R: A short course

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SMEP, October 2009

Overview

I. Hour 1:

   A. What is R: An introduction

   B. Graphical displays and EDA

II. Hour 2:

   A. Multivariate analysis

   B. Programming in R

III. Not covered

   A. The general linear model and its special cases (ANOVA), multilevel models

   B. Advanced graphics

What is R: an introduction

I. What is it

II. How to get it

III. Entering or getting data

IV. Basic descriptive stats

R: statistics for all of us

I. What is it?

II. Why use it?

III. Common (mis)perceptions

IV. Examples for personality and individual differences research

R: What is it?

I.R: An international collaboration

II.R: the open source - public domain version of S/S+

III.R: written by statisticians (and all of us) for statisticians (and the rest of us)

IV.R: an extensible language

Common statistical programs

General	Specialized
R	AMOS
S+	EQS
SAS	LISREL
SPSS	MPlus
STATA	Mx
SYSTAT	your favorite program.

Common statistical programs most are costly

General	Specialized
R	AMO$
$+	EQ$
A	LI$REL
$P$$	MPlu$
$TATA	Mx (open Mx is in R)
YTAT	your favorite program.

R: a way of thinking

(from the R point of view)

- "R is the lingua franca of statistical research. Work in all other languages should be discouraged."
- "This is R. There is no if. Only how."
- "Overall, SAS is about 11 years behind R and S-Plus in statistical capabilities (last year it was about 10 years behind) in my estimation."

Taken from the R.-fortunes (selections from the R.-help list serve)

But it is open source - how can you trust it?

I. Q: When you use it [R], since it is written by so many authors, how do you know that the results are trustable?

II. A:The R engine [...] is pretty well uniformly excellent code but you have to take my word for that. Actually, you don't. The whole engine is open source so, if you wish, you can check every line of it. If people were out to push dodgy software, this is not the way they'd go about it.

Taken from the R.-fortunes (selections from the R.-help list serve)

What is R? : Technically

I. R is an open source implementation of S (S-Plus is a commercial implementation)

II. R is available under GNU Copy-left

III. The current version of R is 2.9.2 (2.10.0 is at alpha release, 2.11 is in development)

IV. R is group project run by a core group of developers (with new releases semiannually)

(Adapted from Robert Gentleman)

R: History

I. 1991-93: Ross Dhaka and Robert Gentleman begin work on R project at U. Auckland

II. 1995: R available by ftp under the GPL

III. 96-97: mailing list and R core group is formed

IV. 2000: John Chambers, designer of S joins the R core (wins a prize for best software from ACM for S)

V. 2001-2005: Core team continues to improve base package

VI. 2009: Becoming the standard for statistics, although other languages are relevant (Python)

VII. Many (>2000) other contributed “packages”

R in Psychology Personality/Psychometrics

I. Some software packages tailored to psychology have been developed (e.g. those in the task view of psychometrics)

II. Some universities are now introducing R to graduate students

III. Some instructors are using it for undergraduates.

Why R?

I. Graphics for data exploration and interpretation

II. Data manipulation including statistics as data

III. Statistical analysis

   A. Standard univariate and multivariate generalizations of the linear model

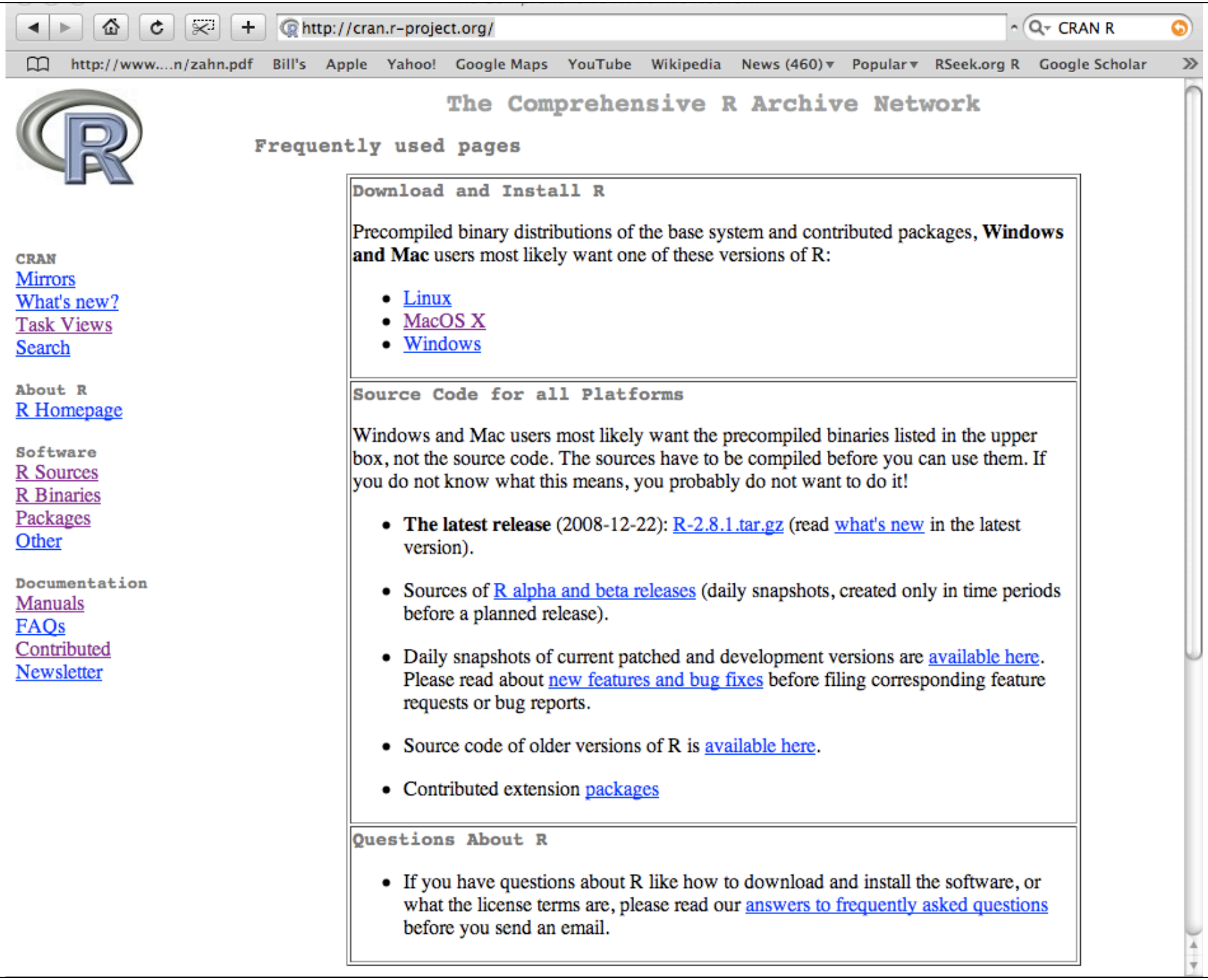
   B. Multivariate-structural extensions

IV. Ease of programming for new applications

Ok, how do I get it

I. CRAN (Comprehensive R Archive Network)

A. http://cran.r-project.org/


http://cran.r-project.org/
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Apple
Yahoo!
Google Maps
YouTube
Wikipedia
News (460)
Popular
RSeek.org R
Google Scholar
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 (2008-12-22): R-2.8.1.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
Questions About R
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.
CRAN
Mirrors
What's new?
Task Views
Search
About R
R Homepage
Software
R Sources
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Packages
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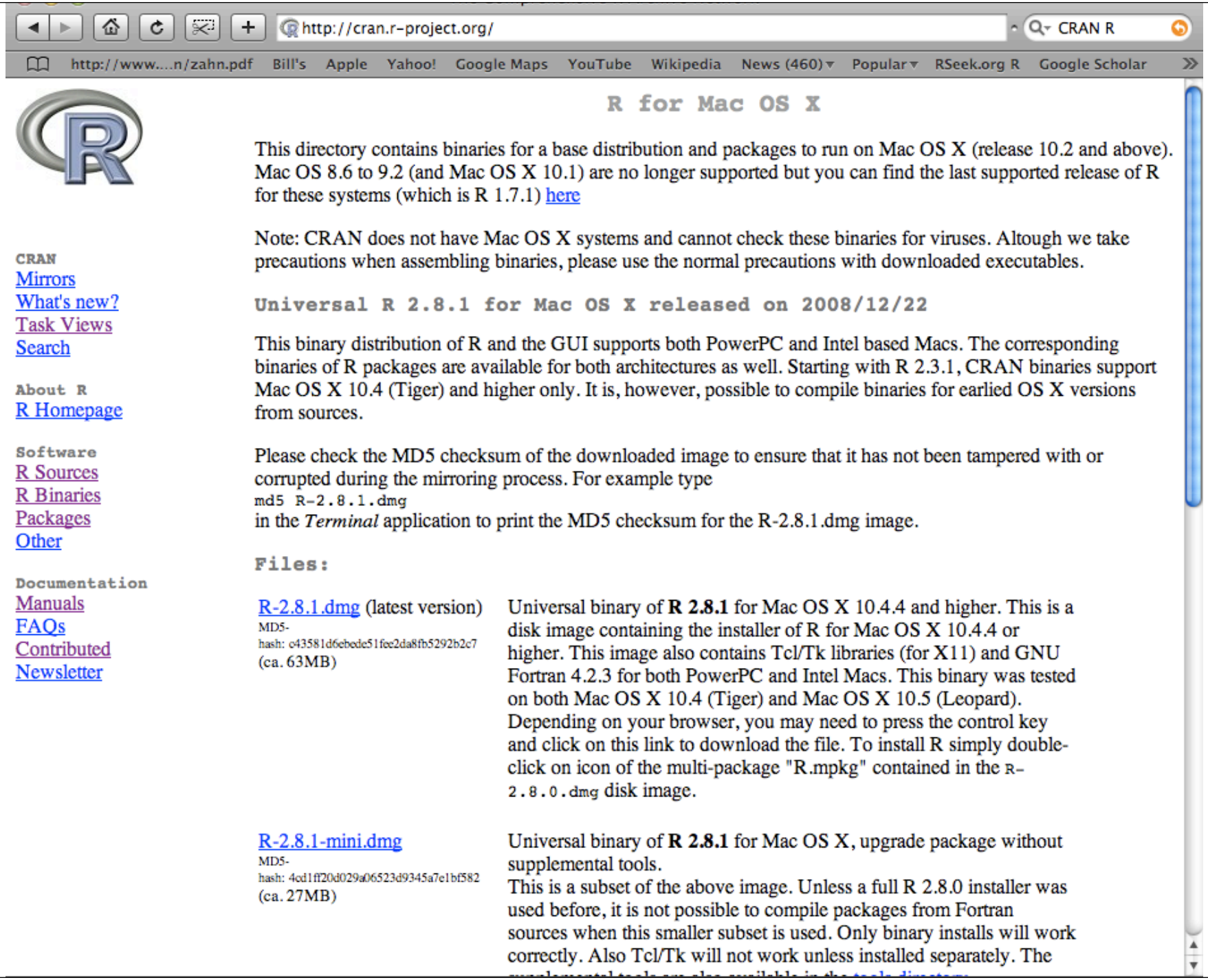
Documentation
Manuals
FAQs
Contributed
Newsletter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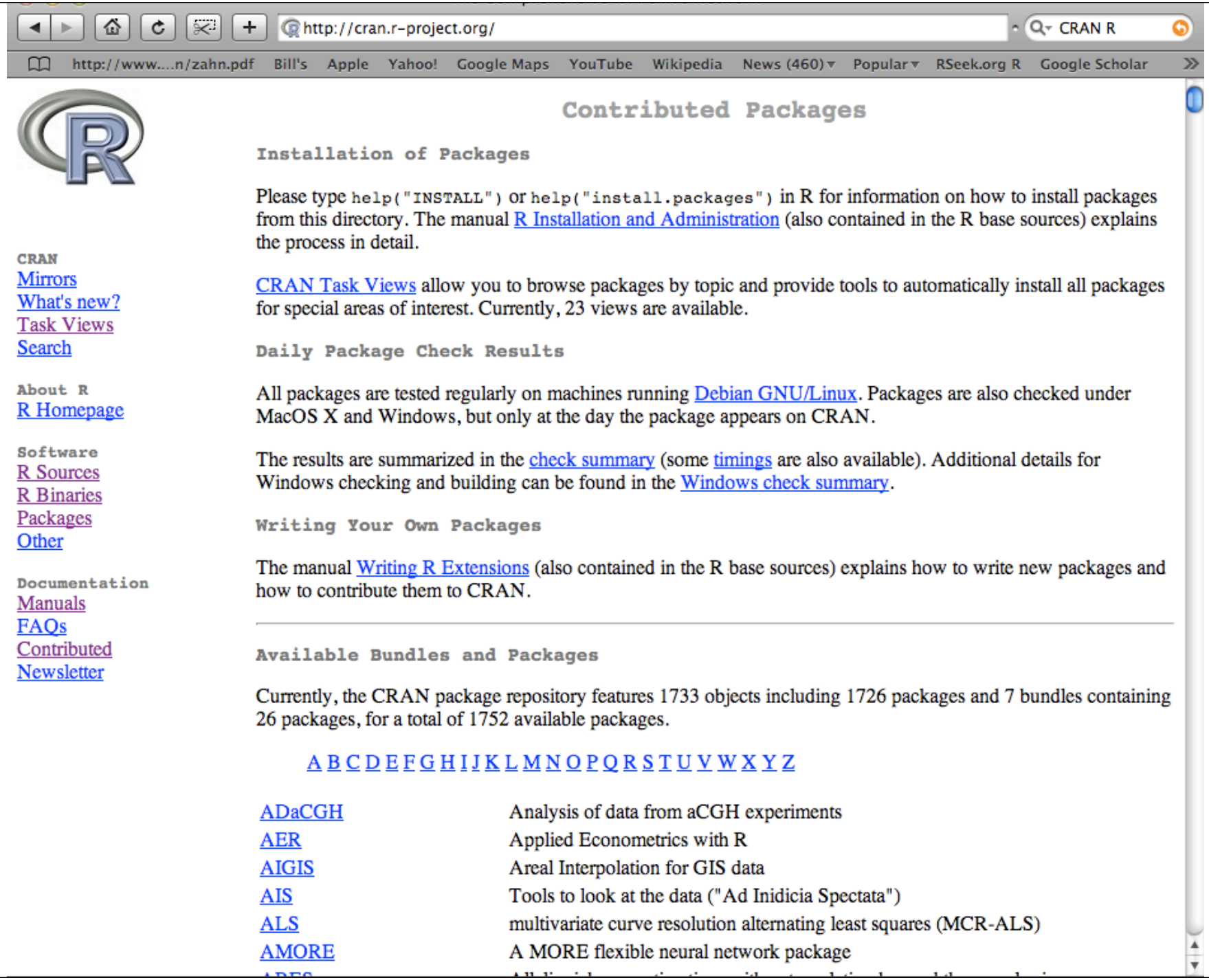
Bill's
Apple
Yahoo!
Google Maps
YouTube
Wikipedia
News (460)
Popular
RSeek.org R
Google Scholar
CRAN
Mirrors
What's new?
Task Views
Search
About R
R Homepage
Software
R Sources
R Binaries
Packages
Other
Documentation
Manuals
FAQs
Contributed
Newsletter
R for Mac OS X
This directory contains binaries for a base distribution and packages to run on Mac OS X (release 10.2 and above). Mac OS 8.6 to 9.2 (and Mac OS X 10.1) are no longer supported but you can find the last supported release of R for these systems (which is R 1.7.1) here
Note: CRAN does not have Mac OS X systems and cannot check these binaries for viruses. Altough we take precautions when assembling binaries, please use the normal precautions with downloaded executables.
Universal R 2.8.1 for Mac OS X released on 2008/12/22
This binary distribution of R and the GUI supports both PowerPC and Intel based Macs. The corresponding binaries of R packages are available for both architectures as well. Starting with R 2.3.1, CRAN binaries support Mac OS X 10.4 (Tiger) and higher only. It is, however, possible to compile binaries for earlied OS X versions from sources.
Please check the MD5 checksum of the downloaded image to ensure that it has not been tampered with or corrupted during the mirroring process. For example type
md5 R-2.8.1.dmg
in the Terminal application to print the MD5 checksum for the R-2.8.1.dmg image.
Files:
R-2.8.1.dmg (latest version)
MD5-hash: c43581d6ebede51fee2da8fb5292b2c7
(ca. 63MB)
Universal binary of R 2.8.1 for Mac OS X 10.4.4 and higher. This is a disk image containing the installer of R for Mac OS X 10.4.4 or higher. This image also contains Tcl/Tk libraries (for X11) and GNU Fortran 4.2.3 for both PowerPC and Intel Macs. This binary was tested on both Mac OS X 10.4 (Tiger) and Mac OS X 10.5 (Leopard). Depending on your browser, you may need to press the control key and click on this link to download the file. To install R simply double-click on icon of the multi-package "R.mpkg" contained in the R-2.8.0.dmg disk image.
R-2.8.1-mini.dmg
MD5-hash: 4cd1ff20d029a06523d9345a7e1bf582
(ca. 27MB)
Universal binary of R 2.8.1 for Mac OS X, upgrade package without supplemental tools.
This is a subset of the above image. Unless a full R 2.8.0 installer was used before, it is not possible to compile packages from Fortran sources when this smaller subset is used. Only binary installs will work correctly. Also Tcl/Tk will not work unless installed separately. The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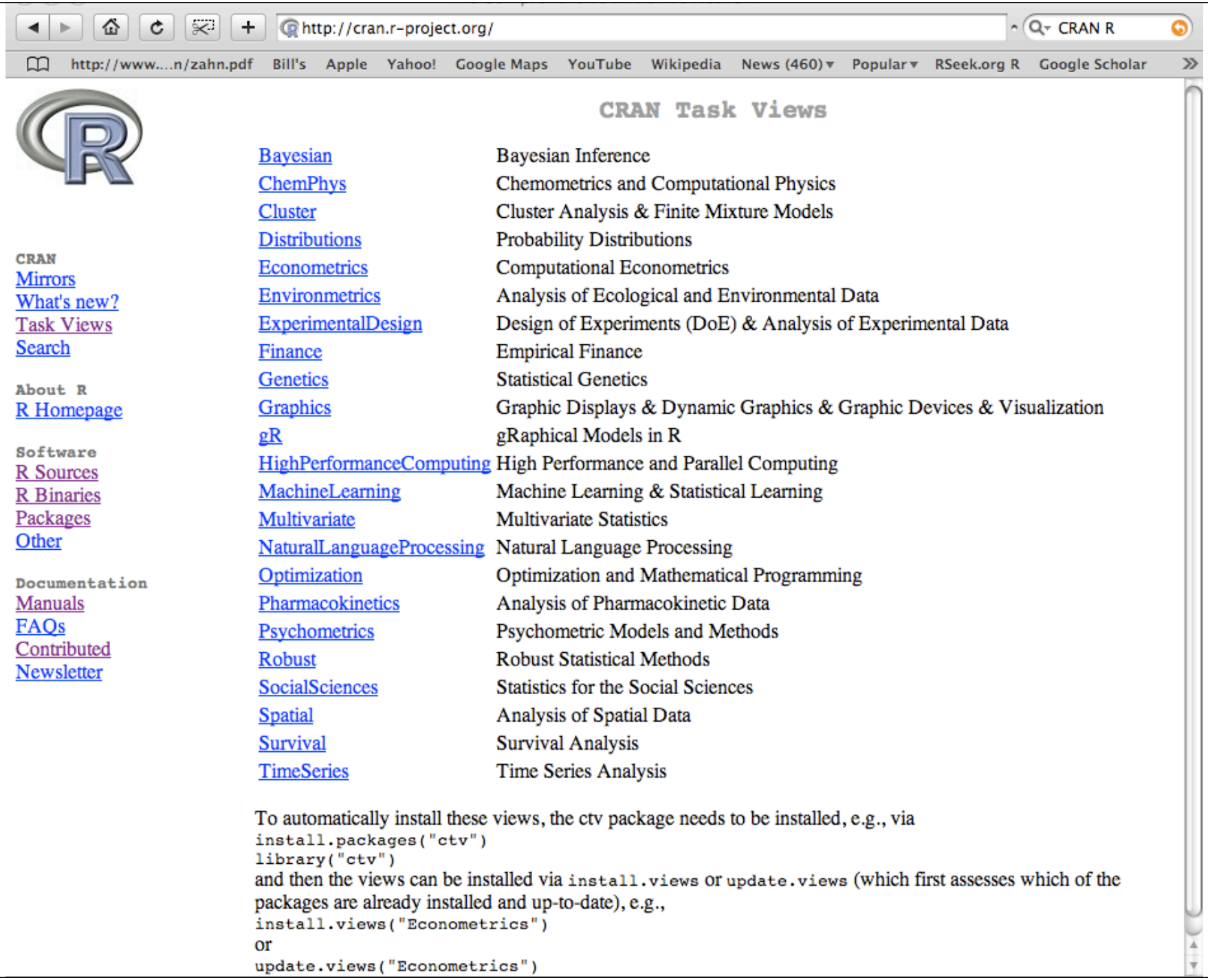
Bill's
Apple
Yahoo!
Google Maps
YouTube
Wikipedia
News (460)
Popular
RSeek.org R
Google Scholar
CRAN
Mirrors
What's new?
Task Views
Search
About R
R Homepage
Software
R Sources
R Binaries
Packages
Other
Documentation
Manuals
FAQs
Contributed
Newsletter
Contributed Packages
Installation of Packages
Please 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, 23 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 1733 objects including 1726 packages and 7 bundles containing 26 packages, for a total of 1752 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
ADaCGH Analysis of data from aCGH experiments
AER Applied Econometrics with R
AIGIS Areal Interpolation for GIS data
AIS Tools to look at the data ("Ad Inidicia Spectata")
ALS multivariate curve resolution alternating least squares (MCR-ALS)
AMORE A MORE flexible neural network package


