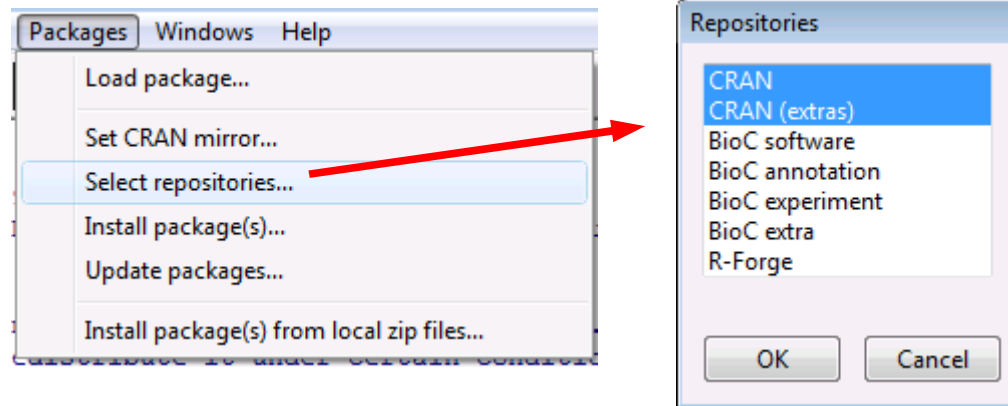
Download from the web

Copy from a USB stick

Packages

Select repository

Which distributor has the necessary packages



```
> setRepositories()  
--- Please select repositories for use in this session ---
```

```
1: + CRAN  
2: + CRAN (extras)  
3:   BioC software  
4:   BioC annotation  
5:   BioC experiment  
6:   BioC extra  
7:   R-Forge
```

```
Enter one or more numbers separated by spaces
```

```
1: |
```

CRAN is the basic R distribution

CRAN (extras) are Contributed R packages

BioC are packages from Bioconductor (bioinformatics/biostatistics, focused on inference using DNA microarrays)

R-forge are packages from Omegahat (umbrella project for S, R and Lisp-stats, focused on statistical tools, with web applications, web services, Java, distributed computing, etc...)

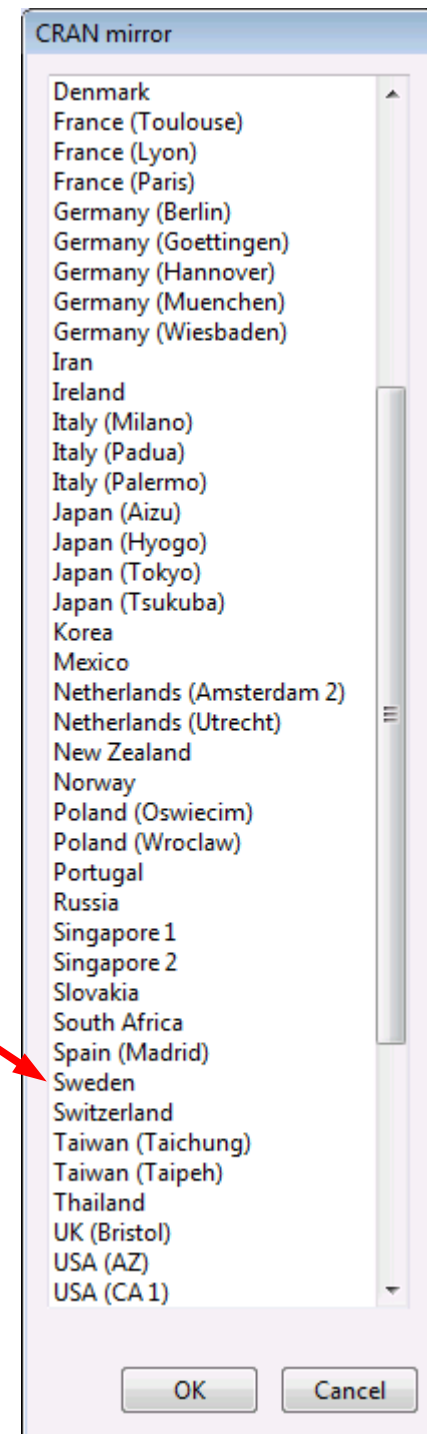
Packages

Set CRAN mirror

Which server is closer or faster/more reliable

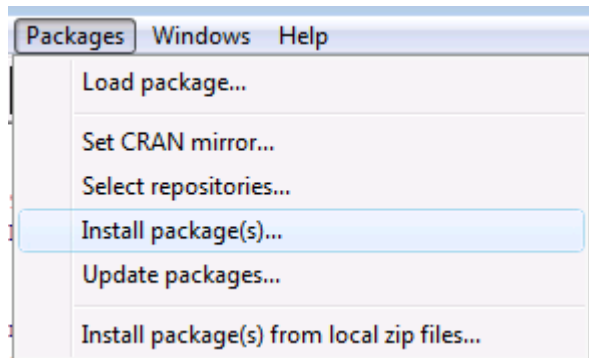
Sweden is the closest

```
> library()  
> chooseCRANmirror()
```



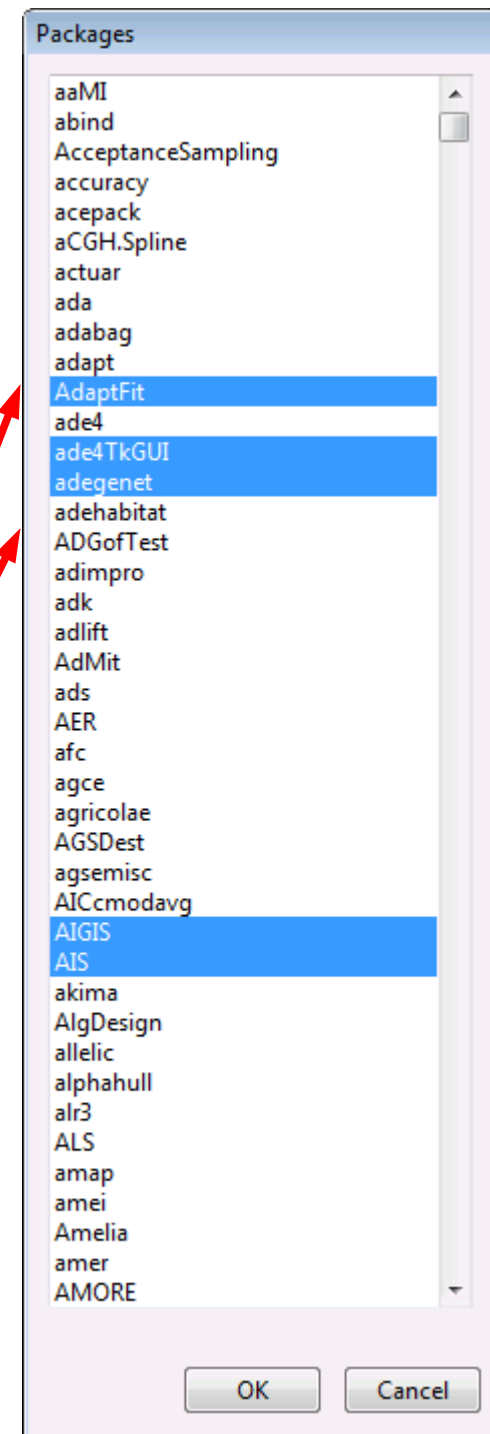
Packages

Install package



If no CRAN mirror was selected in this session, then it will ask for one.

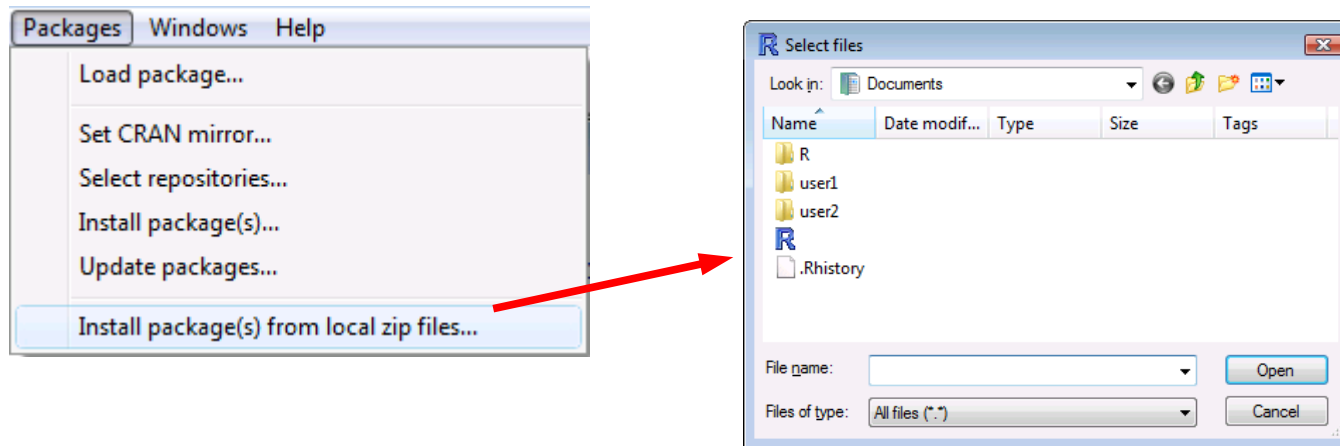
Multiple packages can be chosen by pressing the control key and clicking on the package name.



Packages

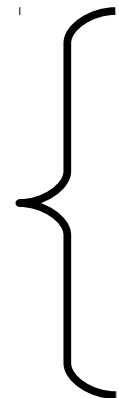
Install package from local zip file

Instead of from the web, for machines without web access



Packages

Functions to work with packages



- available.packages
- old.packages
- new.packages
- download.packages
- update.packages
- install.packages
- remove.packages

`available.packages()` - packages/bundles available at one or more repositories

`old.packages()` - packages/bundles that have newer versions on the repositories

`new.packages()` - uninstalled packages/bundles that are available at the repositories

`download.packages()` - downloads the newest versions of packages/bundles

`update.packages()` - the user will be prompted for which packages/bundles with a newer version to update

`install.packages()` - installs new packages/bundles

`remove.packages()` - removes installed packages/bundles and updates index information as necessary

Packages

When do I need such functions?

`available.packages()` - I want a list of all the existing packages!

`old.packages()` - are there newer versions of the packages/bundles installed?

`new.packages()` - are there new packages/bundles?

`download.packages()` - I want to download packages/bundles.

`update.packages()` - I want to see which packages/bundles have a newer version and decide, interactively, which ones to update.

`install.packages()` - I want to install packages/bundles.

`remove.packages()` - I want to remove installed packages/bundles.

Packages

Other functions:

<code>library()</code>	list all available packages
<code>library(lib.loc = .Library)</code>	list all packages in the default library
<code>library(ada)</code>	load package "ada"
<code>require(ada)</code>	load the package "ada" from inside other functions
<code>library(help = ada)</code>	documentation on package 'ada'
<code>search()</code>	list of attached packages and R objects
<code>.packages</code>	information about package availability
<code>.packages(all.available = TRUE)</code>	return all available as character vector
<code>detach("package:ada")</code>	unload package "ada"

Trying to use function "foo" from a package that is not yet loaded will return an error:
Error: could not find function "foo"

Packages

Loaded packages

search() = .packages() + R objects

Installed packages

library() = .packages(all.available = TRUE) with description

```
> (.packages())
[1] "stats"      "graphics"  "grDevices" "utils"     "datasets"  "methods"   "base"
> .packages(all.available = TRUE)
 [1] "car"          "HSAUR"      "scatterplot3d" "base"      "boot"      "class"     "cluster"    "codetools"  "datasets"  "foreign"
[11] "graphics"    "grDevices"  "grid"        "KernSmooth" "lattice"   "MASS"      "Matrix"     "methods"    "mgcv"      "nlme"
[21] "nnet"        "rpart"      "spatial"     "splines"   "stats"     "stats4"    "survival"   "tcltk"      "tools"     "utils"
> search()
[1] ".GlobalEnv"      "package:stats"  "package:graphics" "package:grDevices" "package:utils"  "package:datasets" "package:methods" "Autoloads"
[9] "package:base"
> library()
```

cluster	Cluster Analysis Extended Rousseeuw et al.
codetools	Code Analysis Tools for R
datasets	The R Datasets Package
foreign	Read Data Stored by Minitab, S, SAS, SPSS, Stata, Systat, dBase, ...
graphics	The R Graphics Package
grDevices	The R Graphics Devices and Support for Colours and Fonts
grid	The Grid Graphics Package
KernSmooth	Functions for kernel smoothing for Wand & Jones (1995)
lattice	Lattice Graphics
MASS	Main Package of Venables and Ripley's MASS
Matrix	Sparse and Dense Matrix Classes and Methods
methods	Formal Methods and Classes
mgcv	GAMs with GCV/AIC/REML smoothness estimation and GAMMs by PQL
nlme	Linear and Nonlinear Mixed Effects Models
nnet	Feed-forward Neural Networks and Multinomial Log-Linear Models
rpart	Recursive Partitioning
spatial	Functions for Kriging and Point Pattern Analysis
splines	Regression Spline Functions and Classes
stats	The R Stats Package
stats4	Statistical Functions using S4 Classes
survival	Survival analysis, including penalised likelihood.
tcltk	Tcl/Tk Interface
tools	Tools for Package Development
utils	The R Utils Package

Packages

To browse packages by topics (views)

<http://cran.r-project.org/web/views/>

CRAN Task Views

Bayesian	Bayesian Inference
ChemPhys	Chemometrics and Computational Physics
ClinicalTrials	Design, Monitoring, and Analysis of Clinical Trials
Cluster	Cluster Analysis & Finite Mixture Models
Distributions	Probability Distributions
Econometrics	Computational Econometrics
Environmetrics	Analysis of Ecological and Environmental Data
ExperimentalDesign	Design of Experiments (DoE) & Analysis of Experimental Data
Finance	Empirical Finance
Genetics	Statistical Genetics
Graphics	Graphic Displays & Dynamic Graphics & Graphic Devices & Visualization
gR	gRaphical Models in R
HighPerformanceComputing	High-Performance and Parallel Computing with R
MachineLearning	Machine Learning & Statistical Learning
MedicalImaging	Medical Image Analysis
Multivariate	Multivariate Statistics
NaturalLanguageProcessing	Natural Language Processing
Optimization	Optimization and Mathematical Programming
Pharmacokinetics	Analysis of Pharmacokinetic Data
Psychometrics	Psychometric Models and Methods
Robust	Robust Statistical Methods
SocialSciences	Statistics for the Social Sciences
Spatial	Analysis of Spatial Data
Survival	Survival Analysis
TimeSeries	Time Series Analysis

CRAN Task View: Statistical Genetics

Maintainer: Giovanni Montana

Contact: gmontana@imperial.ac.uk

Version: 2008-12-08

Maintainer

Great advances have been made in the field of genetic analysis over technology that reduce costs and increase throughput, are enabling for the analysis of genetic data and for related population genetics

Introduction

A number of R packages are already available and many more are

- *Population Genetics* : [genetics](#) implements classes and methods (Weinberg and linkage disequilibria, etc.). [Geneland](#) has fun population genetics simulations. [hapsim](#) simulates haplotype clustering SNP genotype data and SNP simulation from a Markov measures of pairwise LD. [mapLD](#) measures linkage disequilibrium ternary plots (also known as de Finetti diagrams). [Biodem](#) analysis on pedigrees. The [adegenet](#) implements a number of
- *Phylogenetics* : Phylogenetic and evolution analyses can be used for the analysis of phylogenetically simulated data sets and for phylogenetic trees and networks using maximum likelihood,
- *Linkage* : There are few native packages for performing packages that facilitate interface with these stand-alone programs calculated externally to test for genetic linkage with covariates

View description

CRAN packages:

- [adegenet](#)
- [ape](#)
- [apTreeshape](#)
- [Biodem](#)
- [bqtl](#)
- [catmap](#)
- [dlmap](#)
- [gap](#) (core)

Package names sorted alphabetically

Related links:

- [The Rgenetics Project](#)
- [BioConductor](#)
- [R packages from Division of Biostatistics](#)
- [QTL-ALL : provides interfaces between](#)
- [Computer programs by Jing Hua Zhao \(s](#)
- [R Software by David Clayton](#)
- [R Software by David Duffy](#)
- [BayesMendel](#)
- [R code for estimating haplotype frequenc](#)

References

Packages

CRAN task views are categories of contributed packages with simplified installation:

To automatically install these views, the `ctv` package needs to be installed:

```
install.packages("ctv")  
library("ctv")
```

The views can be installed now:

```
install.views("Genetics")  
or  
update.views("Genetics")
```

Data sets

A dataset is a collection of data, usually in a list form or in tabular form, which corresponds, on R, to data types vector and data frame.

a
b
c
d

1	x	j	7
2	y	v	3
3	z	r	9

R loads datasets from:

1. files ending '.R' or '.r' are opened with `source()`
2. files ending '.RData' or '.rda' are opened with `load()`
3. files ending '.tab', '.txt' or '.TXT' are read with `read.table(..., header = TRUE)` into a data frame.
4. files ending '.csv' or '.CSV' are read with `read.table(..., header = TRUE, sep = ";")` into a data frame.

Data set functions:

```
data() # list all available data sets  
try(data(package = "car")) # list the data sets in the car package  
data(car) # load the data set 'car'  
help(car) # give information on data set 'car'  
data(package = .packages(all.available = TRUE)) # lists the data sets in all available packages
```

R comes with some datasets already installed, one is pressure and it is the "Vapor Pressure of Mercury as a Function of Temperature".

```
require(graphics) #just to make sure the graphics library is loaded
```

```
pressure
```

```
?pressure
```

```
mean(pressure)
```

```
median(pressure)
```

```
min(pressure)
```

```
max(pressure)
```

```
quantile(pressure$pressure)
```

```
summary(pressure)
```

```
var(pressure)
```

```
sd(pressure)
```

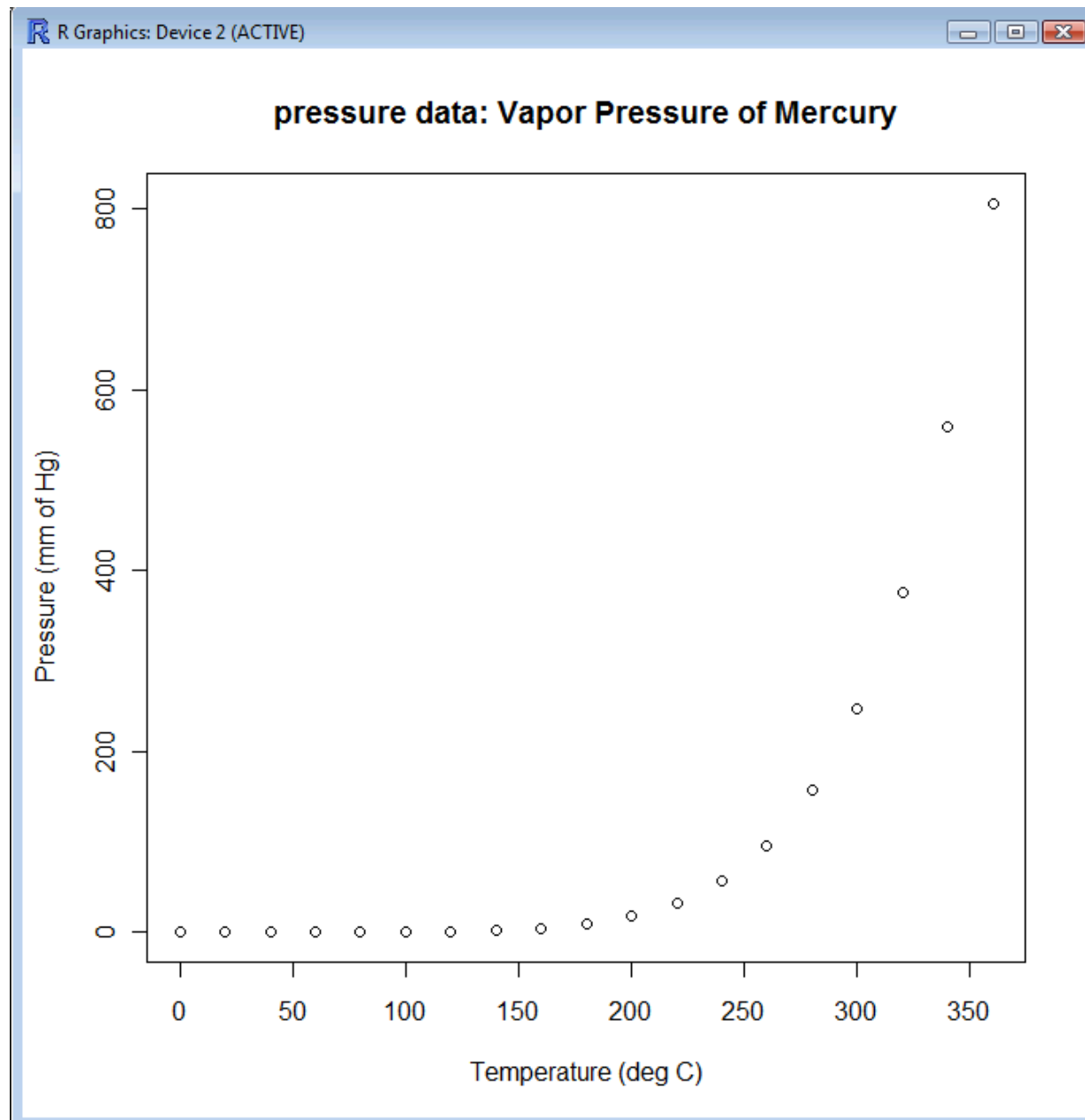
```
cor(pressure)
```

```
boxplot(pressure)
```



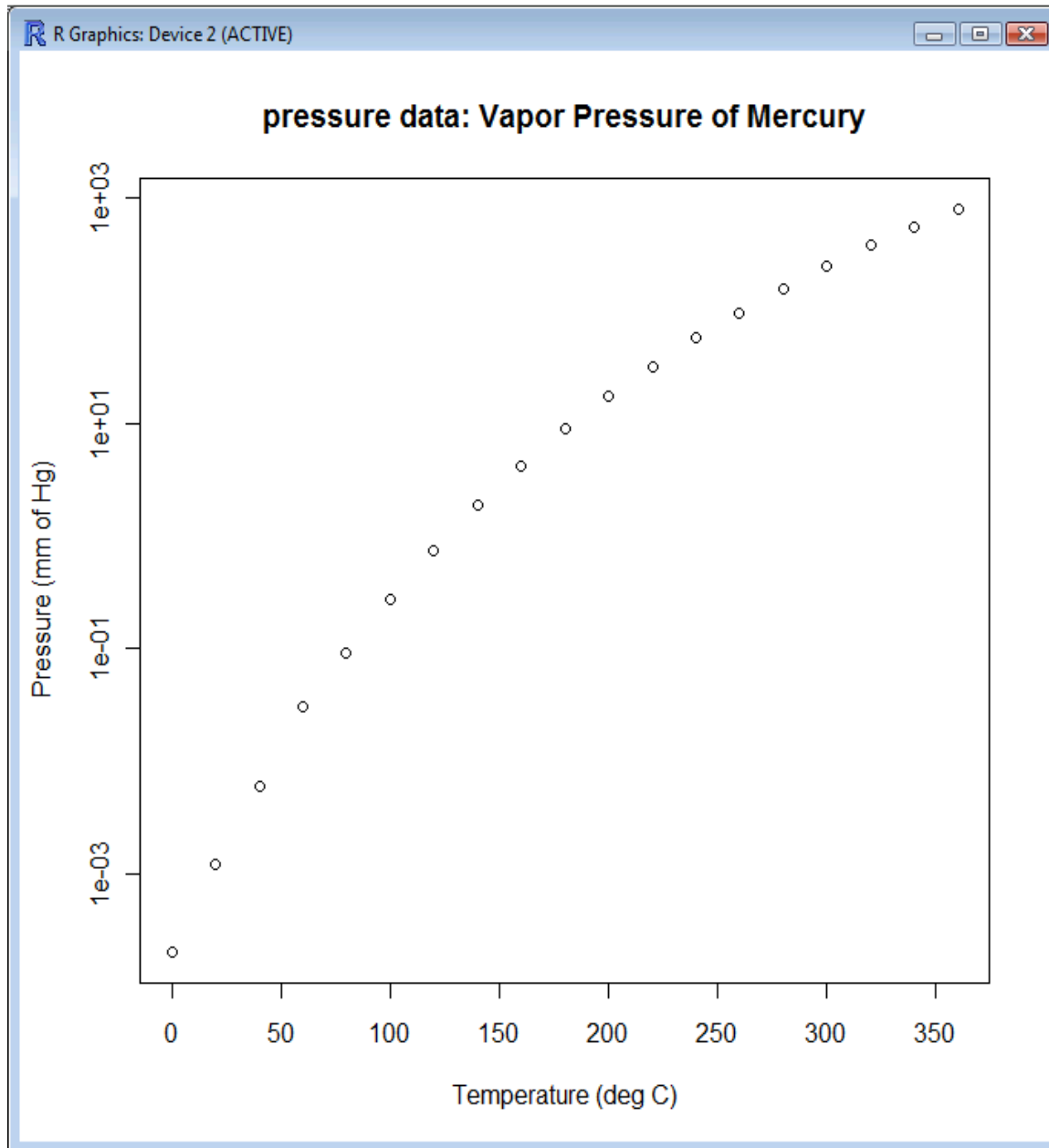
```
#decimal scale
```

```
plot(pressure, xlab = "Temperature (deg C)", ylab = "Pressure (mm of Hg)", main = "pressure data: Vapor Pressure of Mercury")
```



```
#log scale
```

```
plot(pressure, xlab = "Temperature (deg C)", log = "y", ylab = "Pressure (mm of Hg)", main =  
"pressure data: Vapor Pressure of Mercury")
```



Packages

Assignment: packages and help

1. Is the car package loaded?
2. Is the car package installed?
3. Install the car package
4. Load the car package
5. Is there help for the car package?
6. Find out information about the data frame Angell
7. Find out what the function scatterplot does
8. Run an example of scatterplot
9. Unload the car package
10. Uninstall the car package
11. List packages for epidemiology
12. List packages for environmental sciences

<http://cran.r-project.org/web/packages/car/car.pdf>

Packages

1. Is the car package loaded?
2. Is the car package installed?

> # 1. Is the car package loaded?

> (.packages())

```
[1] "stats" "graphics" "grDevices" "utils" "datasets" "methods"  
[7] "base"
```

> # 2. Is the car package installed?

> (.packages(all.available=TRUE))

```
[1] "biglm" "DBI" "ISwR" "leaps"  
[5] "RODBC" "RSQLite" "scatterplot3d" "base"  
[9] "boot" "class" "cluster" "codetools"  
[13] "datasets" "foreign" "graphics" "grDevices"  
[17] "grid" "KernSmooth" "lattice" "MASS"  
[21] "Matrix" "methods" "mgcv" "nlme"  
[25] "nnet" "rpart" "spatial" "splines"  
[29] "stats" "stats4" "survival" "tcltk"  
[33] "tools" "utils"
```

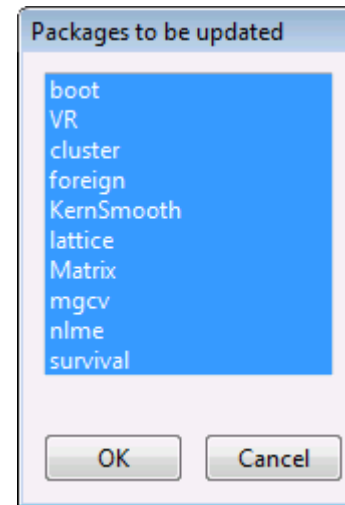
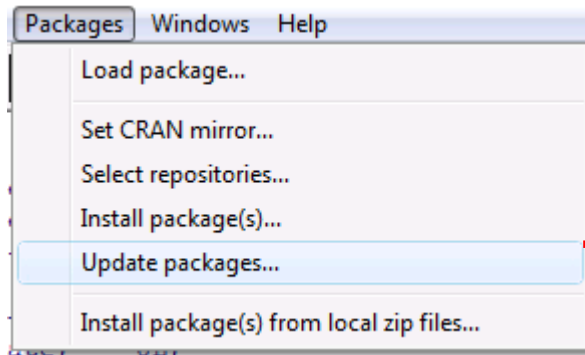
Packages

Before installing a package it is advisable to make sure all installed dependencies have their latest versions.

On the console:

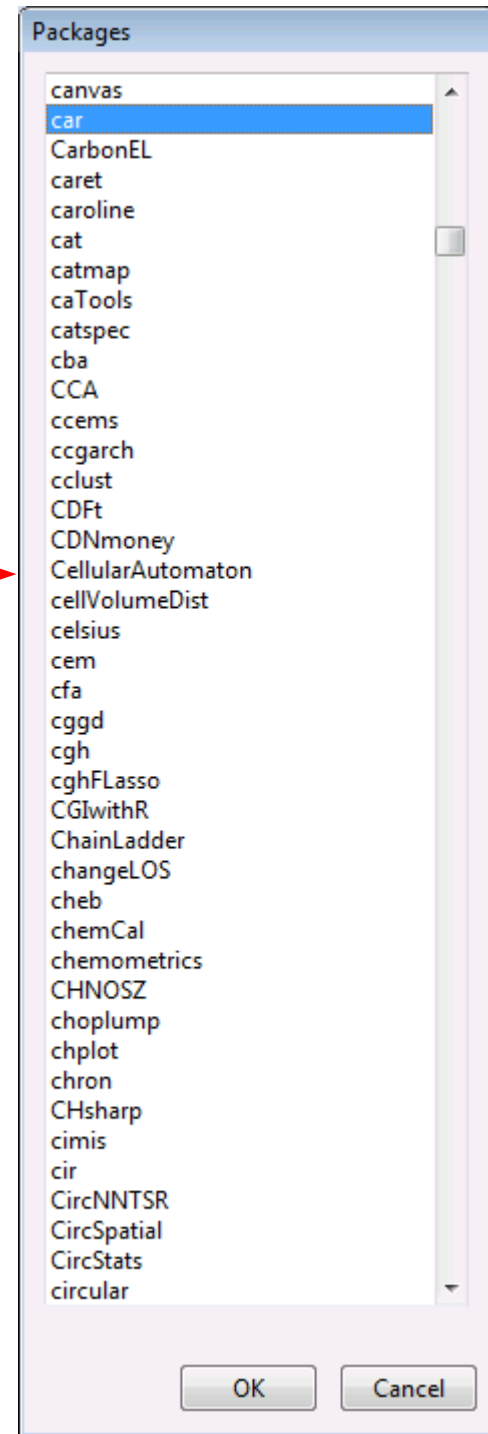
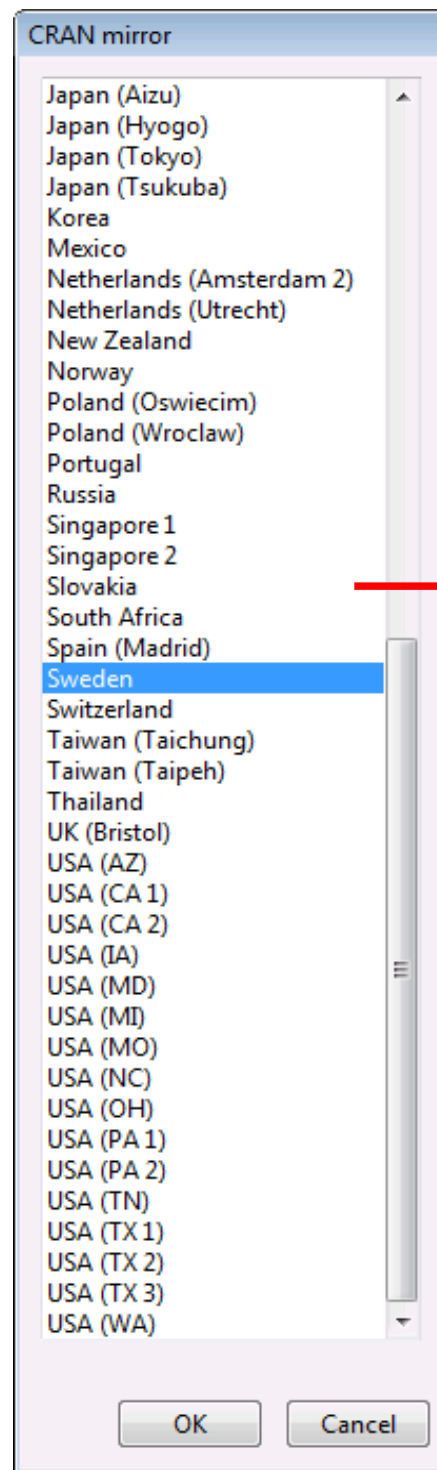
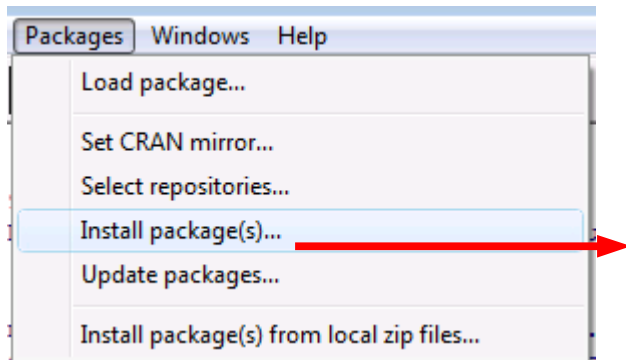
```
update.packages()
```

On RGui:



Packages

3. Install package car with RGui from the web



From the console:

```
install.packages("car",  
dependencies = TRUE)
```

Packages

Install package car from a zip file

The R Project for Statistical Computing

PCA 5 vars
princomp(x = data, cor = cor)

Navigation links:
About R
[What is R?](#)
[Contributors](#)
[Screenshots](#)
[What's new?](#)
Download, Packages
[CRAN](#)

PCA plot showing variables: Fertility, Catholic, Agriculture, Examination, Education. A bar chart below shows a value of 60% for (1-3).

Sweden

<http://ftp.sunet.se/pub/lang/CRAN/>

Swedish University Computer Network, Uppsala

Download and Install R

Precompiled binary distributions of the R:

- [Linux](#)
- [MacOS X](#)
- [Windows](#)

R for Windows

This directory contains binaries for a base distribution and packages to run on i386/x64 Windows.

Note: CRAN does not have Windows systems and cannot check these binaries for viruses. Use the normal procedure.

Subdirectories:

[base](#)

Binaries for base distribution (managed by Duncan Murdoch)

[contrib](#)

Binaries of contributed packages (managed by Uwe Ligges)


Index of /pub/lang/CRAN/bin/windows/contrib

Name	Last modified			
Parent Directory				
1.7/	06-Nov-2004 14:00			
1.8/	27-Jul-2005 14:01			
1.9/	09-Mar-2008 18:33			
2.0/	09-Mar-2008 18:33			
2.1/	09-Mar-2008 18:33			
2.10/	09-Oct-2009 14:26			
2.11/	09-Oct-2009 14:26			
2.2/	09-Mar-2008 18:33			
2.3/	22-Apr-2008 13:27			
2.4/	22-Apr-2008 13:27			
2.5/	25-Nov-2007 14:24			
2.6/	25-Jun-2008 16:25			
2.7/	14-Dec-2008 15:24			
2.8/	10-Oct-2009 06:06			
2.9/	10-Oct-2009 06:06			
canvas_0.1-0.zip	17-Apr-2009 10:09	22K		
car_1.2-16.zip	12-Oct-2009 14:15	711K		
caret_4.25.zip	13-Oct-2009 18:40	2.1M		
caroline_0.1-1.zip	07-Sep-2009 12:22	33K		
cat_0.0-6.2.zip	28-Jul-2009 16:22	149K		
catmap_1.6.zip	04-May-2009 13:27	63K		
catspec_0.93.zip	17-Apr-2009 18:09	80K		
cba_0.2-6.zip	13-Oct-2009 18:40	309K		
ccems_1.03.zip	29-Jun-2009 16:16	623K		
ccgarch_0.1.7.zip	12-Oct-2009 13:11	190K		
cclust_0.6-16.zip	20-Sep-2009 20:39	55K		
cellVolumeDist_1.1.zip	13-Oct-2009 10:36	72K		
celsius_1.0.7.zip	17-Apr-2009 18:09	89K		
cem_1.0.111.zip	13-Oct-2009 15:44	1.1M		



Opening car_1.2-16.zip

You have chosen to open

 **car_1.2-16.zip**

which is a: Compressed (zipped) Folder
from: http://ftp.sunet.se

What should Firefox do with this file?

Open with Windows Explorer (default)

Save File

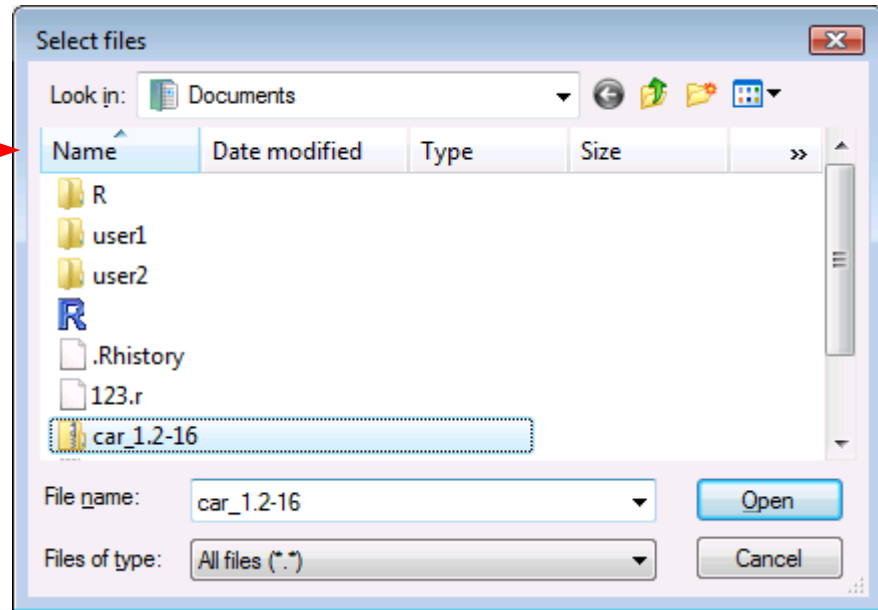
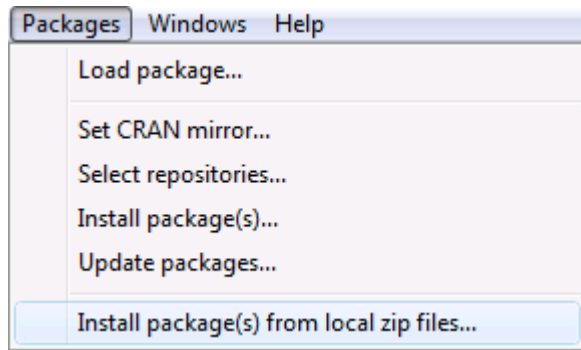
Do this automatically for files like this from now on.

OK Cancel

Packages

Install package car from a zip file

Copy the zip file to the working directory



From the console:

```
install.packages("car_1.2-16.zip")
```

On linux or MacOSx:

```
R CMD INSTALL car.tar.gz
```

Packages

Double check:

Is the car package loaded?
Is the car package installed?

```
> # 1. Is the car package loaded?  
> (.packages())  
[1] "stats"      "graphics"  "grDevices" "utils"      "datasets"  "methods"   "base"  
> # 2. Is the car package installed?  
> .packages(all.available = TRUE)  
[1] "biglm"      "car"       "DBI"       "leaps"      "RODBC"     "RSQLite"   "scatterplot3d" "base"      "boot"      "class"  
[11] "cluster"   "codetools" "datasets"  "foreign"   "graphics"  "grDevices" "grid"         "KernSmooth" "lattice"   "MASS"  
[21] "Matrix"    "methods"   "mgcv"     "nlme"      "nnet"     "rpart"     "spatial"     "splines"   "stats"    "stats4"  
[31] "survival"  "tcltk"     "tools"    "utils"
```



Installed

Packages

4. Load the car package

```
> # 4. Load the car package  
> library("car")
```

Double check:

Is the car package loaded?

```
> # 1. Is the car package loaded?  
> (.packages())  
[1] "car"      "stats"    "graphics" "grDevices" "utils"     "datasets" "methods"  "base"
```

Loaded



Packages

5. Is there help for the car package?

`library(help = car)`

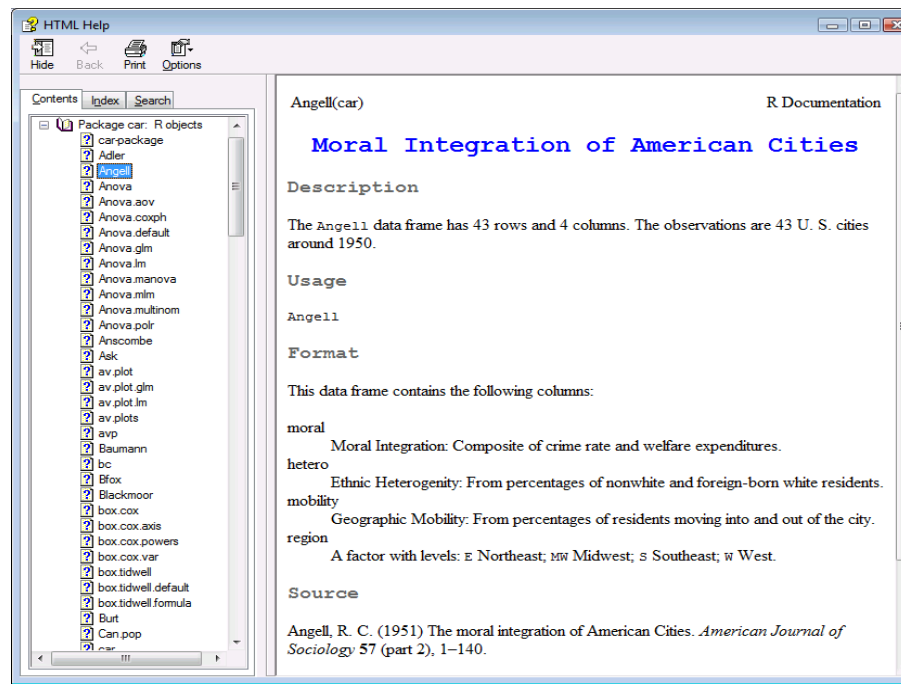
Information on package 'car'

Description:

```
Package:      car
Version:     1.2-16
Date:        2009/10/10
Title:       Companion to Applied Regression
Author:      John Fox <jfox@mcmaster.ca>. I am grateful to Douglas Bates, David Firth, Michael Friendly, Gregor Gorjanc, Spencer Graves, Richard Heiberger, Georges Monette, Henric Nilsson, Derek Ogle, Brian Ripley, Sanford Weisberg, and Achim Zeileis for various suggestions and contributions.
Maintainer:  John Fox <jfox@mcmaster.ca>
Depends:     R (>= 2.1.1), stats, graphics
Suggests:    MASS, nnet, leaps, survival
```

6. Find out information about the data frame Angell

`help(Angell)`



The screenshot shows the R HTML Help window. The left pane displays a tree view of R objects, with 'Angell' selected under the 'car' package. The right pane shows the help page for 'Angell(car)', titled 'Moral Integration of American Cities'. The page includes a description of the data frame (43 rows, 4 columns, 1950 U.S. cities), usage instructions, and the source (Angell, R. C. (1951) The moral integration of American Cities. American Journal of Sociology 57 (part 2), 1-140).

HTML Help

Hide Back Print Options

Contents Index Search

Package car: R objects

- car.package
- Adler
- Angell
- Anova
- Anova.aov
- Anova.coxph
- Anova.default
- Anova.glm
- Anova.lm
- Anova.manova
- Anova.mlm
- Anova.multinom
- Anova.polar
- Anscombe
- Ask
- av.plot
- av.plot.glm
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- box.cox
- box.cox.aaic
- box.cox.powers
- box.cox.var
- box.tidwell
- box.tidwell.default
- box.tidwell.formula
- Burt
- Can.pop
- car

Angell(car) R Documentation

Moral Integration of American Cities

Description

The `Angell` data frame has 43 rows and 4 columns. The observations are 43 U. S. cities around 1950.

Usage

```
Angell
```

Format

This data frame contains the following columns:

- moral**
Moral Integration: Composite of crime rate and welfare expenditures.
- hetero**
Ethnic Heterogeneity: From percentages of nonwhite and foreign-born white residents.
- mobility**
Geographic Mobility: From percentages of residents moving into and out of the city.
- region**
A factor with levels: E Northeast, MW Midwest, S Southeast, W West.

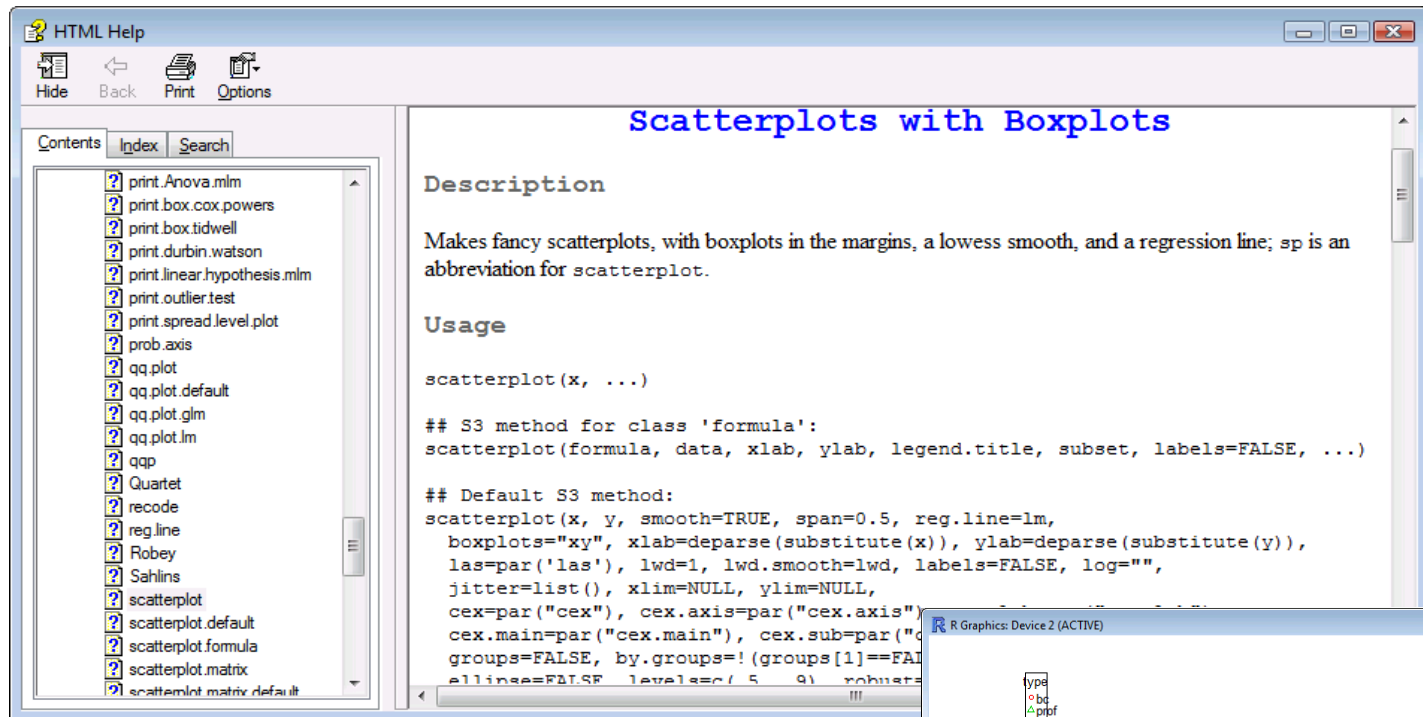
Source

Angell, R. C. (1951) The moral integration of American Cities. *American Journal of Sociology* 57 (part 2), 1-140.