http://cran.r-project.org/
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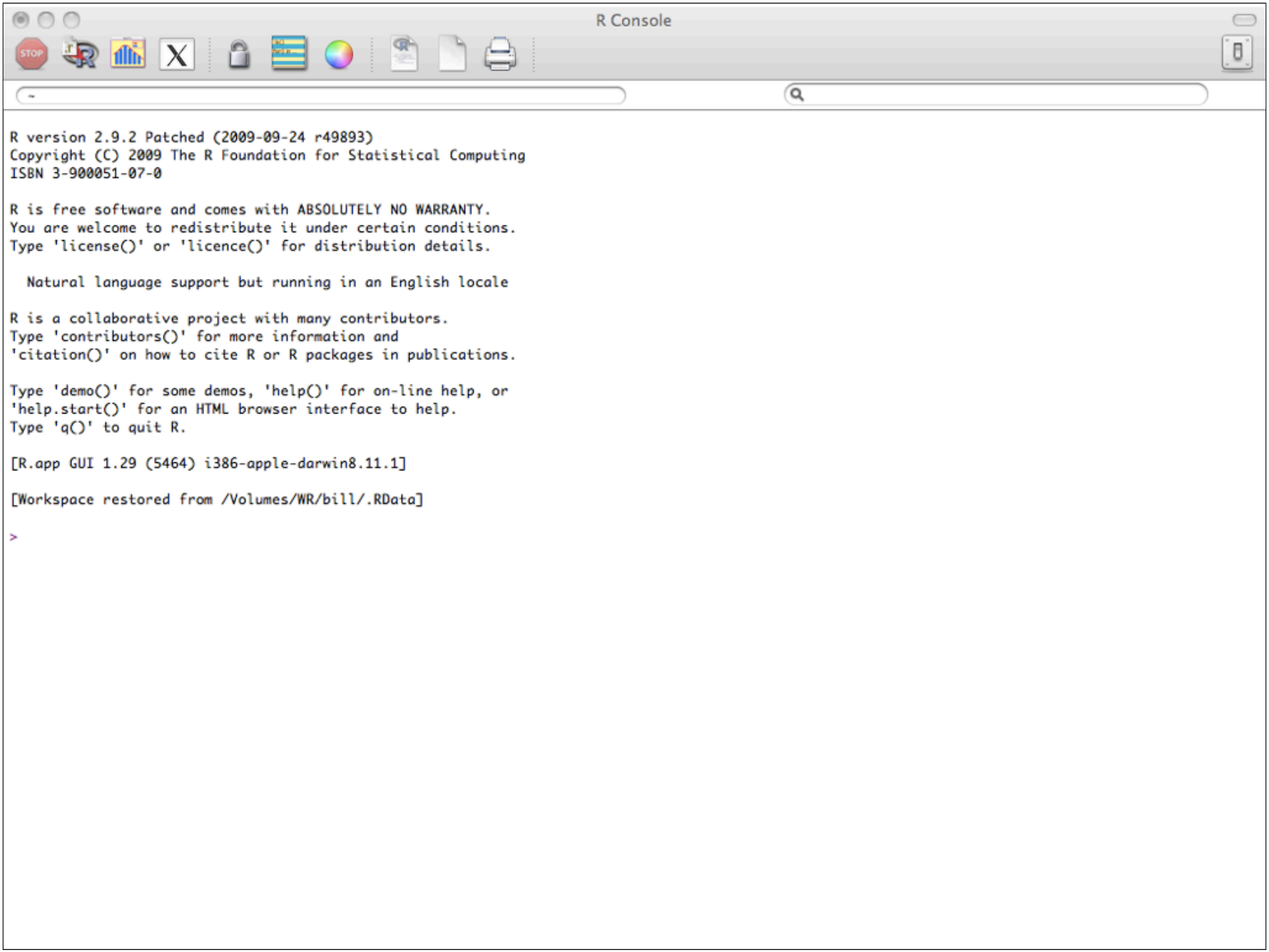
http://www....n/zahn.pdf
Bill's
Apple
Yahoo!
Google Maps
YouTube
Wikipedia
News (460)
Popular
RSeek.org R
Google Scholar
CRAN Task Views
CRAN
Mirrors
What's new?
Task Views
Search
About R
R Homepage
Software
R Sources
R Binaries
Packages
Other
Documentation
Manuals
FAQs
Contributed
Newsletter
Bayesian Bayesian Inference
ChemPhys Chemometrics and Computational Physics
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
MachineLearning Machine Learning & Statistical Learning
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
To automatically install these views, the ctv package needs to be installed, e.g., via
install.packages("ctv")
library("ctv")
and then the views can be installed via install.views or update.views (which first assesses which of the packages are already installed and up-to-date), e.g.,
install.views("Econometrics")
or
update.views("Econometrics")


R Console
~
R version 2.9.2 Patched (2009-09-24 r49893)
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.
[R.app GUI 1.29 (5464) i386-apple-darwin8.11.1]
[Workspace restored from /Volumes/WR/bill/.RData]
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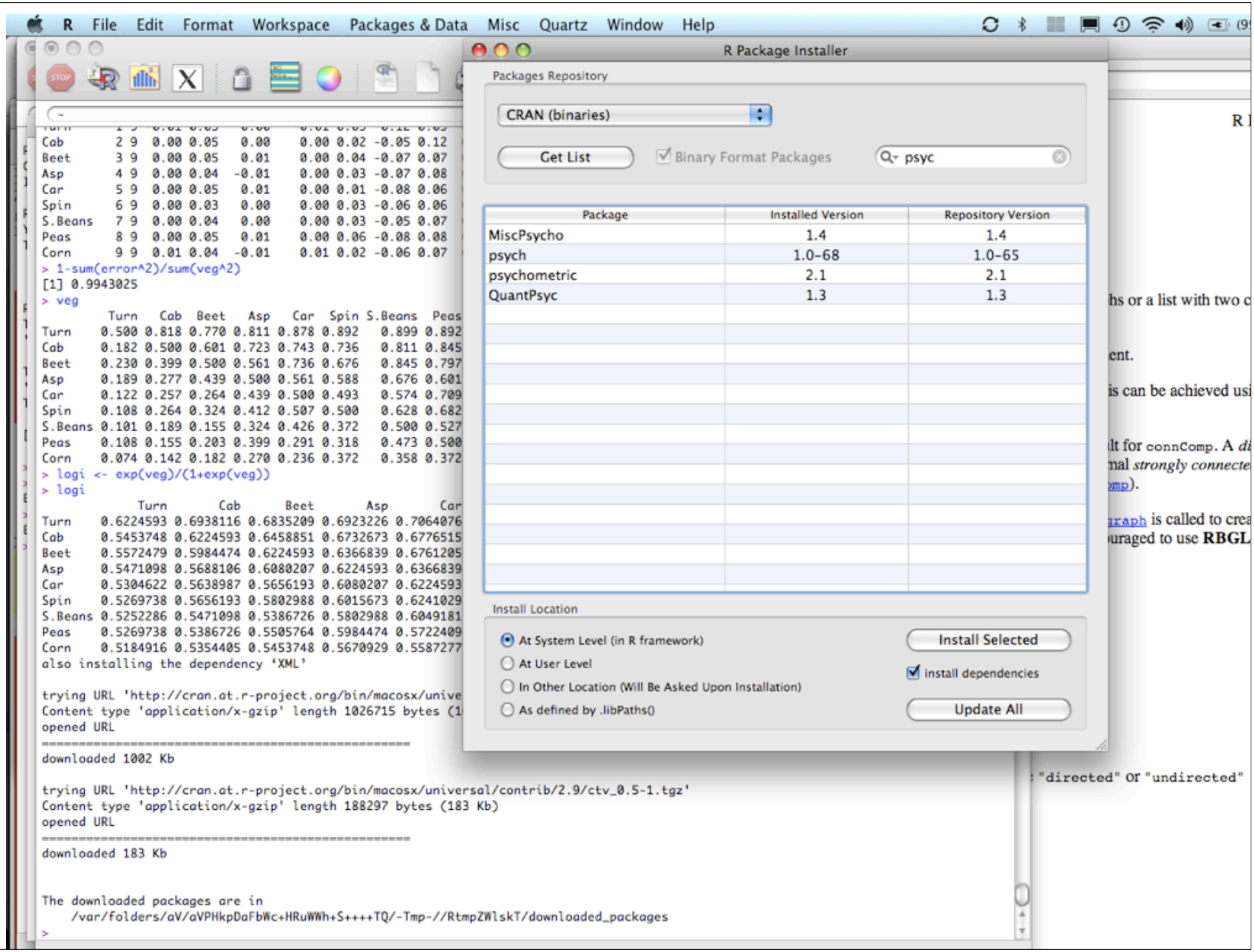
R File Edit Format Workspace Packages & Data Misc Quartz Window Help
R Package Installer
Packages Repository
CRAN (binaries)
Get List
Binary Format Packages
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Installed Version
Repository Version
MiscPsycho 1.4 1.4
psych 1.0-68 1.0-65
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QuantPsyc 1.3 1.3
Install Location
At System Level (in R framework)
At User Level
In Other Location (Will Be Asked Upon Installation)
As defined by .libPaths()
Install Selected
install dependencies
Update All
> 1-sum(error^2)/sum(veg^2)
[1] 0.9943025
> veg
> logi <- exp(veg)/(1+exp(veg))
> logi
also installing the dependency 'XML'
trying URL 'http://cran.at.r-project.org/bin/macosx/universal/contrib/2.9/XML_3.2-0.tgz'
Content type 'application/x-gzip' length 1026715 bytes (1002 Kb)
opened URL
downloaded 1002 Kb
trying URL 'http://cran.at.r-project.org/bin/macosx/universal/contrib/2.9/ctv_0.5-1.tgz'
Content type 'application/x-gzip' length 188297 bytes (183 Kb)
opened URL
downloaded 183 Kb
The downloaded packages are in
/var/folders/aV/aVPHkpDaFbWc+HRuWWh+S++++TQ/-Tmp-//RtmpZWlskT/downloaded_packages
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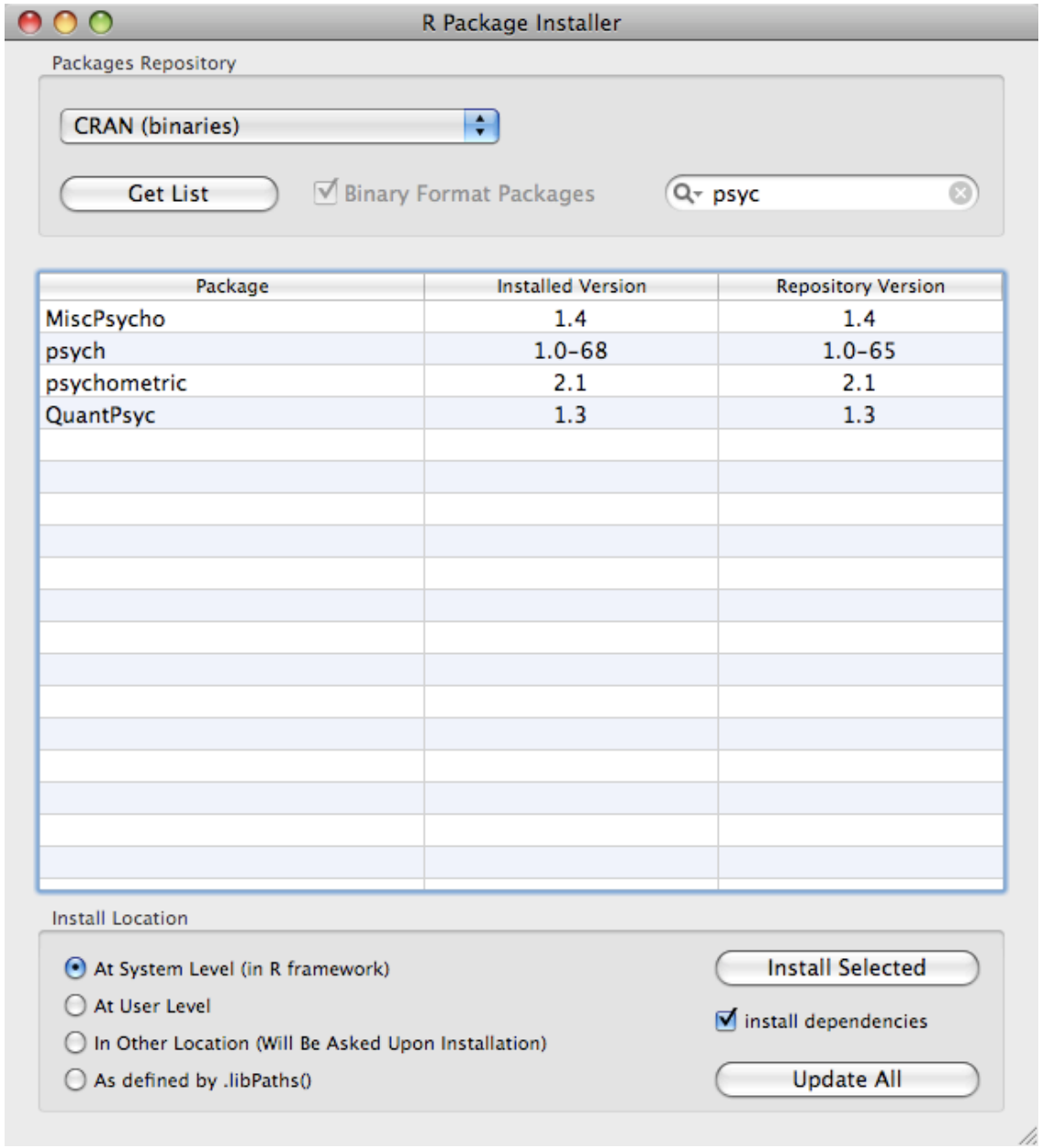
R Package Installer
Packages Repository
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MiscPsycho
1.4
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1.3
Install Location
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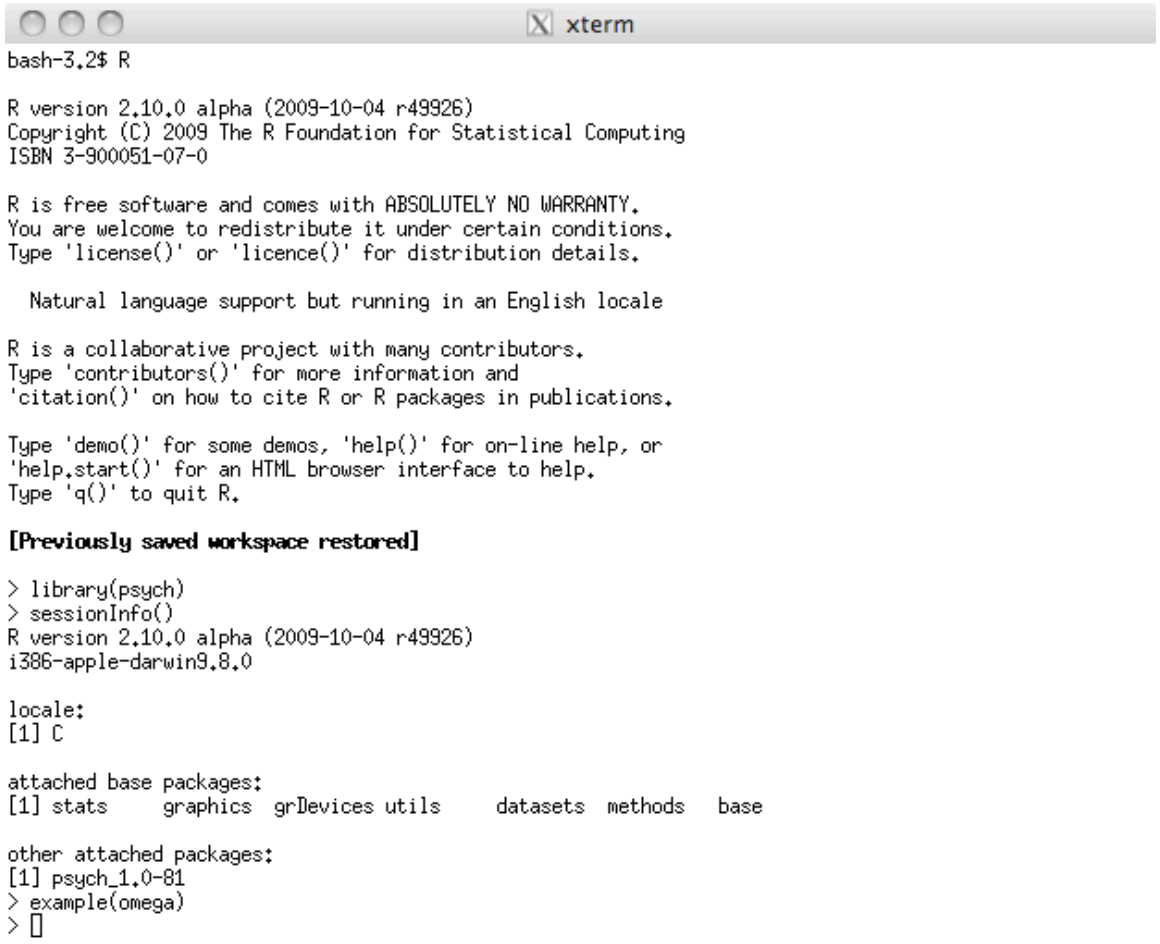
At User Level
In Other Location (Will Be Asked Upon Installation)
As defined by .libPaths()
Install Selected
install dependencies
Update All