Packages

7. Find out what the function scatterplot does

?scatterplot



HTML Help

Hide Back Print Options

Contents Index Search

- ? print.Anova.mlm
- ? print.box.cox.powers
- ? print.box.tidwell
- ? print.durbin.watson
- ? print.linear.hypothesis.mlm
- ? print.outlier.test
- ? print.spread.level.plot
- ? prob.axis
- ? qq.plot
- ? qq.plot.default
- ? qq.plot.glm
- ? qq.plot.lm
- ? qqp
- ? Quartet
- ? recode
- ? reg.line
- ? Robey
- ? Sahlin
- ? scatterplot
- ? scatterplot.default
- ? scatterplot.formula
- ? scatterplot.matrix
- ? scatterplot.matrix.default

Scatterplots with Boxplots

Description

Makes fancy scatterplots, with boxplots in the margins, a loess smooth, and a regression line; `sp` is an abbreviation for `scatterplot`.

Usage

```
scatterplot(x, ...)
```

S3 method for class 'formula':

```
scatterplot(formula, data, xlab, ylab, legend.title, subset, labels=FALSE, ...)
```

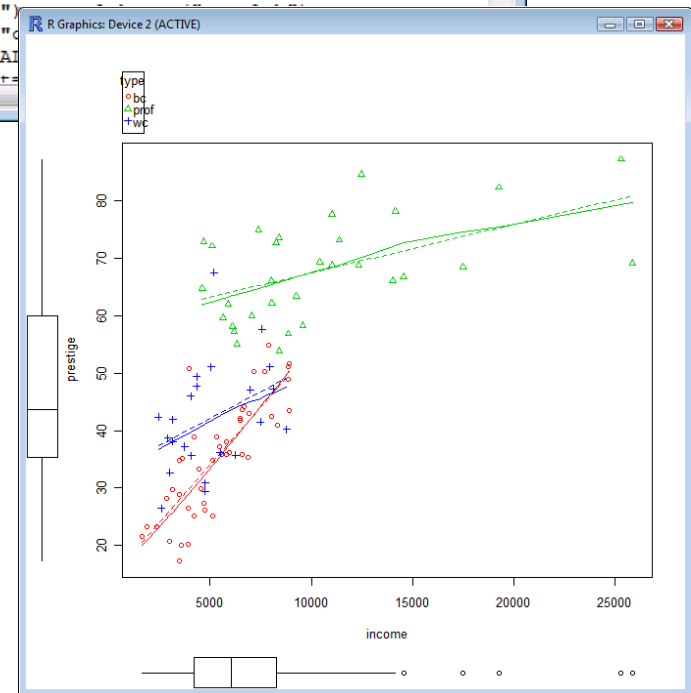
Default S3 method:

```
scatterplot(x, y, smooth=TRUE, span=0.5, reg.line=lm,
  boxplots="xy", xlab=deparse(substitute(x)), ylab=deparse(substitute(y)),
  las=par('las'), lwd=1, lwd.smooth=lwd, labels=FALSE, log="",
  jitter=list(), xlim=NULL, ylim=NULL,
  cex=par("cex"), cex.axis=par("cex.axis"),
  cex.main=par("cex.main"), cex.sub=par("cex.sub"),
  groups=FALSE, by.groups=(groups[1]==FALSE),
  ellipse=FALSE, levels=c(5, 9), robust=FALSE)
```

8. Run an example of scatterplot

scatterplot

```
(prestige ~ income|type, data=Prestige, span=1)
```



Packages

9. Unload the car package
10. Uninstall the car package

```
> # Unload the car package
```

```
> detach("package:car")
```

```
> # Uninstall the car package
```

```
> remove.packages("car")
```

```
Warning in remove.packages("car") :
```

```
argument 'lib' is missing: using C:\Users\user\Documents\R/win-library/2.9
```

```
.libPaths() # get library location  
dir(.libPaths()) # show files and directories on the library location
```

```
# 1. Is the car package loaded?  
# search() is the "usual" command but it also shows R objects (unnecessary info)  
(.packages())  
# 2. Is the car package installed?  
# library() is the "usual" command but it also shows the description (unnecessary info)  
(.packages(all.available=TRUE))
```

```
# 3. Install package car from the web  
install.packages("car", dependencies = TRUE)
```

```
# 2. Is the car package installed?  
(.packages(all.available=TRUE))
```

```
dir(.libPaths()) # show files and directories on the library location
```

```
# 4. Load the car package  
library("car")
```

```
# 1. Is the car package loaded?  
(.packages())
```

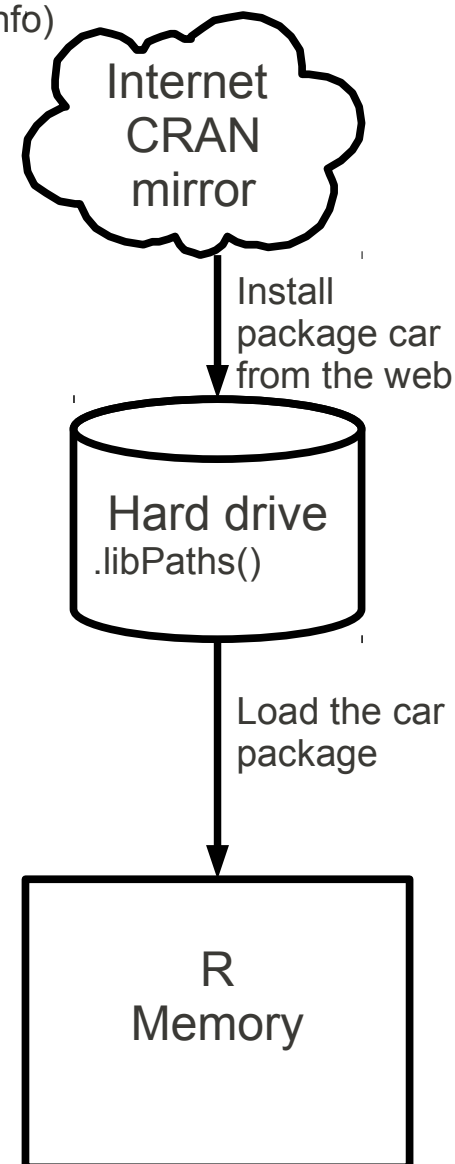
```
# 5. Is there help for the car package?  
library(help=car)
```

```
# 9. Unload the car package
```

```
# 1. Is the car package loaded?  
(.packages())
```

```
# 10. Uninstall the car package
```

```
# 2. Is the car package installed?  
(.packages(all.available=TRUE))  
dir(.libPaths()) # show files and directories on the library location
```



Packages

CRAN Task Views

Bayesian	Bayesian Inference
ChemPhys	Chemometrics and Computational Physics
ClinicalTrials	Design, Monitoring, and Analysis of Clinical Trials
Cluster	Cluster Analysis & Finite Mixture Models
Distributions	Probability Distributions
Econometrics	Computational Econometrics
Environmetrics	Analysis of Ecological and Environmental Data
ExperimentalDesign	Design of Experiments (DoE) & Analysis of Experimental Data
Finance	Empirical Finance
Genetics	Statistical Genetics
Graphics	Graphic Displays & Dynamic Graphics & Graphic Devices & Visualization
gR	gRaphical Models in R
HighPerformanceComputing	High-Performance and Parallel Computing with R
MachineLearning	Machine Learning & Statistical Learning
MedicalImaging	Medical Image Analysis
Multivariate	Multivariate Statistics
NaturalLanguageProcessing	Natural Language Processing
Optimization	Optimization and Mathematical Programming
Pharmacokinetics	Analysis of Pharmacokinetic Data
Psychometrics	Psychometric Models and Methods
Robust	Robust Statistical Methods
SocialSciences	Statistics for the Social Sciences
Spatial	Analysis of Spatial Data
Survival	Survival Analysis
TimeSeries	Time Series Analysis

11. List packages for epidemiology

Check out BioConductor!

12. List packages for environmental sciences

Look at the description of each view,
Spatial has this:

- **Disease mapping and areal data analysis** : [DCluster](#) is a spatial weights, tests for spatial autocorrelation for areal data by known weights. The [spgwr](#) package contains an implementation for detection for case event data. The [gmmBUGS](#) package is a

Packages

11. List packages for epidemiology

?? search the installed help files

For keywords “epidem”, “disease”, “illness”, etc...

R Site Search

<http://search.r-project.org/>

Rseek

<http://www.rseek.org/>

Read and maybe post a question on the Mailing List

R-help -- Main R Mailing List

<https://stat.ethz.ch/mailman/listinfo/r-help>

crantastic, a community site for R packages to search for, review and tag CRAN packages.

<http://crantastic.org/>

sos package

R related Search Engine

<http://cran.r-project.org/web/packages/sos/>

Stack Overflow a programming Q & A site

<http://stackoverflow.com/>

Packages

Contributed Packages

<http://cran.r-project.org/web/packages/> Contributed Packages

Installation of Packages

Please type `help("INSTALL")` or `help("install.packages")` in R for information on how to install packages from this directory. The manual [R Installation and Administration](#) (also contained in the R base sources) explains the process in detail.

[CRAN Task Views](#) allow you to browse packages by topic and provide tools to automatically install all packages for special areas of interest. Currently, 25 views are available.

Daily Package Check Results

All packages are tested regularly on machines running [Debian GNU/Linux](#). Packages are also checked under MacOS X and Windows, but only at the day the package appears on CRAN.

The results are summarized in the [check summary](#) (some [timings](#) are also available). Additional details for Windows checking and building can be found in the [Windows check summary](#).

Writing Your Own Packages

The manual [Writing R Extensions](#) (also contained in the R base sources) explains how to write new packages and how to contribute them to CRAN.

Available Bundles and Packages

Currently, the CRAN package repository features 2031 objects including 2031 packages and 0 bundles containing 0 packages, for a total of 2031 available packages.

[A](#) [B](#) [C](#) [D](#) [E](#) [F](#) [G](#) [H](#) [I](#) [J](#) [K](#) [L](#) [M](#) [N](#) [O](#) [P](#) [Q](#) [R](#) [S](#) [T](#) [U](#) [V](#) [W](#) [X](#) [Y](#) [Z](#)

epiR
epibasix
epicalc
epitools etc...

R Site Search

<http://search.r-project.org/cgi-bin/namazu.cgi>

R Site Search

Query: [\[How to search\]](#)

Display: Description: Sort:

Target:

- Functions
- Vignettes
- R-help 2008-
- Task views
- R-sig-mixed-models
- R-help 2002-2007
- Rhelp 1997-2001
- R-devel

For problems WITH THIS PAGE (not with R) contact baron@psych.upenn.edu.

This search system is powered by [Namazu](#) v

foobar@namazu.org

packages

References/to learn more:

The R book

Michael J. Crawley pp 4

2009 John Wiley & Sons Ltd

Basic statistics using R pp. 16

Jarno Tuimala (CSC) and Dario Greco (HY)

<http://www.csc.fi/english/csc/courses/archive/R2008s>

Statistics with R

Vincent Zoonekynd, pp 115

http://zoonek2.free.fr/UNIX/48_R/all.html

Introductory Statistics with R

Peter Dalgaard, pp 35

2010 Springer

Geographic Data Analysis

Pat Bartlein

<http://geography.uoregon.edu/bartlein/courses/geog417/lectures/lec05.htm>

Quick-R

Rob Kabacoff

<http://www.statmethods.net/interface/packages.html>

R console input

The console will accept R code, functions, expressions, variables and data.

Numbers can be positive or negative, and with a decimal part.

Strings are delimited by double quotes. Strings are text, character data.

Comments are marked with the `#` sign. Everything after a comment is ignored. Comments are useful for explaining the code, otherwise it would be hard trying to guess or remember what the code does.

Examples:

```
> 123
[1] 123
> "Hello world!"
[1] "Hello world!"
> #this is a comment
>
> 123 #this is an integer
[1] 123
> "Hello world!" #this is a string
[1] "Hello world!"
>
```

Using R as a calculator

R can execute expressions directly from the console, like a calculator

```
> 1+1  
[1] 2
```

Type 1+1 and enter

```
>
```

Mathematical operators

```
> 536+278#addition  
[1] 814  
> 536-278#subtraction  
[1] 258  
> 156/23#division  
[1] 6.782609  
> 156%/%23#integer division  
[1] 6  
> 12*13#multiplication  
[1] 156  
> 5^3#power  
[1] 125  
> 159%%13#modulus  
[1] 3
```

Using R as a calculator

Comparison operators

The logical values are TRUE, FALSE and NA for missing values.

```
> 5 < 3 #less than
[1] FALSE
> 8 > 4 #greater than
[1] TRUE
> 5 >= 9 #g.t. or equal
[1] FALSE
> 5 <= 7 #l.t. or equal
[1] TRUE
> 5 == 5 #equals
[1] TRUE
> 5 != 7 #not equals
[1] TRUE
```

Using R as a calculator

Logical operators

The logical values are TRUE, FALSE and NA for missing values.

```
> !FALSE # logical negation
```

```
[1] TRUE
```

```
> TRUE & FALSE # logical AND
```

```
[1] FALSE
```

```
> TRUE | FALSE # logical OR
```

```
[1] TRUE
```

```
> xor(TRUE, FALSE) # logical eXclusive OR
```

```
[1] TRUE
```

```
>
```

```
> TRUE && FALSE # logical AND
```

```
[1] FALSE
```

```
> TRUE || FALSE # logical OR
```

```
[1] TRUE
```

```
>
```

```
> c(T,F,F) & c(F,T,F) # logical AND
```

```
[1] FALSE FALSE FALSE
```

```
> c(T,F,F) | c(F,T,F) # logical OR
```

```
[1] TRUE TRUE FALSE
```

```
> c(T,F,F) && c(F,T,F) # logical AND
```

```
[1] FALSE
```

```
> c(T,F,F) || c(F,T,F) # logical OR
```

```
[1] TRUE
```

Using R as a calculator

Rounding functions

```
> 1 / 3
[1] 0.3333333
> ceiling(1 / 3) #smallest integer not less than the result
[1] 1
> floor(1 / 3) #largest integer not greater than the result
[1] 0
> trunc(1 / 3, 4) #truncate the value toward 0
[1] 0
> round(1 / 3, digits = 4) #round to a number of decimal places
[1] 0.3333
> signif(1 / 3, digits = 4) #round to a number of significant digits
[1] 0.3333
> zapsmall(1 / 3, digits = 4) #rounds to a number of decimal places, numbers close to zero are considered zero
[1] 0.3333
```


Using R as a calculator

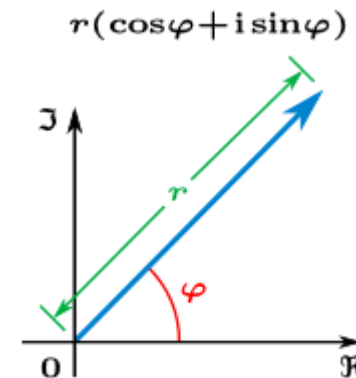
Mathematical functions

```
> sqrt(2) #square root
[1] 1.414214
> exp(1) #exponentiation
[1] 2.718282
> log(2.718282) #natural log
[1] 1
> sum(7,8,9) #sum
[1] 24
> prod(3,4,5) #product
[1] 60
> abs(-1.23) #absolute value
[1] 1.23
> sin(pi/2) #sine
[1] 1
> cos(pi/2) #cosine
[1] 6.123032e-17
> tan(pi/2) #tangent
[1] 1.633178e+16
```

Using R as a calculator

Complex functions

```
> mycomplexvar<-3+5i # a variable with a complex value
> mycomplexvar
[1] 3+5i
> Re(mycomplexvar) # real part
[1] 3
> Im(mycomplexvar) # imaginary part
[1] 5
> Conj(mycomplexvar) # complex conjugate
[1] 3-5i
> Mod(mycomplexvar) # complex modulus
[1] 5.830952
> Arg(mycomplexvar) # complex argument
[1] 1.030377
```



argument $\varphi = \pm \arctan \frac{y}{x}$

modulus $r = |x + iy| = \sqrt{x^2 + y^2}$.

Using R as a calculator

R Built-in Constants

Constants that come with the R base package.

LETTERS: the 26 upper-case letters of the Roman alphabet;

letters: the 26 lower-case letters of the Roman alphabet;

month.abb: the three-letter abbreviations for the English month names;

month.name: the English names for the months of the year;

pi: the ratio of the circumference of a circle to its diameter.

```
pi * 10 # the perimeter of a circumference of diameter 10
```

```
# months in English
```

```
month.name
```

```
# months in your current locale
```

```
format(ISOdate(2009, 1:12, 1), "%B")
```

```
format(ISOdate(2009, 1:12, 1), "%b")
```

R as calculator

References/to learn more:

The R book

Michael J. Crawley pp 9

2010 John Wiley & Sons Ltd

Basic statistics using R pp. 35

Jarno Tuimala (CSC) and Dario Greco (HY)

<http://www.csc.fi/english/csc/courses/archive/R2008s>

Statistics: an introduction using R

Michael J. Crawley pp 281

2008 John Wiley & Sons Ltd

Aprendizaje del software estadístico R: un entorno para simulación y computación estadística

Prof. Alberto Muñoz García

Departamento de Estadística

Universidad Carlos III de Madrid

<http://ocw.uc3m.es/estadistica/aprendizaje-del-software-estadistico-r-un-entorno-para-simulacion-y-computacion-estadistica/resolveUid/6bfdf37a91c966902de8395629e9fef6>

Introductory Statistics with R

Peter Dalgaard, pp 3

2011 Springer

Software Tools, Part 1: introduction to R software

Petri Koistinen

<http://www.rni.helsinki.fi/~pek/s-tools/calculator.r>

R Variables

Assigning values to objects = or <- or ->

```
> myvar <- 123 # to assign value 123 to variable "myvar"  
> print(myvar) # display the variable  
[1] 123  
> #or  
> myvar  
[1] 123  
> x = 5  
> y <- 6  
> 7 -> z  
> x  
[1] 5  
> y  
[1] 6  
> z  
[1] 7  
> (myvar2 <- 456) # assign and display  
[1] 456
```

Multiple assignments

```
> a <- b <- 55  
> a  
[1] 55  
> b  
[1] 55  
>  
> x <- (y <- c(5, 14,234))*2  
> x;y  
[1] 10 28 468  
[1] 5 14 234
```

Multiple commands in one line

R Variables

3 basic types of variables

Numeric

Character

Boolean {true, false}

Functions to test an object's data type

is.integer, is.double, is.numeric,
is.character and is.logical

as.integer is used to pass data to C or Fortran code

```
> ivar <- 57
> is.integer(ivar)
[1] FALSE
> is.double(ivar)
[1] TRUE
> is.numeric(ivar)
[1] TRUE
>
> dvar <- 5.7
> is.integer(dvar)
[1] FALSE
> is.double(dvar)
[1] TRUE
> is.numeric(dvar)
[1] TRUE
>
> iavar <- as.integer(57) #coerce 57 to be of integer type
> is.integer(iavar)
[1] TRUE
> is.double(iavar)
[1] FALSE
> is.numeric(iavar)
[1] TRUE
>
> ivl <- as.numeric("57") #coerce "57" to be of numeric type
> is.numeric(ivl)
[1] TRUE
>
> strcity <- "Oulu"
> is.character(strcity)
[1] TRUE
>
> mybool <- TRUE
> is.logical(mybool)
[1] TRUE
```

R Variables

Variable names

- Case sensitive
- R names depend on the operating system and country within which R is being run (technically on the locale settings)
- All alphanumeric symbols are allowed (and in some countries this includes accented letters) plus '.' and '_', with the restriction that a name must start with '.' or a letter, and if it starts with '.' the second character must not be a digit
- For portable R code (including that to be used in R packages) use only A–Za–z0–9

```
> A <- 567
> A
[1] 567
> a # Case sensitive!
Error: object 'a' not found
> my_str <- "abc"
> my_str
[1] "abc"
> my.str <- "qwe"
> my.str
[1] "qwe"
> my1 <- 265
> my1
[1] 265

> my_ <- 368
> _my <- 35 # a variable name cannot start with "_"
Error: unexpected input in "_"
> my. <- 38
> .my <- 3
> 7my <- 88 # a variable name cannot start with a number
Error: unexpected symbol in "7my"
> . <- 45
>
> my_
[1] 368
> my.
[1] 38
> .my
[1] 3
> .
[1] 45
```

Although legal,
these variable names
are confusing

R Variables

Reserved Words in R

These words should not be used as variable names or function names, to avoid parsing errors.

Reserved words:

if else repeat while function for in next break

TRUE FALSE NULL Inf NaN NA

NA_integer_ NA_real_ NA_complex_ NA_character_

R Variables

Not Available / "Missing" Values

NA is a missing value indicator.

"Missing" Values are common in real world data because of no answers to surveys or missing data from sensors readings.

is.na() returns TRUE for missing elements

is.na() <- sets elements to NA

```
> x <- 5
```

```
> x
```

```
[1] 5
```

```
> is.na(x)
```

```
[1] FALSE
```

```
> y <- NA
```

```
> y
```

```
[1] NA
```

```
> is.na(y)
```

```
[1] TRUE
```

R Variables

Not Available / "Missing" Values

```
> z <- c(3,5,NA,6,7,8) # vector
```

```
> z
```

```
[1] 3 5 NA 6 7 8
```

```
> is.na(z) # which elements are NA
```

```
[1] FALSE FALSE TRUE FALSE FALSE FALSE
```

```
> is.na(z) <- c(1,5) # turn elements at position 1 and position 5 to NA
```

```
> z
```

```
[1] NA 5 NA 6 NA 8
```

```
> # math operators * + - / will return NA
```

```
> 5 * NA
```

```
[1] NA
```

```
> # comparison operators < <= > >= == != will return NA
```

```
> c(5, 5, NA) == c(5, NA, NA)
```

```
[1] TRUE NA NA
```

R Variables

Not Available / "Missing" Values

```
> # NA is "undetermined" for logical expressions
> c(T, F) & c(NA, NA) # FALSE AND whatever is FALSE
[1] NA FALSE
> c(T, F) | c(NA, NA) # TRUE OR whatever is TRUE
[1] TRUE NA
> xor(NA,T)
[1] NA

> myvec <- c(7,4,NA,2,65)
> mean(myvec) # this will return NA
[1] NA
> mean(myvec, na.rm=T) # ignoring NA in a calculation
[1] 19.5
> na.omit(myvec) # omitting NA
[1] 7 4 2 65
attr(,"na.action")
[1] 3
attr(,"class")
[1] "omit"
```

R Variables

```
> x <- c(7, 6, NA, NA, 5)
> x[!is.na(x)] # get the data except the NAs
[1] 7 6 5
> na.omit(x) # get the data except the NAs, proper way
[1] 7 6 5
attr(,"na.action")
[1] 3 4
attr(,"class")
[1] "omit"
> mean(x) # returns NA
[1] NA
> mean(x, na.rm=TRUE) # returns 6
[1] 6
> x[is.na(x)] <- 0 # replace NAs with 0
> x
[1] 7 6 0 0 5
```

Data Collection Issues

Survey Return Rates	2003	2004	2005	2006	2007	2008
Medical Doctors (MDs)	NA	65.1	53.2	75.7	78.0	NA
Doctors of Osteopathy (DOs)	NA	83.6	66.1	54.2	81.6	NA
Physician Assistants	76.9	75.9	43.8	70.1	88.8	NA
Masters Level Psychologists	26.2	24.8	21.9	25.9	19.5	12.0
Clinical Social Workers (LSCSW)	36.0	35.5	35.2	39.1	30.8	18.8
Advanced Registered Nurse Practitioners (ARNPs)	21.3	20.8	11.2	24.1	17.7	23.3
Dentists*	99.6	95.3	NA	97.3	NA	NA
Dental Hygienists*	NA	NA	96.3	NA	96.5	NA

NA=Not Available

Office of Health Assessment, KDHE



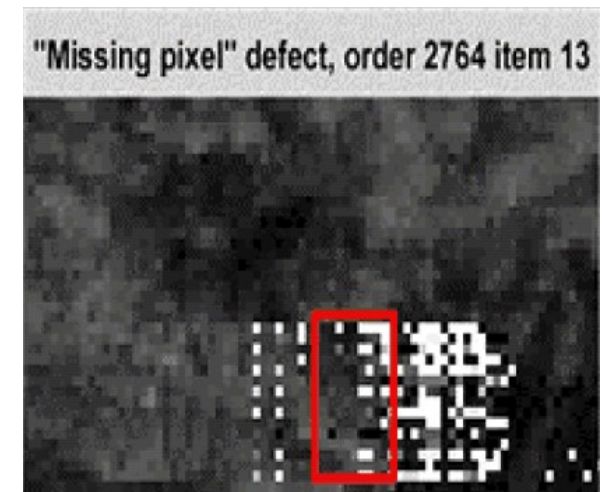
Our Vision – Healthy Kansans Living in Safe and Sustainable Environment

Missing image data LANDSAT 5 - 7

Anomalies description

Missing image data anomaly may be considered under different aspects. The most frequently case of missing data may be called “missing pixels”. Usually, the “missing pixels” anomaly is correlated with others anomalies (shifted swath – speckle - missing swath). Details are also provided about wrong or missing auxiliary data that implies swath misalignment (See also *Anomaly slip 02*). This section describes the following anomalies related to missing image data:

- Missing pixels.
- Missing pixels – shifted swath.
- Missing pixels – missing swath.
- Missing pixels – speckle.
- Corrupted Mirror Scan Correction Data (MSCD) – shifted swath.



TAULUKKO 31.B. Kotona tupakansavulle altistuneiden osuus taustamuuttujien mukaan (%).

TABLE 31.B. Proportion of persons exposed to tobacco smoke at home, by background variables (%).

		Miehet/Males						Naiset/Females							
		Ikäryhmä/Age group						Ikäryhmä/Age group							
		15-24	25-34	35-44	45-54	55-64	Total	15-24	25-34	35-44	45-54	55-64	Total	Total	
SIVILISÄÄTY/ MARITAL STATUS	Naimisissa tai avoliitossa/ Married	34	25	25	26	23	25	40	21	20	27	21	23	24	
	Naimaton/Single	37	28	33	43	38	35	29	20	28	15	13	26	30	
	Eronnut/Divorced	.	25	68	37	31	42	100	45	26	24	33	30	35	
	Leski/Widowed	.	.	100	25	0	25	.	.	0	50	13	24	24	
KOULUTUS/ EDUCATION	0-9 vuotta/0-9 years	39	40	48	40	30	37	30	43	41	35	27	31	34	
	10-12 vuotta/10-12 years	37	40	39	32	23	34	37	30	36	31	17	30	32	
	13 v. tai enemmän/13+ years	32	19	20	19	18	20	24	19	15	21	18	19	20	
ASUNALUE/ LIVING AREA	Uusimaa/South-Finland	44	24	34	33	28	32	33	18	20	29	27	25	28	
	Länsi-Suomi/West-Finland	37	28	26	16	19	25	29	24	26	28	23	26	25	
	Keski-Suomi/Middle Fin.	14	30	31	28	22	25	26	21	13	29	16	21	23	
	Kaakkois-Suomi/South-East	53	8	38	15	34	32	27	17	21	24	18	21	26	
	Itä-Suomi/East-Finland	28	22	19	41	26	29	38	17	18	21	16	21	25	
	Pohjois-Suomi/North-Fin.	59	31	29	42	21	36	40	33	33	18	22	29	32	
SOSIO- EKONOMINEN ASEMA/ SOCIO- ECONOMIC STATUS	Työnantaja,yksityisyrittäjä/ Employer,entrepreneur	50	19	26	24	24	25	0	9	18	16	21	17	22	
	Maanviljelijä,maatalon emäntä/Farmer,farmer's wife	0	50	8	18	20	18	.	0	15	0	9	8	14	
	Ylempi toimihenkilö/Upper white-collar worker	0	9	20	15	21	17	33	14	12	13	11	13	15	
	Alempi toimihenkilö/Lower white-collar worker	22	22	25	22	23	23	29	22	19	28	22	24	23	
	Työntekijä/Blue-collar worker	46	36	39	33	36	37	53	31	33	29	34	33	36	
	Opiskelija/Student	34	21	0	100	.	33	29	17	0	0	.	27	30	
	Eläkeläinen/Pensioned	.	33	75	48	18	26	.	33	67	31	19	22	24	
	Työtön/Unemployed	50	47	46	55	32	45	44	35	44	41	18	35	39	
VUOSI/YEAR	2000-2002	35	25	30	30	24	29	31	23	25	25	20	25	27	
	2003	33	30	23	26	29	28	28	23	26	22	23	24	26	
	2004	37	26	30	29	25	29	31	22	22	26	21	24	26	

Using data from a website:

[\[WW HOME\]](#) [\[CHEMISTRY\]](#) [\[HISTORY\]](#)

[\[SEARCH\]](#)

[\[DISCLAIMER\]](#)

BIRTHDAYS OF SCIENTISTS

January

1 Eugene A. Demarcay, 1852

Roger Adams, 1889

2 Charles Hatchett, 1765

Rudolph Clausius, 1822

4 Astrid V. Grosse, 1905

Joseph Elanger, 1874

5 George W. Carver, 1943

6 John V. N. Dorr, 1872

7 Henry E. Roscoe, 1833

Eilhardt Mitscherlich, 1794

8 Soren P. L. Sorensen, 1868

H. Gobind Khorana, 1922

10 Frederick G. Cottrell, 1877

11 Frederick M. Becket, 1875

Ruth R. Benerito, 1916

12 Konrad Bloch, 1912

Antonia de Ulloa, 1716

13 Pierre J. Robiquet, 1780

Charles F. Mabery, 1850

<td>1</td><td>Eugene A. Demarcay, 1852

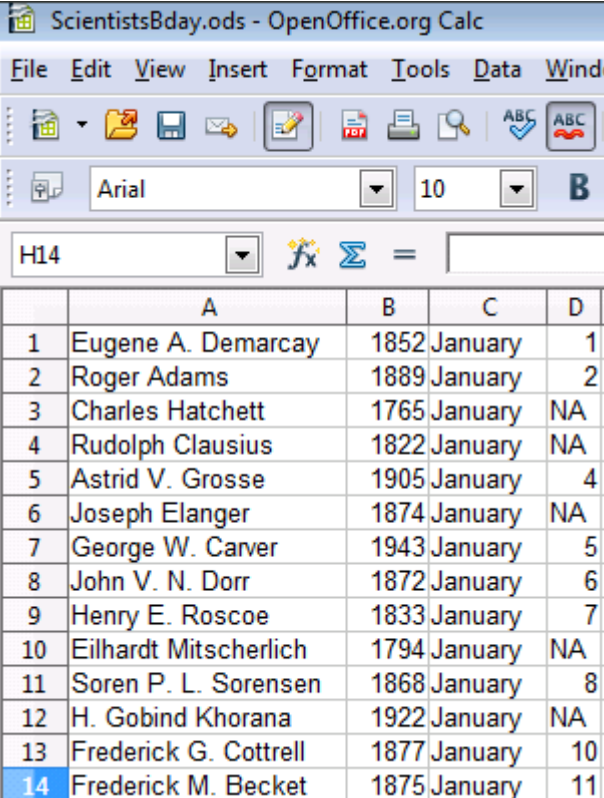
</td></tr><tr><td> 2</td><td>Roger Adams, 1889

Charles Hatchett, 1765

Rudolph Clausius, 1822

</td></tr><tr><td>4</td><td>Astrid V. Grosse, 1905

Joseph Elanger, 1874



ScientistsBday.ods - OpenOffice.org Calc

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	A	B	C	D
1	Eugene A. Demarcay	1852	January	1
2	Roger Adams	1889	January	2
3	Charles Hatchett	1765	January	NA
4	Rudolph Clausius	1822	January	NA
5	Astrid V. Grosse	1905	January	4
6	Joseph Elanger	1874	January	NA
7	George W. Carver	1943	January	5
8	John V. N. Dorr	1872	January	6
9	Henry E. Roscoe	1833	January	7
10	Eilhardt Mitscherlich	1794	January	NA
11	Soren P. L. Sorensen	1868	January	8
12	H. Gobind Khorana	1922	January	NA
13	Frederick G. Cottrell	1877	January	10
14	Frederick M. Becket	1875	January	11

<http://www.woodrow.org/teachers/ci/1992/activities/birthdays.html>

R Variables

Finite Infinite and NaN Numbers

Infinite numbers are the result of finite numbers divided by zero
NaN (Not a Number) are the result of zero divided by zero

Inf ∞

-Inf $-\infty$

NaN undetermined

is.finite() returns TRUE for a finite number

is.infinite() returns TRUE for an infinite number

is.nan() returns TRUE for a NaN

R Variables

```
a <- 1/2
a
is.finite(a)
is.infinite(a)
is.nan(a)

b <- 1/0
b
is.finite(b)
is.infinite(b)
is.nan(b)

c <- 0/0
c
is.finite(c)
is.infinite(c)
is.nan(c)
```

```
> a <- 1/2
> a
[1] 0.5
> is.finite(a)
[1] TRUE
> is.infinite(a)
[1] FALSE
> is.nan(a)
[1] FALSE
>
> b <- 1/0
> b
[1] Inf
> is.finite(b)
[1] FALSE
> is.infinite(b)
[1] TRUE
> is.nan(b)
[1] FALSE
>
> c <- 0/0
> c
[1] NaN
> is.finite(c)
[1] FALSE
> is.infinite(c)
[1] FALSE
> is.nan(c)
[1] TRUE
```

R Variables

Getting info from objects

`class()` returns the class attribute or the implicit class of this object

`is()` returns all the super-classes of this object's class

`mode()` to get or set the type or storage mode of an object

`str()` to compactly display the internal structure of an R object

`length()` to get or set the length of objects

`dim()` to retrieve or set the dimension of an object

`nchar()` to get or set the length of strings

`object.size()` to get an estimate of the memory used to store an R object

Common source of confusion:

`class()` vs `is()` vs `mode()`

`length()` vs `dim()` vs `nchar()`

R Variables

Type on R Editor:

```
Myint <- 567
is(myint)
Myreal <- 8.83
is(myreal)
mycomplex <- 34-7i
is(mycomplex)
mystring <- "quartz"
is(mystring)
myvector_i <- c(6,5,4)
is(myvector_i)
myvector_s <- c("a","b","c")
is(myvector_s)
mymatrix <- matrix(5,2,3)
is(mymatrix)
```

R Variables

is() returns all the super-classes of this object's class

```
> myint <- 567
> is(myint)
[1] "numeric" "vector"
> myreal <- 8.83
> is(myreal)
[1] "numeric" "vector"
> mycomplex <- 34-7i
> is(mycomplex)
[1] "complex" "vector"
>
> mystring <- "quartz"
> is(mystring)
[1] "character"      "vector"          "data.frameRowLabels"
> myvector_i <- c(6,5,4)
> is(myvector_i)
[1] "numeric" "vector"
>
> myvector_s <- c("a","b","c")
> is(myvector_s)
[1] "character"      "vector"          "data.frameRowLabels"
> mymatrix <- matrix(5,2,3)
> is(mymatrix)
[1] "matrix"  "array"   "structure" "vector"
```

All objects are vectors!

Scalars are vectors of length 1

R Variables

On R Editor, go to Edit/Replace and replace “is” with “class”

```
myint <- 567
class(myint)
myreal <- 8.83
class(myreal)
mycomplex <- 34-7i
class(mycomplex)
mystring <- "quartz"
class(mystring)
myvector_i <- c(6,5,4)
class(myvector_i)
myvector_s <- c("a","b","c")
class(myvector_s)
mymatrix <- matrix(5,2,3)
class(mymatrix)
```

Edit/Clear console to clear the previous calculations from the R Console

R Variables

`class()` returns the class attribute or the implicit class of this object

```
> myint <- 567
> class(myint)
[1] "numeric"
> myreal <- 8.83
> class(myreal)
[1] "numeric"
> mycomplex <- 34-7i
> class(mycomplex)
[1] "complex"
> mystring <- "quartz"
> class(mystring)
[1] "character"
> myvector_i <- c(6,5,4)
> class(myvector_i)
[1] "numeric"
> myvector_s <- c("a","b","c")
> class(myvector_s)
[1] "character"
> mymatrix <- matrix(5,2,3)
> class(mymatrix)
[1] "matrix"
```

This is the first class returned by `is()`

`class(myvar) "class 1"`

`is(myvar) "class 1" "class 2" "class 3" ...`

R Variables

On R Editor, go to Edit/Replace and replace “class” with “mode”

```
myint <- 567
mode(myint)
myreal <- 8.83
mode(myreal)
mycomplex <- 34-7i
mode(mycomplex)
mystring <- "quartz"
mode(mystring)
myvector_i <- c(6,5,4)
mode(myvector_i)
myvector_s <- c("a","b","c")
mode(myvector_s)
mymatrix <- matrix(5,2,3)
mode(mymatrix)
```


R Variables

mode() to get or set the type or storage mode of an object

```
> myint <- 567
> mode(myint)
[1] "numeric"
> myreal <- 8.83
> mode(myreal)
[1] "numeric"
> mycomplex <- 34-7i
> mode(mycomplex)
[1] "complex"
> mystring <- "quartz"
> mode(mystring)
[1] "character"
> myvector_i <- c(6,5,4)
> mode(myvector_i)
[1] "numeric"
> myvector_s <- c("a","b","c")
> mode(myvector_s)
[1] "character"
> mymatrix <- matrix(5,2,3)
> mode(mymatrix)
[1] "numeric"
```

The only difference is with matrix, let's try a data frame:

```
> mydataf <- data.frame(1,2,3)
> mode(mydataf)
[1] "list"
> class(mydataf)
[1] "data.frame"
> mydataf <- data.frame("a","b","c")
> mode(mydataf)
[1] "list"
> class(mydataf)
[1] "data.frame"
```

By default, a matrix is stored as numeric data in memory and a data frame as list data in memory. This can be changed, for achieving better performance or for compatibility.

R Variables

On R Editor, go to Edit/Replace and replace “mode” with “length”, “dim” and “nchar”

```
myint <- 567
length(myint)
myreal <- 8.83
length(myreal)
mycomplex <- 34-7i
length(mycomplex)
mystring <- "quartz"
length(mystring)
myvector_i <- c(6,5,4)
length(myvector_i)
myvector_s <-
c("a","b","c")
length(myvector_s)
mymatrix <- matrix(5,2,3)
length(mymatrix)
```

```
myint <- 567
dim(myint)
myreal <- 8.83
dim(myreal)
mycomplex <- 34-7i
dim(mycomplex)
mystring <- "quartz"
dim(mystring)
myvector_i <- c(6,5,4)
dim(myvector_i)
myvector_s <-
c("a","b","c")
dim(myvector_s)
mymatrix <- matrix(5,2,3)
dim(mymatrix)
```

```
myint <- 567
nchar(myint)
myreal <- 8.83
nchar(myreal)
mycomplex <- 34-7i
nchar(mycomplex)
mystring <- "quartz"
nchar(mystring)
myvector_i <- c(6,5,4)
nchar(myvector_i)
myvector_s <-
c("a","b","c")
nchar(myvector_s)
mymatrix <- matrix(5,2,3)
nchar(mymatrix)
```

R Variables

Length() is the number of elements, dim are the dimensions, nchar is the number of characters

```
> myint <- 567
> length(myint)
[1] 1
> myreal <- 8.83
> length(myreal)
[1] 1
> mycomplex <- 34-7i
> length(mycomplex)
[1] 1
> mystring <- "quartz"
> length(mystring)
[1] 1
> myvector_i <- c(6,5,4)
> length(myvector_i)
[1] 3
> myvector_s <- c("a","b","c")
> length(myvector_s)
[1] 3
> mymatrix <- matrix(5,2,3)
> length(mymatrix)
[1] 6
```

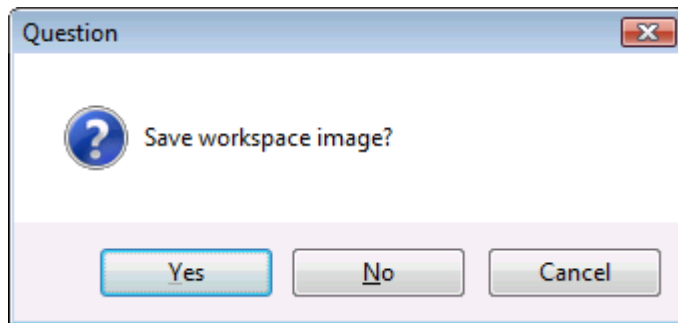
```
> myint <- 567
> dim(myint)
NULL
> myreal <- 8.83
> dim(myreal)
NULL
> mycomplex <- 34-7i
> dim(mycomplex)
NULL
> mystring <- "quartz"
> dim(mystring)
NULL
> myvector_i <- c(6,5,4)
> dim(myvector_i)
NULL
> myvector_s <- c("a","b","c")
> dim(myvector_s)
NULL
> mymatrix <- matrix(5,2,3)
> dim(mymatrix)
[1] 2 3
```

```
> myint <- 567
> nchar(myint)
[1] 3
> myreal <- 8.83
> nchar(myreal)
[1] 4
> mycomplex <- 34-7i
> nchar(mycomplex)
[1] 5
> mystring <- "quartz"
> nchar(mystring)
[1] 6
> myvector_i <- c(6,5,4)
> nchar(myvector_i)
[1] 1 1 1
> myvector_s <- c("a","b","c")
> nchar(myvector_s)
[1] 1 1 1
> mymatrix <- matrix(5,2,3)
> nchar(mymatrix)
      [,1] [,2] [,3]
[1,]  1   1   1
[2,]  1   1   1
```

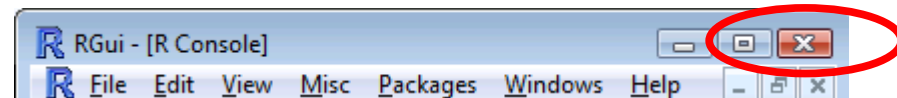
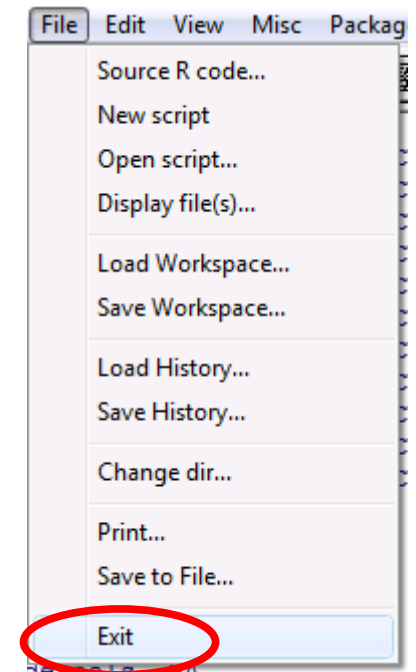
Quitting R

Command `q()`

Or File/Exit or close the editor window (on Windows)



save workspace image?



Yes will save all the objects from memory to a file `.Rdata` and it will also save all the commands typed during the session to a file `.Rhistory`

Both files are saved on `user\documents`

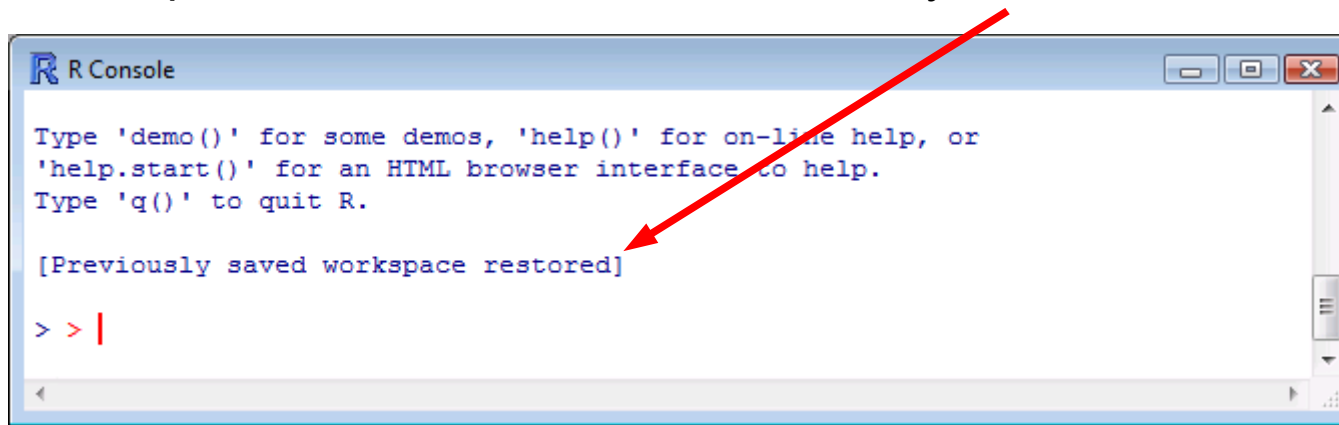
The file `.Rhistory` is plain text and it can be examined or edited.