Running in X11



xterm

```
bash-3.2$ R

R version 2.10.0 alpha (2009-10-04 r49926)
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'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.

> library(psych)
> sessionInfo(
+ )
R version 2.10.0 alpha (2009-10-04 r49926)
i386-apple-darwin9.8.0

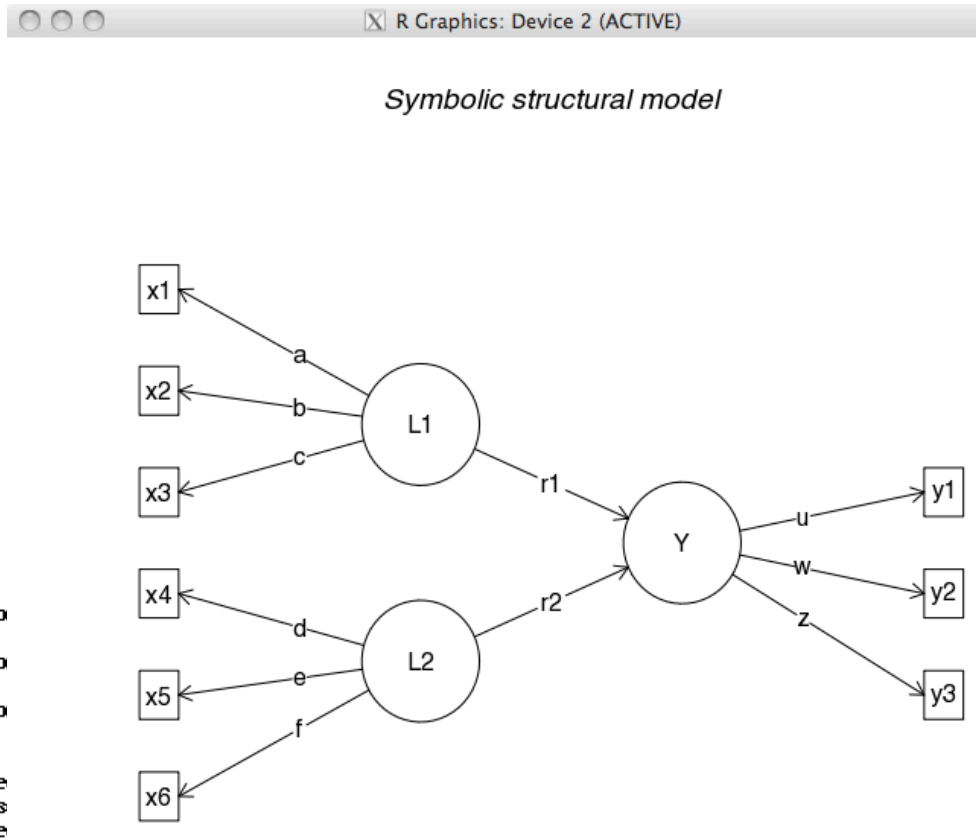
locale:
[1] C

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

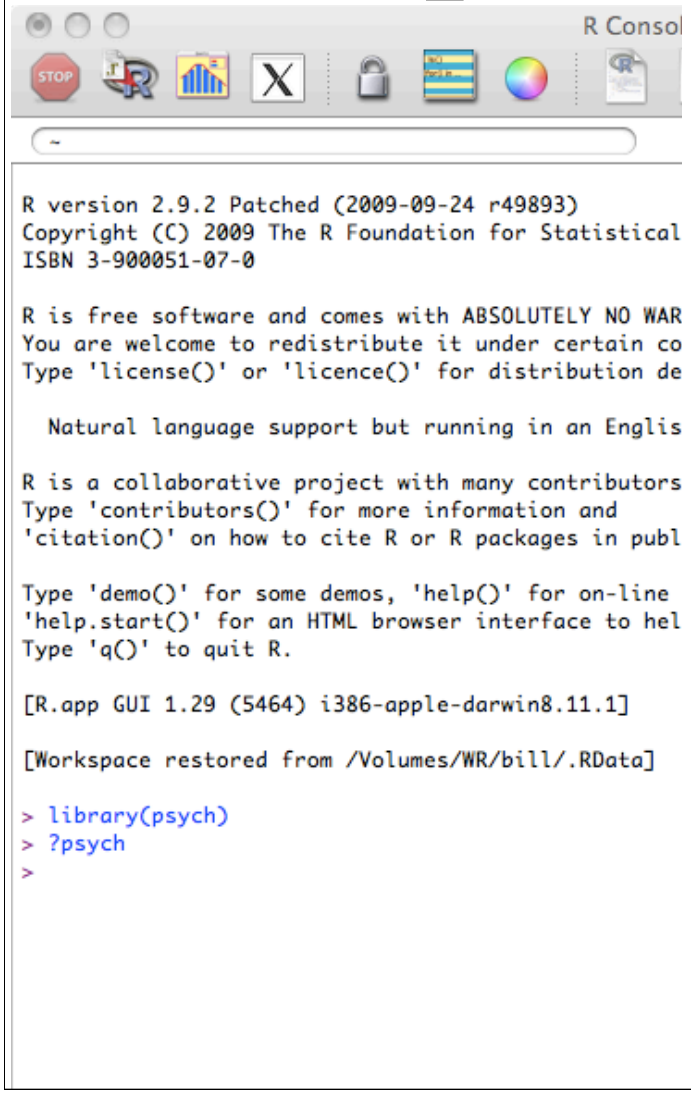
other attached packages:
[1] psych_1.0-82
> test.psych()
too many factors requested for this number of variables to use SMC, 1s used
Loading required package: GPArotation
In fa, too many factors requested for this number of variables to use SMC fo
 are used instead
In fa, too many factors requested for this number of variables to use SMC fo
 are used instead
In fa, too many factors requested for this number of variables to use SMC fo
 are used instead
In smc, the correlation matrix was not invertible, smc's returned as 1s
In factor.stats, the correlation matrix is singular, an approximation is use
In factor.scores, the correlation matrix is singular, an approximation is us
In factor.stats, the correlation matrix is singular, an approximation is use
In factor.scores, the correlation matrix is singular, an approximation is us
Loading required package: MASS
Warning messages:
1: In log(det(m.inv.r)) : NaNs produced
2: In log(det(m.inv.r)) : NaNs produced
3: In test.psych() :
  fa.graph, omega.graph, ICLUST.rgraph, structure.graph require Rgraphviz
>
```

X11

R Graphics: Device 2 (ACTIVE)



Getting Help



00.psych {psych} R Document

A package for personality, psychometric, and psychological resea

Description

Overview of the psych package.

The psych package has been developed at Northwestern University to include functions most useful fo personality and psychological research. Some of the functions (e.g., read.clipboard, describe, pairs.panels, error.bars) are useful for basic data entry and descriptive analyses. Use help(package="psych") for a list of all functions.

Psychometric applications include routines (fa for principal axes (factor.pa), minimum residual (min factor.minres), and weighted least squares (link{factor.wls} factor analysis as well as functions Schmid Leiman transformations (schmid) to transform a hierarchical factor structure into a bifactor solu Factor or components transformations to a target matrix include the standard Promax transformation (Promax), a transformation to a cluster target, or to any simple target matrix (target.rot) as well as th ability to call many of the GPArotation functions. Functions for determining the number of factors in a matrix include Very Simple Structure (VSS) and Minimum Average Partial correlation (MAP). An alterna approach to factor analysis is Item Cluster Analysis (ICLUST). Reliability coefficients alpha (score.ite score.multiple.choice), beta (ICLUST) and McDonald's omega (omega and omega.graph) as well Guttman's six estimates of internal consistency reliability (guttman) and the six measures of Intraclass correlation coefficients (ICC) discussed by Shrout and Fleiss are also available.

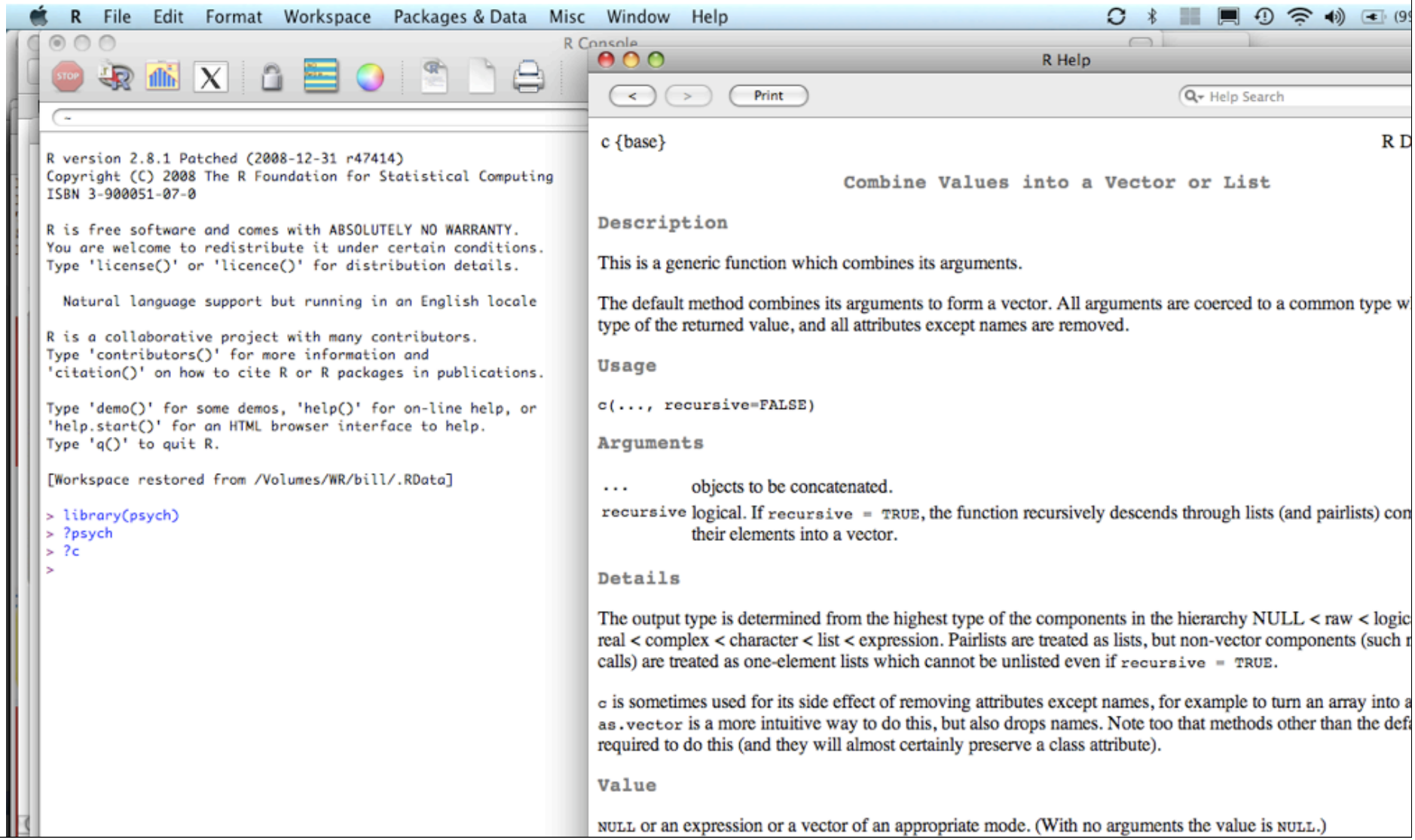
The score.items, and score.multiple.choice functions may be used to form single or multiple sca from sets of dichotomous, multilevel, or multiple choice items by specifying scoring keys.

Additional functions make for more convenient descriptions of item characteristics. Functions under development include 1 and 2 parameter Item Response measures.

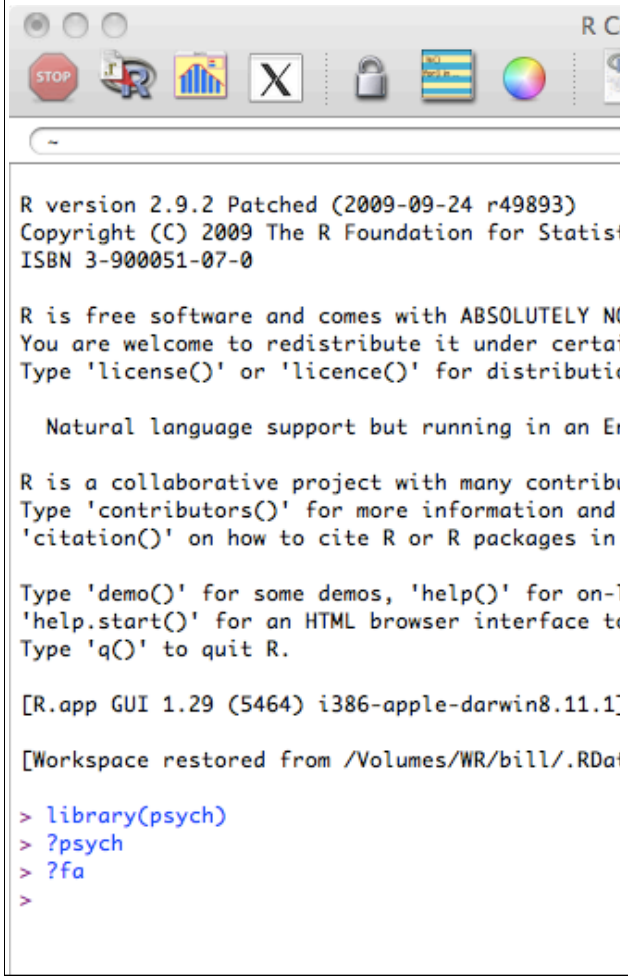
A number of procedures have been developed as part of the Synthetic Aperture Personality Assessmen (SAPA) project. These routines facilitate forming and analyzing composite scales equivalent to using th raw data but doing so by adding within and between cluster/scale item correlations. These functions inc extracting clusters from factor loading matrices (factor2cluster), synthetically forming clusters from correlation matrices (cluster.cor), and finding multiple ((mat.regress) and partial ((partial.r) correlations from correlation matrices.

Functions to generate simulated data with particular structures include sim.circ (for circumplex structu sim.item (for general structures) and sim.congeneric (for a specific demonstration of congeneric measurement). The functions sim.congeneric and sim.hierarchical can be used to create data sets with particular structural properties. A more general form for all of these is sim.structural for genera

Getting help



Getting help



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R version 2.9.2 Patched (2009-09-24 r49893)
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Type 'demo()' for some demos, 'help()' for on-
'help.start()' for an HTML browser interface t
Type 'q()' to quit R.

[R.app GUI 1.29 (5464) i386-apple-darwin8.11.1

[Workspace restored from /Volumes/WR/bill/.RDa

> library(psych)
> ?psych
> ?fa
>
```

R Help

< > Print Help Search

fa {psych} R Documentation

Factor analysis by Principal Axis, MinRes (minimum residual), Weighted Least Squares or Maximum Likelihood

Description

Among the many ways to do factor analysis, one of the most conventional is principal axes. An eigen value decomposition of a correlation matrix is done and then the communalities for each variable are estimated by the first n factors. These communalities are entered onto the diagonal and the procedure is repeated until the sum(diag(r)) does not vary. Another technique is to use Ordinary Least Squares to find the minimum residual (minres) solution. A variation on minres is to do weighed least squares. Yet another estimate procedure is maximum likelihood. For well behaved matrices, maximum likelihood factor analysis (either in the fa or in the factanal fuction) is probably preferred.

Usage

```
fa(r, nfactors=1, residuals = FALSE, rotate = "varimax",n.obs = NA,
scores = FALSE,SMC=TRUE, missing=FALSE,impute="median",min.err = 0.001, digits = 2,

factor.pa(r, nfactors=1, residuals = FALSE, rotate = "varimax",n.obs = NA,
scores = FALSE,SMC=TRUE, missing=FALSE,impute="median",min.err = 0.001, digits = 2,

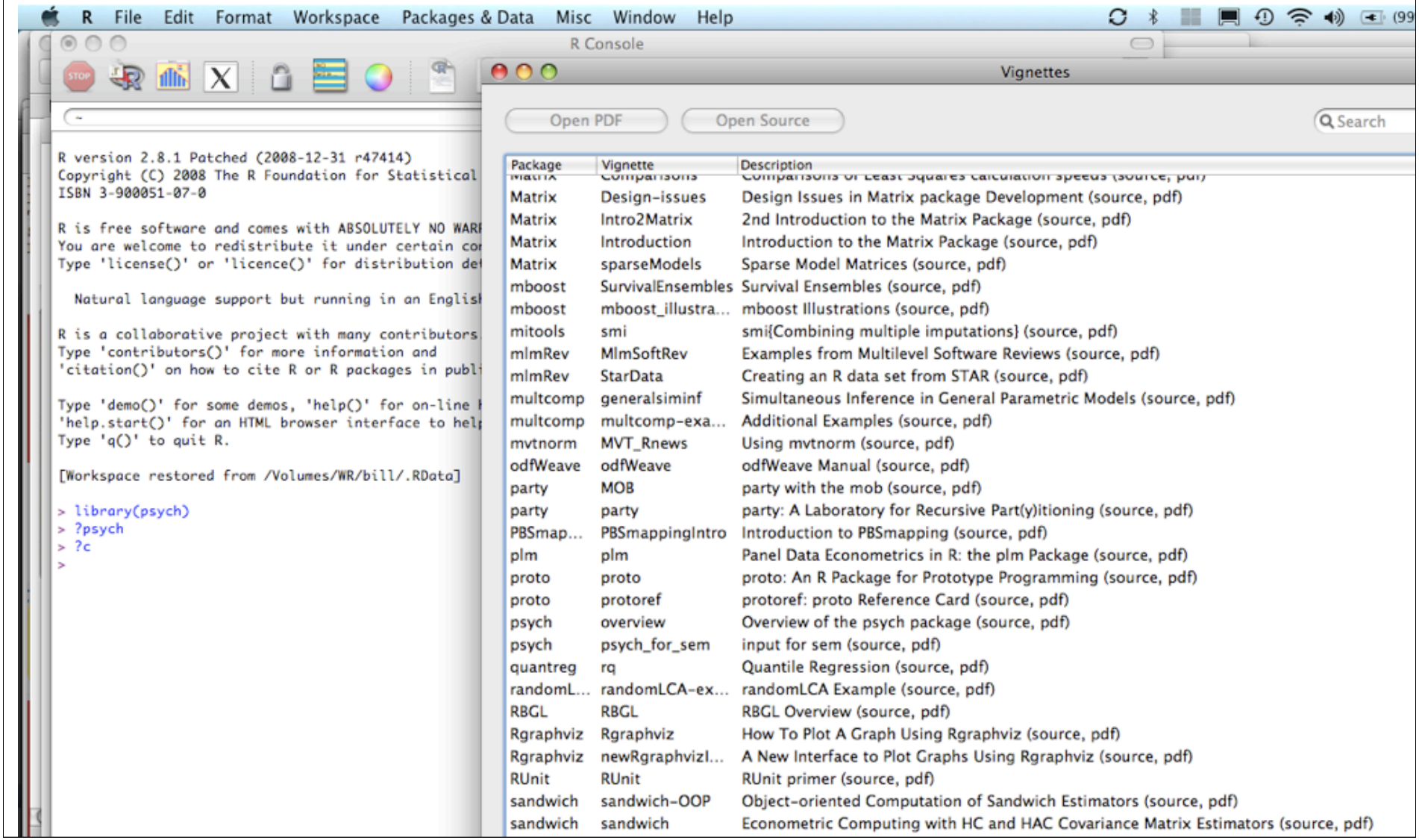
factor.minres(r, nfactors=1, residuals = FALSE, rotate = "varimax",n.obs = NA,
scores = FALSE,SMC=TRUE, missing=FALSE,impute="median",min.err = 0.001, digits = 2,

factor.wls(r,nfactors=1,residuals=FALSE,rotate="varimax",n.obs = NA,
scores=FALSE,SMC=TRUE,missing=FALSE,impute="median", min.err = .001,digits=2,max.ite
```

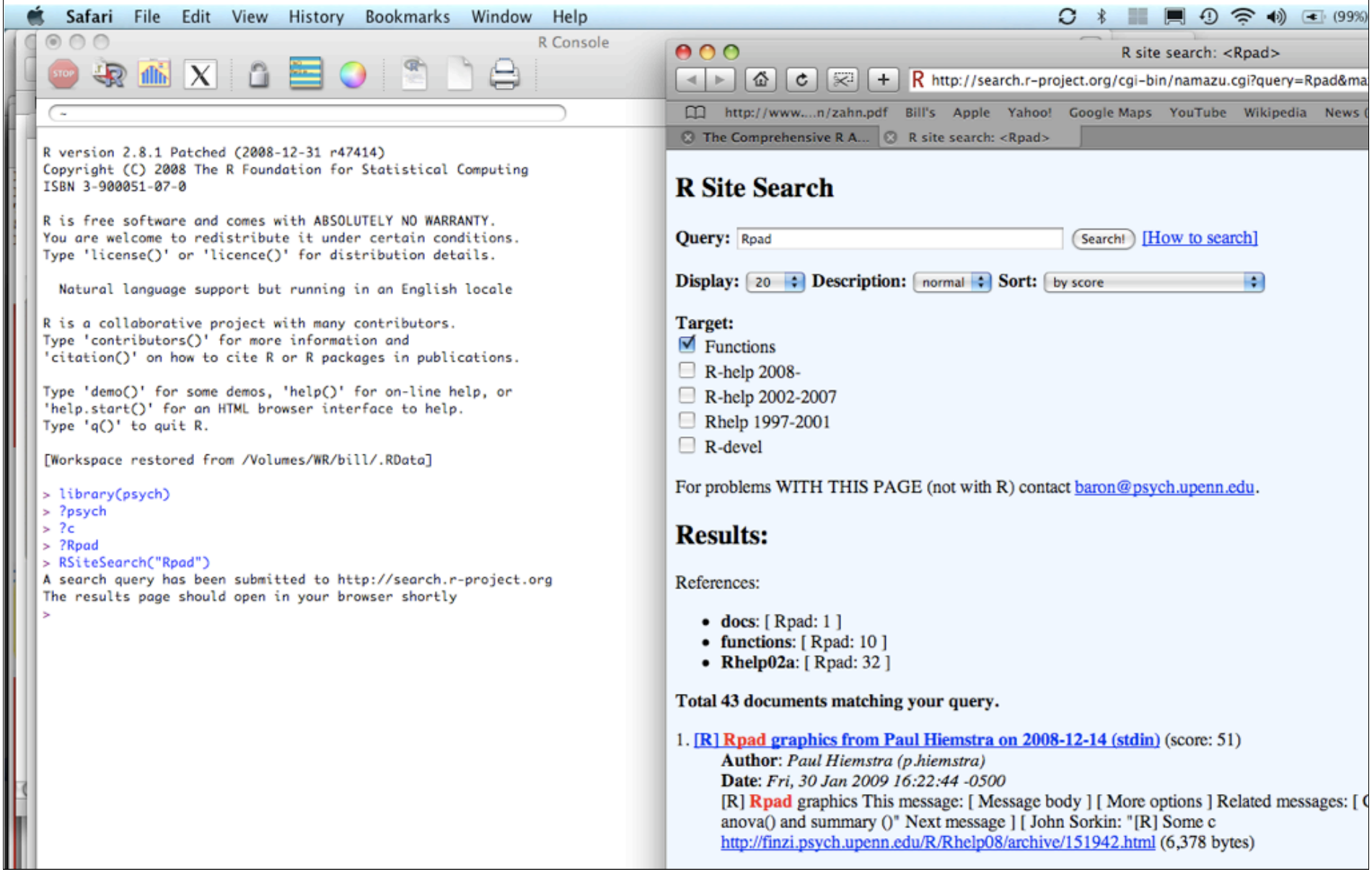
Arguments

r	A correlation matrix or a raw data matrix. If raw data, the correlation matrix will be found using pairwise deletion.
nfactors	Number of factors to extract, default is 1
residuals	Should the residual matrix be shown
rotate	"none", "varimax", "quartimax", "bentlerT", and "geominT" are orthogonal rotations. "promax", "oblimin", "simplimax", "bentlerQ, and "geominQ" or "cluster" are possible rotations or transformations of the solution.
n.obs	Number of observations used to find the correlation matrix if using a correlation matrix. Used for finding the goodness of fit statistics.

Package vignettes



RSiteSearch



Rpad

R/Rpad Reference Card

by Tom Short, EPRI Solutions, Inc., tshort@eprisolutions.com 2005-07-12

Help and basics

Most R functions have online documentation.

help(topic) documentation on topic
?topic id.
help.search("topic") search the help system
apropos("topic") the names of all objects in the search list matching the regular expression "topic"
help.start() start the HTML version of help
str(a) display the internal *str*ucture of an R object
summary(a) gives a "summary" of a, usually a statistical summary but it is *generic* meaning it has different operations for different classes of a
ls() show objects in the search path; specify pat="pat" to search on a pattern
ls.str() str() for each variable in the search path
dir() show files in the current directory
methods(a) shows S3 methods of a
methods(class=class(a)) lists all the methods to handle objects of class a
options(...) set or examine many global options; common ones: width, digits, error
library(x) load add-on packages; library(help=x) lists datasets and functions in package x.
attach(x) database x to the R search path; x can be a list, data frame, or R data file created with save. Use search() to show the search path.
detach(x) x from the R search path; x can be a name or character string of an object previously attached or a package.

Input and output

load() load the datasets written with save
data(x) loads specified data sets
read.table(file) reads a file in table format and creates a data frame from it; the default separator sep="" is any whitespace; use header=TRUE to read the first line as a header of column names; use as.is=TRUE to prevent character vectors from being converted to factors; use comment.char="" to prevent "#" from being interpreted as a comment; use skip=n to skip n lines before reading data; see the help for options on row naming, NA treatment, and others
read.csv("filename",header=TRUE) id. but with defaults set for reading comma-delimited files
read.delim("filename",header=TRUE) id. but with defaults set
cat(..., file="", sep=" ") prints the arguments after coercing to character; sep is the character separator between arguments
print(a, ...) prints its arguments; generic, meaning it can have different methods for different objects
format(x,...) format an R object for pretty printing
write.table(x,file="",row.names=TRUE,col.names=TRUE, sep=" ") prints x after converting to a data frame; if quote is TRUE, character or factor columns are surrounded by quotes ("); sep is the field separator; eol is the end-of-line separator; na is the string for missing values; use col.names=NA to add a blank column header to get the column headers aligned correctly for spreadsheet input
sink(file) output to file, until sink()

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

On windows, the file connection can also be used with description = "clipboard". To read a table copied from Excel, use

```
x <- read.delim("clipboard")
```

To write a table to the clipboard for Excel, use

```
write.table(x,"clipboard",sep="\t",col.names=NA)
```

For database interaction, see packages RODBC, DBI, RMySQL, RPgSQL, and ROracle. See packages XML, hdf5, netCDF for reading other file formats.

Data creation

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

Slicing and extracting data

Indexing lists

x[n]	list with elements n
x[[n]]	n^{th} element of the list
x[["name"]]	element of the list named "name"
x$name	id.

Indexing vectors

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

Indexing matrices

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

Indexing data frames (matrix indexing plus the following)

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

Variable conversion

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

Variable information

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

Data selection and manipulation

which.max(x) returns the index of the greatest element of x

Data Manipulation
Data Entry

I. from console

II. from clipboard (copied from other programs)

III. from file (text files, csv, SPSS, Excel, MySQL)

IV. from the web

R is a desk calculator

```
> 2+2
[1] 4
> 3^4
[1] 81
> pi
[1] 3.141593
> x <- c(1,3,5,7)
> x
[1] 1 3 5 7
> m <- mean(x)
> m
[1] 4
> mean(x)
[1] 4
> sd(x)
[1] 2.581989
>
```

A very fancy desk calculator

```
> set.seed(42)
> V <- seq(1:5)
> M <- matrix(sample(5,15),replace=TRUE,ncol=3,nrow=5)
Error in matrix(sample(5, 15), replace = TRUE, ncol = 3, nrow = 5) :
  unused argument(s) (replace = TRUE)
> M <- matrix(sample(5,15,replace=TRUE),ncol=3,nrow=5)
> V
[1] 1 2 3 4 5
> M
     [,1] [,2] [,3]
[1,]    5    3    3
[2,]    5    4    4
[3,]    2    1    5
[4,]    5    4    2
[5,]    4    4    3
```

But a calculator none the less

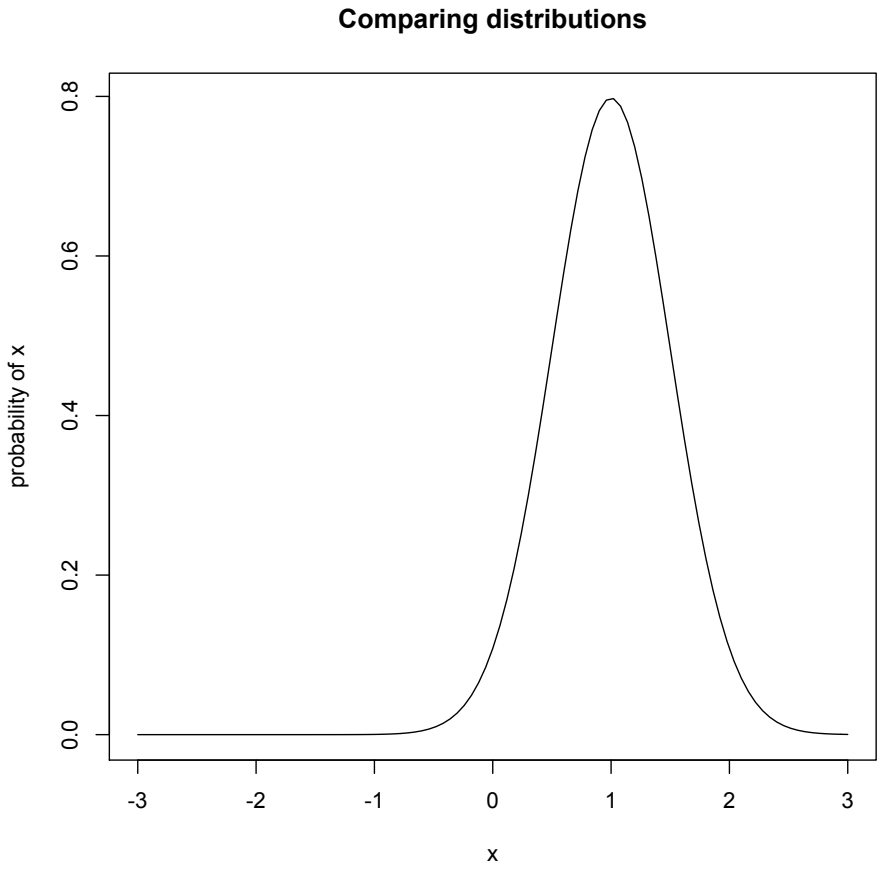
```
> V
[1] 1 2 3 4 5
> M
     [,1] [,2] [,3]
[1,]    5    3    3
[2,]    5    4    4
[3,]    2    1    5
[4,]    5    4    2
[5,]    4    4    3
```

```
> V * M
     [,1] [,2] [,3]
[1,]    5    3    3
[2,]   10    8    8
[3,]    6    3   15
[4,]   20   16    8
[5,]   20   20   15
```