To close R without the question:
`q(save = "no")`

R's workspace

R can save all the objects from memory to a file `.Rdata` and save all the commands typed during the session to a file `.Rhistory`, these are the default file names and they are saved on the working directory

Once a workspace is saved, it will be automatically loaded:



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

[Previously saved workspace restored]

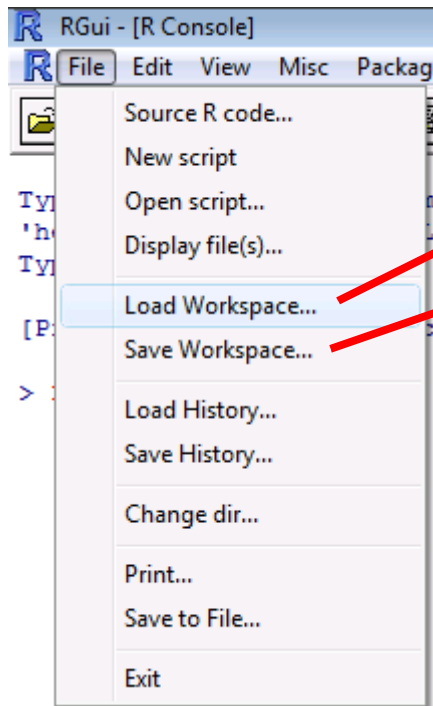
> > |
```

By changing the working directory, many default workspace files can be used, on different directories.

But, the next session will open the default workspace, on the default working directory.

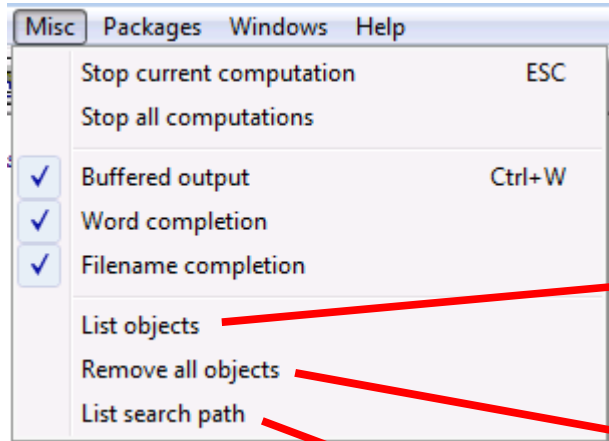
R's workspace

Workspace files can be saved and loaded from the File menu, with no need to change the working directory:



Or on the console:
`load.image()`
and
`save.image()`

R's workspace



shows the contents of the workspace, same as `objects()` or `ls()`

clears the workspace, same as `rm(list = ls(all = TRUE))`

list of attached packages and R objects, same as `search()`

R's workspace

objects() or ls() shows the contents of the workspace

save(var1, var2, varN, file="myfile.R") saves objects var1, var2 and varN to a file "myfile.R"

load("myfile.R") loads objects from file "myfile.R"

rm(var1) removes var1 from the workspace

rm(list = ls(all = TRUE)) clears the workspace

dir() shows the files on the working directory

```
> myvar <- "Hello!"
> myvar2 <- "Goodbye!"
> objects()
[1] "myvar" "myvar2"
> ls()
[1] "myvar" "myvar2"
> save(myvar,myvar2,file="mysession.R")
> dir()
 [1] "123.r"           "desktop.ini"      "hello_world.r.txt" "My Music"
 [9] "user1"          "user2"            "My Pictures"       "My Videos"
 [17] "mysession.R"    "R"
> rm(myvar2)
> ls()
[1] "myvar"
> rm(myvar)
> ls()
character(0)
> load("mysession.R")
> ls()
[1] "myvar" "myvar2"
```


R's working directory

Working Directory

Default setting on Linux is `$R_HOME/bin`

Default setting on Windows is `C:/Users/MyUserName/Documents`

The command "system" executes OS commands

> `getwd()` # get the working directory

[1] "C:/Users/user/Documents"

> `setwd("C:/Users/user/Documents/test123")` # change the working directory

Error in `setwd("C:/Users/user/Documents/test123")` :

cannot change working directory

> `getwd()` # it didn't change because the directory does not exist

[1] "C:/Users/user/Documents"

> `system("md test123")` # create a directory on Linux

Warning message:

In `system("md test123")` : md not found

> `system(paste(Sys.getenv("COMSPEC"), "/c", "md test123"))` # create a directory on

Windows

> `setwd("C:/Users/user/Documents/test123")`

> `getwd()`

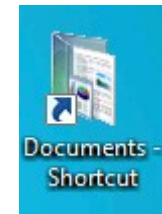
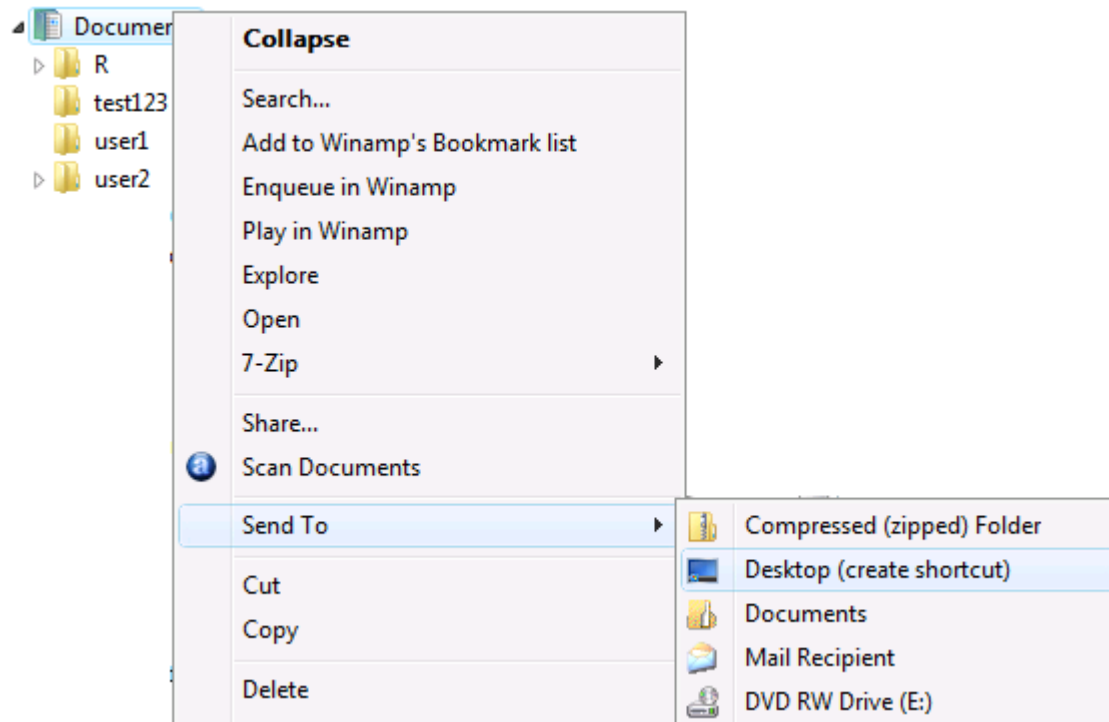
[1] "C:/Users/user/Documents/test123"

R's working directory and workspace

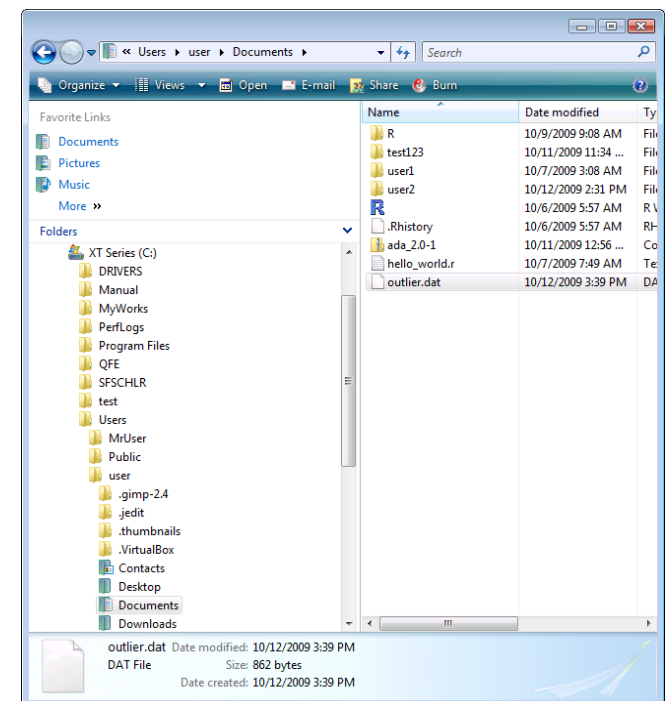
```
getwd()
myvar1 <- "variable 1 is a string"
myvar2 <- -2342.452
dir()
dir(all.files = T)
savehistory() # save the command history to the default file (.Rhistory)
save.image() # save the workspace to the default file (.RData)
dir() # it won't show .Rhistory and .RData
dir(all.files = T) # now it shows all the files!
file.show(".Rhistory") # display the history file, a text file is ok
file.show(".RData") # a binary data can't be displayed
```

R's working directory

Creating a shortcut on the desktop to the working directory



On Windows explorer, right click on the working directory and choose “Send To”, then choose “Desktop (create shortcut)”



programming R workspace

References/to learn more:

Basic statistics using R pp. 76

Jarno Tuimala (CSC) and Dario Greco (HY)

<http://www.csc.fi/english/csc/courses/archive/R2008s>

Aprendizaje del software estadístico R: un entorno para simulación y computación estadística

Prof. Alberto Muñoz García

Departamento de Estadística

Universidad Carlos III de Madrid

<http://ocw.uc3m.es/estadistica/aprendizaje-del-software-estadistico-r-un-entorno-para-simulacion-y-computacion-estadistica/resolveUid/a70c8973cb8798b0bd0e6bdf7abd6ec7>

Introductory Statistics with R

Peter Dalgaard, pp 31

2012 Springer

Quick-R

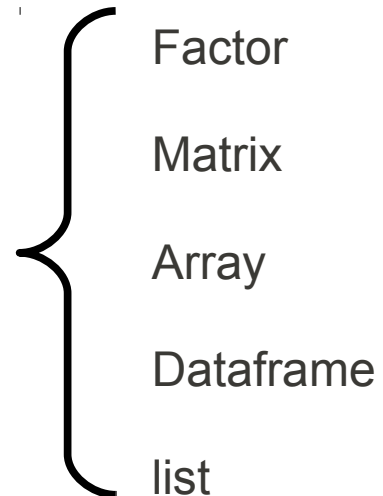
Rob Kabacoff

<http://www.statmethods.net/interface/workspace.html>

Data Structures in R

All objects are vectors

there are five other classes
for the basic data structures



Data Structures in R

Vector

A vector is a dynamic array, that is, a unidimensional array that can be resized and allows elements to be added or removed.



Vector elements are numbered from 1 to n, n is the size of the vector. Elements can be accessed through their index with square brackets [], negative indices = exclusion

3 types of vectors

Numeric

```
> c(734, 985, 43, 952)
```

```
[1] 734 985 43 952
```

Character

```
> c("Helsinki", "Tampere", "Turku")
```

```
[1] "Helsinki" "Tampere" "Turku"
```

Boolean {true, false}

```
> c(T,F,F,F,T,F,T,F,T,T)
```

```
[1] TRUE FALSE FALSE FALSE TRUE  
FALSE TRUE FALSE TRUE TRUE
```

4 ways to create vectors

: - colon operator

c() - "concatenate" function

seq() - "sequence" function

rep() - repetition function

Data Structures in R

: - colon operator

Generates regular sequences from a starting value of the sequence to an end value of the sequence. The values are either a number (numeric or integer) or a factor. The first element is *from* and the next ones' are *from* plus or minus one, up to or down to *to*.

Syntax:
from:to

The increment is always 1 or -1 for numeric arguments.
If *from* is integer then the result is integer, regardless of *to*.

from:to is equivalent to `seq(from, to)`

> 2:5 # sequence of numbers from 2 to 5

[1] 2 3 4 5

> 5:2 # sequence of numbers from 5 down to 2

[1] 5 4 3 2

> -3:4 # sequence of numbers from -3 to 4

[1] -3 -2 -1 0 1 2 3 4

> 0:pi # sequence of numbers from 0 to π

[1] 0 1 2 3

> pi:7 # sequence of numbers from π to 7

[1] 3.141593 4.141593 5.141593 6.141593

$$F(n+1) = F(n) + 1$$

or

$$F(n+1) = F(n) - 1$$

N integer implies $F(n)$ integer

N real implies $F(n)$ real

Data Structures in R

c() - "concatenate" function

Combine Values into a Vector or List.

`c(myobj1, ..., myobjN, recursive=FALSE)` combines all arguments from `myobj1` to `myobjN`, with each element of the object as an element of the resulting vector, unless the object is a list, in which case the list is stored as one element of the resulting vector.

`c(myobj1, ..., myobjN, recursive=TRUE)` recursively combines all arguments from `myobj1` to `myobjN`, with each element of the object as an element of the resulting vector, if the object can be listed, that is split into its elements.

```
> c(734, 985, 43, 952) # numeric vector
```

```
[1] 734 985 43 952
```

```
> c("Helsinki", "Tampere", "Turku") # string vector
```

```
[1] "Helsinki" "Tampere" "Turku"
```

```
> c(T,F,F,F,T,F,T,F,T,T) # logical vector
```

```
[1] TRUE FALSE FALSE FALSE TRUE FALSE TRUE FALSE TRUE TRUE
```

```
> c(23, 10:16) # numeric vector
```

```
[1] 23 10 11 12 13 14 15 16
```



```
> c(T,F,F,5) # numeric vector
```

```
[1] 1 0 0 5
```

```
> c(1:5, 10.5, "next") # string vector
```

```
[1] "1" "2" "3" "4" "5" "10.5" "next"
```


Data Structures in R

The elements of a vectors are of one data type only (Boolean, Numeric or Character) and mixing data types results in automatic data conversion.
Order of conversion: boolean  numeric  character

```
> c(T,F,F,55) # boolean becomes numeric
```

```
[1] 1 0 0 55
```

```
> c(TRUE, FALSE, F, "Turku") # boolean becomes character
```

```
[1] "TRUE" "FALSE" "FALSE" "Turku"
```

```
> c(734, 985, "Turku") # numeric becomes character
```

```
[1] "734" "985" "Turku"
```

```
> c(TRUE, FALSE, F, T, -7.34, 72+9i, "Turku") # boolean and numeric become character
```

```
[1] "TRUE" "FALSE" "FALSE" "TRUE" "-7.34" "72+9i" "Turku"
```

Data Structures in R

seq - "sequence" function

Generate regular sequences:

seq(from = 1, to = 1, by = ((to - from)/(length.out - 1)), length.out = NULL, along.with = NULL, ...)

Arguments

... arguments passed to or from methods.

from, to the starting and (maximal) end value of the sequence.

by number: increment of the sequence.

length.out desired length of the sequence. A non-negative number, which for seq and seq.int will be rounded up if fractional.

along.with take the length from the length of this argument.

> seq(4, 9) # same as 4:9

[1] 4 5 6 7 8 9

$$F(n+1) = F(n) + 1, F(n) [4, 9]$$

> seq(1,10, by= 3) # numbers starting at 1, incrementing by 3, up to 10

[1] 1 4 7 10

$$F(n+1) = F(n) + 3, F(n) [1, 10] \text{ the result is between 1 and 10}$$

> seq(1,15, length.out= 6) # 6 numbers evenly spaced between 1 and 15

[1] 1.0 3.8 6.6 9.4 12.2 15.0

$$F(n+1) = F(n) + x, F(n) [1, 15] x = (15-1)/(6-1)$$

> seq(along.with= 4:8) # the length of this argument will be the length of the output

[1] 1 2 3 4 5

> seq(7) # same as 1:7

[1] 1 2 3 4 5 6 7

> seq(length.out= 7) # same as 1:7

[1] 1 2 3 4 5 6 7

> seq(1,by=3, length.out= 9) # 9 numbers, starting in 1, incremented by 3

[1] 1 4 7 10 13 16 19 22 25

Data Structures in R

rep() - repetition function

Replicate elements of vectors and lists

```
rep(x, times, length.out, each)
```

Arguments

x is a scalar, a vector (including a list) or a pairlist or a factor

... further arguments:

times - a scalar or vector with the number of times repeat each element if times has the same length as the input, or to repeat the whole vector if times has length 1

length.out - an integer with the length of the result

each - an integer with the number of times each element of the input will be repeated

rep(x, times=1, length.out=NA, each=1) this is the default action

Data Structures in R

rep() - repetition function

```
> rep(14,3) # repeat number 14, 3 times
```

```
[1] 14 14 14
```

```
> rep(c(8,3,7),1:3) # repeat number 8, once, number 3, twice and number 7, thrice
```

```
[1] 8 3 3 7 7 7
```

```
> rep(c(8,3,7),1:3,4) # repeat number 8, 3 and 7 but limit the result to 4 elements
```

```
[1] 8 3 7 8
```

```
> rep(c(8,3,7),each=3) # repeat number 8, number 3 and number 7, thrice
```

```
[1] 8 8 8 3 3 3 7 7 7
```

```
> rep(c(8,3,7), length.out=7,each=3) # repeat number 8, number 3 and number 7, thrice -  
but limit the result to 7 elements
```

```
[1] 8 8 8 3 3 3 7
```

```
> rep(c(8,3,7), times=2,each=3) # repeat number 8, number 3 and number 7, thrice - do this  
twice
```

```
[1] 8 8 8 3 3 3 7 7 7 8 8 8 3 3 3 7 7 7
```

```
> rep(c(8,3,7), times=2,length.out=15,each=3) # repeat number 8, number 3 and number 7,  
thrice - do this twice and limit the result to 15 elements
```

```
[1] 8 8 8 3 3 3 7 7 7 8 8 8 3 3 3
```

Data Structures in R

```
rep(14,3) # repeat number 14, 3 times  
rep(14,4)  
rep(14,5)
```

```
rep(c(8,3,7),1:3) # repeat number 8, once, number 3, twice and number 7, thrice  
rep(c(8,3,7),2:4)  
rep(c(8,3,7),3:5)
```

```
rep(c(8,3,7),1:3,4) # repeat number 8, 3, and 7 but limit the result to 4 elements  
rep(c(8,3,7),1:3,5)  
rep(c(8,3,7),1:3,6)
```

```
rep(c(8,3,7),each=3) # repeat number 8, number 3 and number 7, thrice  
rep(c(8,3,7),each=4)  
rep(c(8,3,7),each=5)
```

```
rep(c(8,3,7), length.out=7,each=3) # repeat number 8, number 3 and number 7, thrice -  
but limit the result to 7 elements  
rep(c(8,3,7), length.out=8,each=3)  
rep(c(8,3,7), length.out=9,each=3)
```

```
rep(c(8,3,7), times=2,each=3) # repeat number 8, number 3 and number 7, thrice - do  
this twice  
rep(c(8,3,7), times=3,each=3)  
rep(c(8,3,7), times=4,each=3)
```

Data Structures in R

Extracting vector elements, or subsets

3 ways to extract vector elements

- By the element index(es)
- By a logical expression
- By keys

myvector

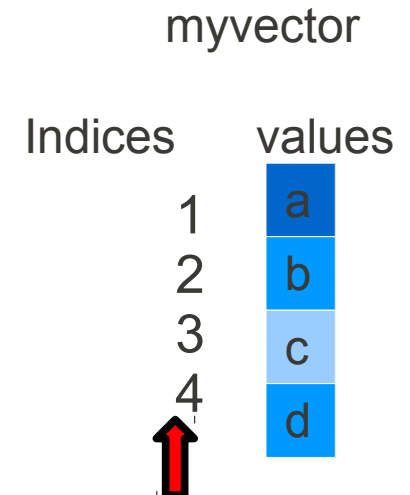
Indices	values
1	a
2	b
3	c
4	d

On vector "myvector"
Element 1 has value "a"

Data Structures in R

Extracting vector elements by the element index(es)

```
> myvec <- c(734, 985, 43, 952, 67, 28, 235, 885, 193)
> myvec
[1] 734 985 43 952 67 28 235 885 193
> myvec[5] # 5th element, starring Bruce Willis
[1] 67
> myvec[c(1,5,7)] # elements 1, 5 and 7
[1] 734 67 235
> myvec[-5] # all but the 5th element
[1] 734 985 43 952 28 235 885 193
> myvec[-c(1,5,7)] # all but elements 1, 5 and 7
[1] 985 43 952 28 885 193
> myvec[4:6] # elements 4 to 6
[1] 952 67 28
```



Data Structures in R


Extracting vector elements by a logical expression

The elements are selected by their value, regardless of their index

```
> myvec <- c(734, 985, 43, 952, 67, 28, 235, 885, 193)
> myvec
[1] 734 985 43 952 67 28 235 885 193
> myvec[myvec > 500] # only elements above 500
[1] 734 985 952 885
> myvec[(myvec %% 2)==0] # only even elements
[1] 734 952 28
> myvec[myvec %in% 100:500] # elements with values from 100 to 500
[1] 235 193
```

myvector

Indices	values
1	a
2	b
3	c
4	d



Data Structures in R

Extracting vector elements by keys

A key (name) can be used to access the vector's elements

The command `names()` will add names to an existing vector, or they can be defined when creating the vector

```
> myvec <- c(734, 985, 43)
> myvec
[1] 734 985 43
> names(myvec) <- c("Helsinki", "Tampere", "Turku")
> myvec
Helsinki Tampere  Turku
   734    985    43
> myvec["Helsinki"]
Helsinki
   734
> myvec[c("Turku", "Tampere")]
Turku Tampere
   43    985
> myvec2 <- c(Helsinki=734, Tampere=985, Turku=43)
> myvec2
Helsinki Tampere  Turku
   734    985    43
```

Data Structures in R

subset

Subset returns subsets of vectors, matrices or data frames

```
subset(x, subset, ...)
```

for matrix or data frame:

```
subset(x, subset, select, drop = FALSE, ...)
```

x object to be subsetted.

subset logical expression indicating elements or rows to keep: missing values are taken as false.

select expression, indicating columns to select from a data frame.

drop passed on to [indexing operator.

... further arguments to be passed to or from other methods.

```
subset(airquality, Temp > 80, select = c(Ozone, Temp))
```

```
subset(airquality, Day == 1, select = -Temp)
```

```
subset(airquality, select = Ozone:Wind)
```

Data Structures in R

Operations on vectors

Most operations for scalars will work on vectors

```
> myvec1 <- c(3,6,7,8,12,23,94)
> 10 + myvec1 # adding a scalar
[1] 13 16 17 18 22 33 104
> 3 * myvec1 # multiplying by a scalar
[1] 9 18 21 24 36 69 282
> myvec1 ^ 2 # power by a scalar
[1] 9 36 49 64 144 529 8836
> log(myvec1) # natural logarithm
[1] 1.098612 1.791759 1.945910 2.079442 2.484907 3.135494 4.543295
> sin(myvec1) # sine
[1] 0.1411200 -0.2794155 0.6569866 0.9893582 -0.5365729 -0.8462204 -0.2452520
> myvec2 <- c(5,7,8,152,71,77,89)
> myvec1 + myvec2 # vector addition
[1] 8 13 15 160 83 100 183
> myvec1 * myvec2 # vector multiplication
[1] 15 42 56 1216 852 1771 8366
```

Data Structures in R

Vector set operations

set operations (union, intersection, asymmetric difference, equality and membership) on two vectors.

Union() is not the same as concatenation c() because c() will duplicate values that are common to both vectors.

```
> myvec1 <- c(3,6,7,8,12,23,94)
> myvec2 <- c(5,7,8,152,71,77)
> union(myvec1, myvec2) # set union
[1] 3 6 7 8 12 23 94 5 152 71 77
> c(myvec1,myvec2) # notice the difference between union() and c()
[1] 3 6 7 8 12 23 94 5 7 8 152 71 77
> intersect(myvec1, myvec2) # set intersection
[1] 7 8
> setdiff(myvec1, myvec2) # set difference
[1] 3 6 12 23 94
> setequal(myvec1, myvec2) # set equality
[1] FALSE
> is.element(4, myvec1) # set membership, is.element and %in% are synonyms
[1] FALSE
> is.element(6, myvec1) # set membership
[1] TRUE
> 4 %in% myvec1 # set membership
[1] FALSE
> 6 %in% myvec1 # set membership
[1] TRUE
```

Data Structures in R

Sorting functions for vectors

```
> myvec <- c(734, NA, 985, 43, NA, 952, 67)
```

```
> myvec
```

```
[1] 734 NA 985 43 NA 952 67
```

```
> sort(myvec) # Sort a vector or factor
```

```
[1] 43 67 734 952 985
```

```
> sort(myvec, decreasing = TRUE) # Sort a vector or factor, decreasing
```

```
[1] 985 952 734 67 43
```

```
> rev(myvec) # Reverse elements
```

```
[1] 67 952 NA 43 985 NA 734
```

```
> unique(myvec) # Get non duplicate elements of a vector
```

```
[1] 734 NA 985 43 952 67
```

```
> order(myvec) # Sort an object, return the indices
```

```
[1] 4 7 1 6 3 2 5
```

```
> order(myvec, na.last = FALSE) # Sort an object, return the indices, NA at the beginning
```

```
[1] 2 5 4 7 1 6 3
```

```
> order(myvec, na.last = TRUE) # Sort an object, return the indices, NA at the end
```

```
[1] 4 7 1 6 3 2 5
```

```
> order(myvec, decreasing = FALSE) # Sort an object, return the indices, increasing
```

```
[1] 4 7 1 6 3 2 5
```

```
> order(myvec, decreasing = TRUE) # Sort an object, return the indices, decreasing
```

```
[1] 3 6 1 7 4 2 5
```

Data Structures in R

Difference and length functions for vectors

```
> myvec <- c(734, 985, 43, 952, 67, 28, 235, 885, 193)
> myvec
[1] 734 985 43 952 67 28 235 885 193
> diff(myvec) # difference between elements
[1] 251 -942 909 -885 -39 207 650 -692
> c(myvec[2]-myvec[1],myvec[3]-myvec[2],myvec[4]-myvec[3],myvec[5]-myvec[4])
[1] 251 -942 909 -885
> diff(myvec, lag = 2) # difference between elements, with a lag of 2
[1] -691 -33 24 -924 168 857 -42
> c(myvec[3]-myvec[1],myvec[4]-myvec[2],myvec[5]-myvec[3])
[1] -691 -33 24
> diff(myvec, differences = 2) # order of the difference of 2
[1] -1193 1851 -1794 846 246 443 -1342
> length(myvec) # Get the length of the vector
[1] 9
> length(myvec) <- 12 # Set the length of the vector
> myvec
[1] 734 985 43 952 67 28 235 885 193 NA NA NA
> length(myvec) # Get the length of the vector
[1] 12
```

Data Structures in R

Statistical functions for vectors

```
> myvec1 <- c(3,6,7,8,12,23,94)
> summary(myvec1) # Min. 1st Qu. Median Mean 3rd Qu. Max.
  Min. 1st Qu. Median Mean 3rd Qu. Max.
  3.00  6.50  8.00 21.86 17.50 94.00
> min(myvec1) # Min
[1] 3
> quantile(myvec1, probs=0.25) # 1st Qu.
25%
6.5
> median(myvec1) # median
[1] 8
> quantile(myvec1, probs=0.5) # median = 2nd Qu.
50%
8
> mean(myvec1) # mean
[1] 21.85714
> quantile(myvec1, probs=0.75) # 3rd Qu.
75%
17.5
> max(myvec1) # max
[1] 94
```

Data Structures in R

Statistical functions for vectors

```
> quantile(myvec1, probs=c(0.25, 0.75)) # 1st Qu. and 3rd Qu.  
25% 75%  
6.5 17.5  
> IQR(myvec1) # inter-quartile range  
[1] 11  
> mad(myvec1) # robust alternative to IQR  
[1] 5.9304  
> sd(myvec1) # standard deviation  
[1] 32.46243  
> var(myvec1) # variance  
[1] 1053.810
```


Data Structures in R

`any(..., na.rm = FALSE)` returns TRUE if at least one value is TRUE

`all(..., na.rm = FALSE)` returns TRUE if all the values are TRUE

`na.rm = TRUE` will ignore all the NAs

> #compare vectors, all elements are equal

> x <- c(7, 5, 6)

> y <- c(7, 5, 6)

> x==y

[1] TRUE TRUE TRUE

> all(x==y)

[1] TRUE

> any(x==y)

[1] TRUE

>

> #compare vectors, one element is equal

> x <- c(7, 5, 6)

> y <- c(7, 8, 9)

> x==y

[1] TRUE FALSE FALSE

> all(x==y)

[1] FALSE

> any(x==y)

[1] TRUE

> #compare vectors, regardless
of element position

> x <- c(7, 5, 6)

> y <- c(5, 7, 6)

> x==y

[1] FALSE FALSE TRUE

> sort(x)==sort(y)

[1] TRUE TRUE TRUE

Data Structures in R

```
> # comparing 2 vectors, by position and with NAs
```

```
> x <- y <- c(7, 6, NA, NA, 5)
```

```
> all(x==y)
```

```
[1] NA
```

```
> all(x==y , na.rm = TRUE)
```

```
[1] TRUE
```

```
> identical(x, y)
```

```
[1] TRUE
```

```
> all.equal(x, y)
```

```
[1] TRUE
```

```
> x[!is.na(x)]==y[!is.na(y)]
```

```
[1] TRUE TRUE TRUE
```

```
> all( x[!is.na(x)]==y[!is.na(y)] )
```

```
[1] TRUE
```

```
>
```

```
> # NA OR TRUE is TRUE
```

```
> # this will return TRUE despite the NAs
```

```
> any(x==y)
```

```
[1] TRUE
```

```
> # this will return NA, not FALSE
```

```
> y <- c(1, NA, 2, 3, 4)
```

```
> any(x==y)
```

```
[1] NA
```

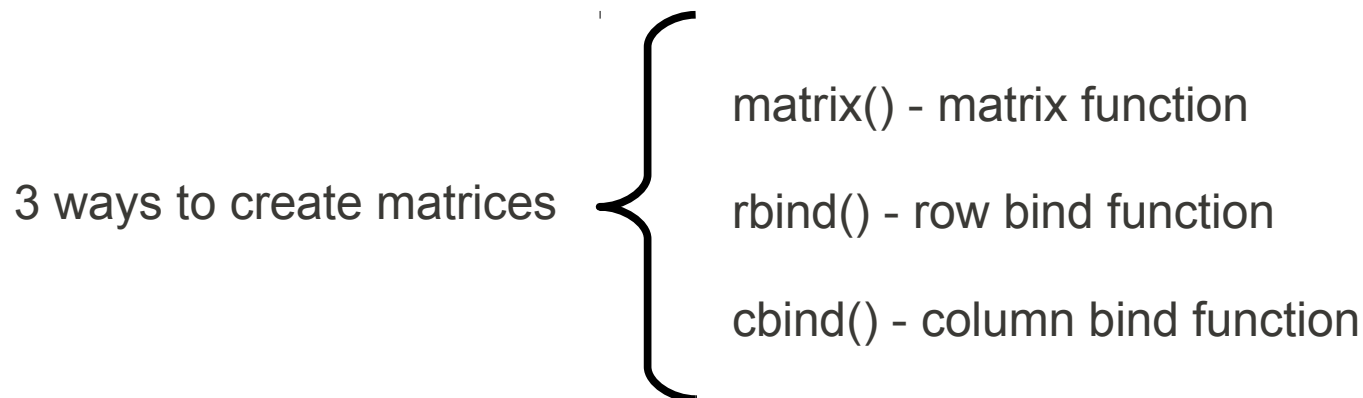
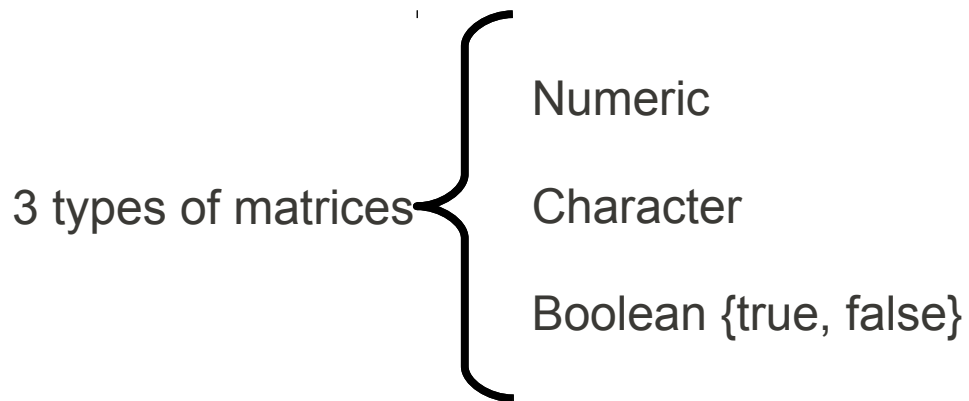
Data Structures in R

a	t	i
b	g	k
c	b	m

Matrix

A matrix is a two-dimensional ($m \times n$) object, like 2 or more vectors of the same size, side by side.

A matrix has only one data type, automatic data conversion like a vector and the functions that apply to vectors also apply to matrices, excluding a few specific ones'.



Data Structures in R

matrix()

matrix creates a matrix from a set of values

```
matrix(data = NA, nrow = 1, ncol = 1, byrow = FALSE, dimnames = NULL)
```

Arguments

data an optional data vector

nrow the desired number of rows

ncol the desired number of columns

byrow if TRUE, the matrix is filled by rows

dimnames list of names for rows or rows and columns

as.matrix tries to convert an object to a matrix.

is.matrix returns TRUE if an object is a matrix

Data Structures in R

```
> matrix(10,3,2) # matrix 3 x 2 with 5's
```

```
  [,1] [,2]  
[1,] 10 10  
[2,] 10 10  
[3,] 10 10
```

```
> matrix(c(1,2,3),3,2)# matrix 3 x 2 with 2 columns with values [1,2,3]
```

```
  [,1] [,2]  
[1,]  1  1  
[2,]  2  2  
[3,]  3  3
```

```
> matrix(c(1,2),3,2,byrow = T)# matrix 3 x 2 with 3 rows with values [1,2]
```

```
  [,1] [,2]  
[1,]  1  2  
[2,]  1  2  
[3,]  1  2
```

```
> matrix(1:6,3,2)# matrix 3 x 2 with ascending values from each column
```

```
  [,1] [,2]  
[1,]  1  4  
[2,]  2  5  
[3,]  3  6
```

```
> matrix(1:6,3,2,byrow = T)# matrix 3 x 2 with ascending values from each row
```

```
  [,1] [,2]  
[1,]  1  2  
[2,]  3  4  
[3,]  5  6
```

Data Structures in R

Setting row and column names

```
> mymatrix <- matrix(1:6,2,3,dimnames = list(c("row1", "row2"),c("col1", "col2", "col3")))
```

```
> mymatrix # row and column names
```

```
  col1 col2 col3  
row1  1  3  5  
row2  2  4  6
```

```
> mymatrix1 <- matrix(1:6,2,3,dimnames = list(c("row1", "row2")))
```

```
> mymatrix1 # row names
```

```
  [,1] [,2] [,3]  
row1  1  3  5  
row2  2  4  6
```

```
> mymatrix2 <- matrix(1:6,2,3,dimnames = list(NULL,c("col1", "col2", "col3")))
```

```
> mymatrix2 # column names
```

```
  col1 col2 col3  
[1,]  1  3  5  
[2,]  2  4  6
```

Data Structures in R

Setting row and column names, or changing them, on an existing matrix

```
> #using colnames, rownames
> mymatrix3 <- matrix(1:6,2,3)
> colnames(mymatrix3) = c("col1", "col2", "col3") # adding column names
> rownames(mymatrix3) = c("row1", "row2") # adding row names
> mymatrix3
  col1 col2 col3
row1  1  3  5
row2  2  4  6
> #using dimnames
> mymatrix4 <- matrix(1:6,2,3)
> dimnames(mymatrix4) = list(c("row1", "row2"),c("col1", "col2", "col3"))
> mymatrix4
  col1 col2 col3
row1  1  3  5
row2  2  4  6
```

Data Structures in R

`cbind()`, `rbind()`

Combine vector, matrix or data frames by columns or rows

```
> myvec <- seq(0,by=2, length.out= 8)
```

```
> rbind(myvec, 1:8)
```

```
      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8]  
myvec  0  2  4  6  8 10 12 14  
      1  2  3  4  5  6  7  8
```

```
> cbind(myvec, 1:8)
```

```
      myvec  
[1,]  0 1  
[2,]  2 2  
[3,]  4 3  
[4,]  6 4  
[5,]  8 5  
[6,] 10 6  
[7,] 12 7  
[8,] 14 8
```


Data Structures in R

Extracting matrix elements

```
> mymatrix <- matrix(1:6*10,3,2)
> mymatrix
  [,1] [,2]
[1,] 10  40
[2,] 20  50
[3,] 30  60
> mymatrix[1,1] # row 1, column 1
[1] 10
> mymatrix[3,2] # row 3, column 2
[1] 60
> mymatrix[1] # row 1, column 1
[1] 10
> mymatrix[2] # row 2, column 1
[1] 20
> mymatrix[2,1:2] # row 2, column 1 and 2
[1] 20 50
> mymatrix[1,] # row 1
[1] 10 40
> mymatrix[2,] # row 2
[1] 20 50
> mymatrix[,1] # column 1
[1] 10 20 30
> mymatrix[,2] # column 2
[1] 40 50 60
```

```
mymatrix <- matrix(1:6*10,3,2)
```

if the row or column index is not specified, the whole row or column is taken

```
mymatrix[1,] # row 1
```

```
mymatrix[1,1:2] # row 1, all columns explicitly selected
```

```
mymatrix[,1] # column 1
```

```
mymatrix[1:3,1] # column 1, all rows explicitly selected
```

mymatrix[,] # if the row and column index are not specified, it's the same

mymatrix # as the whole matrix

a single index will show the matrix elements by the order of insertion

which is columns from top to bottom, rows from left to right

```
mymatrix[1]
```

```
mymatrix[2]
```

```
mymatrix[3]
```

```
mymatrix[4]
```

```
mymatrix[1:6]
```

Data Structures in R

Negative indices remove rows or columns

```
> mymatrix <- matrix(1:6*10,3,2)
```

```
> mymatrix
```

```
  [,1] [,2]  
[1,] 10 40  
[2,] 20 50  
[3,] 30 60
```

```
> mymatrix[-1,-1] # remove row 1 and column 1
```

```
[1] 50 60
```

```
> mymatrix[-1,] # remove row 1
```

```
  [,1] [,2]  
[1,] 20 50  
[2,] 30 60
```

```
> mymatrix[-2,] # remove row 2
```

```
  [,1] [,2]  
[1,] 10 40  
[2,] 30 60
```

```
> mymatrix[, -1] # remove column 1
```

```
[1] 40 50 60
```

```
> mymatrix[, -2] # remove column 2
```

```
[1] 10 20 30
```

Data Structures in R

Extracting matrix elements by row or column names

```
> mymatrix <- matrix(1:6*10,2,3,dimnames = list(c("row1", "row2"),c("col1", "col2", "col3")))
> mymatrix
  col1 col2 col3
row1  10  30  50
row2  20  40  60
> mymatrix["row1","col1"]# row 1, column 1
[1] 10
> mymatrix["row2",]# row 2
col1 col2 col3
 20  40  60
> mymatrix[,c("col1","col3")]# column 1 and column 3
  col1 col3
row1  10  50
row2  20  60
```

Data Structures in R

Matrix info

```
> mymatrix <- matrix(1:6*10,2,3,dimnames = list(c("row1", "row2"),c("col1", "col2", "col3")))
```

```
> mymatrix
```

```
  col1 col2 col3  
row1  10  30  50  
row2  20  40  60
```

```
> dim(mymatrix) # dimensions of the matrix, 2 x 3
```

```
[1] 2 3
```

```
> length(mymatrix) # number of elements
```

```
[1] 6
```

```
> dimnames(mymatrix) # dimension names (rows and columns names')
```

```
[[1]]
```

```
[1] "row1" "row2"
```

```
[[2]]
```

```
[1] "col1" "col2" "col3"
```

```
> colnames(mymatrix) # rows names
```

```
[1] "col1" "col2" "col3"
```

```
> rownames(mymatrix) # columns names
```

```
[1] "row1" "row2"
```

```
> mode(mymatrix) # Storage Mode of this Object
```

```
[1] "numeric"
```

```
> is(mymatrix) # all the super-classes of this object's class
```

```
[1] "matrix" "array" "structure" "vector"
```

```
> class(mymatrix) # class attribute or the implicit class of this object
```

```
[1] "matrix"
```

Data Structures in R

Matrix calculations

```
> myvec <- seq(1,by=3, length.out= 9)
```

```
> mymatrix1 <- matrix(myvec,3,3)
```

```
> mymatrix2 <- matrix(9:1,3,3)
```

```
> # component-wise multiplication
```

```
> mymatrix1 * mymatrix2
```

```
      [,1] [,2] [,3]  
[1,]   9  60  57  
[2,]  32  65  44  
[3,]  49  64  25
```

```
> # matrix multiplication
```

```
> mymatrix1 %*% mymatrix2
```

```
      [,1] [,2] [,3]  
[1,] 222 132  42  
[2,] 294 177  60  
[3,] 366 222  78
```

```
> # matrix transpose
```

```
> t(mymatrix1)
```

```
      [,1] [,2] [,3]  
[1,]   1   4   7  
[2,]  10  13  16  
[3,]  19  22  25
```

```
> myvec
```

```
[1]  1  4  7 10 13 16 19 22 25
```

```
> mymatrix1
```

```
      [,1] [,2] [,3]  
[1,]   1  10  19  
[2,]   4  13  22  
[3,]   7  16  25
```

```
> mymatrix2
```

```
      [,1] [,2] [,3]  
[1,]   9   6   3  
[2,]   8   5   2  
[3,]   7   4   1
```

Data Structures in R

Matrix calculations

```
> diag(1:4) # diagonal matrix 4 X 4
```

```
      [,1] [,2] [,3] [,4]  
[1,]  1  0  0  0  
[2,]  0  2  0  0  
[3,]  0  0  3  0  
[4,]  0  0  0  4
```

```
> diag(1,2) # Identity matrix 2 X 2
```

```
      [,1] [,2]  
[1,]  1  0  
[2,]  0  1
```

```
> mymatrix <- matrix(1:9*10,3,3)
```

```
> det(mymatrix) # Determinant
```

```
[1] -5.32907e-13
```

```
> sum(diag(mymatrix)) # trace of a matrix
```

```
[1] 150
```

```
> eigen(mymatrix)$values # Eigenvalues
```

```
[1] 1.611684e+02 -1.116844e+01 -5.019627e-15
```

```
> eigen(mymatrix)$vectors # Eigenvectors
```

```
      [,1]  [,2]  [,3]  
[1,] -0.4645473 -0.8829060  0.4082483  
[2,] -0.5707955 -0.2395204 -0.8164966  
[3,] -0.6770438  0.4038651  0.4082483
```

Data Structures in R

Matrix calculations

`chol()` Choleski factorization of a real symmetric positive-definite square matrix

`qr()` QR decomposition of a matrix

`svd()` singular-value decomposition of a rectangular matrix

`crossprod()` matrix cross-product

`outer()` outer product of arrays

`scale()` Scaling and centering of matrix

`solve()` Solve a system of equations

`svd()` singular-value decomposition of a rectangular matrix

Data Structures in R

Changing the matrix's elements

> #adding one row

> mymatrix <- matrix(1:6,2,3,byrow=T)

> mymatrix

```
      [,1] [,2] [,3]
[1,]    1    2    3
[2,]    4    5    6
```

> mymatrix <- rbind(mymatrix, 7:9)

> mymatrix

```
      [,1] [,2] [,3]
[1,]    1    2    3
[2,]    4    5    6
[3,]    7    8    9
```

> #adding one column

> mymatrix <- cbind(mymatrix, seq(3.5,by=3,length.out = 3))

> mymatrix

```
      [,1] [,2] [,3] [,4]
[1,]    1    2    3 3.5
[2,]    4    5    6 6.5
[3,]    7    8    9 9.5
```


Data Structures in R

Changing the matrix's elements

```
> #changing an entire row
```

```
> mymatrix[3,] <- 1:4
```

```
> mymatrix
```

```
  [,1] [,2] [,3] [,4]
[1,]  1  2  3 3.5
[2,]  4  5  6 6.5
[3,]  1  2  3 4.0
```

```
> #changing an entire column
```

```
> mymatrix[,4] <- 7:9
```

```
> mymatrix
```

```
  [,1] [,2] [,3] [,4]
[1,]  1  2  3  7
[2,]  4  5  6  8
[3,]  1  2  3  9
```

```
> #deleting one row
```

```
> mymatrix <- mymatrix[-2,]
```

```
> mymatrix
```

```
  [,1] [,2] [,3] [,4]
[1,]  1  2  3  7
[2,]  1  2  3  9
```

```
> #deleting one column
```

```
> mymatrix <- mymatrix[, -4]
```

```
> mymatrix
```

```
  [,1] [,2] [,3]
[1,]  1  2  3
[2,]  1  2  3
```

Data Structures in R

Applying functions on matrix/array elements

`apply()` returns a vector or array or list, after applying a function to each of its members

`apply(object, margin, function, ...)`

object is the input array

margin are the subscripts where to apply the function, 1 indicates rows, 2 indicates columns, `c(1,2)` indicates rows and columns

function

... optional arguments for the function

```
> mymatrix <- matrix(1:6*10,2,3)
```

```
> mymatrix
```

```
  [,1] [,2] [,3]
[1,] 10  30  50
[2,] 20  40  60
```

```
> apply(mymatrix,1,max) # rows
```

```
[1] 50 60
```

```
> apply(mymatrix,2,max) # columns
```

```
[1] 20 40 60
```

```
> apply(mymatrix,c(1,2),max) # rows and columns, useless
```

#try:

```
apply(mymatrix,1,mean) # rows
```

```
apply(mymatrix,2,mean) # columns
```

#try:

```
apply(mymatrix,1,sort) # rows
```

```
apply(mymatrix,2,sort) # columns
```

Data Structures in R

Array

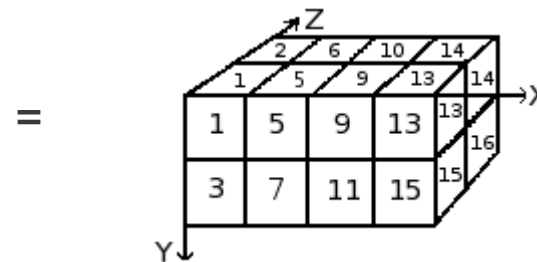
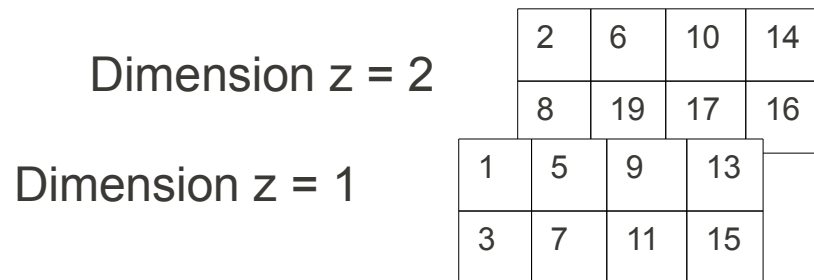
An array is a three-dimensional ($m \times n \times p$) object, like 2 or more matrices of the same dimensions, side by side.

An array has only one data type, automatic data conversion like a vector or matrix and the functions that apply to vectors and matrices also apply to arrays, excluding a few specific ones'.

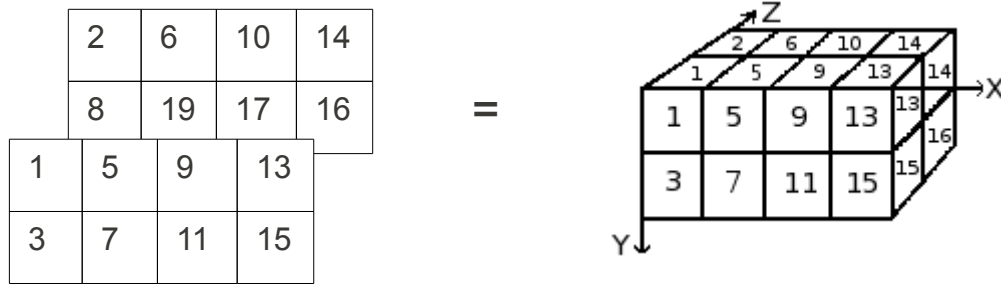
`array(data = NA, dim = length(data), dimnames = NULL)` creates an array from data, dim are the dimensions and dimnames are optional names for the dimensions

`as.array()` tries to convert an object to an array

`is.array()` returns TRUE if the object is an array



Data Structures in R



```
> array(c(1,3,5,7,9,11,13,15,2,8,6,19,10,17,14,16),c(2,4,2))
, , 1
```

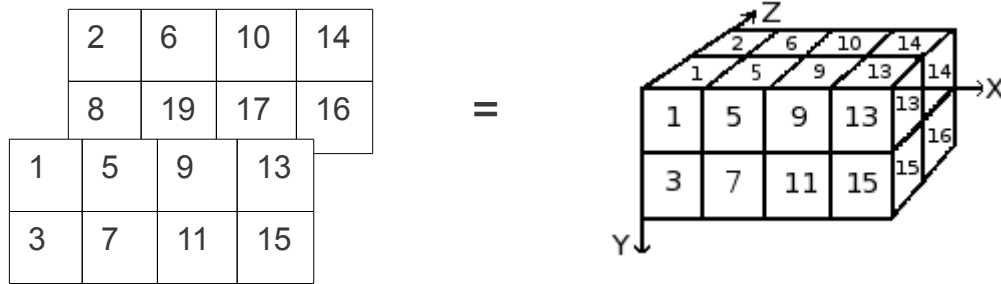
```
      [,1] [,2] [,3] [,4]
[1,]  1   5   9  13
[2,]  3   7  11  15
```

```
, , 2
```

```
      [,1] [,2] [,3] [,4]
[1,]  2   6  10  14
[2,]  8  19  17  16
```

Notice how the element values are inserted by column

Data Structures in R



```
> # turning matrices into arrays
> # passing data by rows
> m1 <- matrix(c(1,5,9,13,3,7,11,15),2,4, byrow=T)
> m2 <- matrix(c(2,6,10,14,8,19,17,16),2,4, byrow=T)
> array(c(m1,m2),c(2,4,2))
,, 1
```

```
      [,1] [,2] [,3] [,4]
[1,]    1    5    9   13
[2,]    3    7   11   15
```

```
,, 2
```

```
      [,1] [,2] [,3] [,4]
[1,]    2    6   10   14
[2,]    8   19   17   16
```

Data Structures in R

Adding dimension names

	City			
	Age	Hgt	Wgt	BPM
Men	56	174	75	77
Women	67	166	55	70

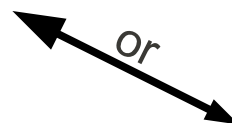
	Countryside			
	Age	Hgt	Wgt	BPM
Men	64	178	78	63
Women	77	170	59	61

This data is fake, can anyone get real data?

```
> myarray<-array(c(56,67,174,166,75,55,77,70,64,77,178,170,78,59,63,61),c(2,4,2))  
> dimnames(myarray) = list(c("men","women"),c("age","height","weight","pulse"),  
+ c("city","countryside"))  
> myarray  
, , city
```

```
      age height weight pulse  
men   56   174    75    77  
women 67   166    55    70  
, , countryside
```

```
      age height weight pulse  
men   64   178    78    63  
women 77   170    59    61
```



```
# dimension names defined directly:  
myarray2<-  
array(c(56,67,174,166,75,55,77,70,64,77,178,170,  
78,59,63,61),c(2,4,2), dimnames =  
list(c("men","women"),c("age","height","weight","pul  
se"),c("city","countryside")))
```

Data Structures in R

> `dimnames(myarray)`

```
[[1]]
[1] "men" "women"
```

```
[[2]]
[1] "age" "height" "weight" "pulse"
```

```
[[3]]
[1] "city" "countryside"
```

Accessing the array's elements

> `myarray["women",,]` # women's all info, all cities

```
city countryside
age      67      77
height  166     170
weight   55     59
pulse    70     61
```

> `myarray["women",,"countryside"]` # women's all info, countryside

```
age height weight pulse
77  170  59  61
```

> `myarray[,,"countryside"]` # all info, countryside

```
age height weight pulse
men   64  178  78  63
women 77  170  59  61
```

> `myarray[, "height",]` # height

```
city countryside
men   174     178
women 166     170
```

Countryside
Age Hgt Wgt BPM

	Men	64	178	78	63
	Women	77	170	59	61
City	Men	56	174	75	77
	Women	67	166	55	70
		Age	Hgt	Wgt	BPM

Same, with indices

```
myarray[2,,] # women's all info, all cities
myarray[2,, 2] # women's all info,
countryside
myarray[,2] # all info, countryside
myarray[, 2,] # height
```



Data Structures in R

Operations on the array's elements

> `apply(myarray,1,max) # rows`

men women Meaningless, age vs htg...
178 170

> `apply(myarray,2,max) # columns`

age height weight pulse Oldest, tallest...
77 178 78 77

> `apply(myarray,c(1,2),max) # rows and columns`

age height weight pulse
men 64 178 78 77 Oldest, tallest... by gender
women 77 170 59 70

		Countryside			
		Age	Hgt	Wgt	BPM
City	Men	64	178	78	63
	Women	77	170	59	61
	Men	56	174	75	77
	Women	67	166	55	70
		Age	Hgt	Wgt	BPM

`apply(myarray,2,mean) # columns mean`

`apply(myarray,c(1,2),mean) # rows and columns mean`

`apply(myarray,2,quantile) # columns quartiles`

`apply(myarray,c(1,2),quantile) # rows and columns quartiles`

`apply(myarray,2,quantile,.5) # columns median`

Data Structures in R

Changing the array's elements

		Countryside			
		Age	Hgt	Wgt	BPM
City	Men	64	178	78	63
	Women	77	170	59	61
	Men	56	174	75	77
	Women	67	166	55	70
		Age	Hgt	Wgt	BPM

```
myarray <- array(c(56,67,174,166,75,55,77,70,64,77,178,170,78,59,63,61),c(2,4,2))
dimnames(myarray) = list(c("men","women"),c("age","height","weight","pulse"),
c("city","countryside"))
```

```
myarray <- myarray[, -4,] # remove pulse, by index
myarray <- myarray[, colnames(myarray) != "age",] # remove age, by column name
```

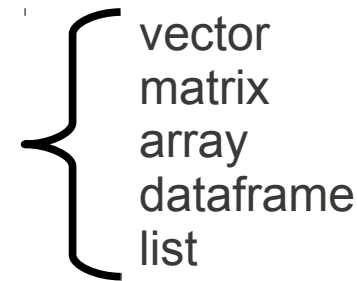
```
myarray <- array(c(myarray,c(167,162,75,60,179,168,77,65)),c(2,2,4)) # adding 2 "places"
dimnames(myarray) = list(c("men","women"),c("height","weight"), c("city","countryside",
"p1","p2"))
```

Data Structures in R

List

A list is a vector containing elements of different types

The elements are accessible by indices, like on a vector, there is just an extra square bracket [] for the list index and there might be other indices from contained elements.



```
> myvec <- 3:8
> mymatrix <- matrix(6:1*10,3,2)
> mydataframe <- as.data.frame(mymatrix)
> mylist <- list(myvec, mymatrix, mydataframe, 56,"test")
> mylist[[1]][1]
[1] 3
> mylist[[1]][2]
[1] 4
> mylist[[2]][1,1]
[1] 60
> mylist[[3]]$V1[2]
[1] 50
> mylist[[4]]
[1] 56
> mylist[[5]]
[1] "test"

> mylist
[[1]]
[1] 3 4 5 6 7 8

[[2]]
      [,1] [,2]
[1,]  60  30
[2,]  50  20
[3,]  40  10

[[3]]
  V1 V2
1 60 30
2 50 20
3 40 10

[[4]]
[1] 56

[[5]]
[1] "test"
```

Data Structures in R

Naming the elements of the list is recommended

Accessing the elements of the list

```
> myvec <- 3:8
> mymatrix <- matrix(6:1*10,3,2)
> mydataframe <- as.data.frame(mymatrix)
> mylist <- list(mv=myvec, mm=mymatrix,
mdf=mydataframe, mn=56,ms="test")
> mylist$mv[1]
[1] 3
> mylist$mv[2]
[1] 4
> mylist$mm[1,1]
[1] 60
> mylist$mdf$V1[2]
[1] 50
> mylist$mn
[1] 56
> mylist$ms
[1] "test"
```

```
> mylist
$mv
[1] 3 4 5 6 7 8

$mm
  [,1] [,2]
[1,] 60  30
[2,] 50  20
[3,] 40  10

$mdf
  V1 V2
1 60 30
2 50 20
3 40 10

$mn
[1] 56

$ms
[1] "test"
```

Data Structures in R

```
myvec <- 3:8
mymatrix <- matrix(6:1*10,3,2)
mydataframe <- as.data.frame(mymatrix)
mylist <- list(myvec, mymatrix, mydataframe, 56,"test")
is(mylist) # list, of course
length(mylist)
dim(mylist) # the dimensions of the elements don't count
mylist[1] # [1] <=> [[1]]
mylist[2]
mylist[3]
mylist[4]
mylist[5]
is(mylist[1]) # each element is a list
is(mylist[2])
is(mylist[3])
is(mylist[4])
is(mylist[5])
mylist[1:3]
```

Data Structures in R

Changing the elements of the list

```
myvec <- 3:8
mymatrix <- matrix(6:1*10,3,2)
mydataframe <- as.data.frame(mymatrix)
mylist <- list(mv=myvec, mm=mymatrix,
mdf=mydataframe, mn=56,ms="test")
# updating one element
mylist$ms <- "new test"
mylist$ms
mylist[[5]] <- "newer test"
mylist$ms
# inserting two elements
mylist <- c(mylist,wname="Friday", mday=13)
mylist
# deleting one element at a time
mylist$ms<- NULL
mylist[["mn"]]<- NULL
mylist[[1]]<- NULL
mylist
```

```
> mylist
$mv
[1] 3 4 5 6 7 8

$mm
  [,1] [,2]
[1,] 60 30
[2,] 50 20
[3,] 40 10

$mdf
  V1 V2
1 60 30
2 50 20
3 40 10

$mn
[1] 56

$ms
[1] "test"
```

Data Structures in R

Using the \$ notation

```
myvec <- 3:8
mymatrix <- matrix(6:1*10,3,2)
mydataframe <- as.data.frame(mymatrix)
mylist <- list(mv=myvec, mm=mymatrix, mdf=mydataframe, mn=56,ms="test")
# inserting one element
mylist <- c(mylist,tree_info=list(family="Fagaceae", genus = "Fagus"))
mylist
mylist$tree_info # this is NULL, must specify the sub-elements
mylist$tree_info.family
mylist$tree_info.genus
mylist[["tree_info.family"]]
```

Data Structures in R

Factors

A factor is a vector that specifies a discrete classification of other vectors. Factors store categorical data, qualitative values, non numeric such as gender, job, color, species, model, brand, etc... Or numeric but meaningless like model numbers or site numbers or zip codes.

```
> student.residence <-
```

```
c("Helsinki", "Tampere", "Turku", "Helsinki", "Helsinki", "Turku", "Oulu", "Tampere", "Helsinki", "Turku", "Tampere", "Helsinki")
```

```
> student.residence
```

```
[1] "Helsinki" "Tampere" "Turku" "Helsinki" "Helsinki" "Turku"
```

```
[7] "Oulu" "Tampere" "Helsinki" "Turku" "Tampere" "Helsinki"
```

```
> fstudent=as.factor(student.residence)
```

```
> fstudent
```

```
[1] Helsinki Tampere Turku Helsinki Helsinki Turku Oulu Tampere
```

```
[9] Helsinki Turku Tampere Helsinki
```

```
Levels: Helsinki Oulu Tampere Turku
```

```
> levels(fstudent)
```

```
[1] "Helsinki" "Oulu" "Tampere" "Turku"
```

```
> summary(fstudent)
```

```
Helsinki Oulu Tampere Turku
```

```
5 1 3 3
```

```
> student.height=c(175,162,170,170,192,170,115,155,150,130,220,160)
```

```
> student.height
```

```
[1] 175 162 170 170 192 170 115 155 150 130 220 160
```

```
> tapply(student.height,fstudent,mean)
```

```
Helsinki Oulu Tampere Turku
```

```
169.4000 115.0000 179.0000 156.6667
```

Data Structures in R

Sorted factors

Factor with levels of hierarchy

function `ordered()` turns a factor into a sorted factor

```
> # sort the cities by increasing longitude
> flevel.residence <- ordered(student.residence,
levels=c("Helsinki", "Turku", "Tampere", "Oulu"))
> flevel.residence
[1] Helsinki Tampere Turku Helsinki Helsinki Turku Oulu Tampere
[9] Helsinki Turku Tampere Helsinki
Levels: Helsinki < Turku < Tampere < Oulu
> # check each student whether he/she lives south of Tampere
> flevel.residence < "Tampere"
[1] TRUE FALSE TRUE TRUE TRUE TRUE FALSE FALSE TRUE TRUE FALSE
TRUE
```


Data Structures in R

Data Frames

Data Frames are matrices with columns of different data types.

```
data.frame(..., row.names = NULL, check.rows = FALSE,  
           check.names = TRUE,  
           stringsAsFactors = default.stringsAsFactors())
```

... value or tag = value

row.names a column to be used as row names, or a vector with the row names

check.rows if TRUE then the rows are checked for consistency of length and names

check.names If TRUE then the names of the variables in the data frame are checked for syntax and uniqueness

stringsAsFactors true if character vectors should be converted to factors

```
> mydataf <- data.frame(age=c(25,22),height=c(174,166),weight=c(75,55),  
                        city=c("Turku","Espoo"),row.names =c("Pekka","Anna"))
```

```
> mydataf
```

```
   age height weight city  
Pekka 25   174    75 Turku  
Anna  22   166    55 Espoo
```

```
> is(mydataf)
```

```
[1] "data.frame" "list"      "oldClass"  "vector"
```

Age Hgt Wgt Name

Pekka	25	174	75	Pekka
Anna	22	166	55	Anna

Data Structures in R

Accessing the data frame's elements

```
> #getting the info for Anna
> mydataf[2,] # by index, row 2
  age height weight  city
Anna 22   166    55 Espoo
> mydataf["Anna",] # by key
  age height weight  city
Anna 22   166    55 Espoo
> #getting the weight for everybody
> mydataf[,3] # by index, column 3
[1] 75 55
> mydataf[,"weight"] # by key
[1] 75 55
> mydataf$weight # by list key
[1] 75 55
```

Data Structures in R

Sorting the data frame's elements

```
mydataf <- data.frame(age=c(25,22,26,28),height=c(174,166,174,170),weight=c(75,55,60,60),  
city=c("Turku","Espoo","Kuopio","Helsinki"),row.names =c("Pekka","Anna","Ari","Tove"))  
mydataf
```

```
#order by height
```

```
order(mydataf$height)
```

```
#order by name
```

```
order(row.names(mydataf))
```

```
#order by height and weight
```

```
order(mydataf$height, mydataf$weight)
```

```
#order by height
```

```
mydataf[order(mydataf$height),]
```

```
#order by name
```

```
mydataf[order(row.names(mydataf)),]
```

```
#order by height and weight
```

```
mydataf[order(mydataf$height, mydataf$weight),]
```

```
#order by height and weight, both decreasing
```

```
mydataf[order(mydataf$height, mydataf$weight, decreasing = T),]
```

```
#order by decreasing height and increasing weight
```

```
mydataf[order(-mydataf$height, mydataf$weight),]
```

Data Structures in R

Changing the data frame's elements

```
> mydataf <- data.frame(age=c(25,22),height=c(174,166),weight=c(75,55),  
city=c("Turku","Espoo"),row.names =c("Pekka","Anna"))
```

```
> mydataf
```

```
  age height weight city  
Pekka 25  174   75 Turku  
Anna  22  166   55 Espoo
```

```
> mydataf <- cbind(mydataf,course=c("Math","Art")) # adding a column
```

```
> mydataf
```

```
  age height weight city course  
Pekka 25  174   75 Turku  Math  
Anna  22  166   55 Espoo  Art
```

```
> mydataf <- data.frame(mydataf, hobby=c("walking","reading")) # adding a column
```

```
> mydataf
```

```
  age height weight city course hobby  
Pekka 25  174   75 Turku  Math walking  
Anna  22  166   55 Espoo  Art reading
```

```
> mydataf <- rbind(mydataf,  
zed=data.frame(age=28,height=199,weight=115,city="Oulu",course="Sports",hobby="sleep")) # adding  
a row
```

```
> mydataf
```

```
  age height weight city course hobby  
Pekka 25  174   75 Turku  Math walking  
Anna  22  166   55 Espoo  Art reading  
zed   28  199  115 Oulu Sports  sleep
```

Data Structures in R

Operations on the data frame's elements

```
> mean(mydataf[,1]) # the mean of all ages
```

```
[1] 23.5
```

```
> mean(mydataf[,c("height","weight")]) # the mean of height, weight
```

```
height weight
```

```
170 65
```

```
> apply(mydataf,2,mean) # ERROR!
```

```
age height weight city
```

```
NA NA NA NA
```

Warning messages:

```
1: In mean.default(newX[, i], ...) :
```

```
argument is not numeric or logical: returning NA
```

```
2: In mean.default(newX[, i], ...) :
```

```
argument is not numeric or logical: returning NA
```

```
3: In mean.default(newX[, i], ...) :
```

```
argument is not numeric or logical: returning NA
```

```
4: In mean.default(newX[, i], ...) :
```

```
argument is not numeric or logical: returning NA
```

```
> apply(mydataf[,1:3],2,mean) # the mean of age, height, weight
```

```
age height weight
```

```
23.5 170.0 65.0
```

Data Structures in R

with() evaluate an expression in a data environment
with(data, expr, ...)

data data to use for constructing an environment, a list, a data frame, or an integer
expr expression to evaluate
... arguments to be passed to future methods

```
library(MASS)
```

```
anorex.1 <- glm(anorexia$Postwt ~ anorexia$Prewt + anorexia$Treat +  
offset(anorexia$Prewt), family = gaussian)  
summary(anorex.1)
```

```
with(anorexia, {  
  anorex.1 <- glm(Postwt ~ Prewt + Treat + offset(Prewt), family = gaussian)  
  summary(anorex.1)  
})
```

Data Structures in R

lapply, sapply applies a function over a list or vector

lapply returns a list of the same length as X, each element of which is the result of applying FUN to the corresponding element of X

sapply is a user-friendly version of lapply by default returning a vector or matrix if appropriate

```
lapply(X, FUN, ...)
```

```
sapply(X, FUN, ..., simplify = TRUE, USE.NAMES = TRUE)
```

X a vector (atomic or list) or an expressions vector

FUN the function to be applied to each element of X

... optional arguments to FUN

simplify if TRUE the result is simplified to a vector or matrix if possible

USE.NAMES if TRUE and if X is character, use X as names for the result unless it had names already

n number of replications

expr expression to evaluate repeatedly

```
at1 <- list(athlete="Johnson",coach="Earp",swimming=c(154,171,165), cycling=c(598,632,621),  
running=c(1046,1102,1095),wetsuit=c(T,F,T))  
# compute the list mean for each list element  
mean(at1)  
mean(at1$swimming) # one at a time...  
lapply(at1,mean)  
sapply(at1,mean)
```

Data Structures in R

Statistical functions

```
mydataf <- data.frame(age=c(25,22),height=c(174,166),weight=c(75,55),  
city=c("Turku","Espoo"),row.names =c("Pekka","Anna"))  
mydataf  
apply(mydataf, mean, na.rm=TRUE)
```

Other functions useful for sapply:

sd, var, min, max, med, range, and quantile

summary will return the Min. 1st Qu. Median Mean 3rd Qu. Max.

```
summary(mydataf)
```

fivenum will return Tukey's five number summary (minimum, lower-hinge, median, upper-hinge, maximum)

```
fivenum(mydataf[1:3])
```


Data Structures in R

string functions

```
# Concatenate strings
```

```
paste("a","b","c")
```

```
paste("a","b","c",sep="")
```

```
# Concatenate a vector of strings
```

```
myvec <- c("a","b","c")
```

```
paste(myvec)
```

```
paste(myvec,sep=" ",collapse="")
```

```
# extract part of the string
```

```
mystr <- "Hello world!"
```

```
substring(mystr, 7, 11)
```

```
# split a string into each character
```

```
mystr <- "Hello world!"
```

```
strsplit(mystr, "")
```

```
# split a string into pieces, using regex
```

```
mystr <- "Hello world!"
```

```
strsplit(mystr, " ")
```

```
strsplit(mystr, "\\s")
```

```
strsplit(mystr, "[\\seo]")
```

Data Structures in R

string functions

```
# find characters within the string, position + length  
regexpr("e", mystr)
```

```
# replace one substring within the string, once only  
sub("l", "+", mystr)
```

```
# replace one substring within the string, for all matches  
gsub("l", "+", mystr)
```

format formats an R object for pretty printing

```
format(x, trim = FALSE, digits = NULL, nsmall = 0L,  
       justify = c("left", "right", "centre", "none"),  
       width = NULL, na.encode = TRUE, scientific = NA,  
       big.mark = "", big.interval = 3L,  
       small.mark = "", small.interval = 5L,  
       decimal.mark = ".", zero.print = NULL, drop0trailing = FALSE, ...)
```

Data Structures in R

date functions

`Sys.Date()` # current date

`date()` # current date and time

Use the `format()` function to print dates

`%d` day of the month (0-31)

`%a` short week day

`%A` long weekday

`%m` month (00-12)

`%b` short month

`%B` long month

`%y` 2-digit year

`%Y` 4-digit year

`format(Sys.Date(), format="%d %B %Y")`

Data Structures in R

Data Type Conversion

Checking the data type

`is.numeric()`, `is.character()`, `is.vector()`, `is.matrix()`, `is.data.frame()`

Explicit conversion

`as.numeric()`, `as.character()`, `as.vector()`, `as.matrix()`, `as.data.frame()`

to from	vector	Factor	Matrix	Array	Dataframe	list
vector	<code>c(x,y)</code>	<code>as.factor(myvec, labels=c("L1", "L2", "L3"))</code> <code>as.factor(myvec, ordered=T, labels=c("L1", "L2", "L3"))</code>	<code>cbind(x,y)</code> <code>rbind(x,y)</code>	<code>array(x)</code>	<code>data.frame(x,y)</code>	<code>list(x)</code>
Factor		<code>ordered(f)</code>				<code>list</code>
Matrix	<code>as.vector(mymatrix)</code>			<code>array(x)</code>	<code>as.data.frame(mymatrix)</code>	<code>list</code>
Array						<code>list</code>
Dataframe	<code>mydataf[n,]</code>		<code>as.matrix(myframe)</code>			<code>list</code>
list	<code>unlist(mylist)</code>					

Data Structures in R

Data Structures in R

Frequencies and Crosstabs

`margin.table()` compute the sum of table entries for a given index

```
margin.table(x, margin=NULL)
```

x an array

margin index number (1 for rows, etc...)

```
m <- matrix(1:9,3)
```

```
m
```

```
# row sum
```

```
margin.table(m,1)
```

```
sum(m[1,]);sum(m[2,]);sum(m[3,])
```

```
apply(m, 1, sum)
```

```
# column sum
```

```
margin.table(m,2)
```

```
sum(m[,1]);sum(m[,2]);sum(m[,3])
```

```
apply(m, 2, sum)
```

```
# note: there are functions for row sum and column sum:
```

```
colSums(m)
```

```
rowSums(m)
```

```
rowMeans(m)
```

```
colMeans(m)
```

Data Structures in R

Frequencies and Crosstabs

`prop.table()` Express table entries as a fraction of the marginal table

```
prop.table(x, margin=NULL)
```

x table

margin index, or vector of indices

```
m <- matrix(1:9,3)
```

```
m
```

```
prop.table(m) # cell percentages
```

```
prop.table(m, 1) # row percentages
```

```
prop.table(m, 2) # column percentages
```

```
prop.table(m) # cell percentages
```

```
m / sum(m)
```

```
sweep(m,1, margin.table(m),"/")
```

```
prop.table(m, 1) # row percentages
```

```
m[1,]/sum(m[1,])
```

```
m[2,]/sum(m[2,])
```

```
m[3,]/sum(m[3,])
```

```
sweep(m,1, margin.table(m,1),"/")
```

```
prop.table(m, 2) # column percentages
```

```
m[,1]/sum(m[,1])
```

```
m[,2]/sum(m[,2])
```

```
m[,3]/sum(m[,3])
```

```
sweep(m,2, margin.table(m,2),"/")
```


Data Structures in R

`table()` Cross tabulation and table creation

```
table(..., exclude = if (useNA == "no") c(NA, NaN), useNA = c("no", "ifany", "always"), dnn =  
list.names(...), deparse.level = 1)
```

... one or more objects which can be interpreted as factors

`exclude` levels to remove from all factors in If set to `NULL`, it implies `useNA="always"`

`useNA` whether to include extra NA levels in the table

`dnn` the names to be given to the dimensions in the result (the `dimnames` names)

`deparse.level` controls how the default `dnn` is constructed. See details

`x` an arbitrary R object, or an object inheriting from class "table" for the `as.data.frame` method

`row.names` a character vector giving the row names for the data frame

`responseName` The name to be used for the column of table entries, usually counts

Data Structures in R

```
x <- sample(c("heads","tails"),5, replace=T)
x
fx <- factor(x)
fx
table(fx)
```

```
mtcars
?mtcars
is(mtcars)
names(mtcars)
dim(mtcars)
rownames(mtcars);colnames(mtcars)
dimnames(mtcars)
# how many cars for each Number of cylinders
table(mtcars$cyl,dnn = list("Number of forward cylinders"))
# how many cars for each Number of cylinders / Number of forward gears
table(mtcars$cyl,mtcars$gear,dnn = list("Number of cylinders","Number of forward
gears"))
# how many cars for each Number of cylinders / Number of forward gears / Transmission
table(mtcars$cyl,mtcars$gear,mtcars$am,dnn = list("Number of cylinders","Number of
forward gears","Transmission"))
```

Data Structures in R

`xtabs()` reate a contingency table from cross-classifying factors

```
xtabs(formula = ~., data = parent.frame(), subset, na.action, exclude = c(NA, NaN),  
drop.unused.levels = FALSE)
```

`formula` a formula object with the cross-classifying variables (separated by `+`) on the right hand side

`data` an optional matrix or data frame containing the variables in the formula

`subset` an optional vector specifying a subset of observations to be used

`na.action` a function which indicates what should happen when the data contain NAs

`exclude` a vector of values to be excluded when forming the set of levels of the classifying factors

`drop.unused.levels` a logical indicating whether to drop unused levels in the classifying factors

```
# convert from table to dataframe
```

```
hair.df=as.data.frame(HairEyeColor)
```

```
# convert from dataframe to table
```

```
xtabs(Freq~Hair+Eye+Sex,data=hair.df)
```

```
# crosstabulation of Hair and Eye
```

```
xtabs(Freq~Hair+Eye,data=hair.df)
```

```
# crosstabulation of Hair and Sex
```

```
xtabs(Freq~Hair+Sex,data=hair.df)
```

```
# crosstabulation of Eye and Sex
```

```
xtabs(Freq~Eye+Sex,data=hair.df)
```

Data Structures in R

`ftable()` create "flat" contingency tables

`ftable(x, ...)`

`x, ...` R objects which can be interpreted as factors

`exclude` values to use in the `exclude` argument of `factor` when interpreting non-factor objects

`row.vars` a vector of integers giving the numbers of the variables, or a character vector giving the names of the variables

`col.vars` a vector of integers giving the numbers of the variables, or a character vector giving the names of the variables

`HairEyeColor`

`dim(HairEyeColor)`

`dimnames(HairEyeColor)`

`rownames(HairEyeColor)`

`colnames(HairEyeColor)`

`# the first variable ($Hair) on the rows`

`ftable(HairEyeColor, row.vars = 1)`

`# the 2nd variable ($Eye) on the rows`

`ftable(HairEyeColor, row.vars = 2)`

`# the 3rd variable ($Sex) on the rows`

`ftable(HairEyeColor, row.vars = "Sex") # by name`

`# the first variable ($Hair) on the rows`

`# on the columns the 2nd and 3rd ($Eye, $Sex)`

`ftable(HairEyeColor, row.vars = 1, col.vars=c(2,3))`

`ftable(HairEyeColor, row.vars = "Hair", col.vars=c("Eye","Sex"))`

Data Structures in R

```
# the first variable ($Hair) on the rows
# on the columns the 3rd and 2nd ($Sex,$Eye )
ftable(HairEyeColor, row.vars = 1, col.vars=c(3,2))
ftable(HairEyeColor, row.vars = "Hair", col.vars=c("Sex","Eye"))

# the first and 2nd variables ($Hair,$Eye) on the rows
ftable(HairEyeColor, row.vars = 1:2)

# the first, 2nd and 3rd variables ($Hair,$Eye,$Sex) on the rows
ftable(HairEyeColor, row.vars = 1:3)
```

Data Structures in R

sweep return an array obtained from an input array by sweeping out a summary statistic

```
sweep(x, MARGIN, STATS, FUN="-", check.margin=TRUE, ...)
```

x an array

MARGIN a vector of indices giving the extents of x which correspond to STATS

STATS the summary statistic which is to be swept out

FUN the function to be used to carry out the sweep

check.margin If TRUE (the default), warn if the length or dimensions of STATS do not match the specified dimensions of x

... optional arguments to FUN

attitude

```
med.att <- apply(attitude, 2, median)
```

med.att

```
sweep(data.matrix(attitude), 2, med.att)# subtract the column medians
```

Data Structures in R

Attach a set of R objects to the search path

```
attach(what, pos = 2, name = deparse(substitute(what)), warn.conflicts = TRUE)
```

Arguments

what a data.frame, list, R data file or an environment

pos position in search() where to attach

name name to use for the attached database

warn.conflicts if true then it shows conflicts from attaching the database

Objects on *what* will be accessible directly through their names

Data Structures in R

```
mydataf <-  
data.frame(age=c(25,22,26,28),height=c(174,166,174,170),weight=c(75,55,60,60),city=c("Turku",  
"Espoo","Kuopio","Helsinki"),row.names =c("Pekka","Anna","Ari","Tove"))  
mydataf  
ls()  
search()  
attach(mydataf)  
ls()  
search()  
detach(mydataf)  
ls()  
search()  
rm(mydataf)  
ls()  
search()
```


Data Structures in R

```
> mydataf <-  
data.frame(age=c(25,22,26,28),height=c(174,166,174,170),weight=c(75,55,60,60),city=c("Turku","Espoo",  
"Kuopio","Helsinki"),row.names =c("Pekka","Anna","Ari","Tove"))  
> ls()  
[1] "mydataf"  
> search()  
[1] ".GlobalEnv"      "package:stats"   "package:graphics"  
[4] "package:grDevices" "package:utils"   "package:datasets"  
[7] "package:methods" "Autoloads"       "package:base"  
> attach(mydataf)  
> ls()  
[1] "mydataf"  
> search()  
[1] ".GlobalEnv"      "mydataf"         "package:stats"  
[4] "package:graphics" "package:grDevices" "package:utils"  
[7] "package:datasets" "package:methods" "Autoloads"  
[10] "package:base"  
> detach(mydataf)  
> ls()  
[1] "mydataf"  
> search()  
[1] ".GlobalEnv"      "package:stats"   "package:graphics"  
[4] "package:grDevices" "package:utils"   "package:datasets"  
[7] "package:methods" "Autoloads"       "package:base"  
> rm(mydataf)  
> ls()  
character(0)  
> search()  
[1] ".GlobalEnv"      "package:stats"   "package:graphics"  
[4] "package:grDevices" "package:utils"   "package:datasets"  
[7] "package:methods" "Autoloads"       "package:base"
```

Data Structures in R

Accessing attached elements from a dataframe

```
mydataf <-  
data.frame(age=c(25,22,26,28),height=c(174,166,174,170),weight=c(75,55,60,60),city=c("Turku",  
"Espoo","Kuopio","Helsinki"),row.names =c("Pekka","Anna","Ari","Tove"))
```

```
> mydataf$weight
```

```
[1] 75 55
```

```
> weight
```

```
Error: object 'weight' not found
```

```
> attach(mydataf) # attach mydataf to the search path
```

```
> weight
```

```
[1] 75 55
```

```
> city
```

```
[1] Turku Espoo
```

```
Levels: Espoo Turku
```

```
> detach(mydataf) # detach mydataf from the search path
```

```
> weight
```

```
Error: object 'weight' not found
```

Data Structures in R

Accessing attached elements from a dataset

```
data()  
ToothGrowth  
names(ToothGrowth) # len supp dose  
supp # error  
ToothGrowth$supp  
attach(ToothGrowth)  
supp  
detach(ToothGrowth)  
supp
```

Data Structures in R

References/to learn more:

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Rob Kabacoff
<http://www.statmethods.net/input/datatypes.html>

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<http://wiener.math.csi.cuny.edu/st/stRmanual/>

Displaying data on R

dir() and **list.files()** lists the files in a directory

```
list.files(path = ".", pattern = NULL, all.files = FALSE, full.names = FALSE, recursive = FALSE, ignore.case = FALSE)
```

```
dir(path = ".", pattern = NULL, all.files = FALSE, full.names = FALSE, recursive = FALSE, ignore.case = FALSE)
```

path vector of full path names; the default is the working directory `getwd()`

pattern match an optional regular expression. Not wildcards!

all.files If TRUE, all file names will be returned, even hidden and system files or not visible for other reason

full.names If TRUE, the directory path is prepended to the file names

recursive logical If TRUE, the listing will recurse into sub-directories

ignore.case If TRUE, the search will be case-insensitive. It's always case-insensitive on Windows

Note:

`R.home()` # the path of R's home directory

Displaying data on R

```
dir()
```

```
list.files()
```

```
dir(pattern="^a") # list all files that start with "a"
```

```
dir(pattern="\.R$") # list all files that end with ".R"
```

```
list.files(path = "c:/temp") # list all files from c:\temp
```

```
list.files(path = "c:/temp", all.files =TRUE) # list all files from c:\temp, even not visible files
```

Displaying data on R

`file.show()` display one or more files, usually text files

```
file.show(..., header = rep("", nfiles), title = "R Information", delete.file = FALSE, pager =  
getOption("pager"), encoding = "")
```

... one or more character vectors containing the names of the files

header character vector (of the same length as the number of files specified in ...) giving a header for each file

title an overall title for the display

delete.file should the files be deleted after display? Used for temporary files

pager the pager to be used

encoding character string giving the encoding to be assumed for the file(s)

`dir()`

`file.show(".Rhistory")`

Displaying data on R

print displays values, expressions or variables

```
print(123) # displaying a number
print("abc") # displaying a string
print(123+567) # displaying an expression
```

cat concatenates and outputs objects
By default it will output to the Console (screen)

```
cat(... , sep = " ", fill = FALSE, labels = NULL)
```

... R objects

sep a character vector of strings to append after each element

fill a logical or (positive) numeric controlling how the output is broken into successive lines. If FALSE (default), only newlines created explicitly by "\n" are printed. Otherwise, the output is broken into lines with print width equal to the option width if fill is TRUE, or the value of fill if this is numeric. Non-positive fill values are ignored, with a warning.

labels character vector of labels for the lines printed. Ignored if fill is FALSE.

```
cat(5,"*",12,"=",5*12,"\n")
cat(5,"*",12,"=",5*12,"\n", sep = "_")
cat(5,"*",12,"=",5*12,"\n", sep = " ")
cat(rep("0123456789",20), fill = T, width=3, labels = c("line 1","line 2","line 3","line 4"))
```


Displaying data on R

paste concatenate vectors to strings

```
paste(..., sep = " ", collapse = NULL)
```

... one or more R objects, to be converted to character vectors

sep a character string to separate the terms. Not NA_character_

collapse an optional character string to separate the results. Not NA_character_

```
paste(1:3) # same as as.character(1:3)
```

```
paste(1:3, sep = "") # separate terms - only 1 term, nothing to do
```

```
paste(c("one", "two", "three"))
```

```
paste(c("one", "two", "three"), sep = "") # separate terms - only 1 term, nothing to do
```

```
paste(c("one", "two", "three"), collapse="****") # separate results OK
```

```
paste(1,2,3)
```

```
paste(1,2,3, sep = "") # separate terms OK
```

```
paste("one", "two", "three")
```

```
paste("one", "two", "three", sep = "") # separate terms OK
```

```
paste("one", "two", "three", collapse="****") # separate results - only 1 result, nothing to do
```

Displaying data on R

Write write data to a connection or file

```
write(x, file = "data", ncolumns = if(is.character(x)) 1 else 5, sep = " ")
```

Arguments

x the data to be written out

file If "", print to the standard output connection

ncolumns the number of columns to write the data in

sep a string used to separate columns. Using sep = "\t" gives tab delimited output; default is " "

```
write("hello", file="")
```

```
write(1:10, file="")
```

```
write(c("one","two","three"), file="")
```

```
write(1:10, file="", sep = " ")
```

```
write(c("one","two","three"), file="", sep = " ")
```

```
write(1:10, file="", ncolumns = 3)
```

```
write(c("one","two","three"), file="", ncolumns = 2)
```

Redirecting data on R

sink redirects R output to a connection

`sink.number()` displays the number of current redirections

```
sink(file = NULL, append = FALSE, type = c("output", "message"),  
      split = FALSE)
```

```
sink.number(type = c("output", "message"))
```

`file` a connection or a file name or `NULL` to stop

`append` If `TRUE`, output will be appended, otherwise, it will be overwritten

`type` either output stream or the messages stream

`split` if `TRUE`, output will be sent to both new and old streams

```
sink("output.txt") # creates a file to store the output  
# the output will now be sent to file "output.txt"  
print("Hello world!")  
print(123*pi)  
sink() # stop sending the output to the file
```

Editing data on R

edit invokes a text editor on an R object

```
edit(name = NULL, file = "", title = NULL, editor = getOption("editor"), ...)
```

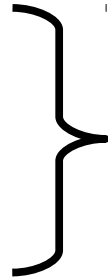
```
vi(name = NULL, file = "")
```

```
emacs(name = NULL, file = "")
```

```
pico(name = NULL, file = "")
```

```
xemacs(name = NULL, file = "")
```

```
xedit(name = NULL, file = "")
```



Invoking a specific editor

name R object or file name to edit

file file name

title a title for the object

editor text editor to use

... further arguments to be passed to or from methods

Editing data on R

```
# open a file
dir()
edit(file="output.txt")

v1 <- c(734, 985, 43, 952)
v2 <- c("Helsinki", "Tampere", "Turku")
v3 <- c(T, F, F, F, T, F, T, F, T, T)
myarray <- array(c(56, 67, 174, 166, 75, 55, 77, 70, 64, 77, 178, 170, 78, 59, 63, 61), c(2, 4, 2))
dimnames(myarray) = list(c("men", "women"), c("age", "height", "weight", "pulse"),
c("city", "countryside"))
mydataf <-
data.frame(age=c(25, 22, 26, 28), height=c(174, 166, 174, 170), weight=c(75, 55, 60, 60), city=c("Turku", "
Espoo", "Kuopio", "Helsinki"), row.names = c("Pekka", "Anna", "Ari", "Tove"))
mymatrix <- matrix(1:6*10, 3, 2)

# open the R Editor with the code to define the variables
edit(v1)
edit(v2)
edit(v3)
edit(myarray)

# open the R Data Editor
edit(mydataf)
edit(mymatrix)
```

Editing data on R

Fix an R object

fix invokes edit on x and then updates x in the user's workspace

fix(x, ...)

x the name of an R object

... arguments to pass to edit

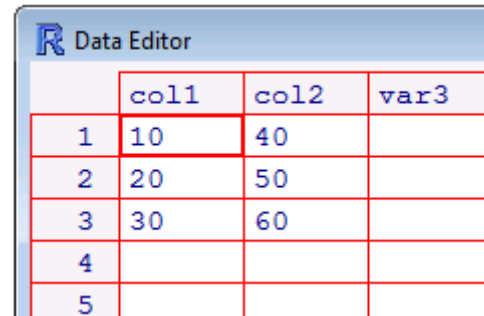
Editing data on R

```
> mymatrix <- matrix(1:6*10,3,2)
```

```
> mymatrix
```

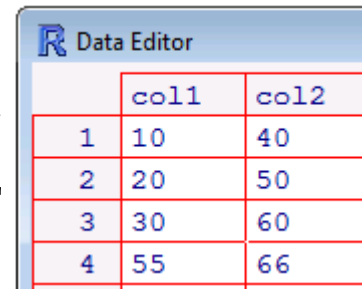
```
  [,1] [,2]  
[1,] 10  40  
[2,] 20  50  
[3,] 30  60
```

```
> edit(mymatrix)
```



	col1	col2	var3
1	10	40	
2	20	50	
3	30	60	
4			
5			

```
  col1 col2  
[1,] 10  40  
[2,] 20  50  
[3,] 30  60  
[4,] 55  66
```



	col1	col2
1	10	40
2	20	50
3	30	60
4	55	66

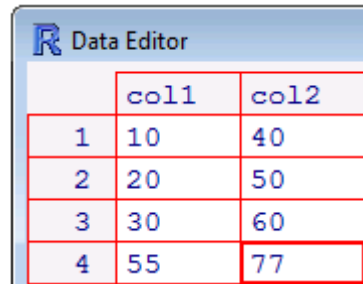
```
> mymatrix
```

```
  [,1] [,2]  
[1,] 10  40  
[2,] 20  50  
[3,] 30  60
```

```
> fix(mymatrix)
```

```
> mymatrix
```

```
  col1 col2  
[1,] 10  40  
[2,] 20  50  
[3,] 30  60  
[4,] 55  77
```



	col1	col2
1	10	40
2	20	50
3	30	60
4	55	77

Data input on R

Reading input from the console

```
> mydata1 <- scan()
```

```
1: 1
```

```
2: 2
```

```
3: 3
```

```
4:
```

```
Read 3 items
```

```
> mydata1
```

```
[1] 1 2 3
```

```
> is(mydata1)
```

```
[1] "numeric" "vector"
```

```
> mydata1 <- scan()
```

```
1: 1 2 3
```

```
4:
```

```
Read 3 items
```

```
> mydata1
```

```
[1] 1 2 3
```

```
> is(mydata1)
```

```
[1] "numeric" "vector"
```

Type

1 Enter 2 Enter 3 Enter Enter

Type

1 Space 2 Space 3 Enter Enter

Same input

Data input on R

Trying to enter text as input:

```
> mydata1 <- scan()
```

```
1: a
```

```
1: b
```

```
Error in scan(file, what, nmax, sep, dec, quote, skip,  
nlines, na.strings, :  
scan() expected 'a real', got 'a'
```

The default input data type is numeric, solution: use the *what* argument

Useful arguments for console input

what input data type logical, integer, numeric, complex, character

nmax maximum number of input values

nlines maximum number of lines of data

na.strings vector of elements interpreted as missing (NA) values

Data input on R

what input data type logical, integer, numeric, complex, character

```
> mydata1 <- scan(what=character())
```

```
1: a b c
```

```
4:
```

```
Read 3 items
```

```
> mydata1
```

```
[1] "a" "b" "c"
```

```
> mydata1 <- scan(what=character())
```

```
1: "one two" "three four"
```

```
3:
```

```
Read 2 items
```

```
> mydata1
```

```
[1] "one two" "three four"
```

Quotes allow space on strings

```
> mydata1 <- scan(what=logical())
```

```
1: T
```

```
2: F
```

```
3: TRUE
```

```
4: FALSE
```

```
5:
```

```
Read 4 items
```

```
> mydata1
```

```
[1] TRUE FALSE TRUE FALSE
```

Logical will not accept 1 or 0

```
> mydata1 <- scan(what=complex())
```

```
1: -6576.9898
```

```
2: 3.54i
```

```
3: -5.543-.68767i
```

```
4:
```

```
Read 3 items
```

```
> mydata1
```

```
[1] -6576.990+0.00000i 0.000+3.54000i
```

```
-5.543-0.68767i
```

5i and 5*i are not the same

```
> mydata1 <- scan()
```

```
1: 25*pi
```

```
1: 15
```

```
Error in scan(file, what, nmax, sep, dec, quote, skip, nlines, na.strings, :
```

```
scan() expected 'a real', got '25*pi'
```

```
> mydata1 <- scan()
```

```
1: sqrt(2)
```

```
1: 5
```

```
Error in scan(file, what, nmax, sep, dec, quote, skip, nlines, na.strings, :
```

```
scan() expected 'a real', got 'sqrt(2)'
```

Constants and functions are not allowed

Data input on R

nmax maximum number of input values

nlines maximum number of lines of data

```
> mydata1 <- scan(nmax=4)
1: 9
2: 8
3: 7
4: 6
Read 4 items
> mydata1
[1] 9 8 7 6
> mydata1 <- scan(nmax=4)
1: 22 33 44 55 66 77 88 99
Read 4 items
> mydata1
[1] 22 33 44 55
```

```
> mydata1 <- scan(nlines=4)
1: 11
2: 22
3: 33
4: 44
Read 4 items
> mydata1
[1] 11 22 33 44
> mydata1 <- scan(nlines=4)
1: 1 2 3 4 5 6 7 8
9: 99 88 77
12: 66 55 44
15: 33 22 11
Read 17 items
> mydata1
[1] 1 2 3 4 5 6 7 8 99 88 77 66 55 44 33 22 11
```

Data input on R

na.strings vector of elements interpreted as missing (NA) values

```
> mydata1 <- scan()  
1: 1 2 NA 3 NA NA 4 5  
9:  
Read 8 items  
> mydata1  
[1] 1 2 NA 3 NA NA 4 5  
> mydata1 <- scan(na.strings="*")  
1: 9 8 * * 7 *  
7:  
Read 6 items  
> mydata1  
[1] 9 8 NA NA 7 NA
```

Data input on R

Reading input from the the web

```
# read a text file from the web to a string
con <- url("http://www.rni.helsinki.fi/~pek/r-koulutus/e2.dat") # open a connection
mytxt <- readLines(con) # read the file
close(con) # close the connection
mytxt
```

```
# execute code from the web
source("http://www.rni.helsinki.fi/~pek/r-koulutus/hello.R")
```

```
# download a file from the web
download.file("http://www.rni.helsinki.fi/~pek/r-koulutus/hello.R",destfile="hello.R")
download.file("http://www.rni.helsinki.fi/~pek/r-koulutus/e2.dat",destfile="e2.dat")
dir() # show the files on the working directory
```

```
# reading a data frame from the web
mydf <- read.table(url('http://www.rni.helsinki.fi/~pek/s-tools/e1.dat'))
mydf
class(mydf)
```

Data input on R

Reading input from a file

Comma-separated values (CSV) files

Text files containing data, each line of text is a row (record) of data and within each line, each column (field) of data is separated by a comma. Usually the first line has the column names.

Rules

- Records are separated by end-of-line characters
- Fields are separated by commas
- Leading or trailing spaces are part of the field data
- Commas within fields are enclosed with double-quotes
- double-quotes within fields are replaced by a pair of double-quotes
- The first line might have the column names

Exceptions

- Line breaks can be placed inside double quotes
- If the comma is used as a decimal sign then semicolons will separate the columns
- Some implementations remove leading or trailing spaces
- Some implementations enclose fields with leading or trailing spaces, within double-quotes
- Some implementations enclose all fields within double-quotes

Data input on R

Reading input from a file

Tab delimited values (TAB) files

Text files containing data, each line of text is a row (record) of data and within each line, each column (field) of data is separated by a tab (ASCII 10). Usually the first line has the column names.

Rules

- Records are separated by end-of-line characters
- Fields are separated by tab
- Leading or trailing spaces are part of the field data
- There are no tabs within fields
- Line breaks can be placed within fields
- The first line might have the column names

Data input on R

Reading input from a file

Fixed Width Text Files

Text files containing data, each line of text is a row (record) of data and within each line, each column (field) of data has a constant, pre-defined number of characters. Usually the first line has the column names.

Rules

- Records are separated by end-of-line characters
- Fields have a fixed size
- Leading or trailing spaces are used as padding, unless another character is chosen for that purpose
- Line breaks can be placed within fields
- The first line might have the column names

Data input on R

Reading input from a file

File "hello.R" from the previous example should be on the working directory, "e2.dat" too.