```
> t(M) %*% M
     [,1] [,2] [,3]
[1,]   95   73   67
[2,]   73   58   50
[3,]   67   50   63
```

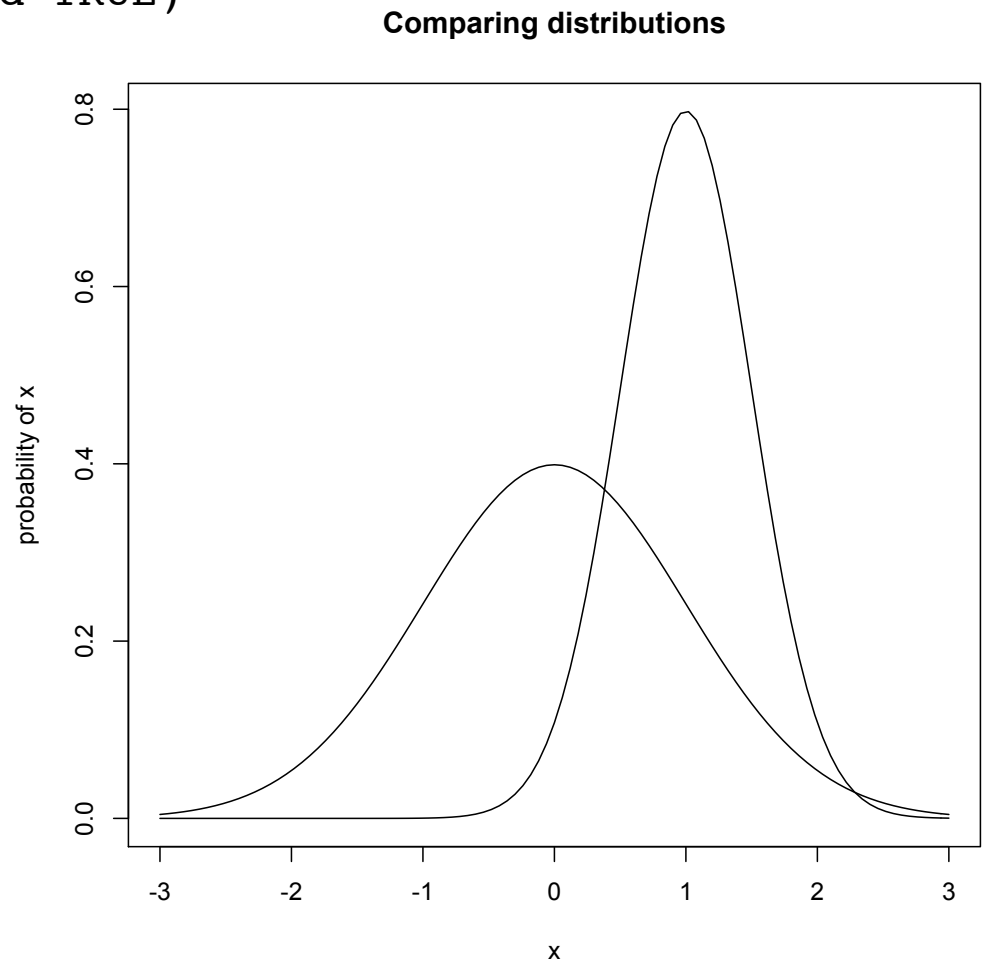
A graphing calculator

```
> curve(dnorm(x,1,0.5),-3,3,ylab="probability of
x",main="Comparing distributions")
```



Add the second line

```
> curve(dnorm(x,1,0.5),-3,3,ylab="probability of x",main="Comparing
distributions")
> curve(dnorm(x,0,1),add=TRUE)
```



R is a stats table

```
> pt(2.0,6) #probability (one tailed of a t > 2.0)
[1] 0.9537868
> pnorm(2.0) #probability of a normal distribution
with value of 2.0)
[1] 0.9772499
> dnorm(-1)  #normal with z value of -1.0
[1] 0.2419707
> pf(3.5,1,20)  #probability of an F statistic
[1] 0.923926
> qf(.95,1,60) # the critical value of an F at the 95
percent value
[1] 4.001191
> qchisq(.95,1) # the critical value for a 1 df #$
\chi^2$
[1] 3.841459
```

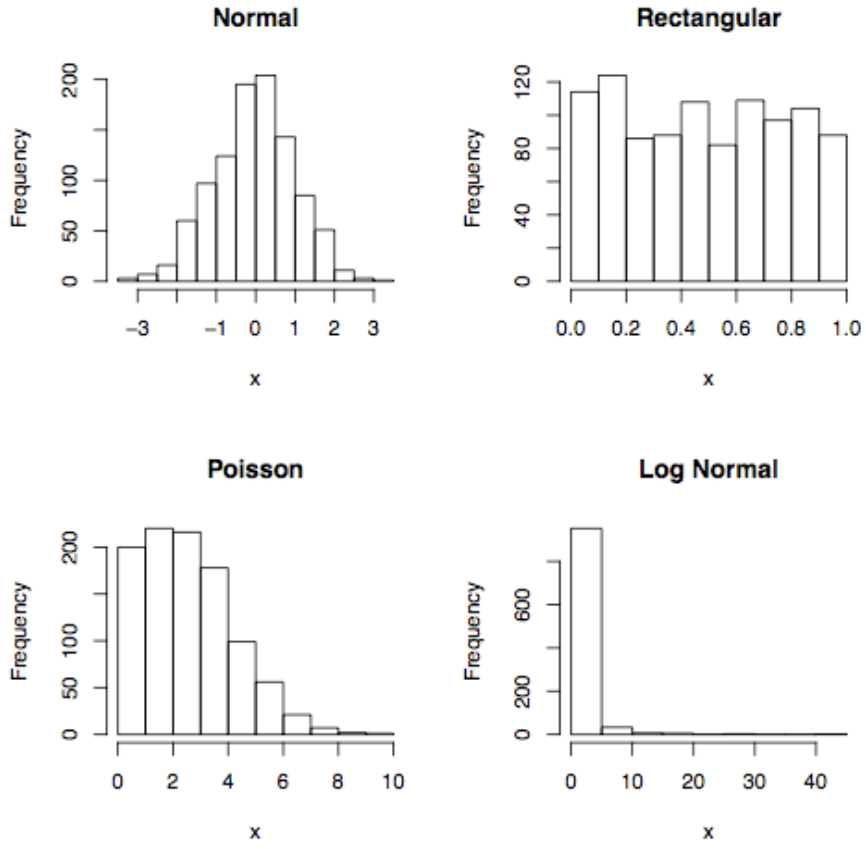
A powerful stats table

```
> z <- seq(0,3,.2)
> z
 [1] 0.0 0.2 0.4 0.6 0.8 1.0 1.2 1.4 1.6 1.8 2.0 2.2 2.4 2.
2.8 3.0
> pnorm(z)
 [1] 0.5000000 0.5792597 0.6554217 0.7257469 0.7881446
0.8413447 0.8849303 0.9192433 0.9452007 0.9640697 0.9772499
0.9860966
[13] 0.9918025 0.9953388 0.9974449 0.9986501
> round(data.frame(z,p=pnorm(z)),3)
     z     p
1  0.0 0.500
2  0.2 0.579
3  0.4 0.655
4  0.6 0.726
5  0.8 0.788
6  1.0 0.841
7  1.2 0.885
8  1.4 0.919
```

Random data

Distribution	base name	P 1	P 2	P 3	example application
Normal	norm	mean	sigma		Most data
Multivariate normal	mvnorm	mean	r	sigma	Most data
Log Normal	lnorm	log mean	log sigma		income or reaction time
Uniform	unif	min	max		rectangular distributions
Binomial	binom	size	prob		Bernuilli trials (e.g. coin flips)
Student's t	t	df		nc	Finding significance of a t-test
Multivariate t	mvt	df	corr	nc	Multivariate applications
Fisher's F	f	df1	df2	nc	Testing for significance of F test
χ^2	chisq	df		nc	Testing for significance of χ^2
Beta	beta	shape1	shape2	nc	distribution theory
Cauchy	cauchy	location	scale		Infinite variance distribution
Exponential	exp	rate			Exponential decay
Gamma	gamma	shape	rate	scale	distribution theoryh
Hypergeometric	hyper	m	n	k	
Logistic	logis	location	scale		Item Response Theory
Poisson	pois	lambda			Count data
Weibull	weibull	shape	scale		Reaction time distributions

Graphics of random data



Graphing commands

```
op <- par(mfrow=c(2,2))

n <- 1000
x <- rnorm(n)
hist(x,main="Normal")
x <- runif(n)
hist(x,main="Rectangular")
x <- rpois(n,3)
hist(x,main="Poisson")
x <- rlnorm(n)
hist(x,main="Log Normal")

op <- par(mfrow=c(1,1))
```

Data Entry example

```
> 5/2            #it is a calculator

[1] 2.5

> 2^8          #still a calculator

[1] 256

> a <- c("A","short","list")  #store this value

> a                          #now show it

[1] "A"     "short" "list"

>
```

Data entry

```
> A <- 1:25  # make a sequence
> A               #show it
 [1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22
23 24 25
> B <- matrix(A,ncol=5) #convert the vector to a matrix
> B                 # show it
     [,1] [,2] [,3] [,4] [,5]
[1,]    1    6   11   16   21
[2,]    2    7   12   17   22
[3,]    3    8   13   18   23
[4,]    4    9   14   19   24
[5,]    5   10   15   20   25
> c <- seq(25,5,by=-5)   #seq can do more interesting stuff
> c
[1] 25 20 15 10  5
```

From the clipboard

Copy this text

```
    V1 V2 V3 V4 V5
S1   1  6 11 16 21
S2   2  7 12 17 22
S3   3  8 13 18 23
S4   4  9 14 19 24
S5   5 10 15 20 25
```

```
library(psych)

> A <- read.clipboard()

> A   #show it
```

```
    V1 V2 V3 V4 V5
S1   1  6 11 16 21
S2   2  7 12 17 22
S3   3  8 13 18 23
S4   4  9 14 19 24
S5   5 10 15 20 25
```

From the clipboard (no headers)

```
> C <- read.clipboard(header=FALSE)

> C  #automatically adds column names!
```

```
  1  6 11 16 21
 2  7 12 17 22
 3  8 13 18 23
 4  9 14 19 24
 5 10 15 20 25
```

```
  V1 V2 V3 V4 V5
1  1  6 11 16 21
2  2  7 12 17 22
3  3  8 13 18 23
4  4  9 14 19 24
5  5 10 15 20 25
```

From built in datasets

```
> data() #show all data sets

> data(sat.act) # get this one

> head(sat.act) #show the first lines

> dim(sat.act)  #show dimensions

[1] 700   6
```

	gender	education	age	ACT	SATV	SATQ
29442	2	3	19	24	500	500
29457	2	3	23	35	600	500
29498	2	3	20	21	480	470
29503	1	4	27	26	550	520
29504	1	2	33	31	600	550
29518	1	5	26	28	640	640

From files or the web

Fn <- file.choose() #uses the system commands to find it

My.data <- read.table(Fn)

> My.data <- read.table(Fn,header=TRUE)

> head(My.data) #show the first 6 lines

	epiE	epiS	epiImp	epilie	epiNeur	bfagree	bfcon	bfext	bfneur	bfopen	bdi	traitanx	stateanx
1	18	10	7	3	9	138	96	141	51	138	1	24	22
2	16	8	5	1	12	101	99	107	116	132	7	41	40
3	6	1	3	2	5	143	118	38	68	90	4	37	44
4	12	6	4	3	15	104	106	64	114	101	8	54	40
5	14	6	5	3	2	115	102	103	86	118	8	39	67
6	6	4	2	5	15	110	113	61	54	149	5	51	38

Getting data from the web

```
> datafilename <- "http://personality-project.org/r/datasets/maps.mixx.epi.bfi.data"
> my.data(datafilename)
Error: could not find function "my.data"
> my.data <- read(datafilename)
Error: could not find function "read"
> my.data <- read.table(datafilename,header=TRUE) #read the data file
>
> dim(my.data)
[1] 231  13
> headtail(mydata)
Error in inherits(x, "data.frame") : object "mydata" not found
> headtail(my.data)
    epiE epiS epiImp epilie epiNeur bfagree bfcon bfext bfneur bfopen bdi traitanx stateanx
1     18   10      7      3       9     138    96   141     51    138   1       24       22
2     16    8      5      1      12     101    99   107    116    132   7       41       40
3      6    1      3      2       5     143   118    38     68     90   4       37       44
4     12    6      4      3      15     104   106    64    114    101   8       54       40
...  ...  ...    ...    ...     ...     ...   ...   ...    ...    ... ...      ...      ...
228   12    7      4      3      15     155   129   127     88    110   9       35       34
229   19   10      7      2      11     162   152   163    104    164   1       29       47
230    4    1      1      2      10      95   111    75    123    138   5       39       58
231    8    6      3      2      15      85    62    90    131     96  24       58       58
```

Looking at the data

> headtail(My.data) #a psych function demonstrating the passing of parameters to functions

```
> > headtail(My.data,5,3)
    epiE epiS epiImp epilie epiNeur bfagree bfcon bfext bfneur bfopen bdi traitanx stateanx
1     18   10      7      3       9     138    96   141     51    138   1       24       22
2     16    8      5      1      12     101    99   107    116    132   7       41       40
3      6    1      3      2       5     143   118    38     68     90   4       37       44
4     12    6      4      3      15     104   106    64    114    101   8       54       40
5     14    6      5      3       2     115   102   103     86    118   8       39       67
...  ...  ...    ...    ...     ...     ...   ...   ...    ...    ... ...      ...      ...
229   19   10      7      2      11     162   152   163    104    164   1       29       47
230    4    1      1      2      10      95   111    75    123    138   5       39       58
231    8    6      3      2      15      85    62    90    131     96  24       58       58
```

Editing the data

Fix(My.data) # edits the object

A <- edit(My.data) #edits and then returns the new version

(Or just edit in your favorite editor)

Why R? Graphics

I. Sample graphics taken from

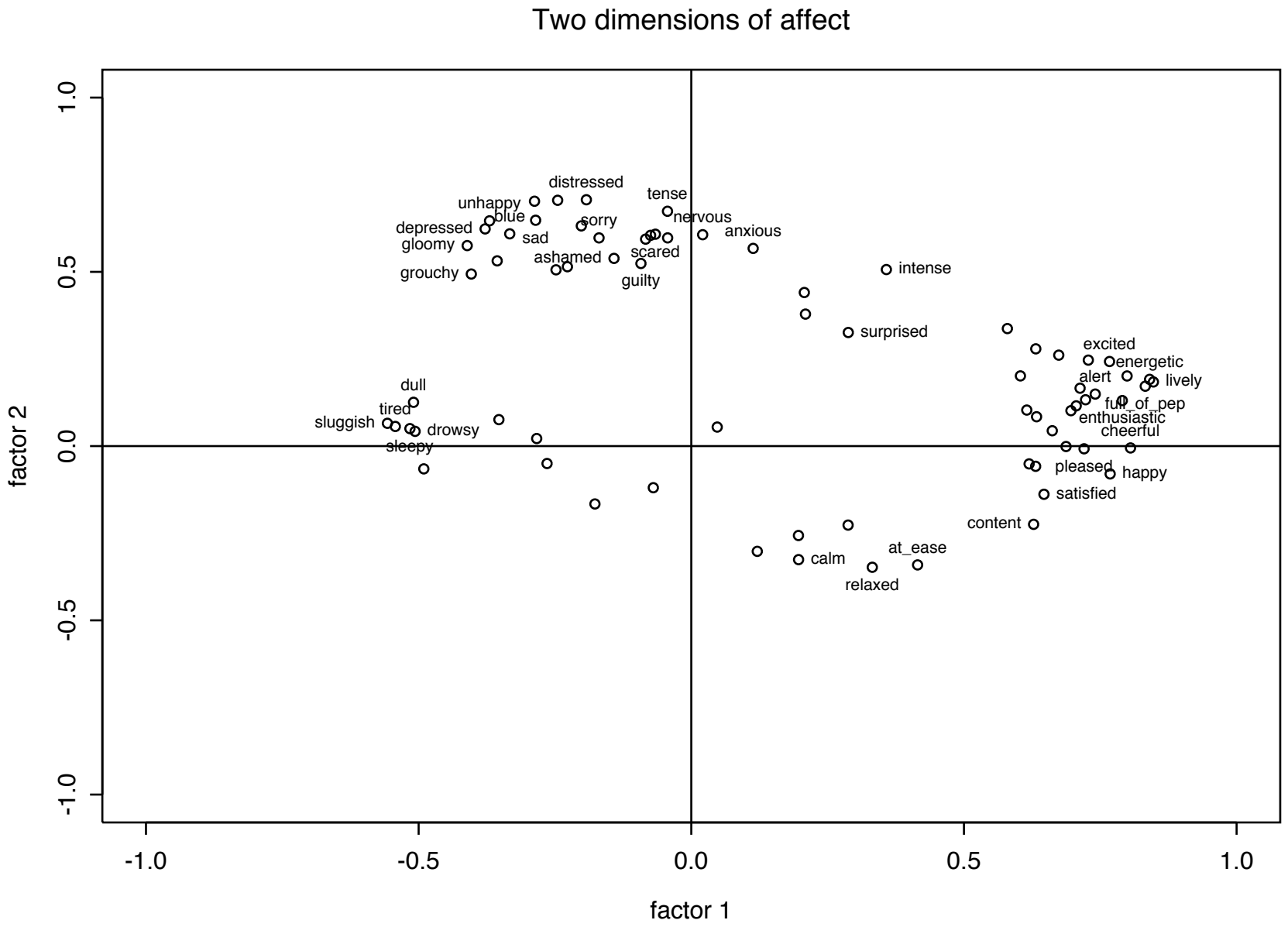
   A. http:personality-project.org/r/

      1. showing what can be done by an amateur

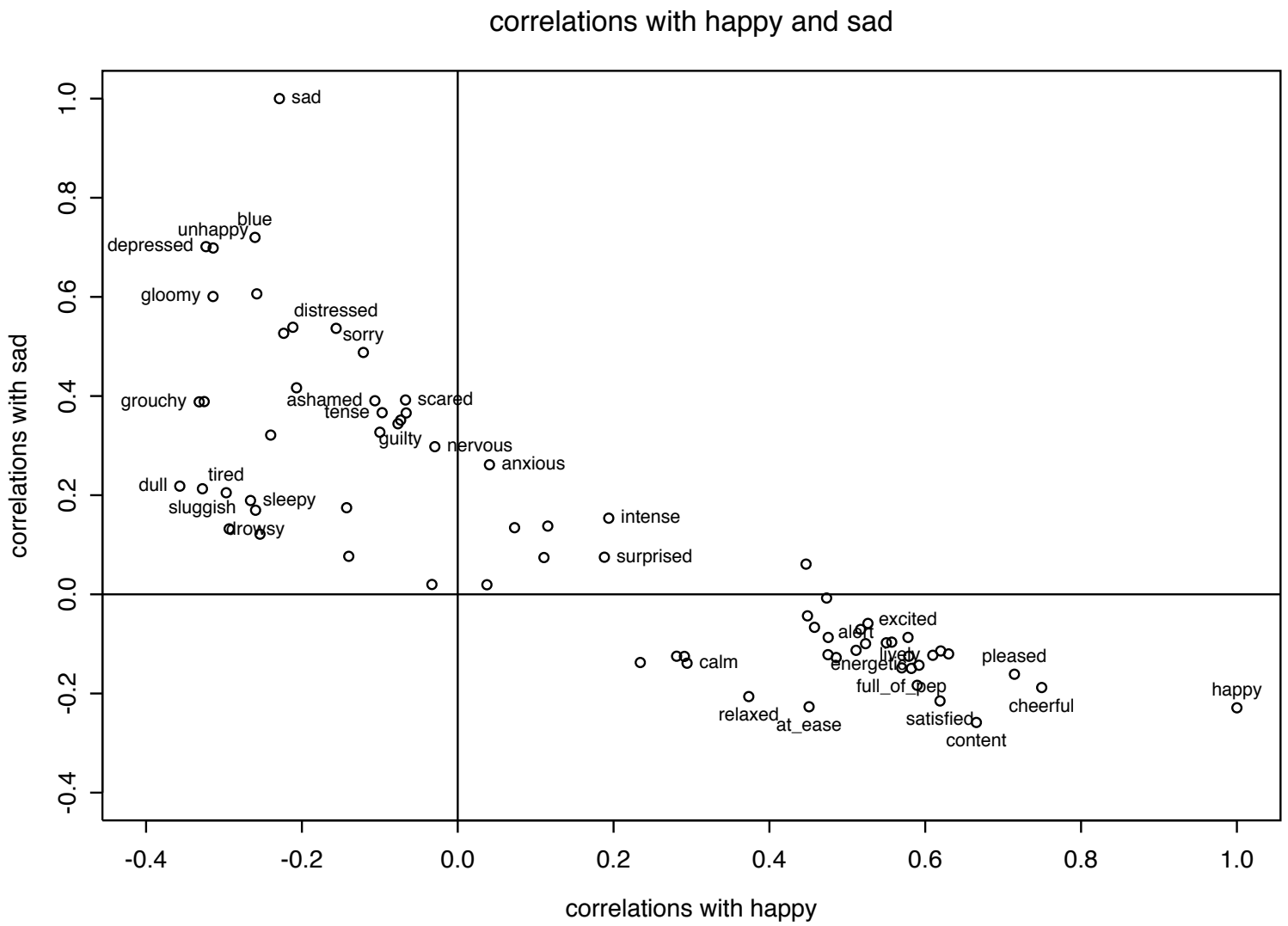
   B. http://addictedtor.free.fr/graphiques/

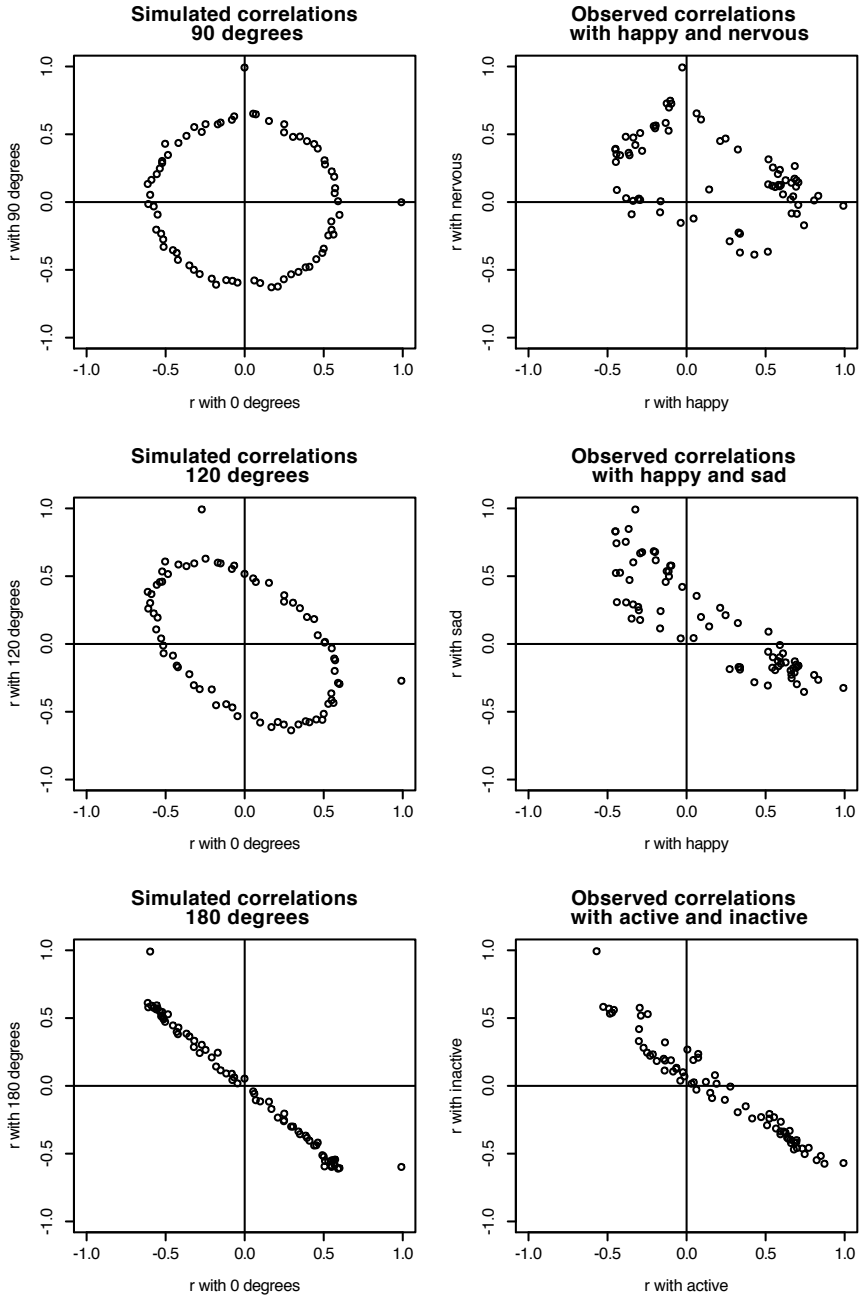
      1. showing some most impressive graphs

Standard Plots of factor loadings



Data points can be dynamically identified

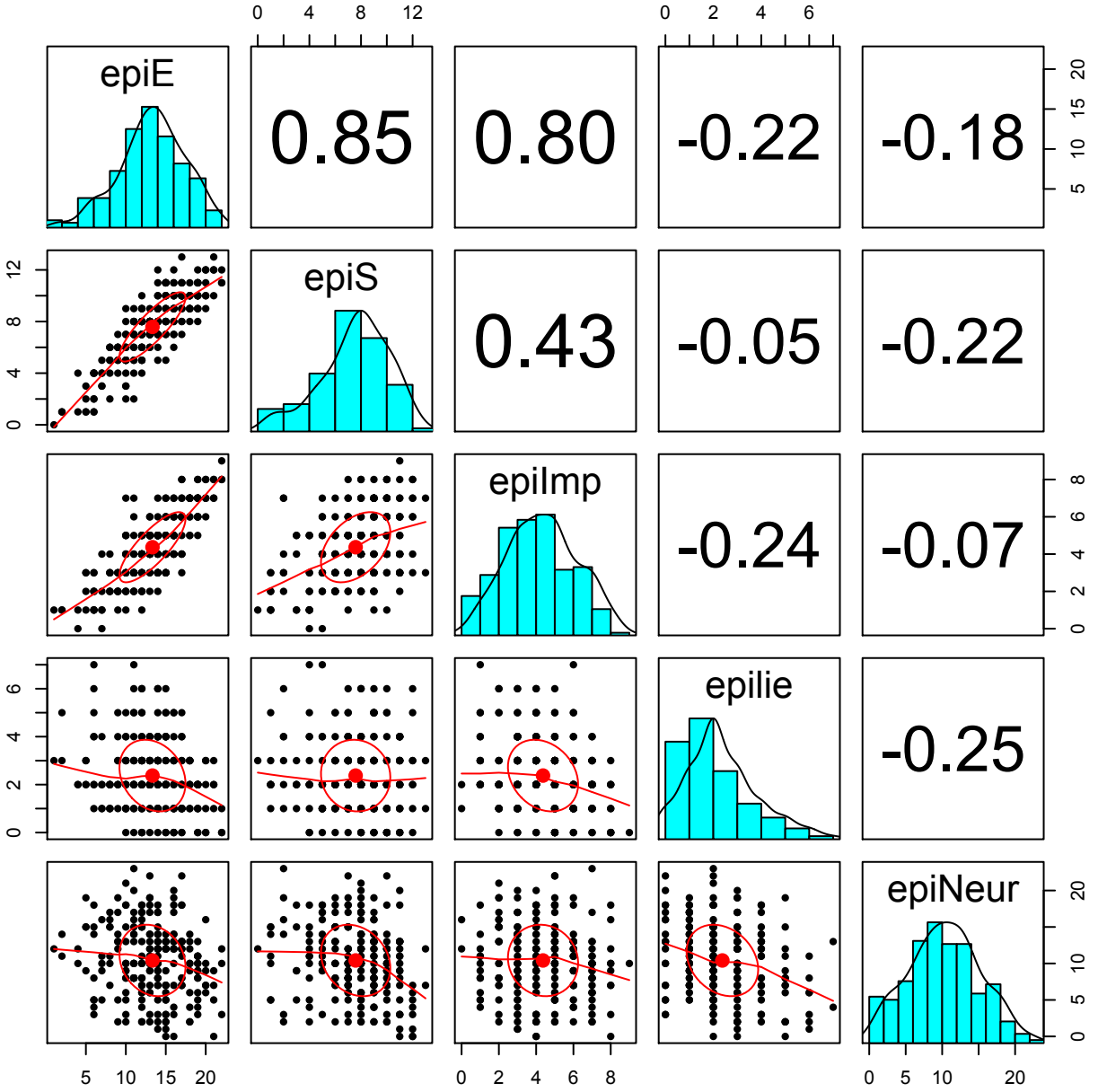




Multi-panel graphs can be labeled separately and organized vertically or horizontally

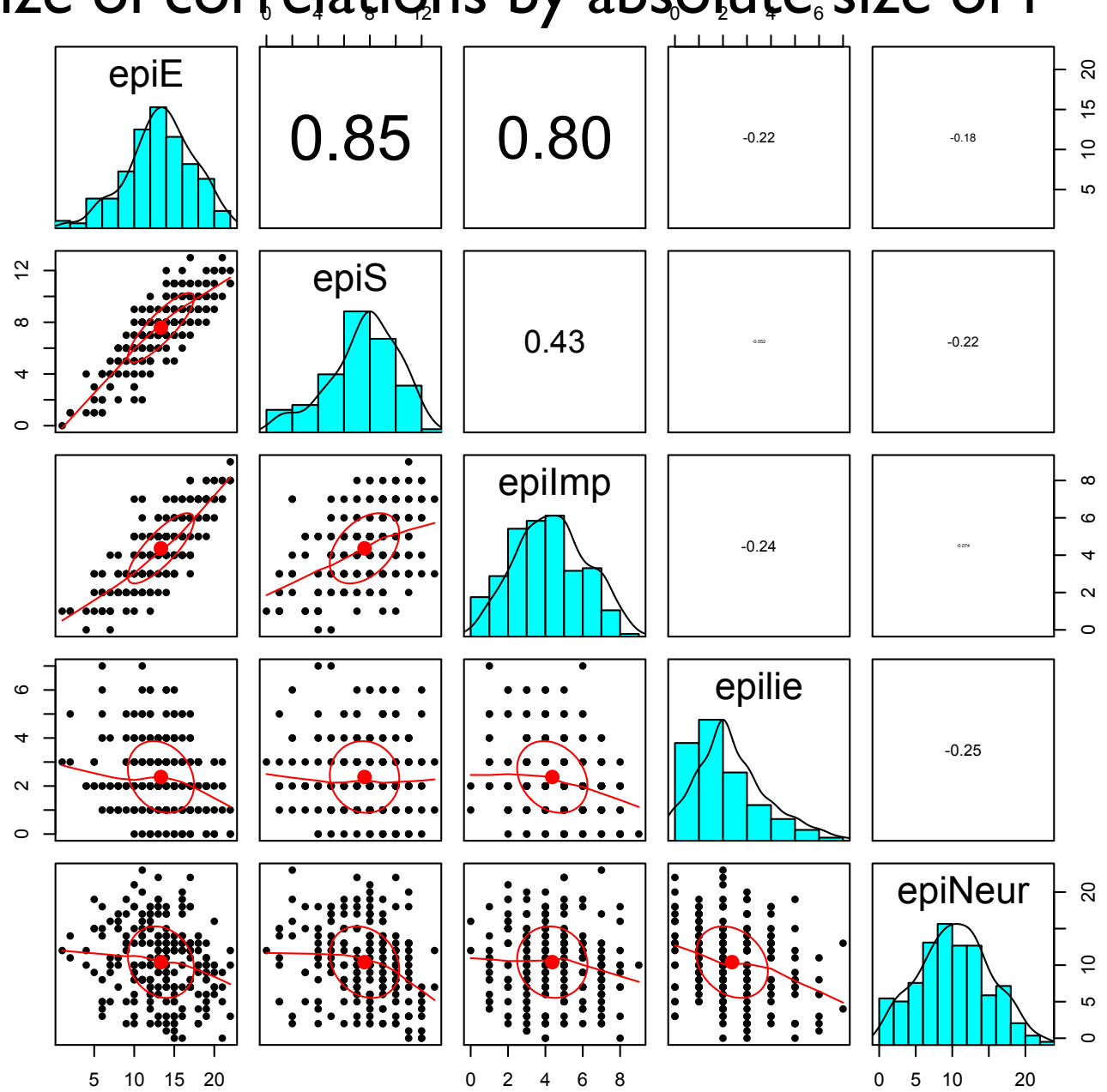
Simulated data can be generated to fit normal, rectangular, binomial, poissen, exponential, etc. distributions

Scatter Plot Matrices can show smoothed fits



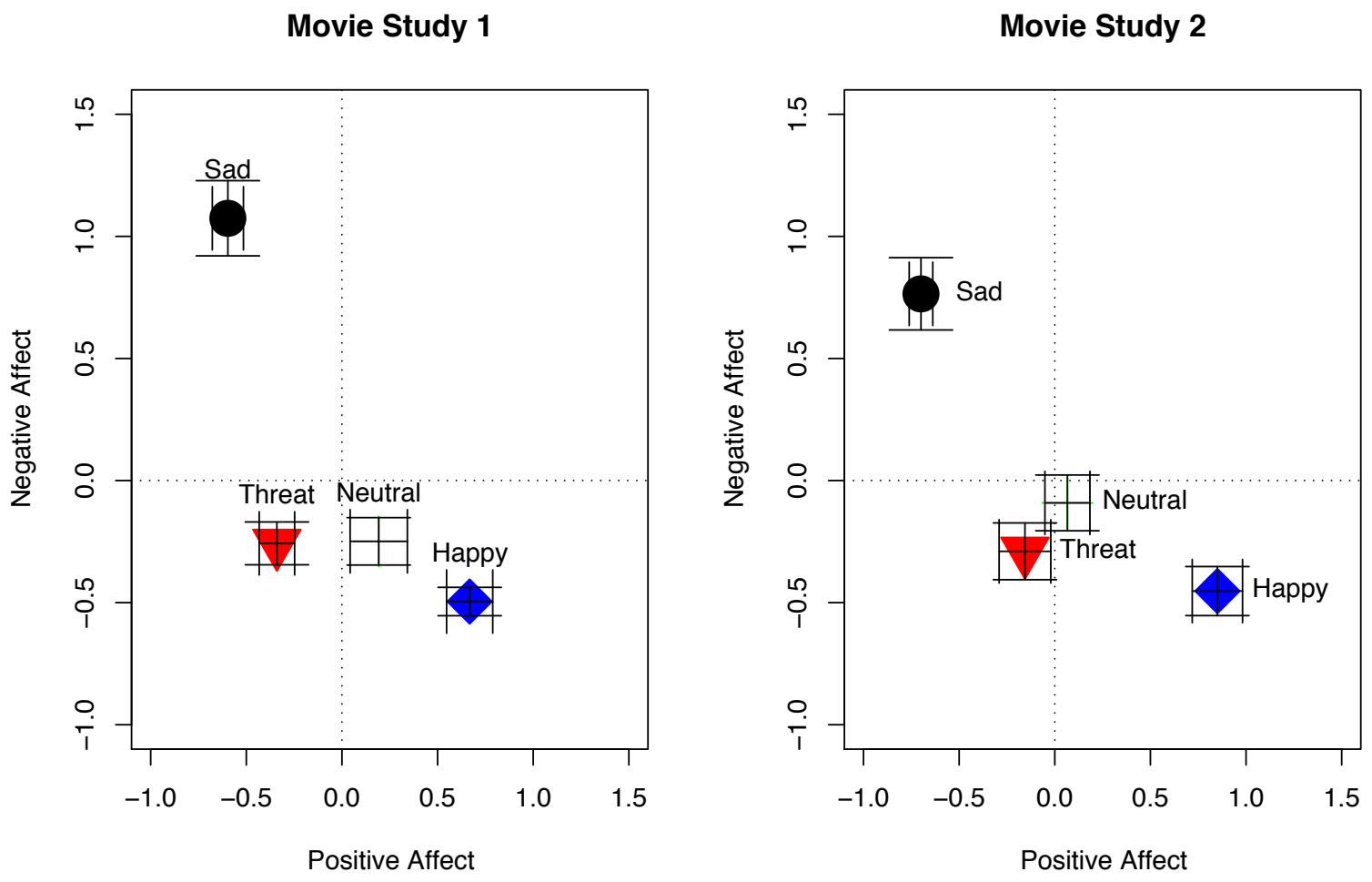