```
# To read and execute it:  
source("hello.R")  
# To open a window for choosing a file to open:  
source( file.choose() )  
  
# read a text file from a file to a string  
con <- file("e2.dat") # open a connection  
mytxt <- readLines(con) # read the file  
close(con) # close the connection  
mytxt
```

Data input on R

Reading input from a file

scan()

Useful arguments for file input

what input data type logical, integer, numeric, complex, character, list

nmax maximum number of input values

nlines maximum number of lines of data

na.strings vector of elements interpreted as missing (NA) values

sep character that delimits fields, the default is white-space or end-of-line (unless within quotes)

dec decimal point character because of "." vs ",",

skip the number of lines to skip from the beginning of the file

blank.lines.skip if true then blank lines are skipped

comment.char a character that marks comment lines, which are skipped

Data input on R

Reading input from a file

```
> mytxt <- scan("e2.dat") # read the file
```

```
Error in scan(file, what, nmax, sep, dec, quote, skip, nlines, na.strings, :  
scan() expected 'a real', got '#'
```

```
> mytxt <- scan("e2.dat", skip=2) # read the file, skip the 1st 2 lines
```

```
Read 14 items
```

```
> mytxt
```

```
[1] 46 148 54 182 48 173 50 166 44 109 42 141 52 166
```

```
> mytxt <- scan("e2.dat", what = list("", ""), skip=2)
```

```
Read 7 records
```

```
> mytxt
```

```
[[1]]
```

```
[1] "46" "54" "48" "50" "44" "42" "52"
```

```
[[2]]
```

```
[1] "148" "182" "173" "166" "109" "141" "166"
```

Data input on R

Reading input from a file

sep character that delimits fields, the default is white-space or end-of-line (unless within quotes)

blank.lines.skip if true then blank lines are skipped

comment.char a character that marks comment lines, which are skipped

```
> cat("12:34:56:78:90",file="numbers.txt") # create a text file with text "12:34:56:78:90"
```

```
> edit(file="numbers.txt")
```

```
> mytxt <- scan("numbers.txt", sep=":") # read the file
```

```
Read 5 items
```

```
> mytxt
```

```
[1] 12 34 56 78 90
```

```
>
```

```
> cat("12:34\n56:78:90",file="numbers.txt") # end-of-line also works
```

```
> edit(file="numbers.txt")
```

```
> mytxt <- scan("numbers.txt", sep=":") # read the file
```

```
Read 5 items
```

```
> mytxt
```

```
[1] 12 34 56 78 90
```

Data input on R

Reading input from a file

```
> # suppose that % is the symbol for lines with comments
> cat("12:ab\n% this is a comment between lines of data\n56:cd",file="numbers.txt")
> mytxt <- scan("numbers.txt", sep=":", what = list("", "")) # read the file
```

Read 3 records

Warning message:

```
In scan(file, what, nmax, sep, dec, quote, skip, nlines, na.strings, :
  number of items read is not a multiple of the number of columns
```

```
> mytxt
```

```
[[1]]
```

```
[1] "12"
```

```
[2] "% this is a comment between lines of data"
```

```
[3] "cd"
```

```
[[2]]
```

```
[1] "ab" "56" ""
```

```
> # the comment was read as data, that is wrong
```

```
> #this is the correct way
```

```
> mytxt <- scan("numbers.txt", sep=":", what = list("", ""), comment.char="%") # read the file
```

Read 2 records

```
> mytxt
```

```
[[1]]
```

```
[1] "12" "56"
```

```
[[2]]
```

```
[1] "ab" "cd"
```

Data input on R

Reading input from a file

read.table()

header if true, the first line of the file contains the names of the variables

sep character that delimits fields, the default is white-space or end-of-line (unless within quotes)

dec decimal point character because of "." vs ",",

row.names a vector with the row names or the number of the column with the row names or the name of the column with the row names

col.names a vector of optional names for the variables ???

na.strings vector of elements interpreted as missing (NA) values

nrows maximum number of rows read

blank.lines.skip if true then blank lines are skipped

comment.char a character that marks comment lines, which are skipped

Data input on R

Reading input from a file

read.table() Reads a text file in table format and creates a data frame from it

<code>read.csv(file, header = TRUE, sep = ",", quote="\"", dec=".", fill = TRUE, comment.char="", ...)</code>	read comma separated value files (CSV)
<code>read.csv2(file, header = TRUE, sep = ";", quote="\"", dec=",", fill = TRUE, comment.char="", ...)</code>	CSV with comma as decimal point and a semicolon as field separator
<code>read.delim(file, header = TRUE, sep = "\t", quote="\"", dec=".", fill = TRUE, comment.char="", ...)</code>	read TAB delimited files (TAB)
<code>read.delim2(file, header = TRUE, sep = "\t", quote="\"", dec=",", fill = TRUE, comment.char="", ...)</code>	TAB with comma as decimal point
<code>read.fwf(file, widths, header = FALSE, sep = "\t", skip = 0, row.names, col.names, n = -1, buffersize = 2000, ...)</code>	read a table of fixed width formatted data

Data input on R

```
mydataf <- data.frame(age=c(25,22,26,28),height=c(174,166,174,170),weight=c(75,55,60,60),
city=c("Turku","Espoo","Kuopio","Helsinki"),row.names =c("Pekka","Anna","Ari Wan","Tove"))
mydataf
```

```
# saving with default values: separator = space, strings within "" and row names on the 1st line
write.table(mydataf, file = "z.txt")
edit(file="z.txt")
mydataf2 <- read.table("z.txt")
mydataf2
```

```
# saving as CSV
write.csv(mydataf, file = "z.csv")
edit(file="z.csv")
mydataf2 <- read.table("z.csv")
mydataf2
mydataf2 <- read.csv("z.csv")
mydataf2
```

```
# saving as TAB-delimited
write.table(mydataf, file = "z.tab", sep="\t")
edit(file="z.tab")
mydataf2 <- read.table("z.tab", sep="\t")
mydataf2
```

```
# saving as TAB-delimited, no "", no row names
write.table(mydataf, file = "z.tab", sep="\t",quote=F,row.names=F)
edit(file="z.tab")
mydataf2 <- read.table("z.tab", sep="\t",quote="")
mydataf2
```


Data input on R

read.ftable(), **write.ftable()** read, write "flat" contingency tables

Usage

```
read.ftable(file, sep = "", quote = "\"", row.var.names, col.vars, skip = 0)
```

```
write.ftable(x, file = "", quote = TRUE, append = FALSE, digits = getOption("digits"))
```

file either a character string naming a file or a connection which the data are to be read from or written to

sep character that delimits fields, the default is white-space or end-of-line (unless within quotes)

quote a character string giving the set of quoting characters for read.ftable

row.var.names a character vector with the names of the row variables

col.vars a list giving the names and levels of the column variables

skip the number of lines of the data file to skip before beginning to read data

x an object of class "ftable"

append If TRUE, the output from write.ftable is appended to the file

digits an integer giving the number of significant digits

Data input on R

Write an object to a file in ASCII format or read an object from a file

dget() and dput()

dget(filename) reads an R object from file "filename"

dput(obj, filename) writes an object "obj" to a file "filename", in ASCII format

```
> mydataf <- data.frame(age=c(25,22),height=c(174,166),weight=c(75,55),  
city=c("Turku","Espoo"),row.names =c("Pekka","Anna"))
```

```
> dput(mydataf,"mydf.dat")
```

```
> mydataf2 <- dget("mydf.dat")
```

```
> mydataf2 == mydataf
```

```
   age height weight city  
Pekka TRUE  TRUE  TRUE TRUE  
Anna  TRUE  TRUE  TRUE TRUE
```

Data input on R

`dump(list, file = "dumpdata.R", append = FALSE, control = "all", envir = parent.frame(), evaluate = TRUE)`

list vector with names of one or more R objects to be dumped.

file either a character string naming a file or a connection. "" indicates output to the console.

append if TRUE and file is a character string, output will be appended to file; otherwise, it will overwrite the contents of file.

`source()` reads R code from a file or a connection

`source(file, local = FALSE, echo = verbose, print.eval = echo, verbose = getOption("verbose"), prompt.echo = getOption("prompt"), max.deparse.length = 150, chdir = FALSE, encoding = getOption("encoding"), continue.echo = getOption("continue"), skip.echo = 0, keep.source = getOption("keep.source"))`

file a connection or a character string giving the pathname of the file or URL to read from

echo if TRUE, each expression is printed after parsing, before evaluation

print.eval if TRUE, the result of `eval(i)` is printed for each expression `i`; defaults to the value of `echo`

verbose if TRUE, more diagnostics (than just `echo = TRUE`) are printed during parsing and evaluation of input, including extra info for each expression

prompt.echo character; gives the prompt to be used if `echo = TRUE`

encoding The encoding(s) to be assumed when file is a character string: see file

skip.echo if `echo = TRUE`, how many lines to skip from the beginning

Data input on R

```
a <- 543.86
dump(a, "test_a.R") # error!
dump(ls(pattern="a"), "test_a.R") # works...
dir(pattern="test")
ls()
rm(a)
a
ls()
source("test_a.R")
a
ls()
```

```
# to choose a file interactively:
source(file.choose())
```

Data input on R

```
mydataf <-  
data.frame(age=c(25,22,26,28),height=c(174,166,174,170),weight=c(75,55,60,60),city=c("Turku",  
"Espoo","Kuopio","Helsinki"),row.names =c("Pekka","Anna","Ari","Tove"))  
dump(ls("mydataf"), file ="test_mydataf.R") # error!  
ls()  
search()  
attach(mydataf)  
ls()  
search()  
dump(ls("mydataf"), file ="test_mydataf.R")  
dir(pattern="test")  
detach(mydataf)  
rm(mydataf)  
ls()  
search()  
source("test_mydataf.R")  
ls()  
search() # "age"  "city"  "height" "weight"!  
mydataf # got attached!  
edit(file="test_mydataf.R") # this is why!
```

Data input on R

Write write data to a connection or file

```
write(x, file = "data", ncolumns = if(is.character(x)) 1 else 5, sep = " ")
```

Arguments

x the data to be written out

file If "", print to the standard output connection

ncolumns the number of columns to write the data in

sep a string used to separate columns. Using sep = "\t" gives tab delimited output; default is " "

```
write("hello", file="hello.txt")
```

```
write(1:10, file="1to10.txt")
```

```
write(c("one","two","three"), file="123.txt")
```

```
write(1:10, file="1to10b.txt", sep = "")
```

```
write(c("one","two","three"), file="123b.txt", sep = "")
```

```
write(1:10, file="1to10c.txt", ncolumns = 3)
```

```
write(c("one","two","three"), file="123c.txt", ncolumns = 2)
```

```
myvector<-c(1,2,3,4,5)
```

```
write(myvector,"myvector.txt")
```

```
mymatrix<-matrix(1:9,ncol=3,byrow=T)
```

```
write(t(mymatrix),"mymatrix.txt",ncol=ncol(mymatrix))
```

Data input on R

cat concatenates and outputs objects, also to a file
By default it will output to the Console (screen)

```
cat(... , file = "", sep = " ", fill = FALSE, labels = NULL, append = FALSE)
```

... R objects

file file name to get the output

sep a character vector of strings to append after each element

fill a logical or (positive) numeric controlling how the output is broken into successive lines. If FALSE (default), only newlines created explicitly by "\n" are printed. Otherwise, the output is broken into lines with print width equal to the option width if fill is TRUE, or the value of fill if this is numeric. Non-positive fill values are ignored, with a warning.

labels character vector of labels for the lines printed. Ignored if fill is FALSE.

append if TRUE, the output is appended at the end of the file

```
cat("Hello world!", file = "cattest.txt")
```

```
edit(file="cattest.txt")
```

```
cat("Hello aliens!", file = "cattest.txt", append = TRUE)
```

```
edit(file="cattest.txt")
```

Data input on R

save() saves R objects

```
save(..., list = character(0L),  
      file = stop("'file' must be specified"),  
      ascii = FALSE, version = NULL, envir = parent.frame(),  
      compress = !ascii, eval.promises = TRUE, precheck = TRUE)
```

... the names of the objects to be saved

list A vector containing the names of objects to be saved

file a connection or the name of the file where the data will be saved

ascii if TRUE, an ASCII representation of the data is written

compress if TRUE, the file is compressed

precheck if TRUE, the existence of the objects is checked before saving

load() loads datasets saved with save()

```
v1 <- c(734, 985, 43, 952)
```

```
v2 <- c("Helsinki", "Tampere", "Turku")
```

```
save(v1, v2, file = "v1v2.Rdata")
```

```
#remove all objects
```

```
rm(list=ls(all=TRUE))
```

```
v1;v2
```

```
load("v1v2.Rdata")
```

```
v1;v2
```

```
save(v1, v2, file = "v1v2.Rdata", ascii = TRUE)
```

```
edit(file="v1v2.Rdata")
```


Data input on R

References/to learn more:

The R book

Michael J. Crawley pp 97

2014 John Wiley & Sons Ltd

Basic statistics using R pp. 57

Jarno Tuimala (CSC) and Dario Greco (HY)

<http://www.csc.fi/english/csc/courses/archive/R2008s>

Statistics: an introduction using R

Michael J. Crawley pp 286

2012 John Wiley & Sons Ltd

Statistics with R

Vincent Zoonekynd, pp 91

http://zoonek2.free.fr/UNIX/48_R/all.html

Aprendizaje del software estadístico R: un entorno para simulación y computación estadística

Prof. Alberto Muñoz García

Departamento de Estadística

Universidad Carlos III de Madrid

<http://ocw.uc3m.es/estadistica/aprendizaje-del-software-estadistico-r-un-entorno-para-simulacion-y-computacion-estadistica/resolveUId/81279218bad3be4326b943c4c3e62e4d>

Introductory Statistics with R

Peter Dalgaard, pp 46

2014 Springer

Software Tools, Part 1: introduction to R software

Petri Koistinen

<http://www.rni.helsinki.fi/~pek/s-tools/data-input.r>

Quick-R

Rob Kabacoff

<http://www.statmethods.net/input/index.html>

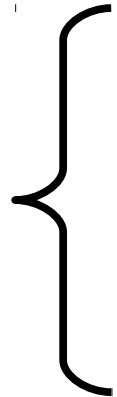
The Stem and Tendril simplified R manual

Professors Franzblau, Poje and Verzani of the College of Staten Island

<http://wiener.math.csi.cuny.edu/st/stRmanual/>

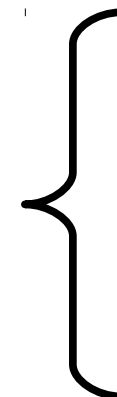
Control Flow

Conditional
statements



if
ifelse
switch

Loop
statements



for
while
repeat

Control Flow

if - Conditional statement

if(condition) expression # if the condition is true then the expression will execute
if(condition) expression else alternate.expression # if the condition is true then the expression will execute, otherwise the alternate.expression will execute

condition - a logical result, not NA. Only the first element of a vector is considered.

expression, alternate.expression - Either a simple expression, one command only, or a so called compound expression { expression1 ; expression2 } or:

```
{  
expression1  
expression2  
}
```

To separate several expressions can be done with ; or newline but newline is more clear and understandable.

A newline before an else statement will cause an error.

```
> if (5 > 3) print ("OK") # this always returns "OK"  
[1] "OK"
```

Control Flow

This code should be tested on the R editor, selecting a block if code + ctrl r

```
# get a random integer number from 1 to 10, say if it is greater than 5 or not
if (sample(1:10, 1) > 5) print ("random number > 5") else print ("random number < 5")
```

```
# same as above but in separate lines of code
if (sample(1:10, 1) > 5)
print ("random number > 5") else
print ("random number < 5")
```

```
# get a random integer number from 1 to 10, if greater than 5 then show its square value
# otherwise show it multiplied by 4
myrnd <- sample(1:10, 1)
if (myrnd > 5) {myrnd2 <- myrnd^2;print (myrnd2)} else {myrnd2 <- myrnd*4;print (myrnd2)}
```

```
# same as above but in separate lines of code
myrnd <- sample(1:10, 1)
if (myrnd > 5)
{
  myrnd2 <- myrnd^2
  print (myrnd2)
} else
{
  myrnd2 <- myrnd*4
  print (myrnd2)
}
```

Control Flow

"If" can be used as a function within expressions:

```
> x <- 5  
> strwhartx <- if(is.complex(x)) "imaginary" else "real"  
> strwhartx  
[1] "real"
```

Control Flow

Conditional Element Selection

ifelse - returns 1 out of 2 elements, depending on a logical condition.

```
ifelse(condition, condition.true.expression, condition.false.expression)
```

```
> x <- 5-7i
```

```
> ifelse(is.complex(x), "imaginary", "real") # if x is complex, return "imaginary", otherwise "real"
```

```
[1] "imaginary"
```

```
> x <- 16
```

```
> ifelse(is.complex(x), "imaginary", "real") # if x is complex, return "imaginary", otherwise "real"
```

```
[1] "real"
```

Control Flow

Ifelse on multiple elements

Ifelse can affect elements from vectors, matrices, etc... directly, with no need for loops or for "apply" functions

```
# get the sign (-1, 0, 1) from numbers
> ifelse(myvec >0, 1, ifelse(myvec <0, -1, 0))
[1] -1 -1 -1 0 1 1 1
```

```
# replace numbers with a word
# NA MISSING
# Inf INFINITY
# >0 POSITIVE
# <0 NEGATIVE
# =0 ZERO
myvec <- c(-3:3, Inf, NA)
myvec
myvec <- sample(myvec) # random permutation
myvec
myvec.str <- ifelse(is.na(myvec),"MISSING",
  ifelse(is.infinite(myvec),"INFINITY",
    ifelse(myvec>0,"POSITIVE",
      ifelse(myvec<0,"NEGATIVE",
        "ZERO"
      )))
myvec.str
```

Control Flow

switch - choose from several results depending upon an expression

It is not a statement like the C or C++ switch statement but a function, like the CASE WHEN THEN from SQL.

```
switch(expression, alternative1,alternative2,alternative3,alternative4,...)
```

```
> for(ch in c("c","k","a","B","A","b")) print(switch(EXPR = ch,a=,A="ai",b="bee",c="see","????"))
```

```
[1] "see"
```

```
[1] "????"
```

```
[1] "ai"
```

```
[1] "????"
```

```
[1] "ai"
```

```
[1] "bee"
```

a=,A="ai" both "a" and "A" will return the same value

"????" is the default value (aka "otherwise") for values not in the alternatives' list

Numeric EXPR has no "otherwise"

```
> for(i in c(-1:3,9)) print(switch(i, 1,2,3,4))
```

```
NULL
```

```
NULL
```

```
[1] 1
```

```
[1] 2
```

```
[1] 3
```

```
NULL
```


Control Flow

for

```
for (var in seq) expr  
break  
next
```

for will cycle through the elements of a vector sequentially until it reaches the last element or the *break* command is found within the loop. *Next* skips the current iteration.

```
> for(i in 4:7) print(i)
```

```
[1] 4
```

```
[1] 5
```

```
[1] 6
```

```
[1] 7
```

Loop through a sequence of numbers

```
> for(i in c(734, 985, 43, 952)) print(i)
```

```
[1] 734
```

```
[1] 985
```

```
[1] 43
```

```
[1] 952
```

Loop through a vector of numbers

```
> for(i in c("Helsinki", "Tampere", "Turku")) print(i)
```

```
[1] "Helsinki"
```

```
[1] "Tampere"
```

```
[1] "Turku"
```

Loop through a vector of strings

Control Flow

```
> for(i in 1:10)
+ {
+ print(i)
+ if (i==3) break
+ }
```

break exits the loop

```
[1] 1
[1] 2
[1] 3
```

```
>
```

```
> for(i in 1:10)
+ {
+ if (i/2==i %/%2) next
+ print(i)
+ }
```

next skips the current iteration

```
[1] 1
[1] 3
[1] 5
[1] 7
[1] 9
```

All the even numbers are skipped

Control Flow

while

```
while(cond) expr  
break  
next
```

while will test a condition and execute an expression if the condition is TRUE, then it will test the condition again and so forth.

break exits the loop

next skips the current iteration, it will cause an infinite loop unless the variable is updated before the *next* statement

Control Flow

example of using while

```
n <- 1
while (n < 5)
{
  print(n)
  n <- n+1
}
```

example of using while and next

```
n <- 0
while ((n <- n+1) < 5)
{
  if (n==2) next
  print(n)
}
```

The code before *next* is executed
The code after *next* is skipped

The loop variable must be updated before reaching the next, otherwise the loop will be infinite

example of using while and next

```
n <- 0
while (n < 5)
{
  n <- n+1
  if (n==2) next
  print(n)
}
```

The code before *next* is executed
The code after *next* is skipped

example of using while and break

```
n <- 1
while (n < 5)
{
  if (n==2) break
  print(n)
  n <- n+1
}
```

The code before *break* is executed
The code after *break* is skipped and the loop ends

Control Flow

```
print("Game: I will choose 3 numbers between 1 and 8, you have to guess them to win this
game")
x <- sample(1:8,3)
user.score <- c()
while (length(x)>0)
{
print("Give me a number between 1 and 8")
user.try <- scan(,what=numeric(),1)
if (user.try %in% x)
{
user.score <- c(user.score, user.try)
x <- x[x != user.try]
print("Correct!")
}
else print("Wrong!")
if (length(x)==0)
{
print("You win! Now give 10 euros to the instructor and play again!")
}
else
{
cat("You already guessed", ifelse((length(user.score)==0),"nothing!", paste(user.score,
collapse=", ")), " Try again!\n" )
}
}
```

Control Flow

repeat

repeat expr
break

repeat will execute an expression and, from within that expression, test a condition, if the condition is TRUE, it will use *break* to stop, otherwise it will execute the expression again and so forth.

break exits the loop

Control Flow

example of using repeat

```
n <- 1
repeat
{
print(n)
n <- n+1
if (n == 5) break
}
```

The code before *break* is executed
The code after *break* is skipped and
the loop ends

```
n <- 0
repeat
{
n <- n+1
print(n)
if (n == 4) break
}
```

example of using repeat and next

```
n <- 0
repeat
{
n <- n+1
if (n == 2) next
print(n)
if (n == 4) break
}
```

The code before *next* is executed
The code after *next* is skipped

The loop variable
must be updated
before reaching the
next, otherwise the
loop will be infinite

Control Flow

while vs repeat

while checks the conditional expression before entering the loop, it might not execute all at.

repeat executes the loop and then it checks the conditional expression anywhere from within the loop, usually, it will execute once, at least partially.

Control Flow

References/to learn more:

The R book

Michael J. Crawley pp 58

2015 John Wiley & Sons Ltd

Statistics: an introduction using R

Michael J. Crawley pp 283

2013 John Wiley & Sons Ltd

Statistics with R

Vincent Zoonekynd, pp 26

http://zoonek2.free.fr/UNIX/48_R/all.html

Aprendizaje del software estadístico R: un entorno para simulación y computación estadística

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Departamento de Estadística

Universidad Carlos III de Madrid

<http://ocw.uc3m.es/estadistica/aprendizaje-del-software-estadistico-r-un-entorno-para-simulacion-y-computacion-estadistica/resolveUId/a70c8973cb8798b0bd0e6bdf7abd6ec7>

Introductory Statistics with R

Peter Dalgaard, pp 44

2015 Springer

Software Tools, Part 1: introduction to R software

Petri Koistinen

<http://www.rni.helsinki.fi/~pek/s-tools/cond.r>

Quick-R

Rob Kabacoff

<http://www.statmethods.net/management/controlstructures.html>

The Stem and Tendril simplified R manual

Professors Franzblau, Poje and Verzani of the College of Staten Island

<http://wiener.math.csi.cuny.edu/st/stRmanual/>

Function Syntax

R commands are R functions, syntax:

calling a function, passing no parameters, the parenthesis are mandatory

```
result <- my_function()
```

calling a function, passing parameters by position

```
result <- my_function(arg1,arg2,...,argN)
```

calling a function, passing parameters by name

```
result <- my_function(arg_nameN=argN,arg_name1=arg1,...,arg_name2=arg2)
```

calling a function, passing parameters by position and with optional parameters

```
result <-  
my_function(arg1,arg2,...,argN,optional_arg1=value1,optional_arg2=value2,...optional_N=valueN)
```

Calling a function without parenthesis will return its code, unless it is an internal function.

```
> Sys.info()  
  sysname      release      version  
"Windows"     "Vista"   "build 6000"
```

```
> new.packages()  
 [1] "aaMI"  
 [6] "aCGH.Spline"  
[11] "AdaptFit"  
[16] "ADGofTest"  
[21] "ads"  
[26] "AGSDest"
```

```
> Sys.info  
function ()  
  .Internal(Sys.info())  
<environment: namespace:base>
```

```
> new.packages  
function (lib.loc = NULL, repos = getOption("repos"), contriburl = contrib.url(repos,  
  type), instPkgs = installed.packages(lib.loc = lib.loc),  
  method, available = NULL, ask = FALSE, ..., type = getOption("pkgType"))  
{  
  ask  
  if (is.null(lib.loc))
```

Functions

To get the arguments of a function:

`args()` will return the arguments

`args(plot)` # get the arguments for function plot
`args(graphics::plot)` # specify package

Functions

$$y = f(x)$$

input(independent variable or argument)

output(dependent variable or value)

Example: quadratic function

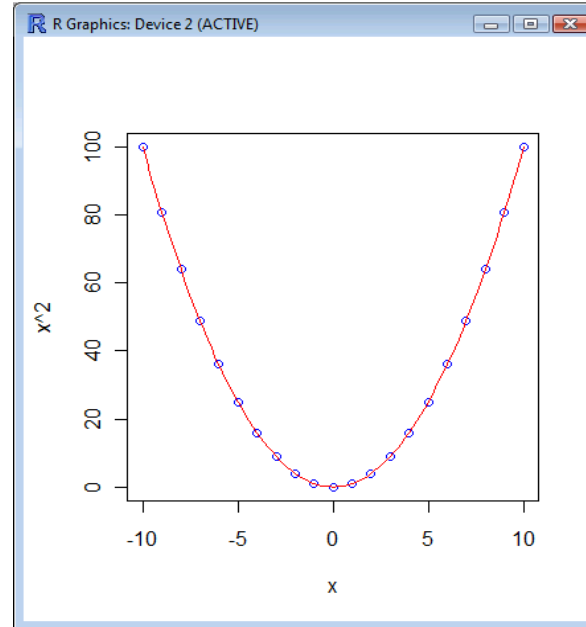
$$y = f(x) = x^2$$

f: [-10,10] \rightarrow [0,100]

```
X <- -10:10
```

```
plot(x, x^2, col = "red", type="l")
```

```
points(x,x^2,col="blue")
```



Argument List of a Function

args() returns the argument names and corresponding default values of a function or primitive

Functions

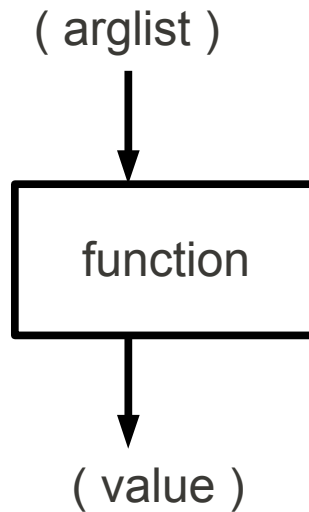
Function Definition

```
function( arglist ) expr  
return(value)
```

Arguments

arglist Empty or one or more terms
value An expression to be returned

The *return* command is unnecessary if the function end with the expression to be returned



A simple function

```
fncube <- function(x) x^3
```

Function name

declaration

Function body
(code)

```
fncube(7)  
fncube(1:5)
```

Functions

Example of using return

Improve the function fncube by returning 0 when the input is a character

```
fncube <- function(x) x^3
```

```
fncube2 <- function(x)  
{  
  if (is.character(x)) return(0) else return(x^3)  
}
```

```
fncube(123)  
fncube("a")
```

```
fncube2(123)  
fncube2("a")
```

Functions

A function with multiple parameters

```
fnpower <- function(x, n) x^n  
fnpower(5, 3)  
fnpower(1:5, 3)  
fnpower(5, 1:3)  
fnpower(1:8, 1:2)  
c(1^1, 2^2, 3^1, 4^2, 5^1, 6^2, 7^1, 8^2)  
fnpower(1:8, 1:4)  
c(1^1, 2^2, 3^3, 4^4, 5^1, 6^2, 7^3, 8^4)  
fnpower(1:8, 1:6) # error!
```

Functions

A recursive function

Fibonacci sequence, each element is the sum of the previous and the one before

Fibonacci $F(n) = F_{n-1} + F_{n-2}$, $F(0)=0$, $F(1)=1$
 $n=0, 1, 2, \dots$ $F(n) = 0, 1, 1, 2, 3, 5, 8, 13, 21$

iterative implementation

```
Fibonacci <- function(v)
{
  if (v<2) return(v)
  t <- c(1, 1)
  for (n in 3:v) t <- c(t, t[n-1]+t[n-2])
  return(t[v])
}
```

```
Fibonacci2 <- function(n) ifelse(n==0, 0,ifelse(n==1 | n==2, 1, Fibonacci2(n-1)+Fibonacci2(n-2) ) )
```

```
Fibonacci(8)
sapply(0:8,Fibonacci)
```


Functions

Default values

An argument can be optional and have a default value

```
my.foo <- function(x, y) {  
  return( x^3 + y*9 )  
}
```

```
# calling the function  
# passing arguments by position  
my.foo(4, 3)  
my.foo(4) # error!  
# passing arguments by name  
my.foo(y=3, x=4)
```

```
# default values  
my.foo <- function(x, y=3) {  
  return( x^3 + y*9 )  
}
```

```
# calling using the default value  
my.foo(4)
```

Functions

Passing functions as arguments

```
# passing a function as an argument
my.foo <- function(x, y=3, foo2) {
  return( foo2(x^3 + y*9) )
}
```

```
my.foo(2, 3, sin)
sin(2^3 + 3*9)
```

```
# passing a function as an argument, with parameters for that function
my.foo <- function(x,y=3, foo2, ...) {
  return( foo2(x, x^3 + y*9, ...) )
}
```

```
my.foo(2:20,3, plot,col = "blue",type="l")
```

Functions

Passing an arbitrary number of arguments

```
my.foo <- function(x,y=3, ...) {  
  return( x^3 + y*9 +mean( ... ) )  
}
```

```
my.foo(2,3,76,45,43,976,34)  
2^3 + 3*9 +mean(76,45,43,976,34)
```

Functions

References/to learn more:

The R book

Michael J. Crawley pp 47
2016 John Wiley & Sons Ltd

Statistics: an introduction using R

Michael J. Crawley pp 292
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Statistics with R

Vincent Zoonekynd, pp 27
http://zoonek2.free.fr/UNIX/48_R/all.html

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Introductory Statistics with R

Peter Dalgaard, pp 46
2016 Springer

Software Tools, Part 1: introduction to R software

Petri Koistinen

<http://www.rni.helsinki.fi/~pek/s-tools/f-own.r>

Chem 351 Archives Page

David Harvey

<http://fs6.depauw.edu:50080/~harvey/Chem%20351/PDF%20Files/Handouts/RDocs/Writing%20Functions%20Using%20R.pdf>

Quick-R

Rob Kabacoff

<http://www.statmethods.net/management/userfunctions.html>

The Stem and Tendril simplified R manual

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<http://wiener.math.csi.cuny.edu/st/stRmanual/>

Graphics on R

The "graphics" package contains many functions for drawing graphics

high level functions

- plot
- barplot
- dotchart
- stripchart
- pie
- hist
- boxplot
- pairs
- stem
- mosaicplot
- qqnorm
- contour
- persp
- image

low level functions
(add details to the
graphic)

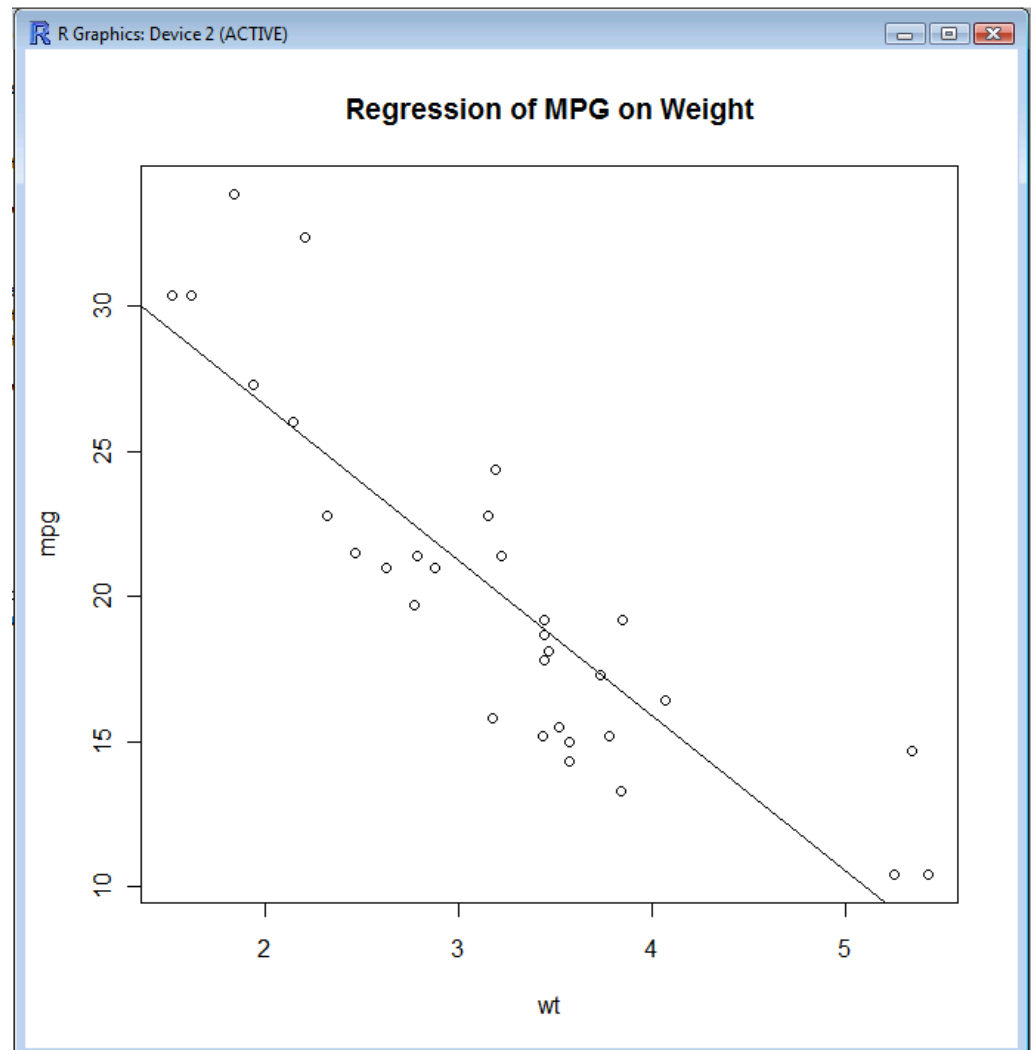
- axis
- title
- text
- legend
- points
- lines
- abline
- polygon
- qqline

Graphics on R

```
mtcars  
?mtcars
```

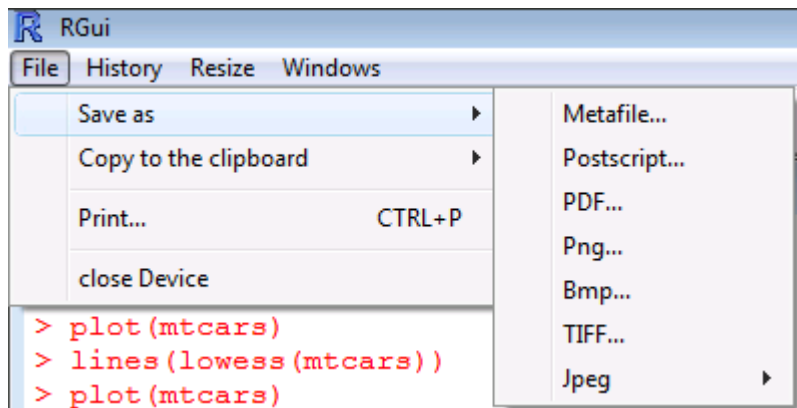
```
attach(mtcars)  
plot(wt, mpg)  
abline(lm(mpg~wt))  
title("Regression of MPG on Weight")  
detach(mtcars)
```

```
# instead of attach, "with" would work,  
not adding to the search path  
with(mtcars, {  
plot(wt, mpg)  
abline(lm(mpg~wt))  
title("Regression of MPG on Weight")  
})
```



Graphics on R

The graphic can be saved as an image file from the menu:



Or from code:

```
win.metafile("MPGonWeight.wmf")  
postscript("MPGonWeight.ps")  
pdf("MPGonWeight.pdf")  
png("MPGonWeight.png")  
bmp("MPGonWeight.bmp")  
tiff("MPGonWeight.jpg")  
jpeg("MPGonWeight.jpg")
```

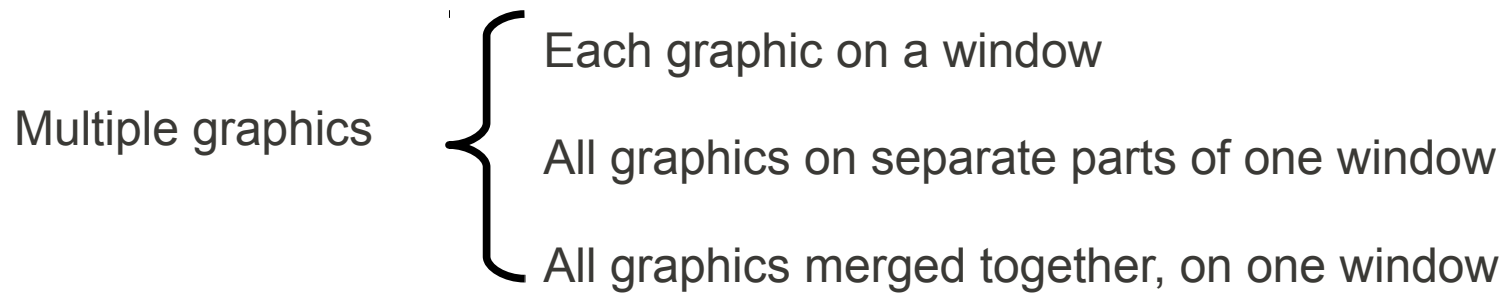
Graphics on R

Plotting the sine and a parabola:

```
plot(sin, -pi, 2*pi)  
plot(function(r) r^2, -pi, 2*pi)
```

The second plot will overwrite the first one

If that is not the effect wanted:



Graphics on R

Several graphic windows (graphic devices)

To create a graphic device (different commands for different OSs), that will become the active graphic device:

`windows()` or `win.graph()` Windows
`X11()` Unix
`macintosh()` Mac

The first device is device 2, then device 3, etc...

To make a graphic device the active one:

`dev.set(2)` # set active graphic device 2

To close the active graphic device

`dev.off()`

To close the graphic device 5

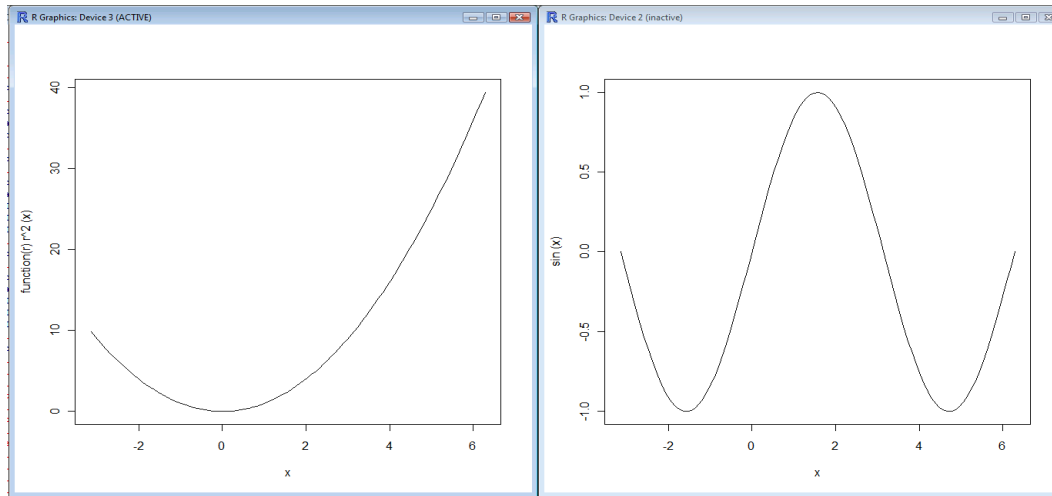
`dev.off(5)`

Graphics on R

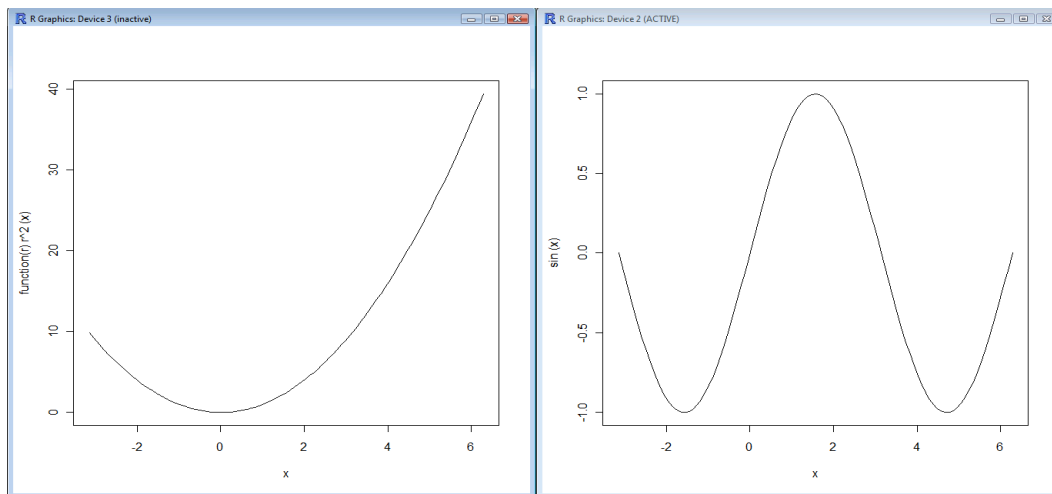
```
plot(sin, -pi, 2*pi)
```

```
windows()
```

```
plot(function(r) r^2, -pi, 2*pi)
```

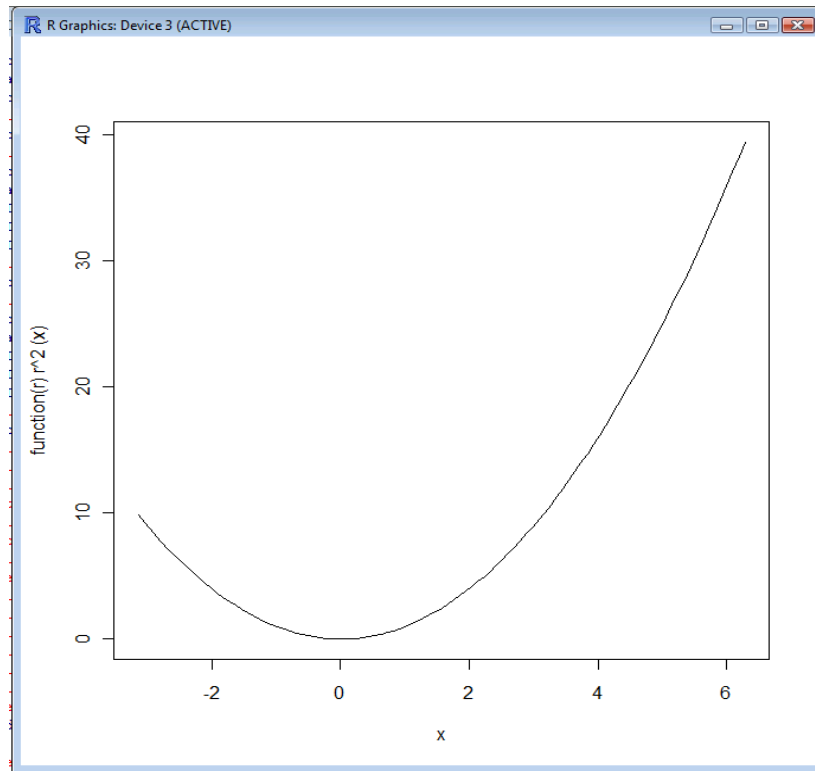


```
dev.set(2) # set active graphic device 2
```



Graphics on R

```
dev.off() # close the active graphic device
```



```
dev.off() # close the active graphic device
```

This graph is gone too

Graphics on R

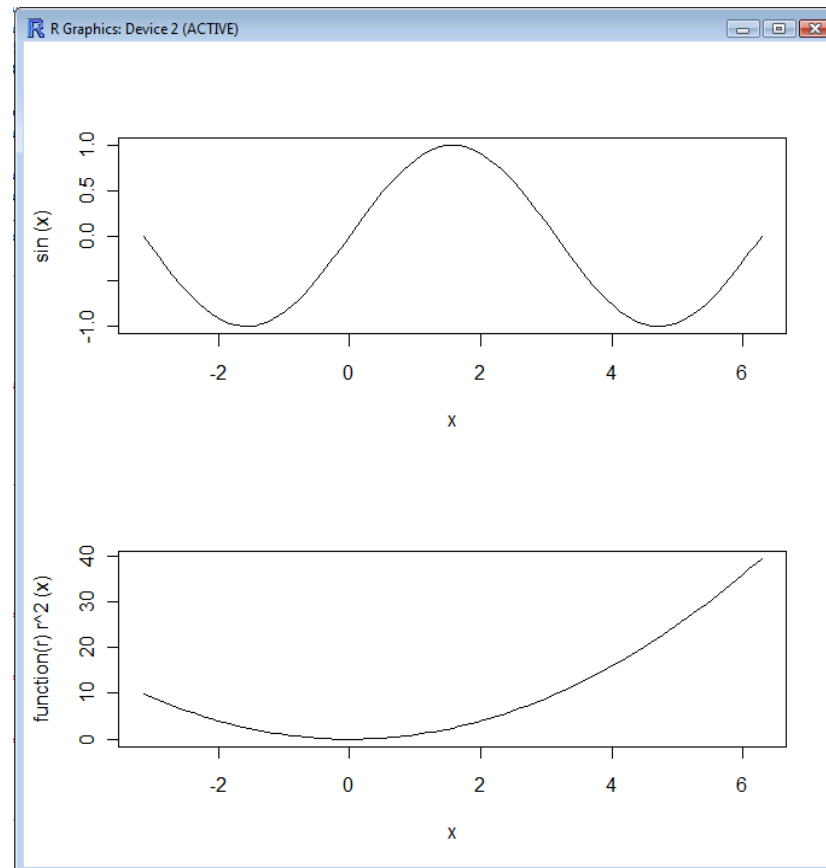
Multiple graphs in one window

`par()` set or query graphical parameters

Many parameters but the one needed:

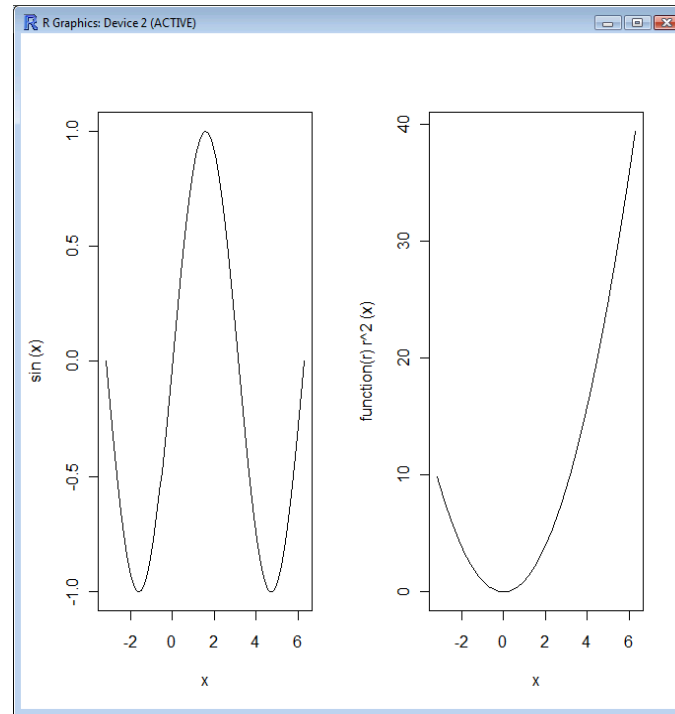
`mfc`, `mfr` A vector of the form `c(nr, nc)`. Subsequent figures will be drawn in an `nr`-by-`nc` array on the device by columns (`mfc`), or rows (`mfr`)

```
par(mfrow=c(2,1))  
plot(sin, -pi, 2*pi)  
plot(function(r) r^2, -pi, 2*pi)
```

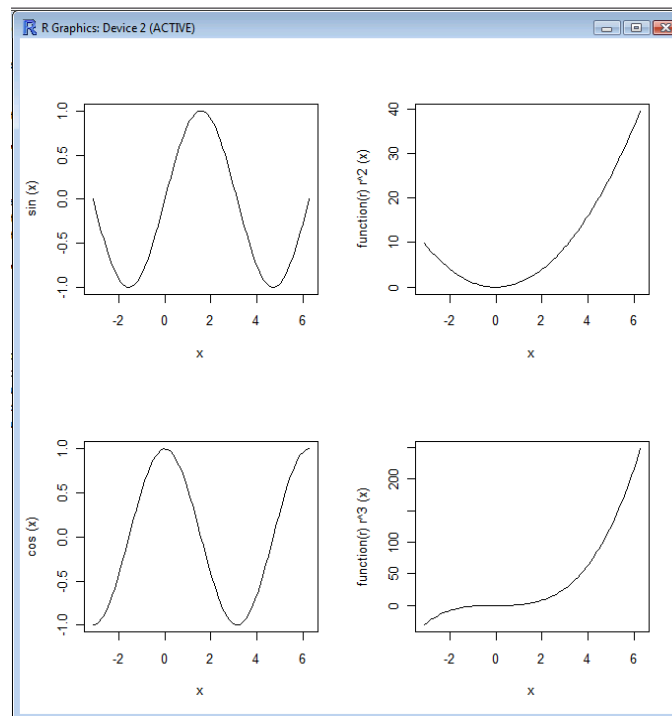


Graphics on R

```
par(mfrow=c(1,2))  
plot(sin, -pi, 2*pi)  
plot(function(r) r^2, -pi, 2*pi)
```



```
par(mfrow=c(2,2))  
plot(sin, -pi, 2*pi)  
plot(function(r) r^2, -pi, 2*pi)  
plot(cos, -pi, 2*pi)  
plot(function(r) r^3, -pi, 2*pi)
```



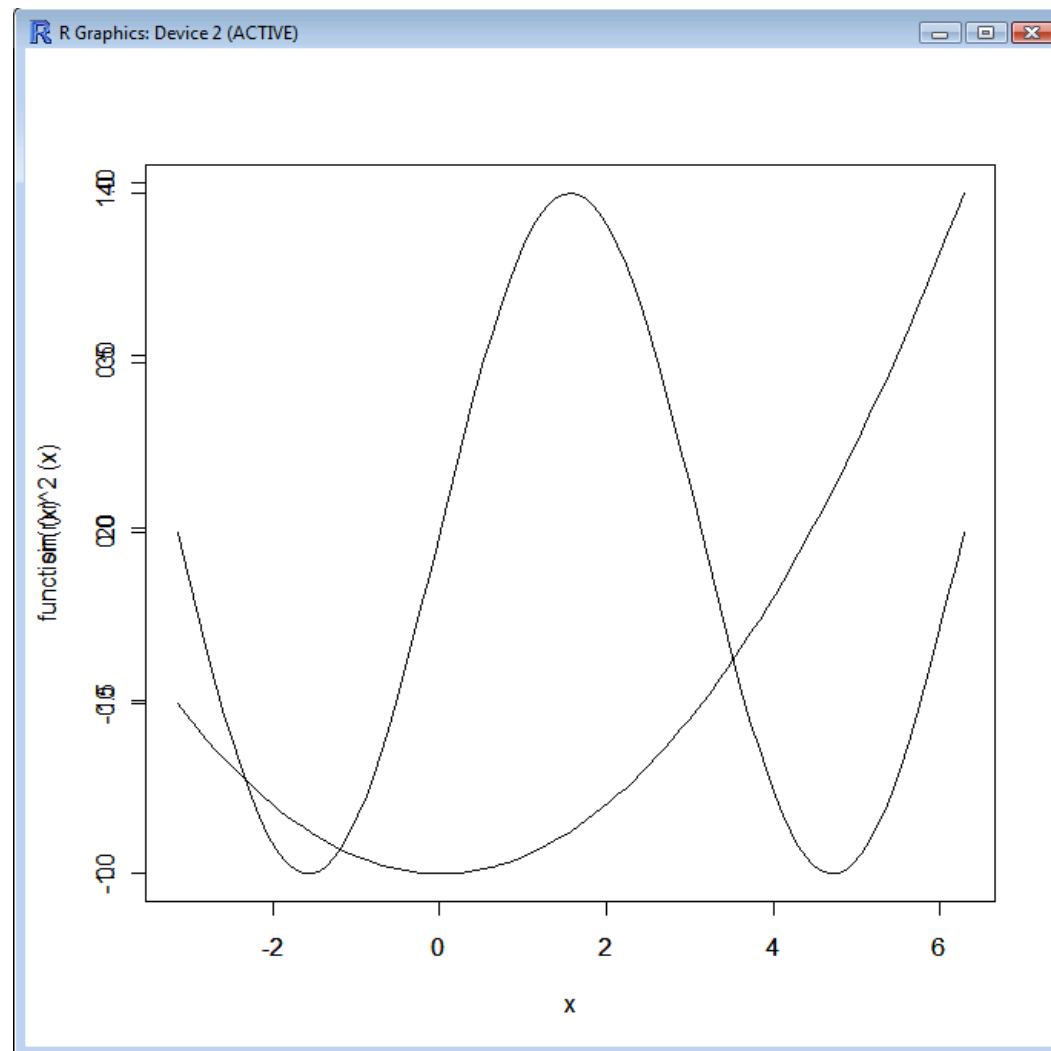
Graphics on R

graphics merged together, on one window

```
plot(sin, -pi, 2*pi)  
par(new=T)  
plot(function(x) x^2, -pi, 2*pi)
```

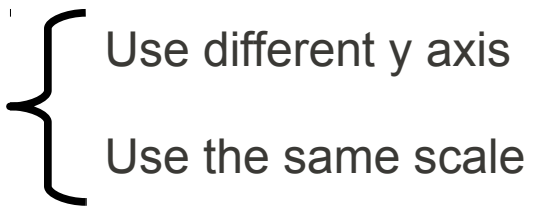
The y axis has a different title and scale, making the overlay look funny...

But the two graphs are there!



Graphics on R

Overlaying graphs with different scales



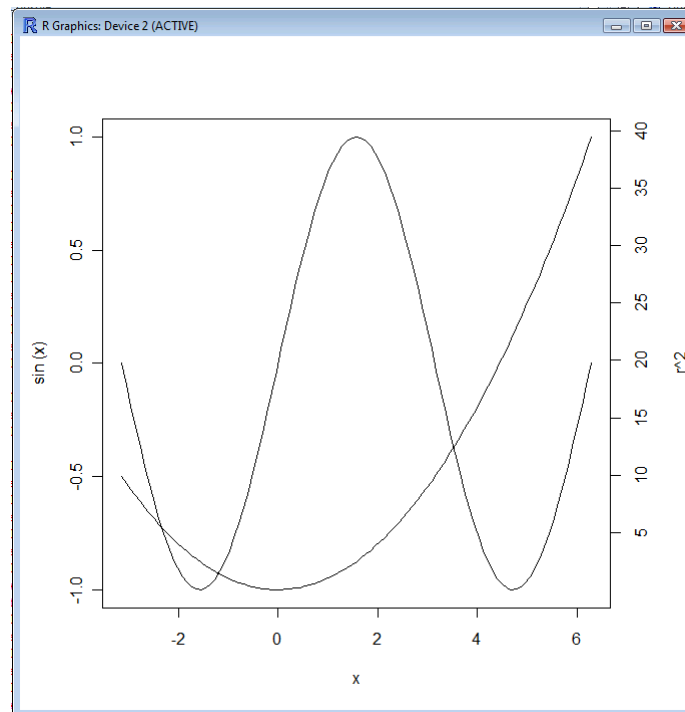
- Use different y axis
- Use the same scale

Graphics on R

Using different y axis on the same plot

Usually misleading, this seldom used but it is just an example of R's graphing capabilities

```
par(mar = c(5, 4, 4, 4) + 0.3) # Leave space for z axis  
plot(sin, -pi, 2*pi)  
par(new = TRUE)  
plot(function(r) r^2, -pi, 2*pi, axes = FALSE, bty = "n", xlab = "", ylab = "")  
axis(side=4, at = pretty( c(pi^2, 4*pi^2) ))  
mtext("r^2", side=4, line=3)
```

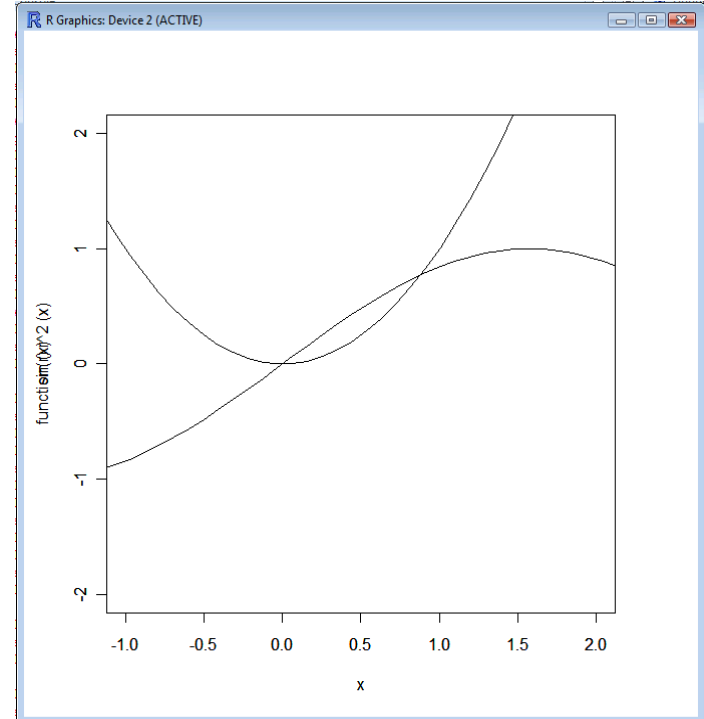
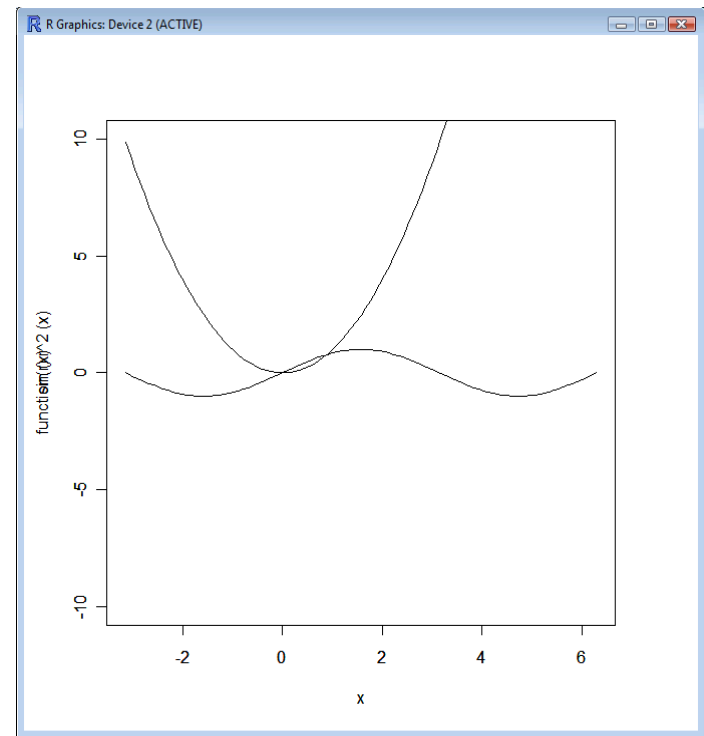


Graphics on R

Choosing a range for the x or y axis

```
plot(sin, -pi, 2*pi, ylim=c(-10,10))  
par(new=T)  
plot(function(r) r^2, -pi, 2*pi, ylim=c(-10,10))
```

```
plot(sin, -pi, 2*pi, xlim=c(-1,2), ylim=c(-2,2))  
par(new=T)  
plot(function(r) r^2, -pi, 2*pi, xlim=c(-1,2),  
ylim=c(-2,2))
```




Graphics on R

plot()

The plot() function is very versatile and very useful

plot() can draw



- simple plot
- function plot
- line chart
- scatterplot
- density plot

Graphics on R

Simple plot

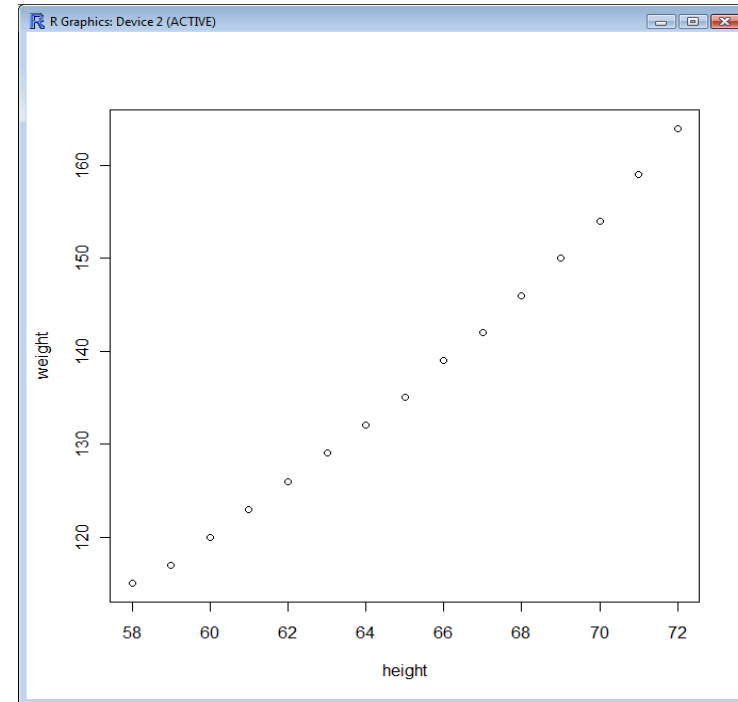
A simple plot `plot(X)` has each element of a discrete variable `X` plotted on the y-axis and the element's index on the x-axis

```
# simple plot  
women  
plot(women)
```

Function plot

A function plot is a simple plot for a continuous variable

```
# function plot  
x = seq(-2,2)  
y = x^2  
# edgy graph!  
plot(x,y,type="l",xlab="X axis",ylab="Y axis",main="Parabola", col = "red")  
# better  
sp <- spline(x, y) # spline interpolation of data points  
lines(sp, col = "blue")  
# much better  
sp <- spline(x, y,n=20) # interpolation at n points spanning [xmin, xmax]  
lines(sp, col = "green")
```



Graphics on R

Line chart

A line chart is a simple plot with consecutive plots connected by lines

line chart

```
x <- c(1:5); y <- x # create some data
par(pch=22, col="blue") # plotting symbol and color
par(mfrow=c(2,4)) # all plots on one page
opts = c("p","l","o","b","c","s","S","h")
for(i in 1:length(opts))
{
  heading = paste("type=",opts[i])
  plot(x, y, main=heading)
  lines(x, y, type=opts[i])
}
```

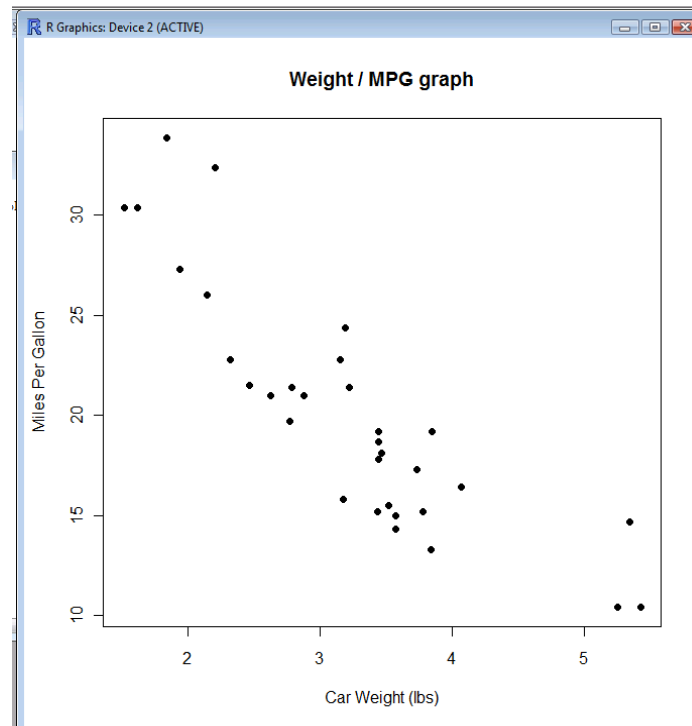
```
x <- c(1:5); y <- x^4 # create some data
par(pch=22, col="blue") # plotting symbol and color
par(mfrow=c(2,4)) # all plots on one page
opts = c("p","l","o","b","c","s","S","h")
for(i in 1:length(opts))
{
  heading = paste("type=",opts[i])
  plot(x, y, main=heading)
  lines(x, y, type=opts[i])
}
```

Graphics on R

Scatterplot

A scatterplot `plot(X, Y)` has each element of a variable `Y` plotted on the y-axis and the corresponding element for variable `X` on the x-axis

```
# scatterplot  
attach(mtcars)  
plot(wt, mpg, main="Weight / MPG graph", xlab="Car Weight (lbs)", ylab="Miles Per  
Gallon", pch=19)
```



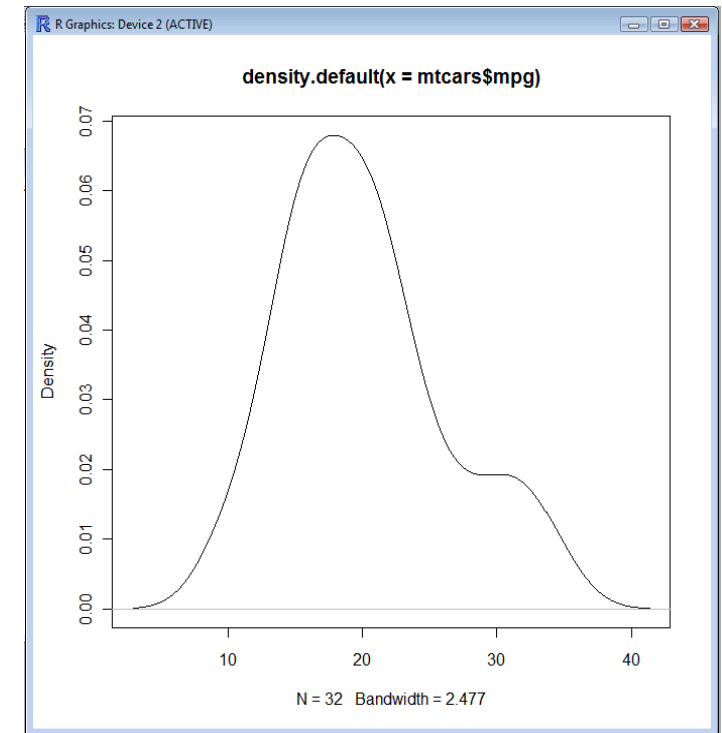
Graphics on R

Kernel density plots

Kernel density plots nicely visualize the shape of a distribution. They can be better than histograms, even with normal curves because histograms are strongly affected by the number of bins used and by outliers.

```
# Kernel density plot  
d <- density(mtcars$mpg) # kernel density estimates  
plot(d)
```

```
# Filled density plot  
d <- density(mtcars$mpg)  
plot(d, main="Kernel Density of Miles Per Gallon")  
polygon(d, col="red", border="blue")
```



Graphics on R

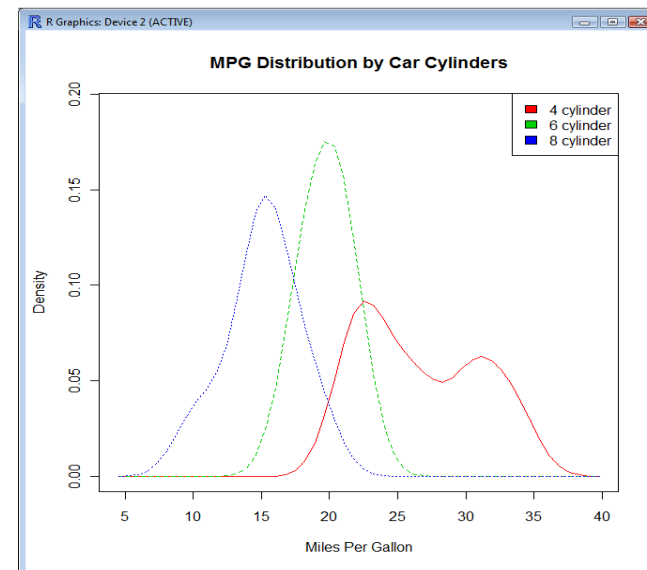
Kernel density for comparing groups

To compare the kernel density plots of two or more groups, the `sm` package has the function `sm.density.compare()`:

```
sm.density.compare(x, factor)
```

`x` numeric vector

`factor` grouping variable



```
# Compare MPG distributions for cars with 4,6, or 8 cylinders
```

```
library(sm)
```

```
attach(mtcars)
```

```
# create value labels
```

```
cyl.f <- factor(cyl, levels= c(4,6,8), labels = c("4 cylinder", "6 cylinder", "8 cylinder"))
```

```
# plot densities
```

```
sm.density.compare(mpg, cyl, xlab="Miles Per Gallon")
```

```
title(main="MPG Distribution by Car Cylinders")
```

```
# add legend
```

```
colfill<-c(2:(2+length(levels(cyl.f))))
```

```
legend("topright", levels(cyl.f), fill=colfill)
```

Graphics on R

barplot

boxplot(X) is a plot that, if X is a vector, the vector elements are the heights of the bars in the plot, if X is a matrix, the matrix columns are the heights of the bars in the plot, stacked after the first bar (column)

If the argument beside=TRUE, then the values in each column are juxtaposed, not stacked. The argument horiz=TRUE creates an horizontal barplot.

VADeaths

```
class(VADeaths)
```

```
dimnames(VADeaths)
```

```
# simple barplot
```

```
barplot(VADeaths[, "Rural Male"])
```

```
# stacked barplots
```

```
barplot(VADeaths[,c("Rural Male", "Rural Female")])
```

```
# juxtaposed barplots
```

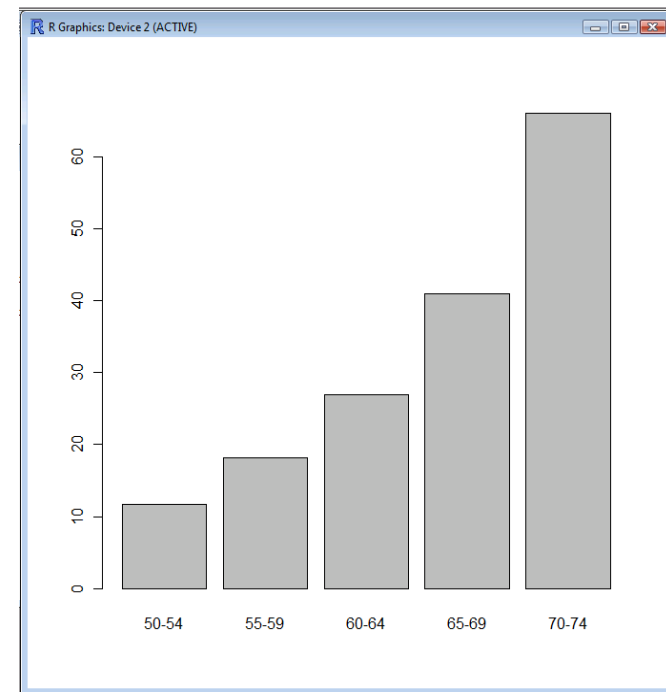
```
barplot(VADeaths[,c("Rural Male", "Rural Female")], beside=T)
```

```
# stacked barplots
```

```
barplot(VADeaths)
```

```
# juxtaposed barplots
```

```
barplot(VADeaths, beside=T)
```



Graphics on R

dotchart

dotchart(X) plots a dot chart or dot plot which plots the values of variable X in groups

Simple Dotplot

```
dotchart(mtcars$mpg, labels=row.names(mtcars), cex=.7,  
main="Gas Milage for Car Models", xlab="Miles Per Gallon")
```

Dotplot: Grouped Sorted and Colored

Sort by mpg, group and color by cylinder

```
x <- mtcars[order(mtcars$mpg),] # sort by mpg
```

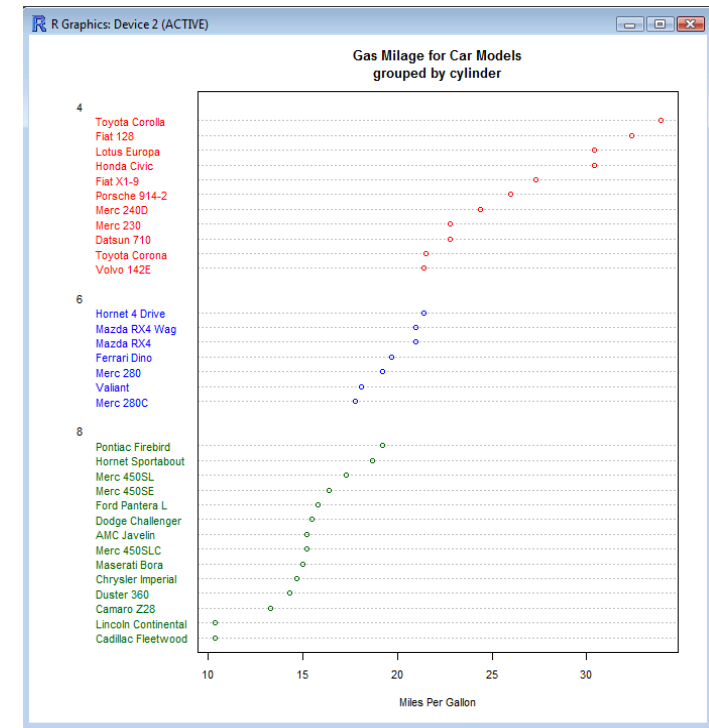
```
x$cyl <- factor(x$cyl) # it must be a factor
```

```
x$color[x$cyl==4] <- "red"
```

```
x$color[x$cyl==6] <- "blue"
```

```
x$color[x$cyl==8] <- "darkgreen"
```

```
dotchart(x$mpg, labels=row.names(x), cex=.7, groups= x$cyl, main="Gas Milage for Car  
Models\ngrouped by cylinder", xlab="Miles Per Gallon", gcolor="black", color=x$color)
```



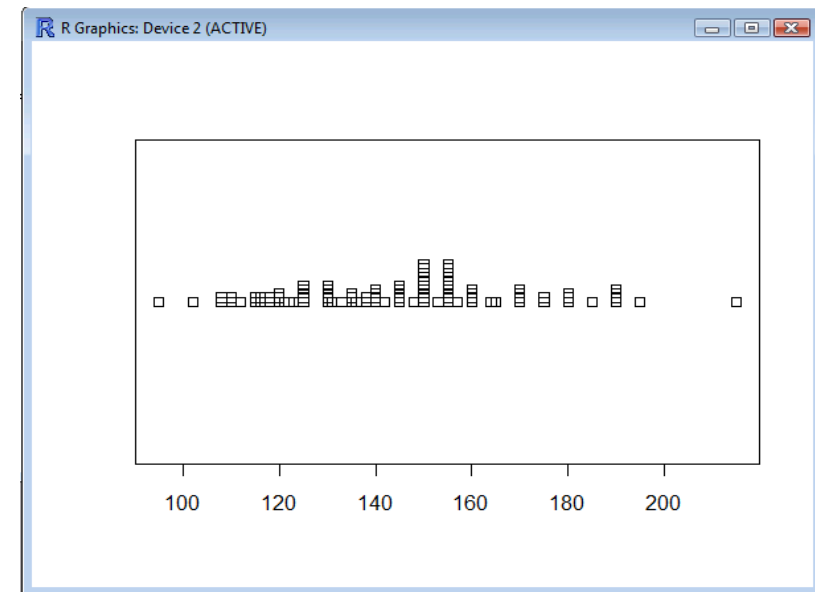
stripchart

A stripchart(X) plots a one dimensional or dot plot of the variable X, this is a good alternative to boxplots when sample sizes are small

Data from Cartoon Guide to Statistics, from Larry Gonick, Woollcott Smith, Collins Reference, 1993

The weights of some Penn State students, in 1992

```
mydataf2 <- read.csv("PennState92.csv", header=F,row.names=1)
mydataf2
# put all the data in one vector
v1 <- c(as.matrix(mydataf2[1,]),as.matrix(mydataf2[2,]))
v1 <- v1[!is.na(v1)]
# nice strip chart
stripchart(v1)
# nice strip chart with groups
stripchart(v1, method = "stack",xlim = c(min(v1),max(v1)))
```



Graphics on R

pie

pie(x) draws a circle (pie) cut into segments (slices), each slice represents a unique value from the elements of x and the size of the slice and the relative frequency of each unique value is represented by the size of the slice.

```
# simple pie
```

```
pie(unique(mtcars$cyl), labels = unique(mtcars$cyl), main="Pie Chart of N. of cylinders")
```

```
# pie with percentages and colors
```

```
with(mtcars, {
```

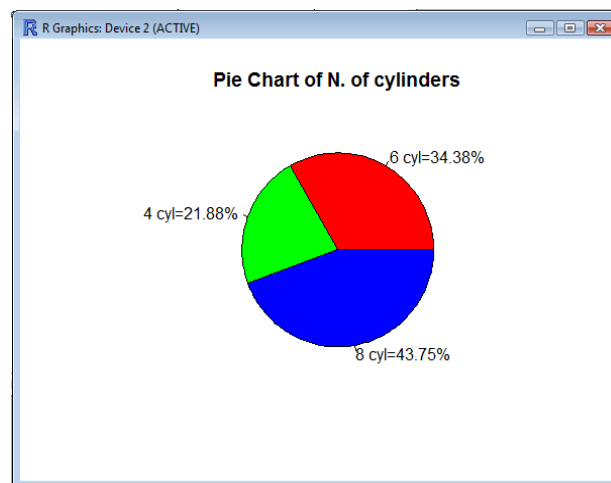
```
n.cyl <- unique(cyl)
```

```
percent.cyl <- round(table(cyl)/dim(mtcars)[1]*100,2)
```

```
lbls <- paste(n.cyl, " cyl=", percent.cyl, "%", sep="")
```

```
pie(n.cyl, labels = lbls , main="Pie Chart of N. of cylinders", col=rainbow(length(lbls)))
```

```
})
```



Graphics on R

hist

hist(X) is an histogram, a bar plot with the frequencies of the values in X on the y-axis and the ranges of values on the x-axis

A cumulative distribution curve is the proportion of X on the y-axis, up to the current position on the x-axis

```
# simple histogram
```

```
hist(faithful$waiting, prob=TRUE)
```

```
# Frequency polygon
```

```
# http://addictedtor.free.fr/graphiques/RGraphGallery.php?graph=101
```

```
h <- hist(faithful$waiting, prob=TRUE, plot=FALSE)
```

```
# compute the frequency polygon
```

```
diffBreaks <- h$mids[2] - h$mids[1]
```

```
xx <- c( h$mids[1]-diffBreaks, h$mids, tail(h$mids,1)+diffBreaks )
```

```
yy <- c(0, h$density, 0)
```

```
# draw the histogram
```

```
hist(faithful$waiting, prob = TRUE, xlim=range(xx),border="gray", col="gray90")
```

```
# adds the frequency polygon
```

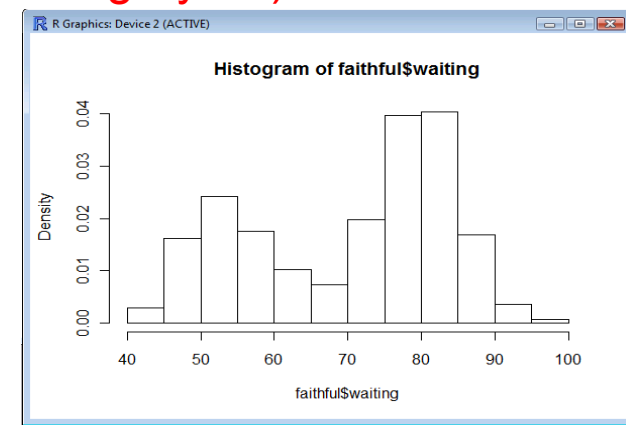
```
lines(xx, yy, lwd=2, col = "royalblue")
```

```
# cumulative distribution
```

```
h <- hist(faithful$waiting)
```

```
h$counts <- cumsum(h$counts)
```

```
plot(h)
```

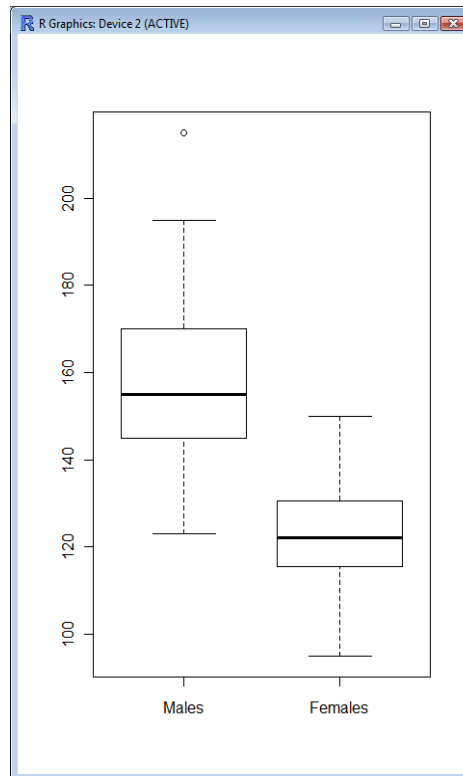


Graphics on R

boxplot

boxplot(X) is a box-and-whisker plot with the values of variable X, this is an effective way to summarize larger datasets

```
mydataf2 <- read.csv("PennState92.csv", header=F, row.names=1)
mydataf2
# plot the data for Males and Females
apply(mydataf2, 1, summary)
boxplot(as.numeric(mydataf2[1,]), as.numeric(mydataf2[2,]), names=c("Males", "Females"))
```



Graphics on R

Changing the scale

```
mydataf2 <- read.csv("PennState92.csv", header=F, row.names=1)  
mydataf2
```

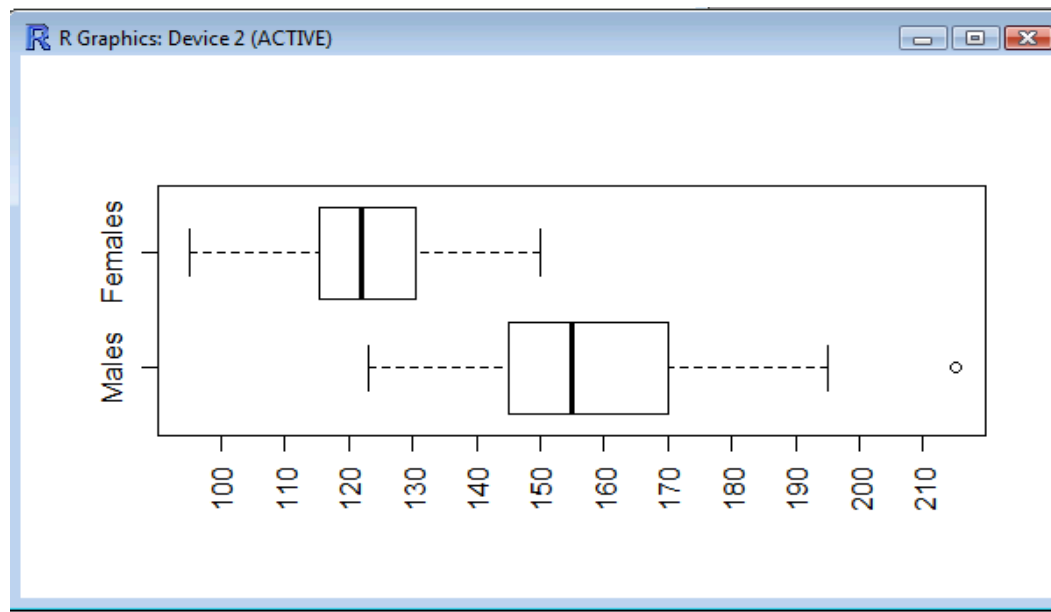
```
# plot the data for Males and Females
```

```
apply(mydataf2, 1, summary)
```

```
# use a y-axis scale of 10
```

```
boxplot(as.numeric(mydataf2[1,]), as.numeric(mydataf2[2,]), names=c("Males", "Females"),  
horizontal=T, xaxt = "n")
```

```
axis(1, 10:21*10, las = 2)
```



Graphics on R

Adding references to points

```
mydataf2 <- read.csv("PennState92.csv", header=F, row.names=1)  
mydataf2
```

```
# plot the data for Males and Females
```

```
# summary points on the y-axis
```

```
boxplot(as.numeric(mydataf2[1,]), as.numeric(mydataf2[2,]), names=c("Males", "Females"), horizontal=T,  
las = 2)
```

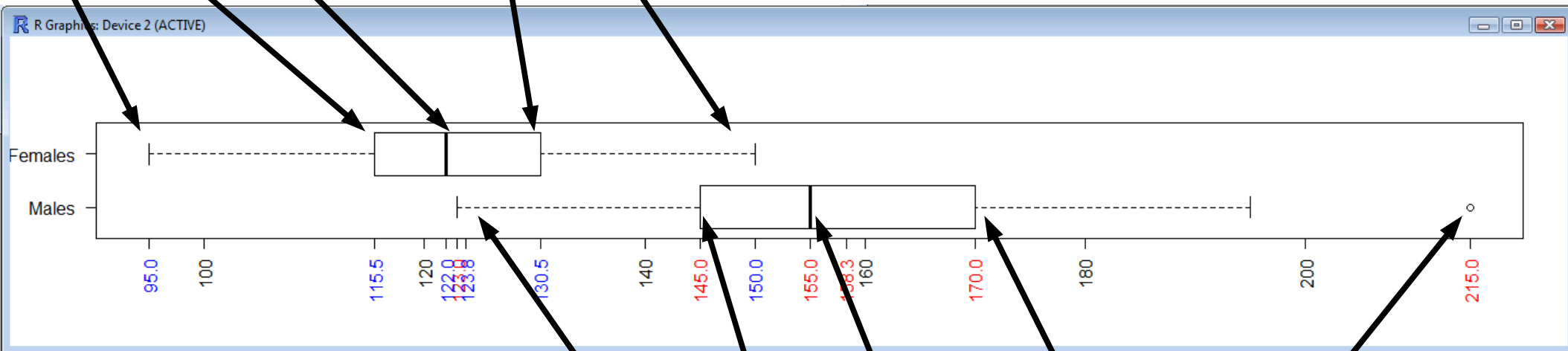
```
summdtf <- apply(mydataf2, 1, summary)
```

```
axis(1, summdtf$Males, las = 2, col.axis="red")
```

```
axis(1, summdtf$Females, las = 2, col.axis="blue")
```

\$Females

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	NA's
95.0	115.5	122.0	123.8	130.5	150.0	22.0



```
> apply(mydataf2, 1, summary)
```

\$Males

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
123.0	145.0	155.0	158.3	170.0	215.0

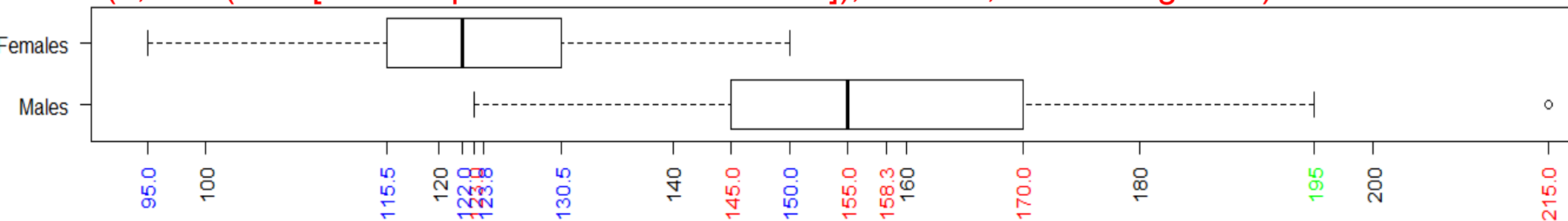
Graphics on R

Calculating the whiskers

```
boxplot(as.numeric(mydataf2[1,]), as.numeric(mydataf2[2,]), names=c("Males","Females"),  
horizontal=T, las = 2)  
summdtf <- apply(mydataf2, 1, summary)  
axis(1, summdtf$Males, las = 2, col.axis="red")  
axis(1, summdtf$Females, las = 2, col.axis="blue")
```

```
female <- as.numeric(mydataf2[2,])  
female <- female[!is.na(female)]  
male <- as.numeric(mydataf2[1,])  
IQRmale <- IQR(male, na.rm =T) # interquartile range  
IQRfemale <- IQR(female, na.rm =T) # interquartile range  
q1male <- quantile(male,.25, na.rm =T)  
q3male <- quantile(male,.75, na.rm =T)  
q1female <- quantile(female,.25, na.rm =T)  
q3female <- quantile(female,.75, na.rm =T)  
# whiskers = Q1 - 1.5 * IQR and Q3 + 1.5 * IQR  
min(female[female > q1female - 1.5 * IQRfemale])  
max(female[female < q3female + 1.5 * IQRfemale])  
min(male[male > q1male - 1.5 * IQRmale])  
max(male[male < q3male + 1.5 * IQRmale])
```