```
> data(epi.bfi)
>pairs.panels(epi.bfi[1:5])
```

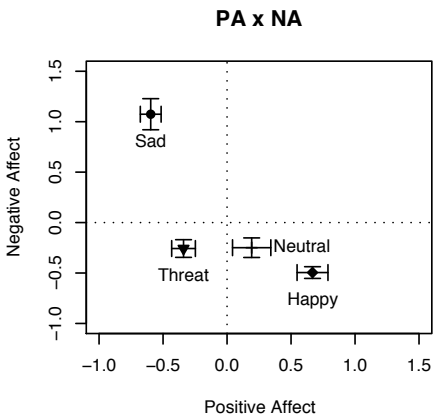
Can scale font size of correlations by absolute size of r

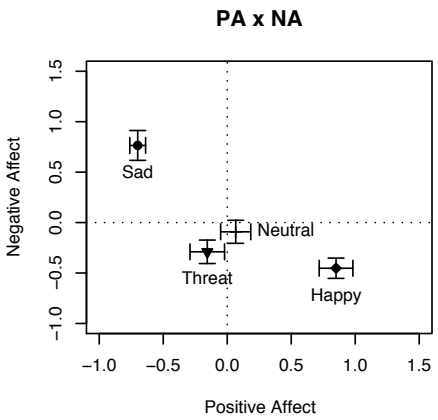


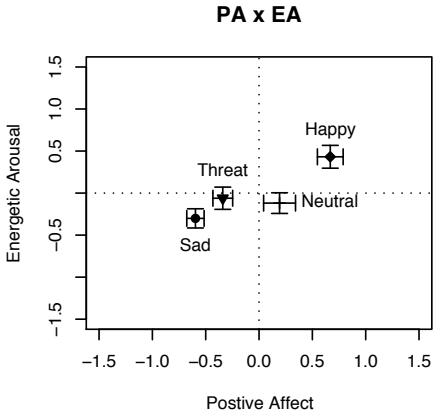