```
axis(1, max(male[male < q3male + 1.5 * IQRmale]), las = 2, col.axis="green")
```

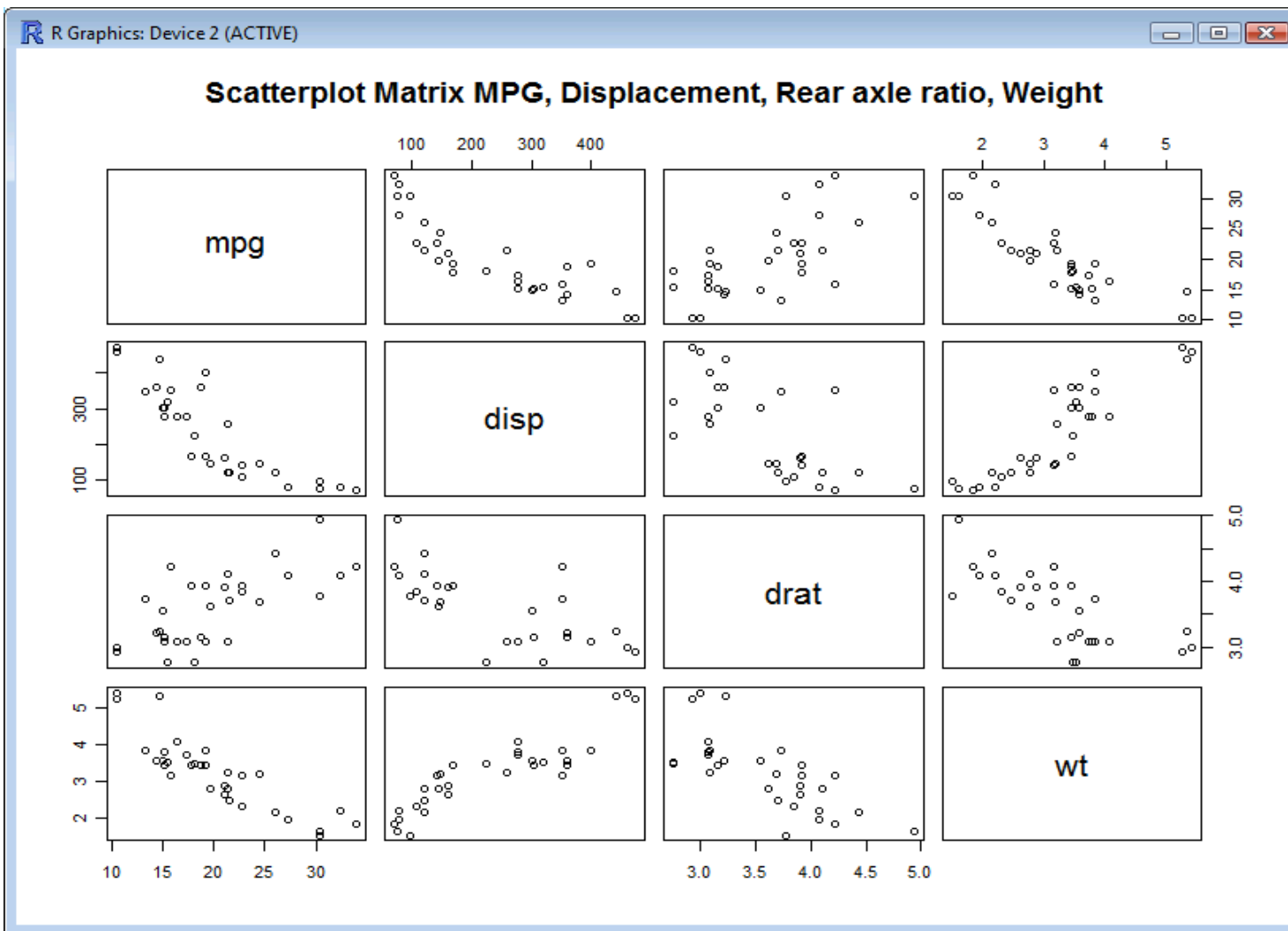


Graphics on R

pairs

pairs() shows a matrix with all the scatterplots for the columns of variable X

pairs(~mpg+disp+drat+wt,data=mtcars, main="Scatterplot Matrix MPG, Displacement, Rear axle ratio, Weight")



Graphics on R

stem

stem(X) creates a stem-and-leaf plot, which shows the shape of a distribution and displays each observation, useful for small datasets

```
mydataf2 <- read.csv("PennState92.csv", header=F,row.names=1)
mydataf2
# put all the data in one vector
v1 <- c(as.matrix(mydataf2[1,]),as.matrix(mydataf2[2,]))
v1 <- v1[!is.na(v1)]
# stem-and-leaf plot
stem(v1)
```

The decimal point is 1 digit(s) to the right of the |

```
8 | 5
10 | 288002556688
12 | 000123555550000013555688
14 | 000025555800000000003555555557
16 | 000045000055
18 | 000500005
20 | 5
```



Graphics on R

Details about the R stem()

Data from Basic Biostatistics, by Burt Gertsman, chapter 3

```
stem(x, scale = 1, width = 80, atom = 1e-08)
```

x a numeric vector

scale This controls the plot length

width The desired width of plot

atom a tolerance

```
myvec <- c(14, 17, 18, 19, 22, 22, 23, 24, 24, 26, 26, 27, 28, 29, 30, 30, 30, 31, 32, 33, 34, 34, 35, 36, 37, 38)
```

```
stem(myvec) # this is wrong!
```

```
length(myvec) # n=26
```

```
stem(myvec,atom =26) # OK!
```

```
# Too squished to see shape
```

```
# Split stem
```

```
stem(myvec,atom =1) # OK!
```

```
myvec <- c(14, 17, 18, 19, 22, 22, 23, 24, 26, 26, 27, 28, 29, 30, 30, 30, 31, 32, 33, 34, 34, 35, 36, 37, 38)
```

```
stem(myvec) # this is wrong!
```

```
length(myvec) # n=25
```

```
stem(myvec,atom =25) # OK!
```

```
# Too squished to see shape
```

```
# Split stem
```

```
stem(myvec) # OK!
```

Graphics on R

mosaicplot

mosaicplot() draws a mosaic plot, a relationship between two or more categorical variables, the width of the bars is horizontally and vertically proportional to the probabilities associated with the categorical variables

```
mosaicplot(Titanic, main = "Survival on the Titanic", color = TRUE)
```

```
## Formula interface for tabulated data:
```

```
mosaicplot(~ Sex + Age + Survived, data = Titanic, color = TRUE)
```

```
## Formula interface for raw data: visualize cross-tabulation of numbers
```

```
## of gears and carburetors in Motor Trend car data.
```

```
mosaicplot(~ gear + carb, data = mtcars, color = TRUE, las = 1)
```

```
# color recycling
```

```
mosaicplot(~ gear + carb, data = mtcars, color = 2:3, las = 1)
```

Graphics on R

Examples to explain mosaicplot()

```
Titanic
is(Titanic)
dim(Titanic)
dimnames(Titanic) # Class Sex Age Survived

# Overall gender proportion the Titanic
mosaicplot(~ Sex, main = "Overall gender proportion on the Titanic", data = Titanic, color =
TRUE)
# ladies first
mosaicplot(~ Sex, main = "Overall gender proportion on the Titanic", data = Titanic[,2:1,,],
color = TRUE)

# split vertically by survival rate
mosaicplot(~ Sex+ Survived, main = "Overall gender/survival proportion on the Titanic", data =
Titanic[,2:1,,], color = TRUE)

#Overall age/survival proportion on the Titanic
mosaicplot(~ Age+ Survived, main = "Overall age/survival proportion on the Titanic", data =
Titanic, color = TRUE)
```

Graphics on R

qqnorm and qqline

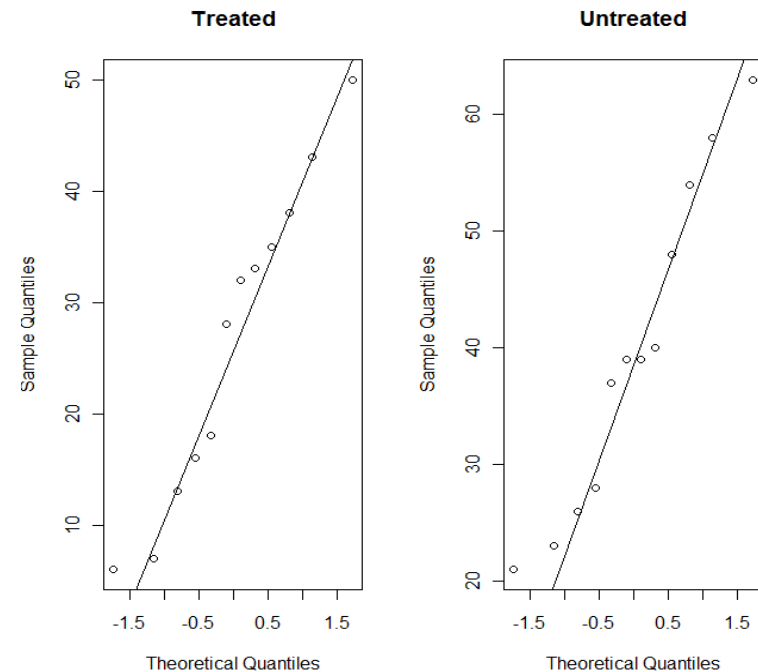
qqnorm(X) draws a normal probability chart for variable X, with the values of variable X on the y-axis and their associated probability based on a cumulative frequency on the x-axis, assuming a normal distribution

qqline(X) draws the expected linear relationship, assuming a normal distribution

Data from Transcriptomics Bioinformatics, by Attila Gyenesei

"An experiment was conducted to evaluate the effectiveness of a treatment for tapeworm in the stomachs of sheep. A random sample of 24 worm-infected lambs of the same age and health was randomly divided into two groups. 12 were injected with the drug and the remaining 12 were left untreated. After a 6-month period the worm counts were recorded"

```
sheep <- read.table("sheep.txt", sep="\t", header=T)
par(mfrow=c(1,2))
qqnorm(sheep$treated, main="Treated")
qqline(sheep$treated)
qqnorm(sheep$untreated, main="Untreated")
qqline(sheep$untreated)
```



Graphics on R

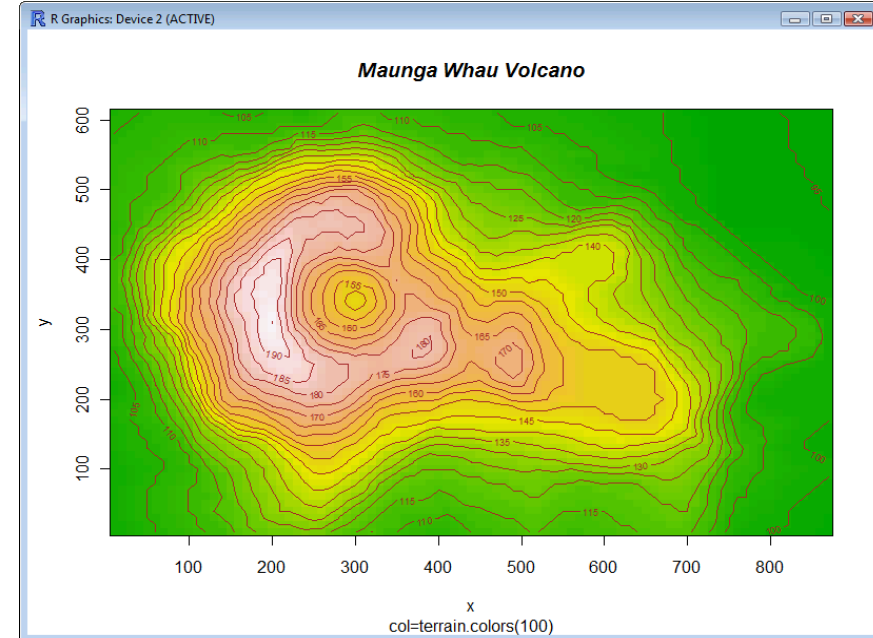
contour

`contour(X,Y,Z)` draws a contour plot, with vector X for the rows, vector Y for the columns and matrix X for the data

Example from R Graph Gallery by Romain François
<http://addictedtor.free.fr/graphiques/RGraphGallery.php?graph=22>

contour plot Maunga Whau Volcano

```
x <- 10*(1:nrow(volcano)); x.at <- seq(100, 800, by=100)
y <- 10*(1:ncol(volcano)); y.at <- seq(100, 600, by=100)
# Using Terrain Colors
image(x, y, volcano, col=terrain.colors(100),axes=FALSE)
contour(x, y, volcano, levels=seq(90, 200, by=5), add=TRUE, col="brown")
axis(1, at=x.at)
axis(2, at=y.at)
box()
title(main="Maunga Whau Volcano", sub = "col=terrain.colors(100)", font.main=4)
```



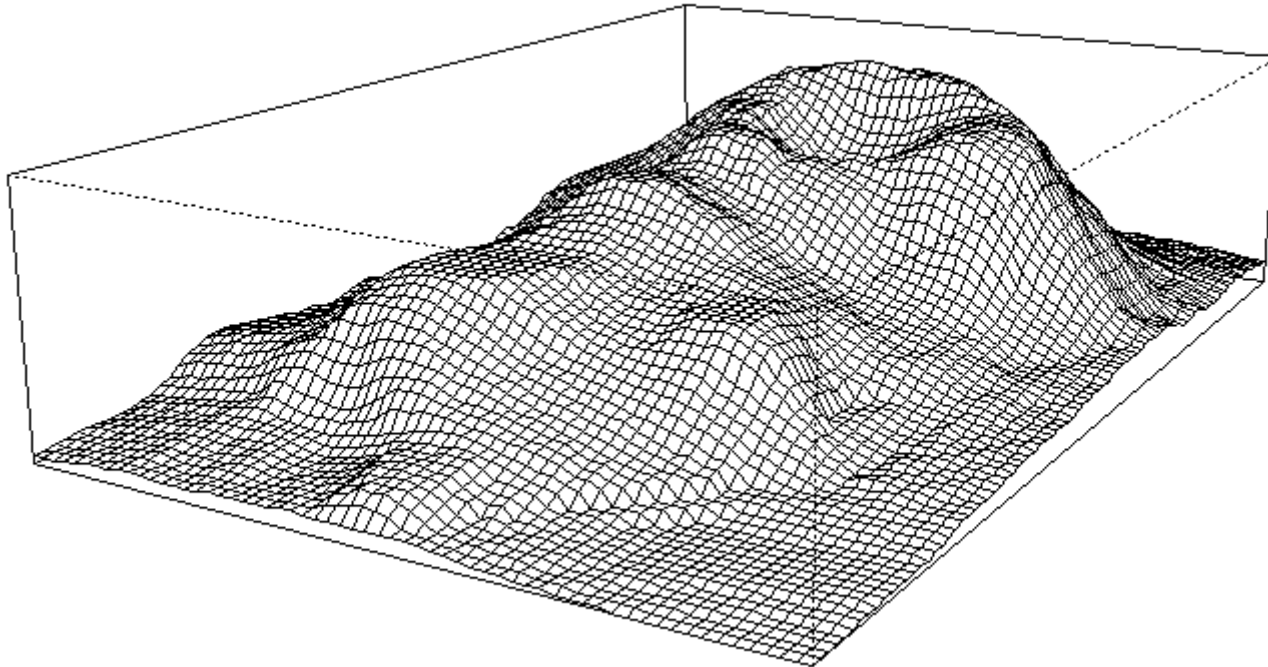
Graphics on R

persp

`persp(X,Y,Z)` draws a 3d graph, with vector X for the rows, vector Y for the columns and matrix X for the data

(2) Visualizing a simple DEM model

```
z <- 2 * volcano      # Exaggerate the relief  
x <- 10 * (1:nrow(z)) # 10 meter spacing (S to N)  
y <- 10 * (1:ncol(z)) # 10 meter spacing (E to W)  
persp(x, y, z, theta = 120, phi = 15, scale = FALSE, axes = FALSE)
```



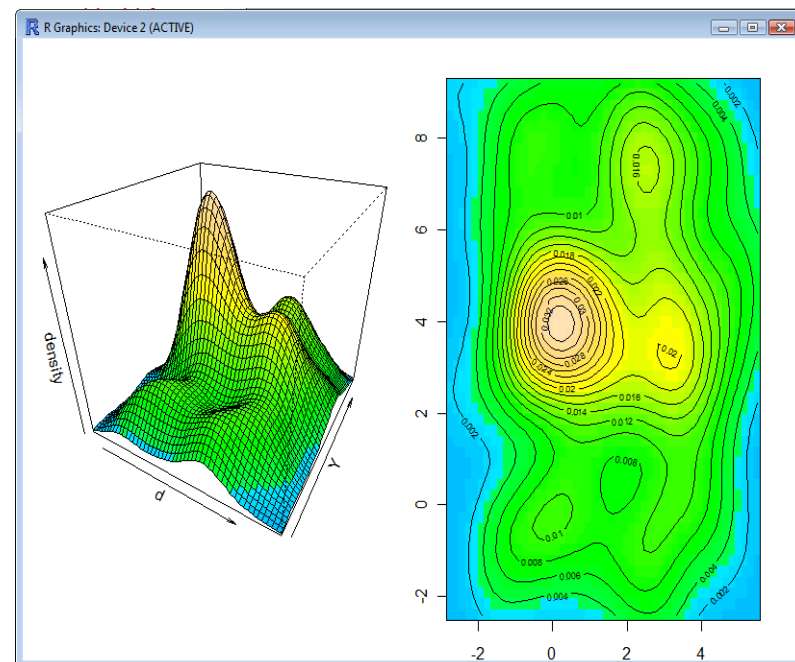
Graphics on R

Example from R Graph Gallery by Romain François

<http://addictedtor.free.fr/graphiques/RGraphGallery.php?graph=1>

Kernel density estimator in R2 Perspective plot and contour plot

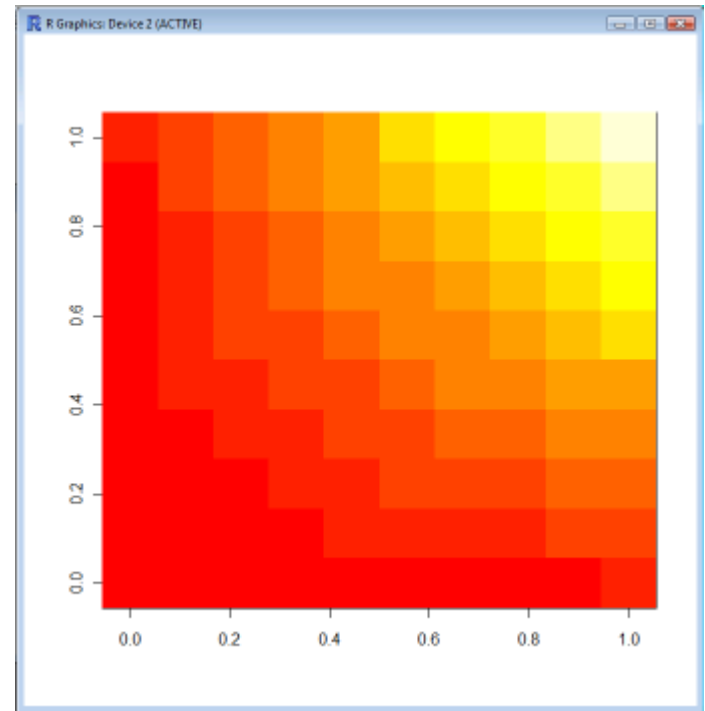
```
require(MASS)
set.seed(125)
x <- rnorm(150,mean=3*rbinom(150,prob=.5,size=1),sd=1)
y <- rnorm(150,mean=4*rbinom(150,prob=.5,size=2),sd=1)
d <- kde2d(x,y,n=50)
kde2dplot <- function(d,          # a 2d density computed by kde2D
                     ncol=50,    # the number of colors to use
                     zlim=c(0,max(z)), # limits in z coordinates
                     nlevels=20, # see option nlevels in contour
                     theta=30,   # see option theta in persp
                     phi=30)    # see option phi in persp
{
  z <- d$z
  nrz <- nrow(z)
  ncz <- ncol(z)
  couleurs <- tail(topo.colors(trunc(1.4 * ncol)),ncol)
  fcol <- couleurs[trunc(z/zlim[2]*(ncol-1))+1]
  dim(fcol) <- c(nrz,ncz)
  fcol <- fcol[-nrz,-ncz]
  par(mfrow=c(1,2),mar=c(0.5,0.5,0.5,0.5))
  persp(d,col=fcol,zlim=zlim,theta=theta,phi=phi,zlab="density")
  par(mar=c(2,2,2,2))
  image(d,col=couleurs)
  contour(d,add=T,nlevels=nlevels)
  box()
}
kde2dplot(d)
```



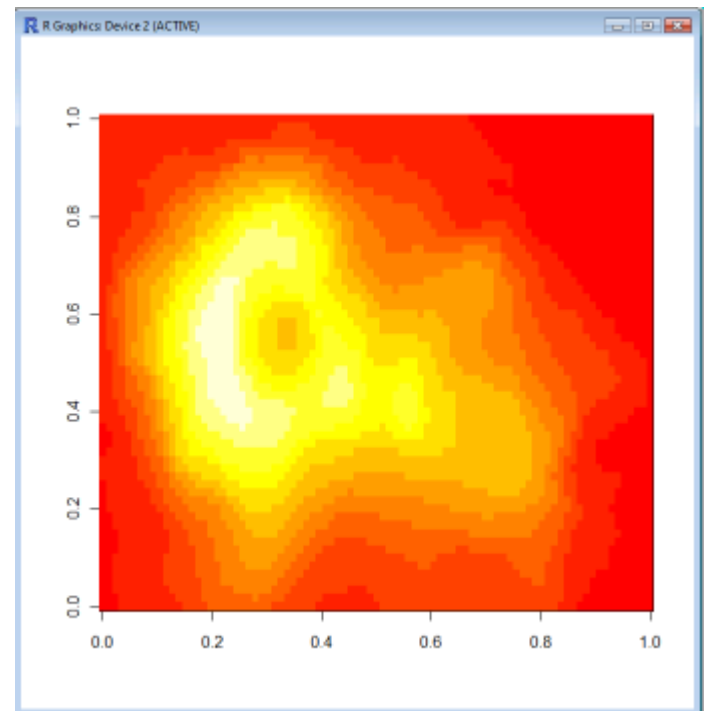
Graphics on R

image() Creates a grid of colored or gray-scale rectangles with colors corresponding to the values in z

```
x <- 1:10  
y <- 1:10  
m <- outer(x,y)  
m  
image(m)
```



```
volcano  
image(volcano)
```



Graphics on R
References/to learn more:

The R book
Michael J. Crawley pp 135
2017 John Wiley & Sons Ltd

Basic statistics using R pp. 110
Jarno Tuimala (CSC) and Dario Greco (HY)
<http://www.csc.fi/english/csc/courses/archive/R2008s>

Statistics: an introduction using R
Michael J. Crawley pp 297
2015 John Wiley & Sons Ltd

Statistics with R
Vincent Zoonekynd, pp 147
http://zoonek2.free.fr/UNIX/48_R/all.html

Aprendizaje del software estadístico R: un entorno para simulación y computación estadística
Prof. Alberto Muñoz García
Departamento de Estadística
Universidad Carlos III de Madrid
<http://ocw.uc3m.es/estadistica/aprendizaje-del-software-estadistico-r-un-entorno-para-simulacion-y-computacion-estadistica/resolveUid/a68d739b891b9a30368f756ba473b81d>

Introductory Statistics with R
Peter Dalgaard, pp 71
2017 Springer

Geographic Data Analysis
Pat Bartlein
<http://geography.uoregon.edu/bartlein/courses/geog417/lectures/lec02.htm>

Software Tools, Part 1: introduction to R software
Petri Koistinen
<http://www.rni.helsinki.fi/~pek/s-tools/g-intro.r>

Chem 351 Archives Page
David Harvey
<http://fs6.depauw.edu:50080/~harvey/Chem%20351/PDF%20Files/Handouts/RDocs/Graphing%20Data%20in%20R%20-%20A%20Gallery%20of%20Plots.pdf>

Thomas AP Statistics
thomasmathematics.com
<http://www.thomasmathematics.com/Aims/Ch1Aim50001.pdf>

Quick-R
Rob Kabacoff
<http://www.statmethods.net/graphs/index.html>

The Stem and Tendril simplified R manual
Professors Franzblau, Poje and Verzani of the College of Staten Island
<http://wiener.math.csi.cuny.edu/st/stRmanual/>

Sexual Discrimination at Berkeley

UCBAdmissions(datasets)

This data set is frequently used for illustrating Simpson's paradox, see Bickel et al. (1975). At issue is whether the data show evidence of sex bias in admission practices. There were 2691 male applicants, of whom 1198 (44.5%) were admitted, compared with 1835 female applicants of whom 557 (30.4%) were admitted. This gives a sample odds ratio of 1.83, indicating that males were almost twice as likely to be admitted. In fact, graphical methods (as in the example below) or log-linear modelling show that the apparent association between admission and sex stems from differences in the tendency of males and females to apply to the individual departments (females used to apply more to departments with higher rejection rates).

Simpson's paradox

http://en.wikipedia.org/wiki/Simpson%27s_paradox

Admissions by Department

Male Female

Department A Admitted 512 89

Rejected 313 19

Department B Admitted 353 17

Rejected 207 8

Department C Admitted 120 202

Rejected 205 391

Department D Admitted 138 131

Rejected 279 244

Department E Admitted 53 94

Rejected 138 299

Department F Admitted 22 24

Rejected 351 317

Gender Admitted Rejected %Admitted

Male 1198 1493 44.5

Female 557 1278 30.4

More males are admitted than females is this discrimination?

```
UCBAdmissions
is(UCBAdmissions) # contingency table!
dim(UCBAdmissions)
rownames(UCBAdmissions)
colnames(UCBAdmissions)
dimnames(UCBAdmissions)
```

```
# creating the table Gender Admitted Rejected %Admitted
```

```
> apply(UCBAdmissions, 1:2, sum)
```

```
Gender
```

```
Admit   Male Female
```

```
Admitted 1198  557
```

```
Rejected 1493 1278
```

```
> apply(UCBAdmissions, 1:2, sum)[1,]/apply(UCBAdmissions, 2, sum)
```

```
Male  Female
```

```
0.4451877 0.3035422
```

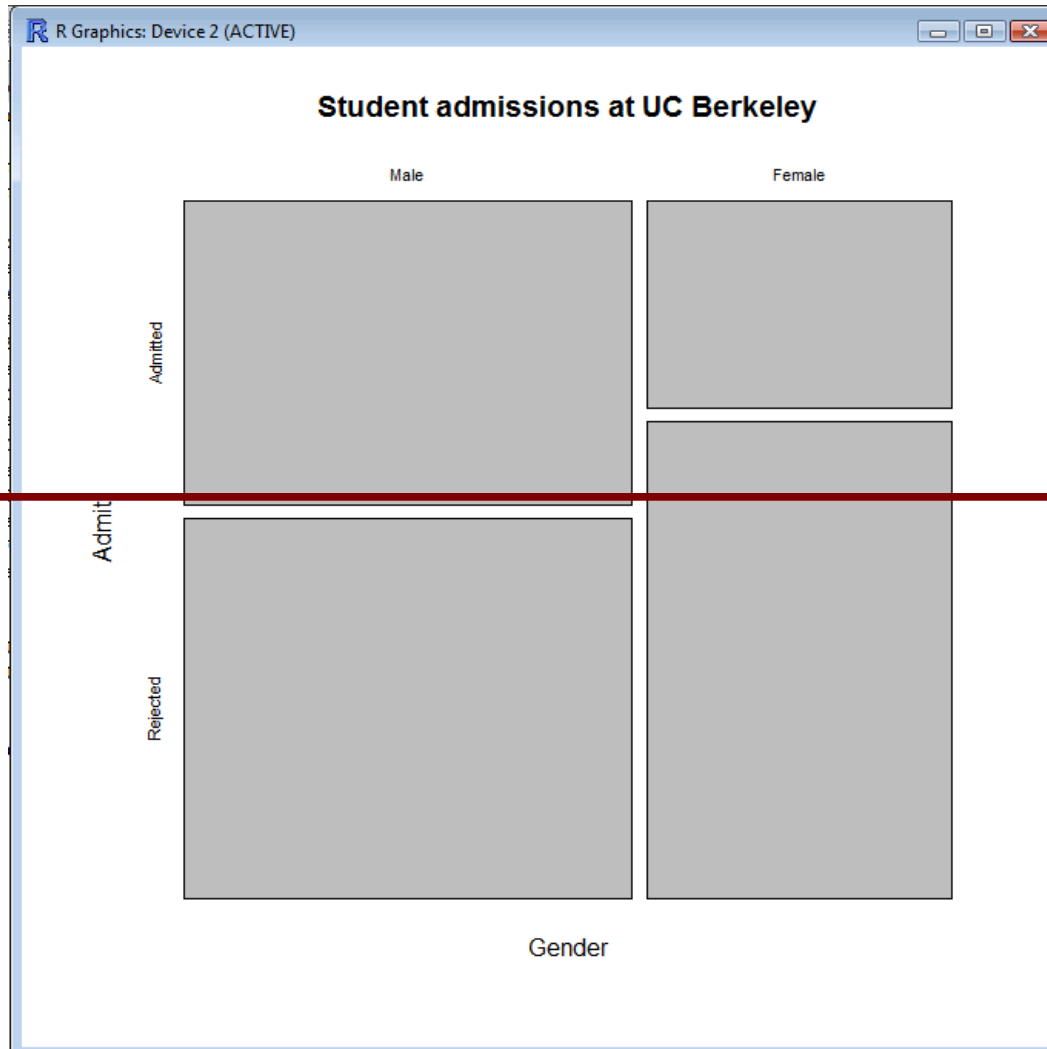
```
# creating the table Admissions by Department
```

```
xtabs(Freq~Dept+Gender+Admit,data=UCBAdmissions)
```

```
apply(UCBAdmissions, c(3,2,1), sum)
```

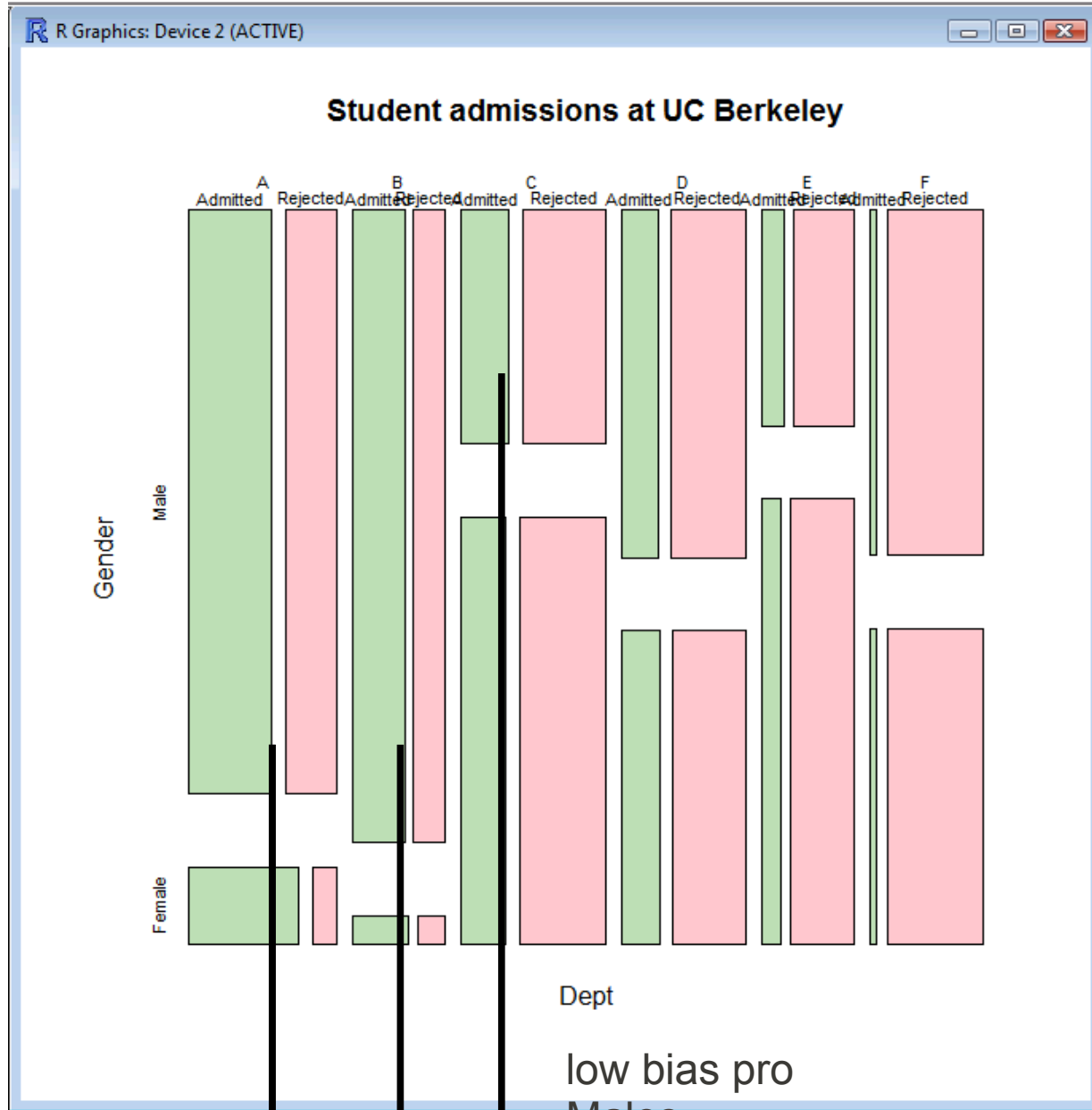
On a mosaicplot, 2 variables are independent when their proportions are the same, this is not the case

```
mosaicplot(apply(UCBAdmissions, c(2, 1), sum), main = "Student admissions at UC Berkeley")
```



More males are admitted!

mosaicplot(UCBAdmissions, sort = 3:1,col = hcl(c(120, 10)),main = "Student admissions at UC Berkeley")



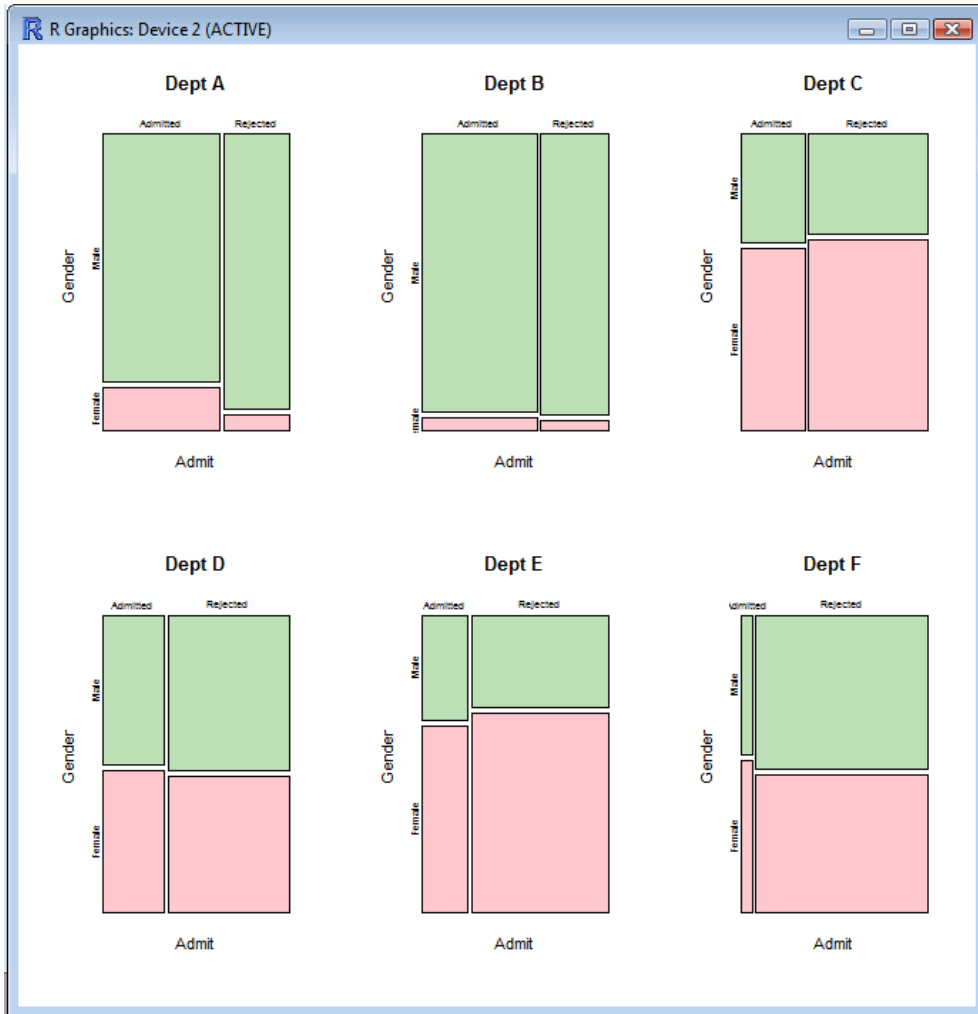
High bias pro
Females

low bias pro
Females

low bias pro
Males

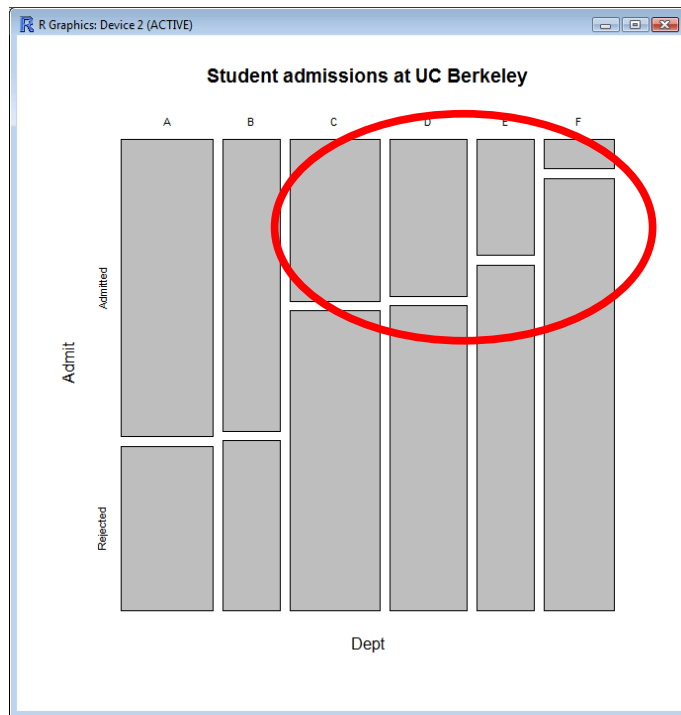
More clear picture:

```
par(mfrow = c(2,3))  
for (dpt in LETTERS[LETTERS <= "F"]) mosaicplot(UCBAdmissions[,dpt], sort = c(1,2), main  
= paste("Dept",dpt),col = hcl(c(120, 10)))
```

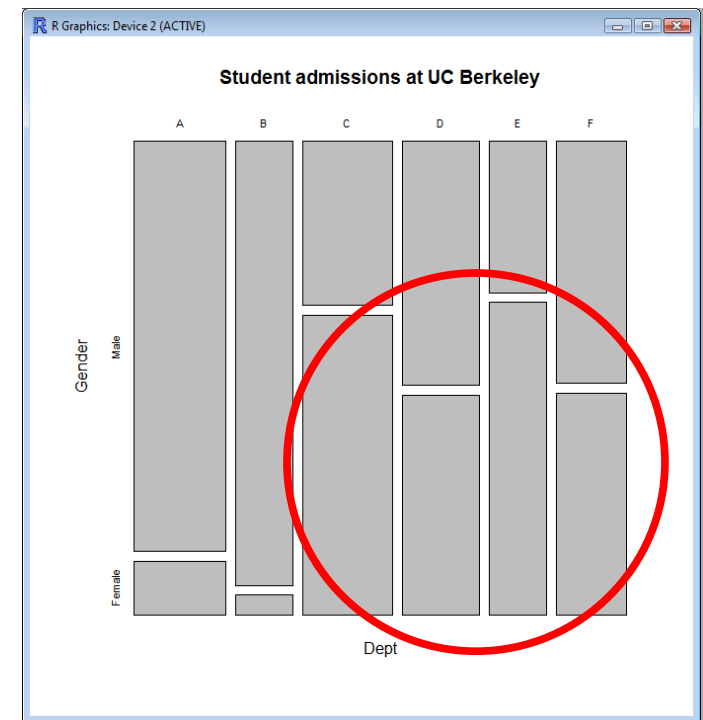


There is very low bias and it favors females, so, why the huge disparity in admissions?

```
# which departments admitted less
people?
mosaicplot(apply(UCBAdmissions, c(3, 1),
sum), main = "Student admissions at UC
Berkeley")
```



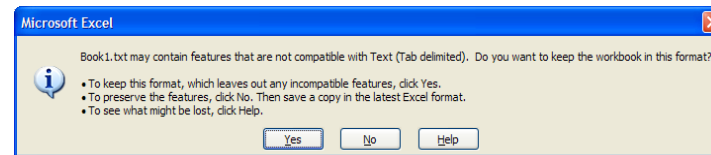
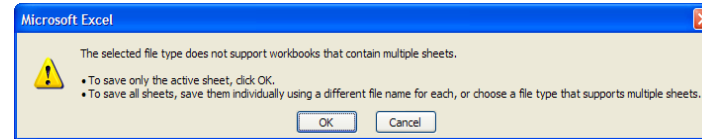
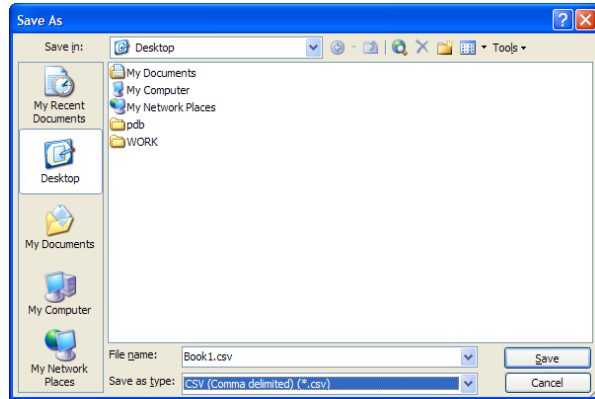
```
# which departments did females
applied to mostly?
mosaicplot(apply(UCBAdmissions, c(3,
2), sum), main = "Student admissions
at UC Berkeley")
```



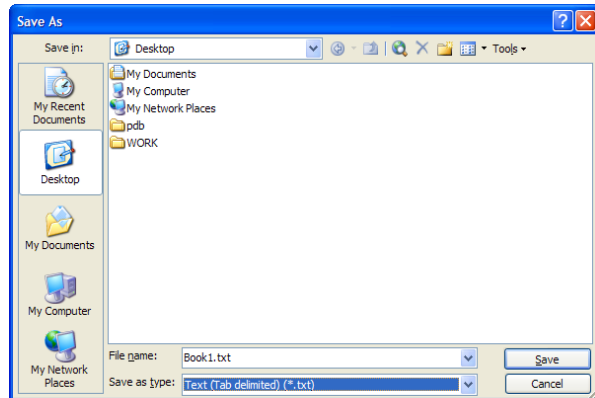
Females applied mostly to departments that admitted less people, basically competing against each other, while males took the departments more accessible

Saving CSV and TAB from Excel

Height (inches)	Weight (lbs)	Color of eyes (1=blue, 2=green, 3=brown, 4=other)	gender (1=male, 2=female)	Year
Height	Weight	Eyecolor	Gender	Year
72	190		1	2001
66	130		2	2001
63	98		3	2001
72.5	210		1	2001
73	175		4	2001



Save as height_weight2.csv



data from:

ECO 231W Econometrics, Summer 07, Session A

Instructor: Tak Wai Chau

http://troi.cc.rochester.edu/~tchau/eco231/height_weight.xls

Let's read the table and check out its data:

```
DataStudents<-read.csv("height_weight2.csv",skip=1)
DataStudents # Height Weight Eyecolor Gender Year
```

(a) Calculate the sample means and standard deviations from each variable.

```
mean(DataStudents$Height)
mean(DataStudents$Weight)
sd(DataStudents$Height)
sd(DataStudents$Weight)
# or
mean(DataStudents[,c("Height","Weight")]) # the mean of height, weight
sd(DataStudents[,c("Height","Weight")]) # the sd of height, weight
```

(b) Calculate the sample means and standard deviations for height and weight, this time by gender.

```
mean(DataStudents[which(DataStudents$Gender==1),c("Height","Weight")]) # the mean of
height, weight
mean(DataStudents[which(DataStudents$Gender==2),c("Height","Weight")]) # the mean of
height, weight
sd(DataStudents[which(DataStudents$Gender==1),c("Height","Weight")]) # the sd of height,
weight
sd(DataStudents[which(DataStudents$Gender==2),c("Height","Weight")]) # the sd of height,
weight
# or
aggregate(DataStudents[,c(1,2,4)], list(DataStudents[,4]), mean)
aggregate(DataStudents[,c(1,2,4)], list(DataStudents[,4]), sd)
```

(c) Calculate the sample means and standard deviations for height and weight, this time by color of eyes.

```
aggregate(DataStudents[,1:3], list(DataStudents[,3]), mean)
```

```
aggregate(DataStudents[,1:3], list(DataStudents[,3]), sd)
```

(d) Suppose it is a random sample of students in the university, test the null hypothesis that the mean weight is 200lb for male students against a two-sided alternative.

Null hypothesis $H_0: \mu = 200$ Alternative hypothesis $H_1: \mu \neq 200$

5% significance level

$m = 177.9864$

$s = 28.42943$

$n = \text{length}(\text{which}(\text{DataStudents}\$Gender == 1)) = 147$

$T = (177.9864 - 200) / (28.42943 / \text{sqrt}(147)) = -9.388184$

On R:

```
t.test(DataStudents$Weight[DataStudents$Gender==1], NULL, "two.sided", mu = 200, paired = FALSE,
var.equal = FALSE, conf.level = 0.95)
```

One Sample t-test

data: DataStudents\$Weight[DataStudents\$Gender == 1]

$t = -9.3882$, $df = 146$, $p\text{-value} < 2.2e-16$

alternative hypothesis: true mean is not equal to 200

95 percent confidence interval:

173.3522 182.6206

sample estimates:

mean of x

177.9864

200 is over the confidence interval, in the rejection zone, so it has to be rejected

(e) Suppose it is a random sample of students in the university, test the null hypothesis that mean weights are the same for male and female students.

null hypothesis: mean weights are the same for male and female students

Null hypothesis $H_0: \mu_1 = \mu_2$ Alternative hypothesis $H_1: \mu \neq \mu_2$

5% significance level

$m_1 = 177.9864$

$m_2 = 133.5093$

$s_1 = 28.42943$

$s_2 = 20.10362$

$n_1 = \text{length}(\text{which}(\text{DataStudents}\$Gender == 1)) = 147$

$n_2 = \text{length}(\text{which}(\text{DataStudents}\$Gender == 2)) = 54$

$T = (177.9864 - 133.5093) / \sqrt{(28.42943^2 / 147 + 20.10362^2 / 54)} = 12.34402$

On R:

```
t.test(DataStudents$Weight[DataStudents$Gender==1],  
DataStudents$Weight[DataStudents$Gender==2], "two.sided", paired = FALSE, var.equal = FALSE,  
conf.level = 0.95)
```

Welch Two Sample t-test

data: DataStudents\$Weight[DataStudents\$Gender == 1] and

DataStudents\$Weight[DataStudents\$Gender == 2]

$t = 12.344$, $df = 133.349$, $p\text{-value} < 2.2e-16$

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

95 percent confidence interval:

37.35046 51.60382

sample estimates:

mean of x mean of y

177.9864 133.5093

Null hypothesis rejected

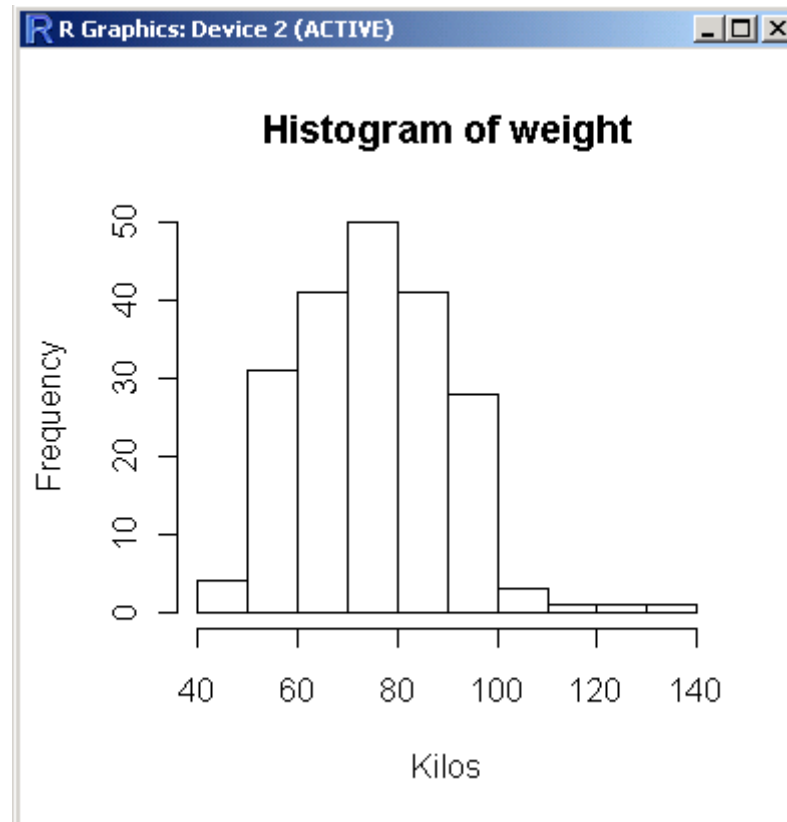
To do a dot plot in R:

```
dotchart(DataStudents$Weight, main='Students Weight',xlab='Weight in pounds')
```

```
stripchart(DataStudents$Weight, method = "stack",xlim =  
c(min(DataStudents$Weight),max(DataStudents$Weight)))
```

To examine a distribution of the weight, an histogram is quite useful:

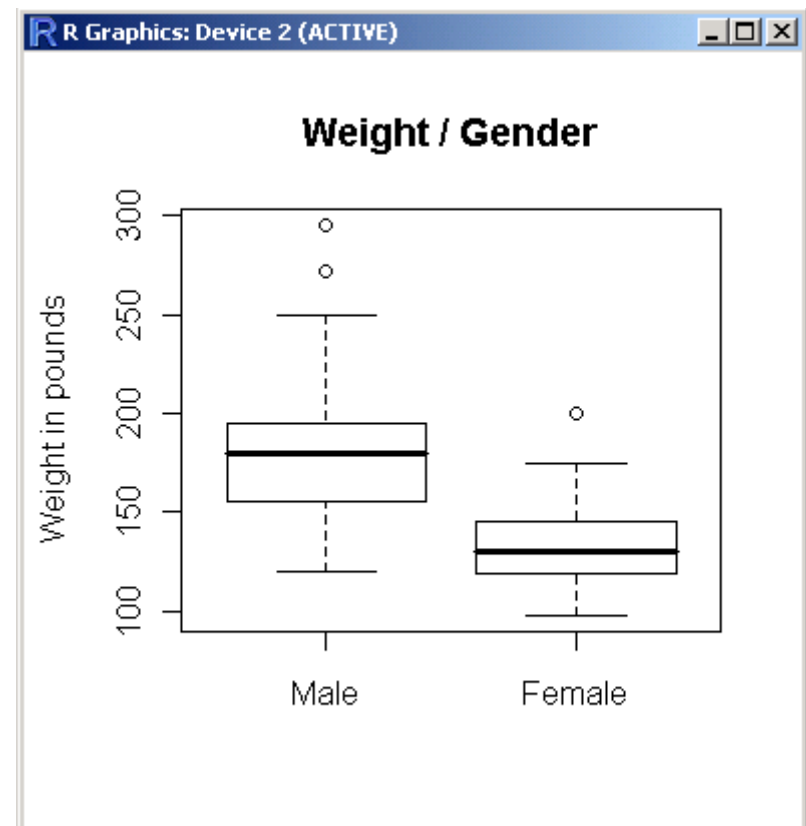
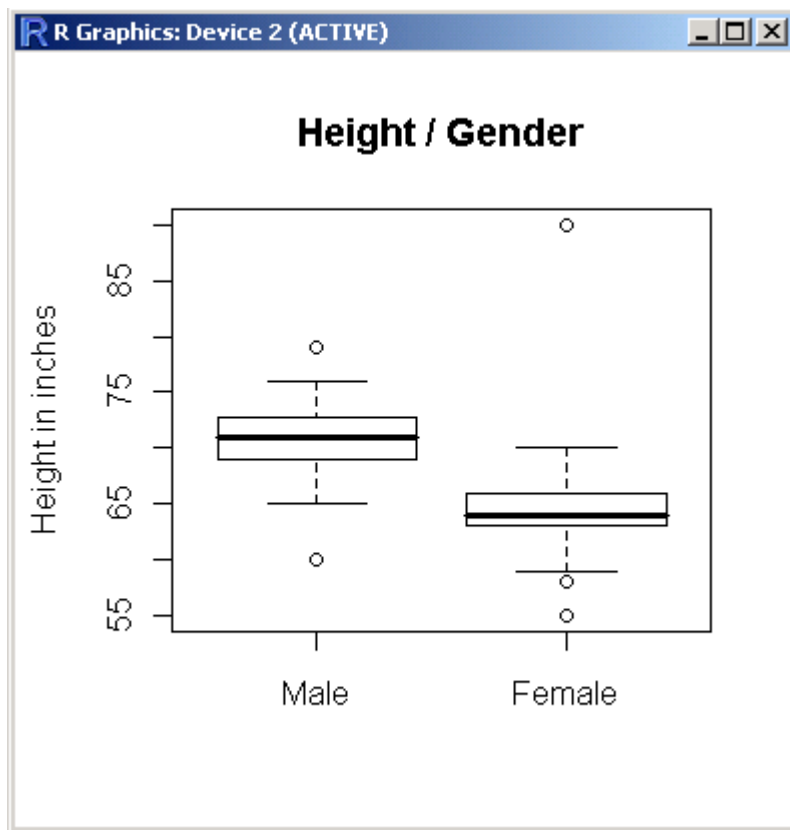
```
hist(DataStudents$Weight*0.45359237,main='Histogram of weight',xlab='Kilos')
```



Are men taller and heavier than women?

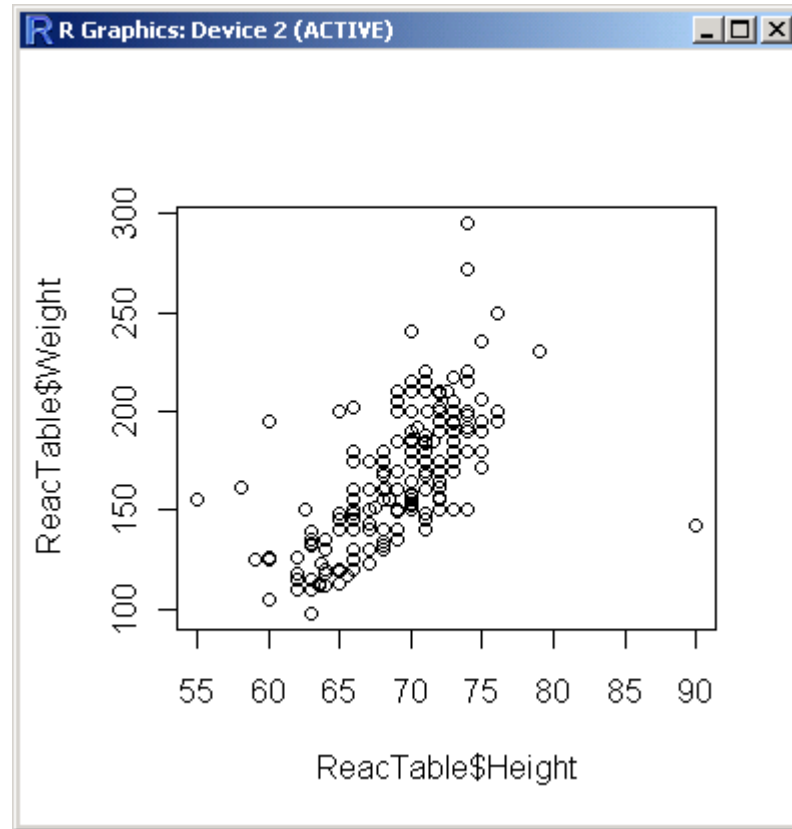
```
boxplot(DataStudents$Height ~ DataStudents$Gender, main='Height / Gender',  
ylab='Height in inches',names=c('Male','Female'))
```

```
boxplot(DataStudents$Weight ~ DataStudents$Gender, main='Weight / Gender',  
ylab='Weight in pounds',names=c('Male','Female'))
```



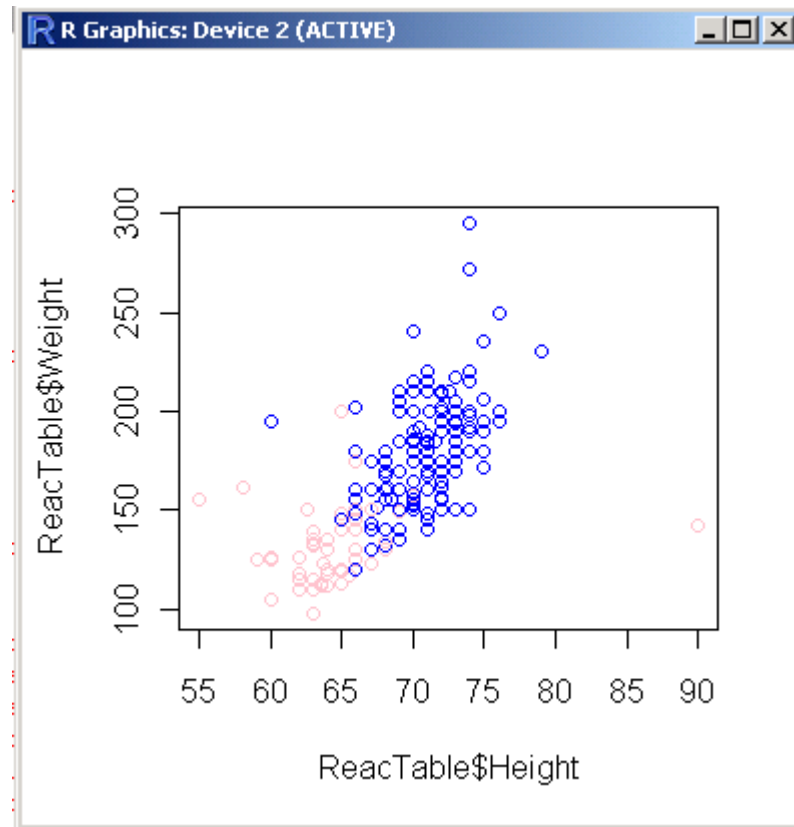
How are weight and height related? A scatter plot will show all the data.

```
plot(DataStudents$Height, DataStudents$Weight)
```



That could be more interesting if the gender was also involved:

```
sex<-ifelse(DataStudents$Gender==1,'blue','pink')  
plot(DataStudents$Height, DataStudents$Weight, col=sex)
```



Who's fat?

Using the BMI(Body Mass Index) formula, BMI Overweight ≥ 25

$BMI = (\text{weight in pounds} * 703) / \text{height in inches}^2$

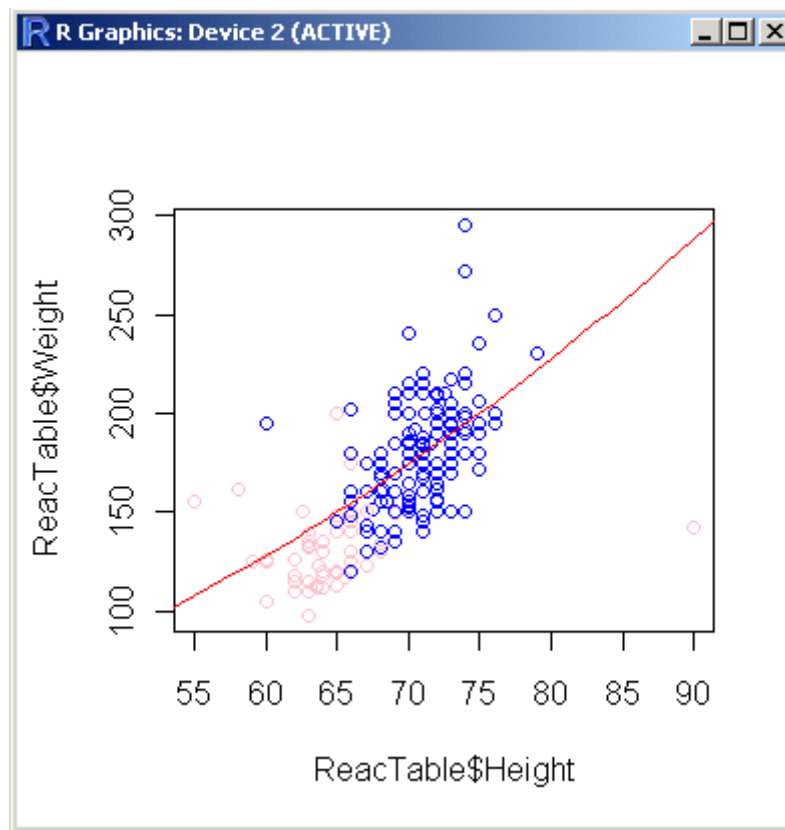
So, the curve that separates Overweight people from the rest is:

$\text{weight} = (25 * \text{height in inches}^2) / 703$

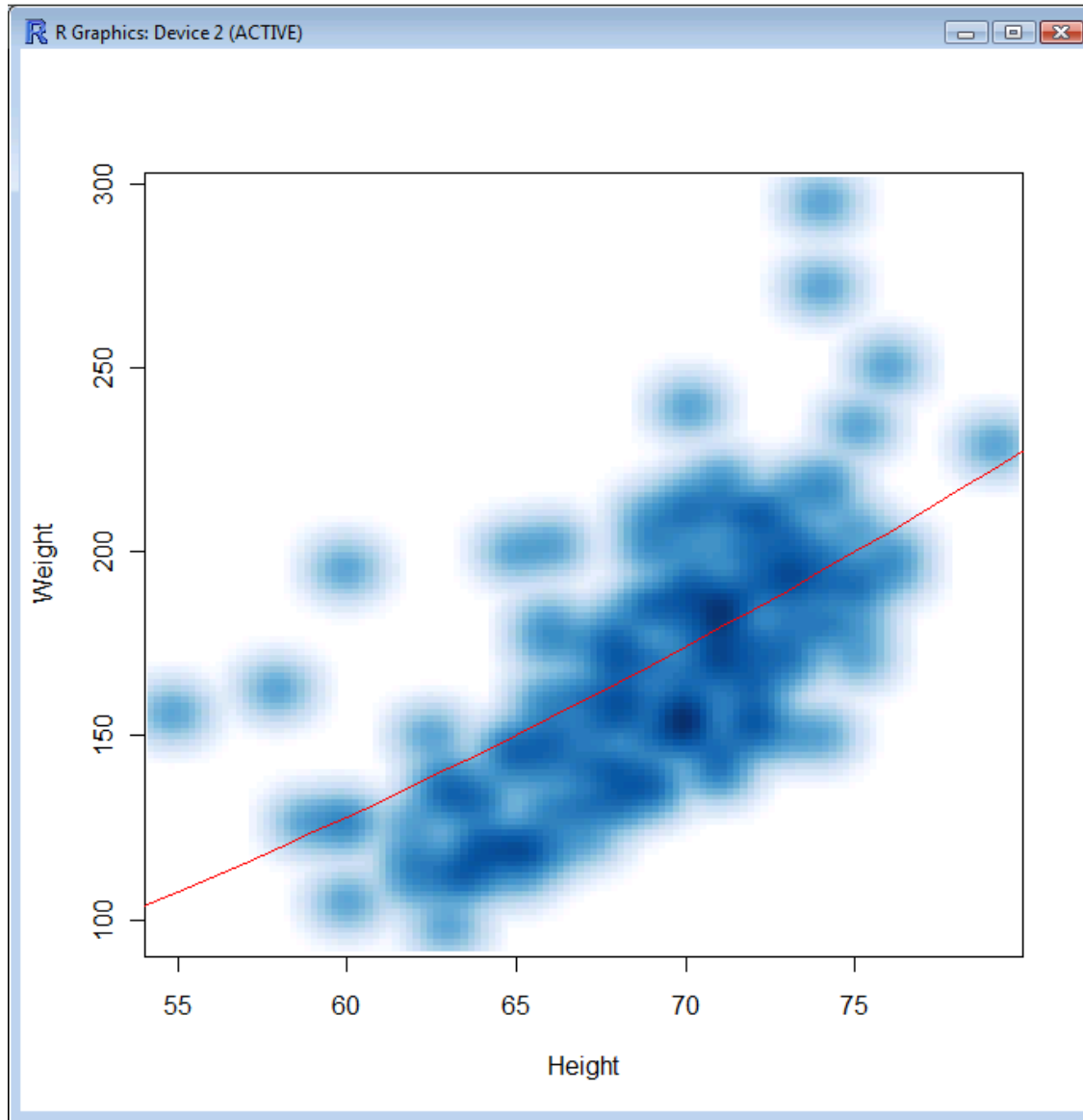
In R:

```
sex<-ifelse(DataStudents$Gender==1,'blue','pink')
plot(DataStudents$Height, DataStudents$Weight, col=sex)
x1<- 50:100 #height
y1<- 25 * x1 * x1 / 703 #weight
points(x1, y1,type='l',col='red')
```

It seems like more men than women are Overweight in this sample data. But there are almost 3 times more men than women and the scatter plot shows one plot for one or more coincident data values and draws the blue over the pink!



```
smoothScatter(DataStudents, nrpoints=0)
x1<- 50:100 #height
y1<- 25 * x1 * x1 / 703 #weight
points(x1, y1,type='l',col='red')
```



Connecting to Excel through ODBC

```
library(RODBC)
connection <- odbcConnectExcel("Forbes2000.xls", readOnly = TRUE)
#odbcConnectExcel2007
connection
sqlTables(connection)

odbcGetInfo(connection)

sqlFetch(connection, 'Sheet1$')
sqlQuery(connection, "select * from [Sheet1$]")
dfForbes2000 <- sqlFetch(connection, 'Sheet1$')

class(dfForbes2000)
# names of the columns
names(dfForbes2000)
colnames(dfForbes2000)
# names of the rows are the row numbers, usually plenty of them!
rownames(dfForbes2000)

close(connection)

layout(matrix(1:2, nrow = 2))
hist(dfForbes2000$marketvalue)
hist(log(dfForbes2000$marketvalue))
```

Problem: the data from a chemical analysis comes in several columns (table 1), each for a different concentration, 10, 20 and 30. AUC is area under the concentration-time curve. The concentration value is stored with the column name, but some statistical analysis would require it to be on a column of its own (table 2)

reactime	AUC10	AUC20	AUC30
10	361	729	1105
25	541	1089	1645
55	721	1449	2185
80	901	1809	2725
85	1081	2169	3265
105	1261	2529	3805
110	1441	2889	4345
135	1621	3249	4885
150	1801	3609	5425
155	1981	3969	5965

Table 1

The data is on a TAB delimited file datawnoise.txt and it will have to be converted and saved onto file datawnoise2.txt

ReacTime	Concentration	AUC
10	10	361
10	20	729
10	30	1105
25	10	541
25	20	1089
25	30	1645
55	10	721
55	20	1449
55	30	2185
80	10	901
80	20	1809
80	30	2725
85	10	1081
85	20	2169
85	30	3265
105	10	1261
105	20	2529
105	30	3805
110	10	1441
110	20	2889
110	30	4345
135	10	1621
135	20	3249
135	30	4885
150	10	1801
150	20	3609
150	30	5425
155	10	1981
155	20	3969
155	30	5965

Table 2

```
# read table data, TAB separated
RTable<-read.table("datawnoise.txt", header = T, sep = "\t")
# examine the data
RTable
# store the number of rows and columns
iNrows<-dim(RTable)[1]
iNrows
iNcols<-dim(RTable)[2]
iNcols
# reactime values are needed for each AUC value
rep(RTable$reactime,iNcols-1)
# sort the repeated reactime values
ReactTime<-sort(rep(RTable$reactime,iNcols-1))
ReactTime
#get the AUC col names
sColName<-colnames(RTable)[-1]
sColName
# the concentration values are extracted from the AUC column names'
sub( "\\D+", "", sColName,perl = TRUE)
# concentration values are needed for each original row
Concentration<-rep(sub( "\\D+", "", sColName,perl = TRUE),iNrows)
Concentration
# convert to vector, by columns
AUC<-c(t(as.matrix(RTable[-1])))
#create a matrix with the new data
newdata<-cbind(ReactTime,Concentration,AUC)
# save the new data
write.table(newdata, file = "datawnoise2.txt", sep = "\t",row.names =FALSE, quote =FALSE)
```

Example from R Graph Gallery by Romain François

<http://addictedtor.free.fr/graphiques/RGraphGallery.php?graph=139>

Scatterplots with smoothed densities color representation

```
library("geneplotter") ## from BioConductor  
require("RColorBrewer") ## from CRAN
```

```
x1 <- matrix(rnorm(1e4), ncol=2)  
x2 <- matrix(rnorm(1e4, mean=3, sd=1.5), ncol=2)  
x <- rbind(x1,x2)
```

```
layout(matrix(1:4, ncol=2, byrow=TRUE))  
op <- par(mar=rep(2,4))  
smoothScatter(x, nrpoints=0)  
smoothScatter(x)  
smoothScatter(x, nrpoints=Inf,  
              colramp=colorRampPalette(brewer.pal(9,"YlOrRd")),  
              bandwidth=40)  
colors <- densCols(x)  
plot(x, col=colors, pch=20)
```

```
par(op)
```


Open PennState92.xls

Save as

PennState92.csv

```
PennStudents<-read.csv("PennState92.csv",row.names=1,header =F)
```

```
PennStudents
```

Statistical Inference

Distributions

standard univariate discrete distributions




binom	Binomial Distribution
nbinom	Binomial negative Distribution
pois	Poisson Distribution
geom	Geometric Distribution
hyper	Hipergeometric Distribution

Statistical Inference

Distributions

standard univariate continuous distributions



unif	Uniform Distribution
norm	Normal Distribution
lnorm	Log-normal Distribution
chisq	Chi Square Distribution
t	Student t Distribution
f	f Distribution Distribution
exp	Exponential Distribution
gamma	Gamma Distribution
weibull	Weibull Distribution
cauchy	Cauchy Distribution
beta	Beta Distribution
logis	Logistic
signrank	Wilcoxon Signed Rank Statistic
wilcox	Wilcoxon Rank Sum Statistic

Statistical Inference

Distributions

Multivariate continuous distributions

mvrnorm multivariate normal (pkg MASS)
wish Wishart (pkg MCMCpack)
iwish inverse Wishart (pkg MCMCpack)
dirichlet Dirichlet (pkg MCMCpack)
mvnorm multivariate normal (pkg mvtnorm)
mvt multivariate t (pkg mvtnorm)

Multivariate discrete distributions

{ multinom multinomial

Statistical Inference

Distributions

Functions for distribution
"dist"

`ddist(x, ... params ..., log=FALSE)` density function or probability density function, `log=TRUE` for log-likelihoods

`pdist(q, ... params ..., lower.tail=TRUE, log.p=FALSE)` distribution function (cumulative density function), `lower.tail=FALSE` for one-tailed upper p-values, `log.p=TRUE` for very small p-values

`qdist(p, ... params ..., lower.tail=TRUE, log.p=FALSE)` quantile function (inverse cumulative density function)

`rdist(n, ... params ...)` random deviate generator, `n` is the number of deviates

Statistical Inference

Distributions

R has several algorithms for pseudo random number generators (RNG), these algorithms will generate the same sequence of pseudo random numbers by specifying the seed for the algorithm (to start the sequence) and the version number (the algorithms are updated for bugs and improvements)

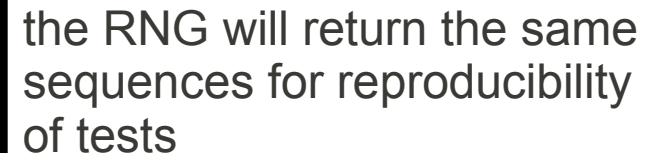
RNG functions

RNGkind
RNGversion
set.seed

For simplicity, the examples will use the default RNG and change the seed to assure reproducibility of results

```
rnorm(5) # draw a sample of size 5 from a normal distribution  
rnorm(5) # draw a sample of size 5 from a normal distribution  
rnorm(5) # draw a sample of size 5 from a normal distribution  
set.seed(2012) # setting a seed for the RNG  
rnorm(5) # draw a sample of size 5 from a normal distribution  
rnorm(5) # draw a sample of size 5 from a normal distribution  
rnorm(5) # draw a sample of size 5 from a normal distribution  
set.seed(2012) # setting a seed for the RNG  
rnorm(5) # draw a sample of size 5 from a normal distribution  
rnorm(5) # draw a sample of size 5 from a normal distribution  
rnorm(5) # draw a sample of size 5 from a normal distribution
```

the RNG will return the same sequences for reproducibility of tests



Statistical Inference

Distributions

```
rnorm(1) # draw a sample of size 1 from a normal distribution  
rnorm(5) # draw a sample of size 5 from a normal distribution  
rnorm(5,mean=1,sd=3) # draw a sample of size 5 from a normal distribution with mean 1 and  
standard deviation 3  
rnorm(60, 4, 7) # draw a sample of size 60 from a normal distribution with mean 4 and standard  
deviation 7
```

```
dnorm(0) # density for the normal distribution on point 0  
dnorm(1) # density for the normal distribution on point 1  
dnorm(3) # density for the normal distribution on point 3  
pnorm(0) # acumulated probability for the normal distribution below point 0  
pnorm(3) # acumulated probability for the normal distribution below point 3  
qnorm(0.5) # quantile 50% of the normal distribution is 0  
qnorm(0.9986501) # quantile for pnorm(3)  
x<-seq(-4,4,length=200) # create a sequence of 200 values [-4, 4]  
plot(x,dnorm(x),type="l") # plot a normal distribution
```

```
rpois(50, lambda=3) # draw a sample of size 50 from a Poisson distribution with lambda=3
```

```
rbinom(100, 40, .25) # draw a sample of size 100 from a Binomial distribution with size=40 and  
prob=.25
```

Statistical Inference

Sampling

sample draws a random sample from a population, replacement=T for sampling with replacement

```
sample(5) # random permutation of sequence [1, 5]
```

```
sample(20) # random permutation of sequence [1, 20]
```

```
sample(seq(3:45), 10) # random sample of size 10 from [3, 45]
```

```
sample(4, 10, prob = c(0.3, 0.5, 0.1, 0.1), replace = T) # random sample of size 10 from sequence [1, 4] with different probabilities of being chosen P(1)=.3, P(2)=.5 etc...
```

```
sample(c(0,1), 20, replace = TRUE) # 20 Bernoulli trials
```

```
sample(c("heads","tails"),1) # flipping a coin once
```

```
sample(c("heads","tails"),5, replace=T) # flipping a coin 5 times
```

```
sample(6,1) # rolling a dice once
```

```
sample(6,20,replace=T) # rolling a dice 20 times
```

```
sample(c("rock","paper", "scissors"),1) # draw rock-paper-scissors once
```

```
sample(39, 7) # drawing lottery numbers
```


Statistical Inference

Tests

One-Sample and Paired Data



t.test t-test
wilcox.test Wilcoxon signed rank

Two-Sample



t.test t-test
wilcox.test Wilcoxon 2-sample rank-sum

k-Sample



kruskal.test Kruskal-Wallis
oneway.test One-way ANOVA

Unified Unpaired Nonparametric Tests



spearman2

Statistical Inference

Tests

```
# Student's sleep data  
plot(extra ~ group, data = sleep)  
# t test  
t.test(extra ~ group, data = sleep)
```

Statistical Inference

Tests

Explanatory response	continuous	categorical
categorical	Logistic regression	Cpntgency tables, 2x2, Chi2, Fisher
continuous	Regression, correlation	Anova, t-test

Statistical Inference

Correlations

`cor()` correlations

`cov()` covariances

`cor.test()` test a single correlation coefficient

`corrgram()` plot correlograms

```
# Correlations/covariances among numeric variables in  
# dataframe mtcars. Use listwise deletion of missing data.  
cor(mtcars, use="complete.obs", method="kendall")  
cov(mtcars, use="complete.obs")
```

```
# Correlation matrix from mtcars  
# with mpg, cyl, and disp as rows  
# and hp, drat, and wt as columns  
x <- mtcars[1:3]  
y <- mtcars[4:6]  
cor(x, y)
```

Statistical Inference

Correlations

First Correlogram Example

```
library(corrgram)  
corrgram(mtcars, order=TRUE, lower.panel=panel.shade, upper.panel=panel.pie,  
text.panel=panel.txt, main="Car Milage Data in PC2/PC1 Order")
```

Second Correlogram Example

```
library(corrgram)  
corrgram(mtcars, order=TRUE, lower.panel=panel.ellipse, upper.panel=panel.pts,  
text.panel=panel.txt, diag.panel=panel.minmax, main="Car Milage Data in PC2/PC1 Order")
```

Third Correlogram Example

```
library(corrgram)  
corrgram(mtcars, order=NULL, lower.panel=panel.shade, upper.panel=NULL,  
text.panel=panel.txt, main="Car Milage Data (unsorted)")
```

<http://www.statmethods.net/stats/correlations.html>

Statistical Inference

Linear Regression

Model Fitting

Multiple linear regression: `lm`, `ols` [Residuals: `residuals.ols`]
General linear model: `glm`, `glmD` (just change `glm` to `glmD` in call)
Binary logistic model: `glm`, `lrm`
Ordinal logistic model: `lrm` [Residuals: `residuals.lrm`]
Parametric survival models: `survreg`, `psm`
Cox proportional hazards model: `coxph`, `cph` [Residuals: `residuals.coxph`,
`residuals.cph`]
Buckley-James censored least squares regression: `bj`

After-Fitting Analysis

Specifications for predictor transformations used by `Design`: `specs`
Predictions and confidence intervals: `predict.Design`
Overly influential observations: `which.influence`
Sensitivity to unmeasured confounder in `lrm`: `sensuc`
Create S function to evaluate fitted equation: `Function`
Compose LATEX code for typesetting algebraic expressions containing model fit:
`latex.Design`
Odds and hazard ratios and effect differences: `summary.Design`
General contrasts and CLs: `contrast.Design`
ANOVA: `anova.Design`
Fast backward stepdown variable selection: `fastbw`
Huber-White-Efron robust covariance matrix estimator with optional cluster
sampling adjustment: `robcov`
Bootstrap nonparametric covariance matrix estimator with optional cluster
sampling adjusting: `bootcov`
Generate data frame with predictor combinations: `gendata`

Statistical Inference

Linear Regression

Years of experience and executive salaries in millions

```
exec.df = read.delim("salary.txt",col.names=c("years.experience","exec.salary"), header =  
F)
```

```
class(exec.df)
```

```
plot(exec.df)
```

```
attach(exec.df)
```

```
exec.salary.lm = lm(exec.salary~years.experience) # regression
```

```
abline(exec.salary.lm) # regression line
```

```
summary(exec.salary.lm) # SUMMARY OF THE REGRESSION PROCESS
```

```
exec.salary.lm$residuals # check residuals
```

```
plot(exec.salary.lm$residuals) # plot residuals
```

```
abline(h=0)
```

```
# horizontal line on  $y=0$  because residuals are centered around it
```

```
# data far from this line was not predicted well by the regression model, because the  
residual is high
```

```
exec.salary.lm$fitted.values # predicted salary for each executive, by the adjusted model
```

```
predict.lm(exec.salary.lm,data.frame(years.experience=0)) # to predict the salary for a new  
executives, with 0 years of experience
```

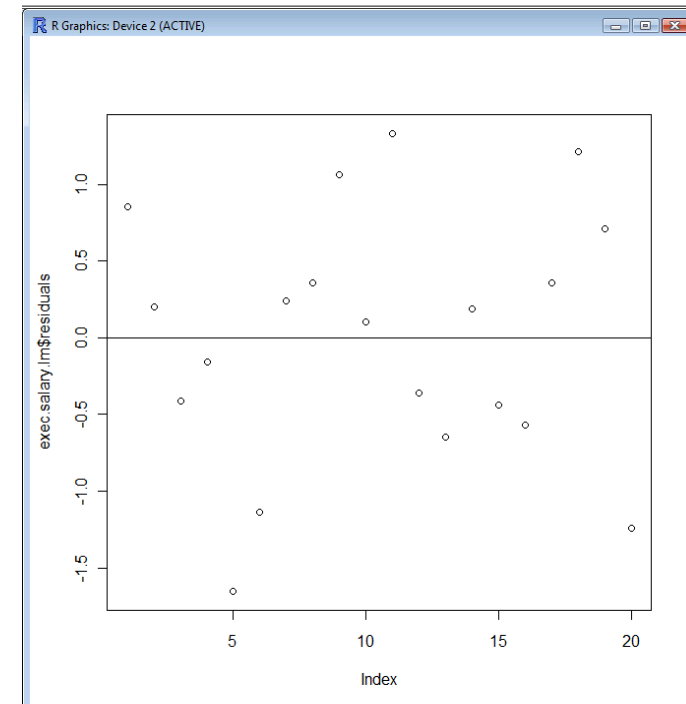
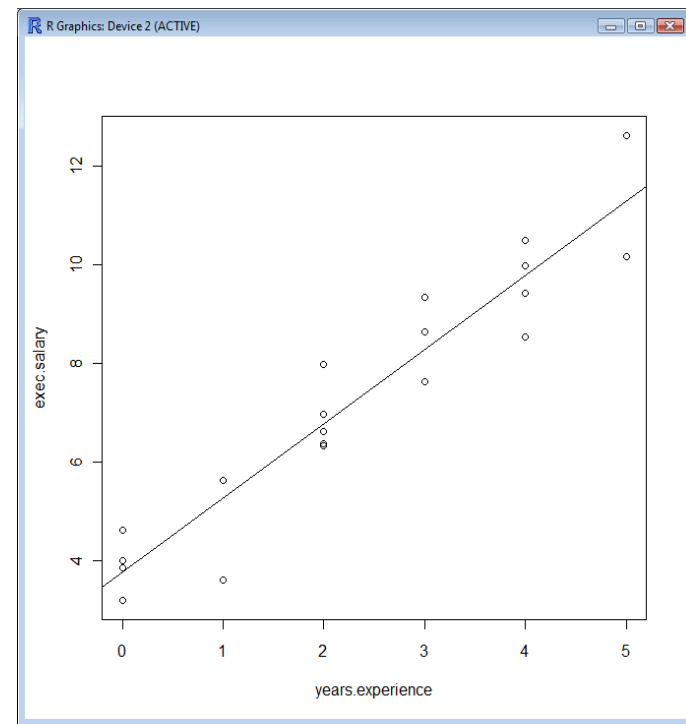
```
predict.lm(exec.salary.lm,data.frame(years.experience=c(1.5,2,3.5))) # to predict the salary  
for 3 new executives, with 1.5, 2 and 3.5 years of experience
```

Statistical Inference

Linear Regression

Simple Linear Regression

0	4.61
2	6.97
2	6.36
2	6.61
1	3.61
5	10.15
0	4.00
3	8.63
3	9.34
0	3.86
5	12.62
4	9.42
3	7.63
4	9.97
2	6.33
0	3.19
1	5.62
2	7.98
4	10.49
4	8.54



Statistical Inference

Linear Regression

Multiple linear regression

Instead of a regression line there is a regression plane

```
data(mtcars) # load dataset
```

```
attach(mtcars)
```

```
cars.lm = lm(mpg~hp+wt) # explain gas milleage in function of power and weight
```

```
summary(cars.lm)
```

```
# the model is: gas milleage = 37.22 - 0.03 power - 3.87 weight
```

```
# the more powerful the car, the lower the MPG, less milles per gallon
```

```
# the heavier the car, the lower the MPG, less milles per gallon
```

```
# R-Squared is 82%, these 2 variables explain the gas milleage very well
```

```
# let's draw the residuals to check if any car behaves differently
```

```
plot(cars.lm$residuals)
```

```
abline(h=0)
```

```
# to predict how many milles per gallon a car with 150 horse power and weight 2.t tons:
```

```
predict.lm(cars.lm,data.frame(hp=150,wt=2.5))
```

Statistical Inference

ANOVA

When is Anova Used?

- All explanatory variables are categorical—unquantified and unordered
- The explanatory variables are called ‘factors’; each has two or more levels.
- If there is one factor with two levels, use Student’s t.
- If there is one factor with three+ levels, use one-way Anova.
- If there are two factors, use two-way Anova.
- For three factors, use three-way Anova, and so on...
- If every combination of factors is present, you have a factorial design, allowing you to study interactions between variables (and order no longer matters!).

Statistical Inference

ANOVA

Modelling the mileage (mpg) with variables weight (wt), transmission type (am), and/or the number of cylinders (cyl), 3 models:

```
data(mtcars) # load dataset
res.lm = lm(mpg ~ wt, data = mtcars)
res.lm2 = lm(mpg ~ wt + cyl, data = mtcars)
res.lm3 = lm(mpg ~ wt + cyl + am, data = mtcars)
```

```
#Applying anova() to a single model object produces an analysis of variance for computing the F-test of whether the constant mean model is appropriate
anova(res.lm)
```

```
# there is a relationship between mpg and wt
```

```
# Applying anova() to two model objects for test if nested models produces an analysis of variance for computing the F-test of whether the extra term is warranted.
```

```
anova(res.lm, res.lm2)
```

```
# the differences are significant, the number of cylinders seems to have a statistically significant effect.
```

```
# Applying anova() to three nested models produces sequential F-tests.
anova(res.lm, res.lm2, res.lm3)
```

```
# This shows that in the model mpg modeled by wt and cyl, the cyl variable is statistically significant.
# However, in the full model of mpg modeled by wt, cyl, and am, the variable am is not statistically significant.
```

```
# http://wiener.math.csi.cuny.edu/st/stRmanual/anova.pdf
```

Statistical Inference

References/to learn more:

The R book

Michael J. Crawley pp 370

2018 John Wiley & Sons Ltd

Basic statistics using R pp. 213

Jarno Tuimala (CSC) and Dario Greco (HY)

<http://www.csc.fi/english/csc/courses/archive/R2008s>

Statistics: an introduction using R

Michael J. Crawley pp 125

2016 John Wiley & Sons Ltd

Statistics with R

Vincent Zoonekynd, pp 620

http://zoonek2.free.fr/UNIX/48_R/all.html

Aprendizaje del software estadístico R: un entorno para simulación y computación estadística

Prof. Alberto Muñoz García

Departamento de Estadística

Universidad Carlos III de Madrid

<http://ocw.uc3m.es/estadistica/aprendizaje-del-software-estadistico-r-un-entorno-para-simulacion-y-computacion-estadistica/resolveUid/4b28fd8154f6521f963aa058ec6baf31>

Introductory Statistics with R

Peter Dalgaard, pp 109

2018 Springer

Geographic Data Analysis

Pat Bartlein

<http://geography.uoregon.edu/bartlein/courses/geog417/lectures/lec10.htm>

Software Tools, Part 1: introduction to R software

Petri Koistinen

<http://www.rni.helsinki.fi/~pek/s-tools/test-ci.r>

Chem 351 Archives Page

David Harvey

<http://fs6.depauw.edu:50080/~harvey/Chem%20351/PDF%20Files/Handouts/RDocs/Using%20R%20for%20Linear%20Regression.pdf>

Thomas AP Statistics

thomasmathematics.com

<http://www.thomasmathematics.com/Aims/Ch3Aim30001.pdf>

Quick-R

Rob Kabacoff

<http://www.statmethods.net/stats/correlations.html>

The Stem and Tendril simplified R manual

Professors Franzblau, Poje and Verzani of the College of Staten Island

<http://wiener.math.csi.cuny.edu/st/stRmanual/>

- The rgdal Package

October 17, 2008

Title for the Geospatial Data Abstraction Library

Version .5-27

Date -10-09

Depends (>= 2.3.0), methods, sp

LazyLoad

Description bindings to Frank Warmerdam's Geospatial Data Abstraction Library (GDAL) (>= 1.3.1) and access to projection/transformation operations from the PROJ.4 library. The GDAL and PROJ.4 libraries are external to the package, and, when installing the package from source, must be correctly installed first. Both GDAL raster and OGR vector map data can be imported into R, and GDAL raster data and OGR vector data exported. Use is made of classes defined in the sp package.

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Maintainer Bivand <Roger.Bivand@nhh.no>

License (>= 2)

URL ://www.gdal.org, <http://rgdal.sourceforge.net/>, <http://sourceforge.net/projects/rgdal/>

System Requirements for building from source:GDAL >= 1.3.1 library from <http://www.gdal.org/download.html> and PROJ.4 (proj >= 4.4.9) from <http://proj.maptools.org/>

- OGR Simple Feature Library

The OGR Simple Features Library is a C++ open source library (and commandline tools) providing read (and sometimes write) access to a variety of vector file formats including ESRI Shapefiles, S-57, SDTS, PostGIS, Oracle Spatial, and Mapinfo mid/mif and TAB formats.

OGR is a part of the GDAL library.

<http://www.gdal.org/ogr/>

R and GIS

R has several packages that can work with GIS data, the most commonly used is the rgdal Package. The acronym rgdal stands for "R Geospatial Data Abstraction Library".

The rgdal Package provides bindings to Frank Warmerdam's Geospatial Data Abstraction Library (GDAL), this library can work with both raster and vector data in many of the available GIS formats in use. The vector library (OGR) is incorporated into GDAL (raster library) and it is fine to mention either one as separate libraries or GDAL as a whole. RGDAL can work with GDAL raster and OGR vector map files, and it can use both together.

Using rgdal

Loading the library:

```
> library(rgdal)
```

```
Loading required package: sp
```

```
Geospatial Data Abstraction Library extensions to R successfully loaded
```

```
Loaded GDAL runtime: GDAL 1.5.3, released 2008/09/09
```

```
GDAL_DATA: C:/PROGRA~1/R/R-28~1.0/library/rgdal/gdal
```

```
Loaded PROJ.4 runtime: Rel. 4.6.1, 21 August 2008
```

```
PROJ_LIB: C:/PROGRA~1/R/R-28~1.0/library/rgdal/proj
```

```
>
```

To get a list of the available drivers:

```
> getGDALDriverNames()
```

	name	long_name	create	copy
1	AAIGrid	Arc/Info ASCII Grid	FALSE	TRUE
2	ADRG	ARC Digitized Raster Graphics	TRUE	FALSE
3	AIG	Arc/Info Binary Grid	FALSE	FALSE

```
...
```

These are just the first 3, there are over 70, including geoTIFF, ESRI HDR, Erdas IMG, Idrisi RST, USGS DEM, etc...

```
# To get the gdal version:
getGDALVersionInfo()

# Loading dem30m_erdas.img (about 5 Megs):
dem30 <- readGDAL('dem30m_erdas.img')

# Getting the projection, datum, etc...
proj4string(dem30)

# What kind of variable is dem30?
class(dem30)

# Getting detailed information about dem30:
summary(dem30)

# dimensions and their names
dim(dem30)
names(dem30)

# Plotting a density map:
plot(density(dem30$band1))

# read as GDALReadOnlyDataset
dem30 <- GDAL.open('dem30m_erdas.img', read.only = TRUE)
# Displaying the raster
displayDataset(dem30, offset=c(0,0), region.dim=dim(dem30), reduction=1, band=1)

# Lattice (trellis) plot method for spatial data with attributes
spplot(as(dem30, "SpatialGridDataFrame"))
```

```
# storing the elevation on a matrix
rt <- as.matrix(getRasterTable(dem30)[,3])

# fixing the dimensions
rm<-matrix(rt,dim(dem30)[1],dim(dem30)[2],byrow=T)
dim(rt)
dim(rm)

# using function image to show the DEM
image(1:dim(dem30)[1],1:dim(dem30)[2],rm)

# using function persp to show the DEM
v1 <- seq(1,dim(dem30)[1],100)
v2 <- seq(1,dim(dem30)[2],100)
persp(1:length(v1), 1:length(v2),rm[v1,v2] )
```


Cholera mortalities, Soho

Load unit0_slides.R

and read unit0_slides-2x2.pdf

To learn more:

One-day introductory course on Spatial Data Analysis with R
www.bias-project.org.uk/ASDARcourse

Geographic Data Analysis
Geog 4/517, Pat Bartlein
<http://geography.uoregon.edu/bartlein/courses/geog417/syll09.htm>

R for Medicine and Biology
Paul D. Lewis pp 58
Jones and Bartlett Series in Biomedical Informatics

Applied Spatial Data Analysis with R
<http://www.amazon.com/Applied-Spatial-Data-Analysis-Use/dp/0387781706>