```
> pairs.panels(epi.bfi[1:5],scale=TRUE)
```

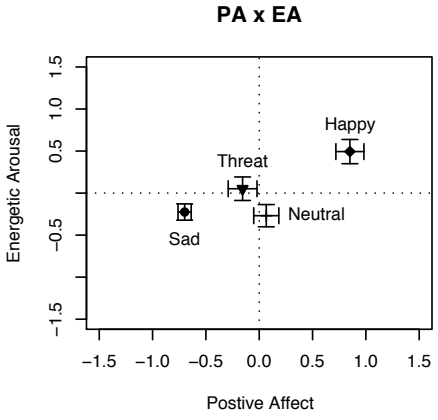
Error bars on two dimensions

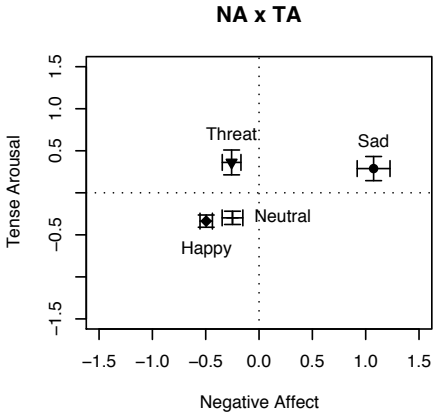


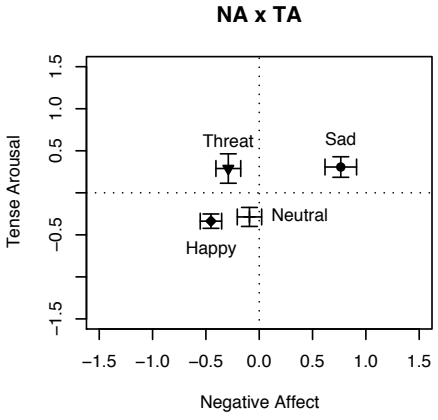








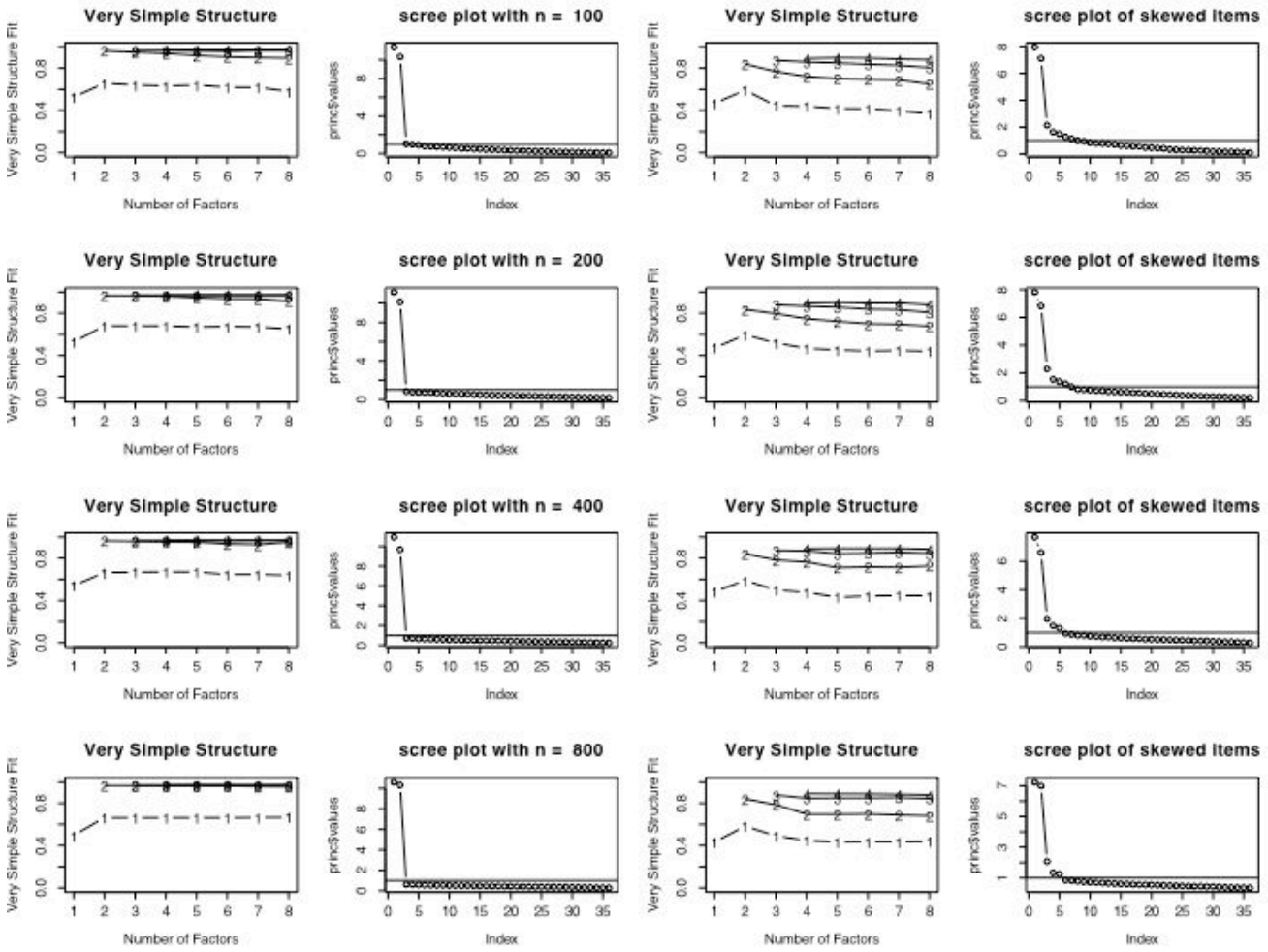




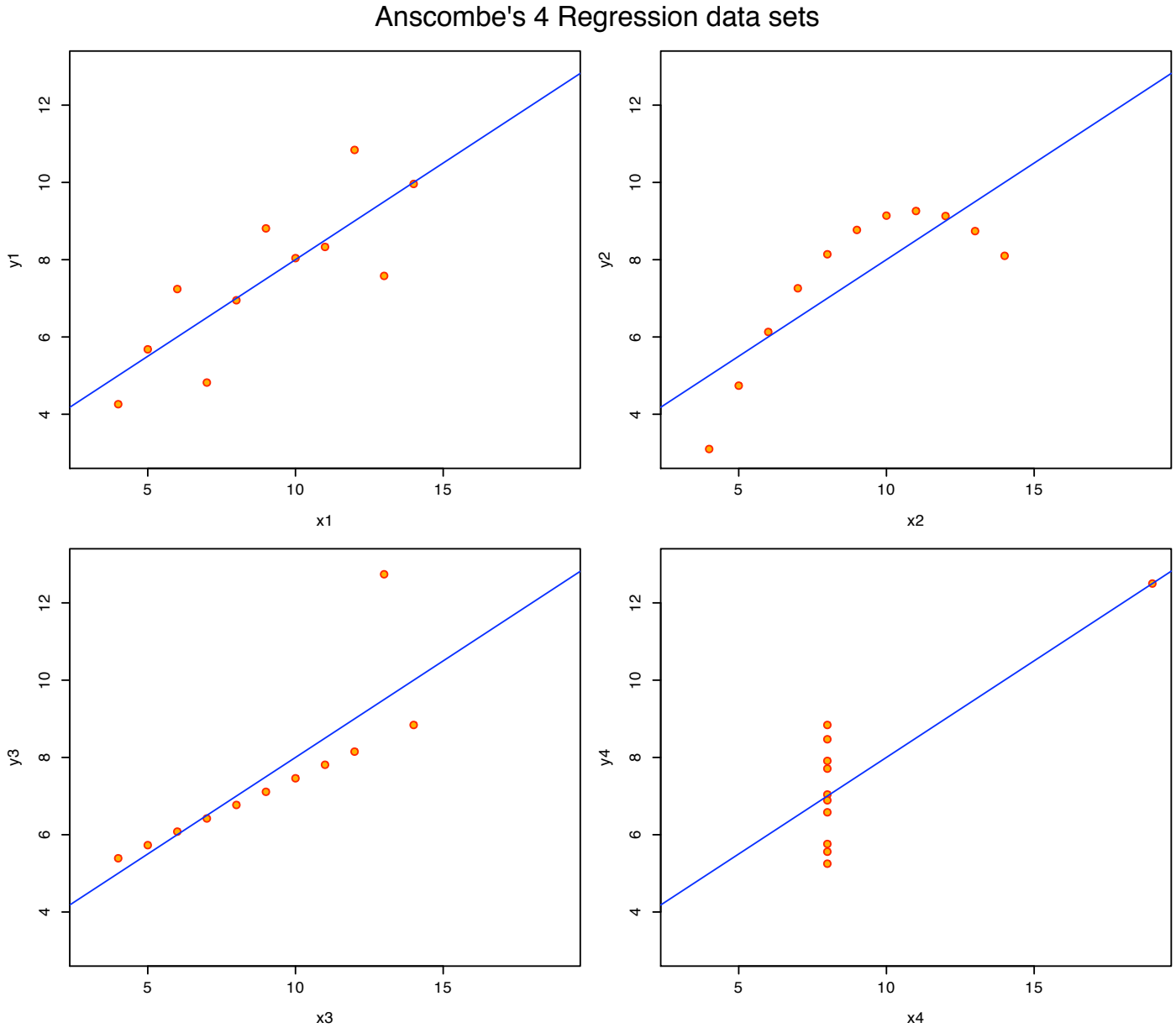
Presentation graphics scale to fit page and produce output for pdf presentations

Window or page size is controllable

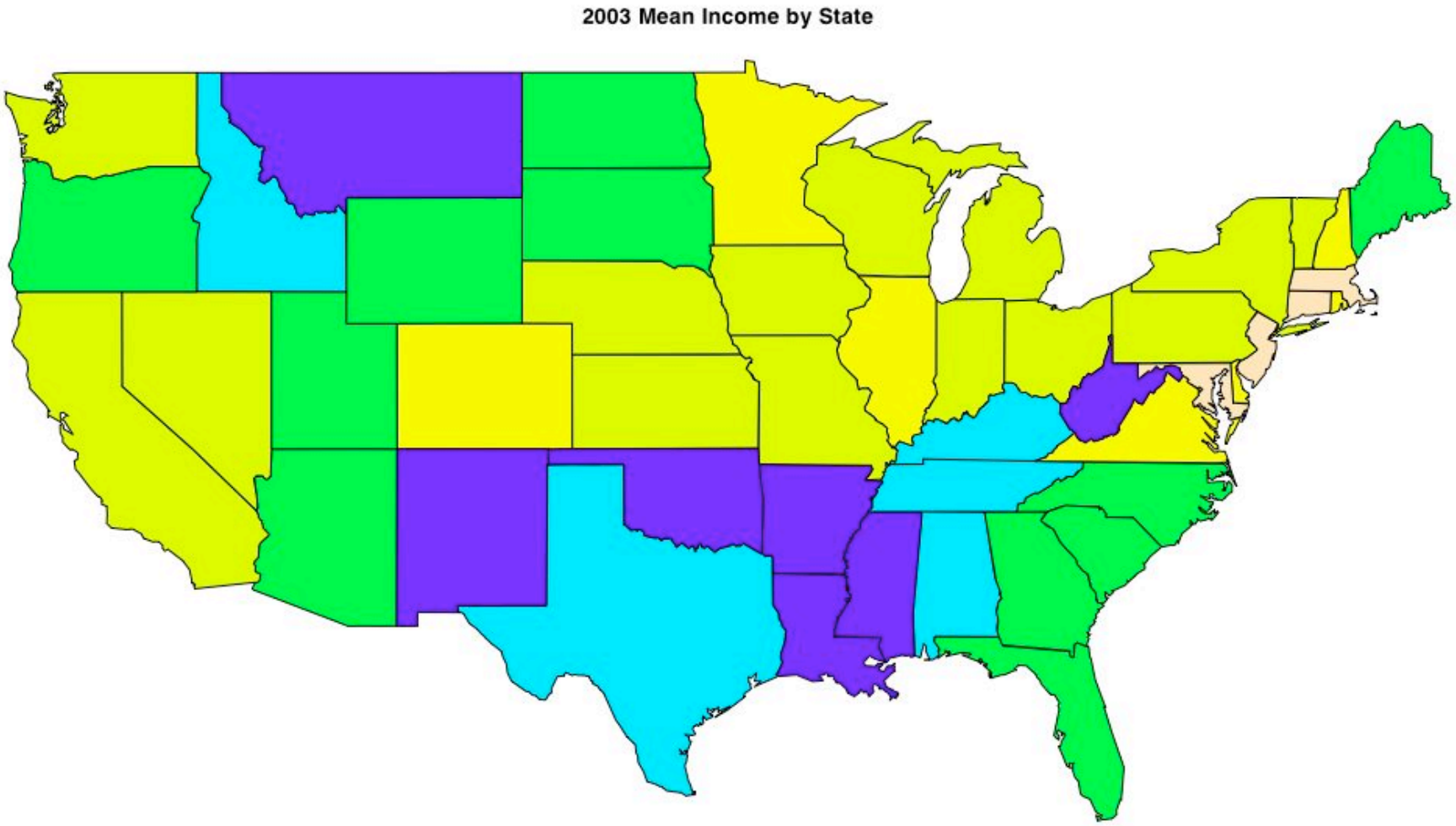
Graphic output can be taken from multiple programs (e.g. Very Simple Structure, factor analysis



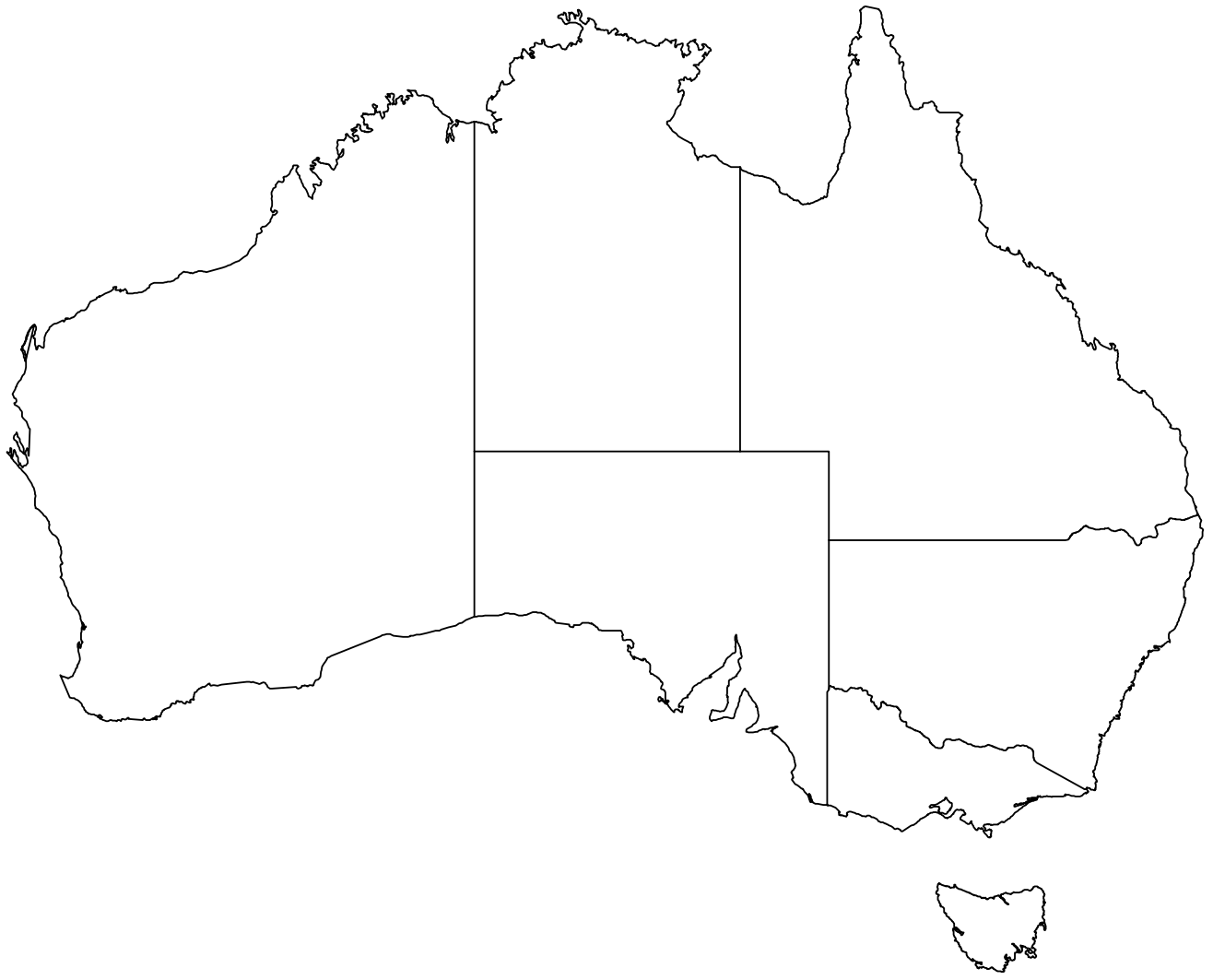
Built-in data sets provide useful demonstrations of stats



Mapping data (GIS) may be combined with descriptive data

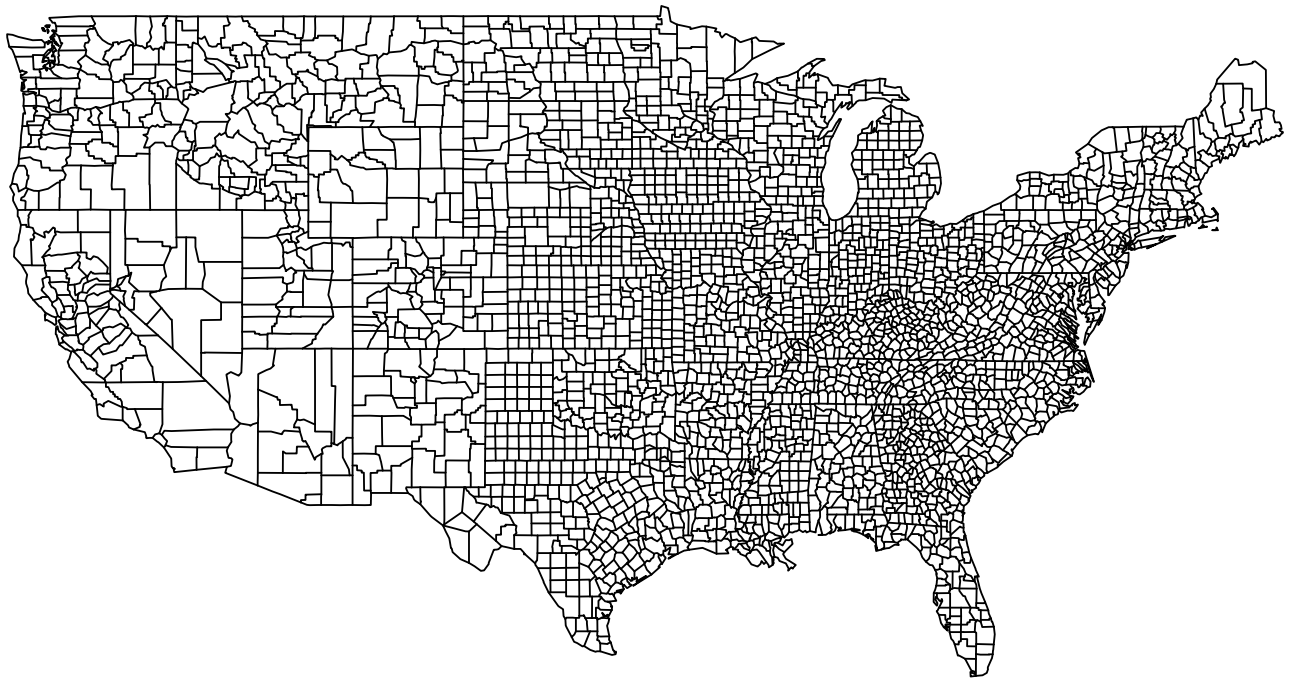


Many GIS map files are available for download from ESRI



GIS maps detail regional boundaries

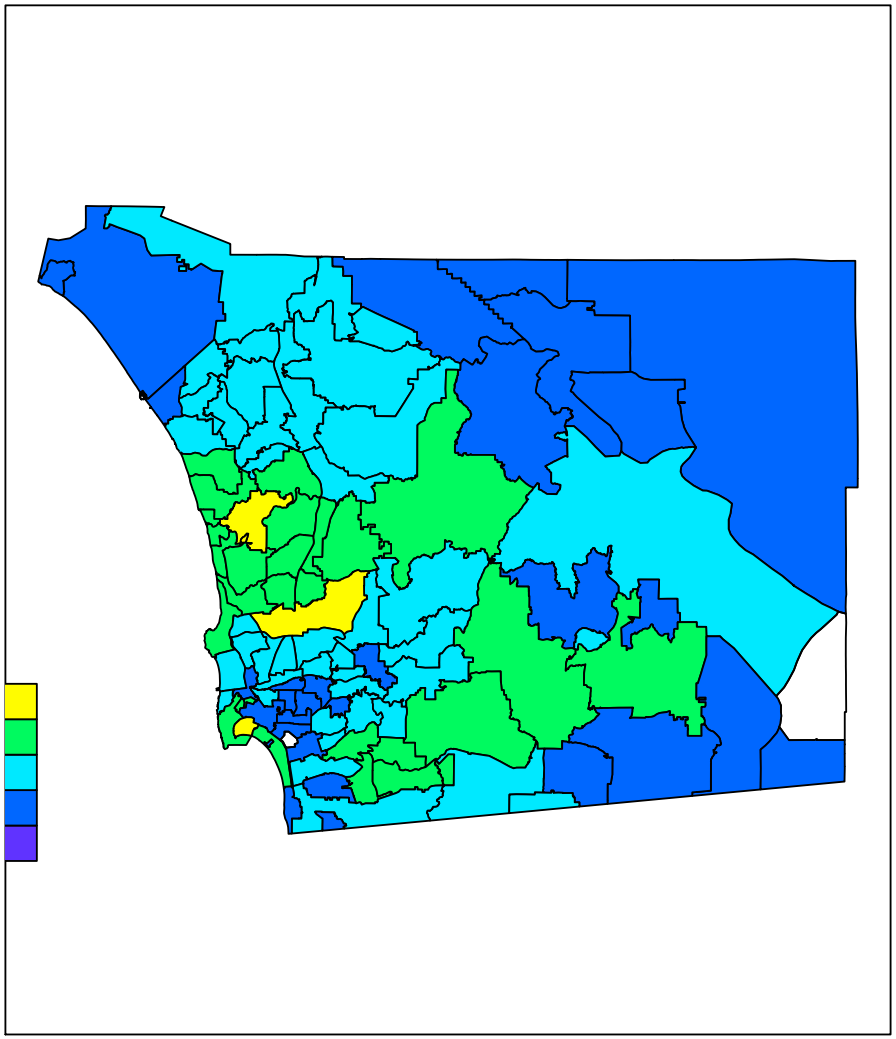
US counties



Counties of California

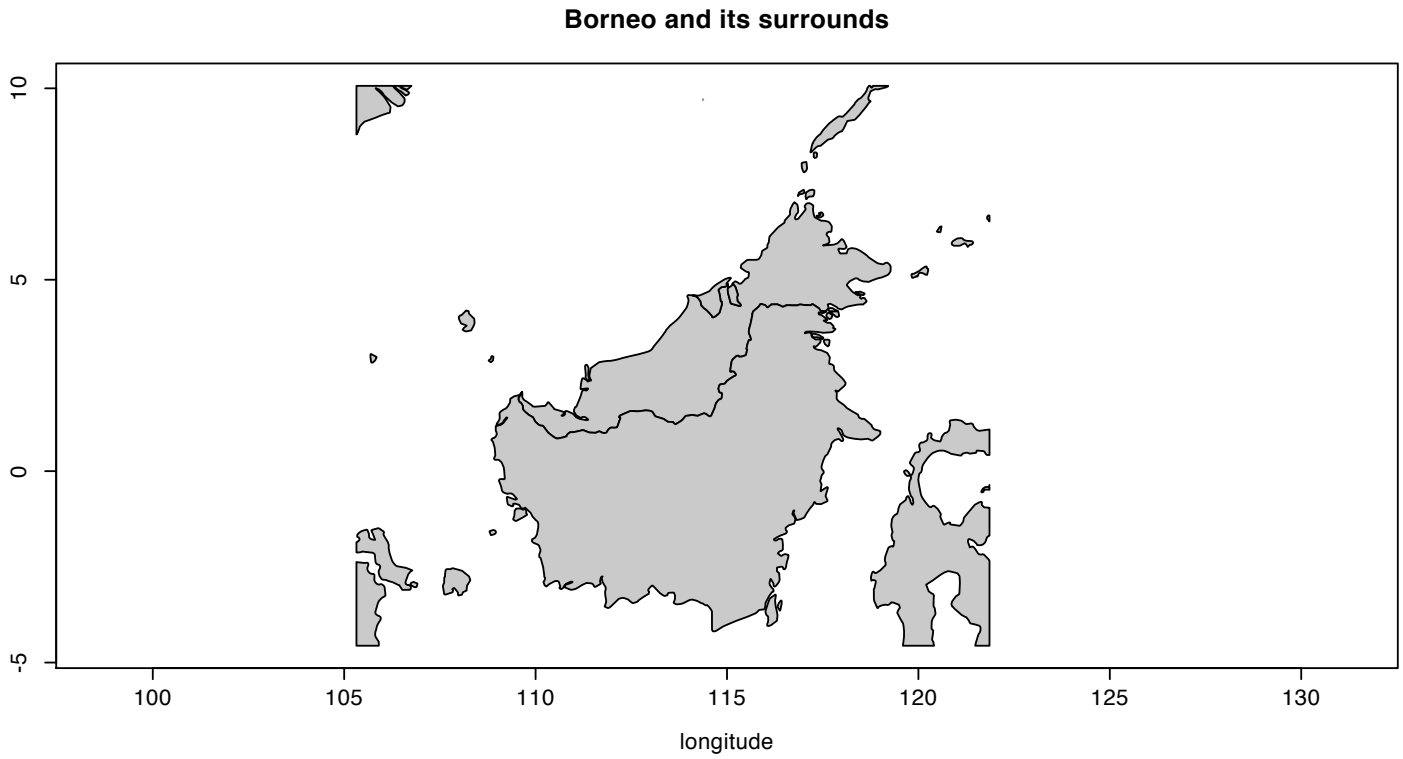
Combine income data from 2000 census with zipcode map of San Diego County

Median Household Income for 2000

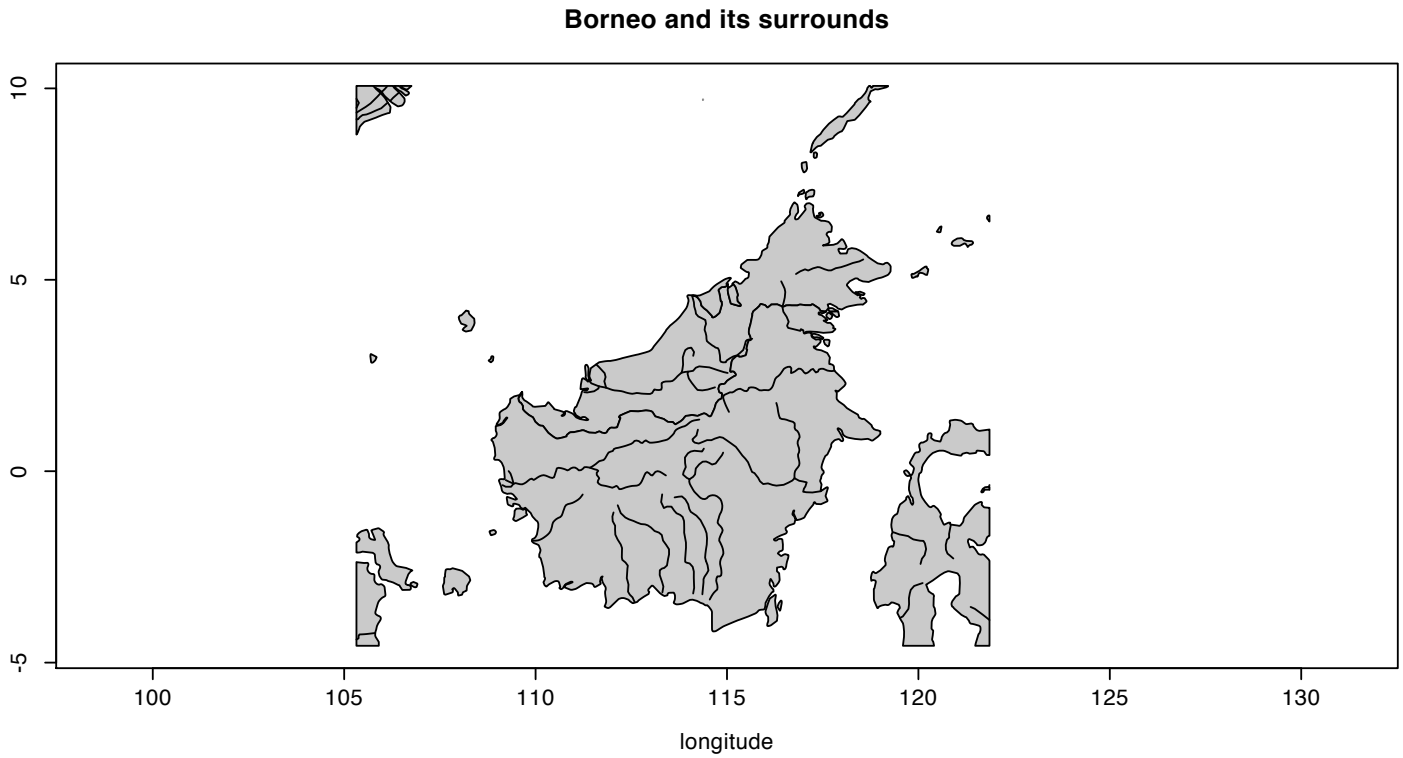


2000 median household income for zip codes

GIS files of Borneo can show country boundaries (e.g., Malaysia, Brunei, Indonesia)



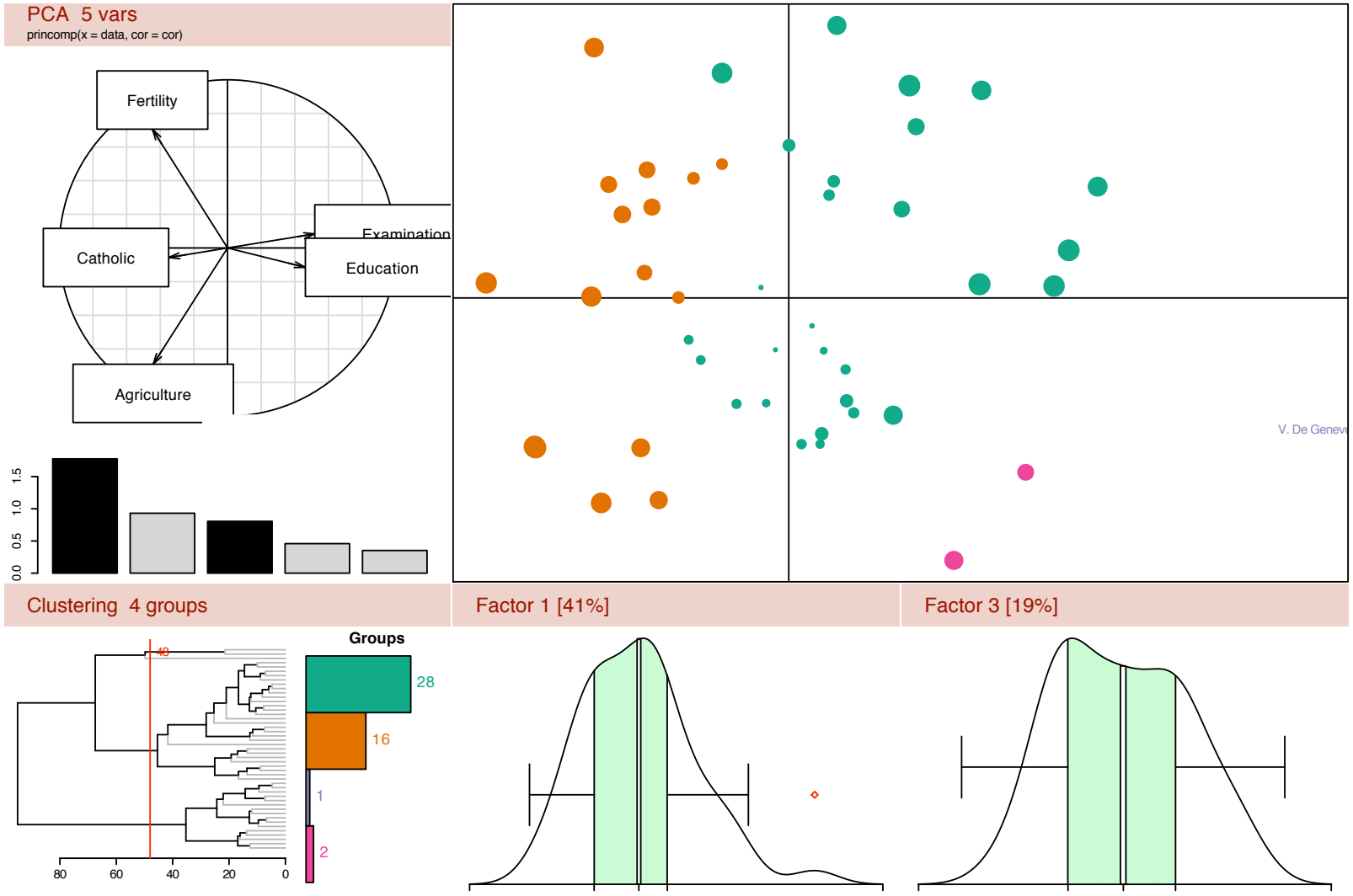
Public access GIS files include rivers and roads



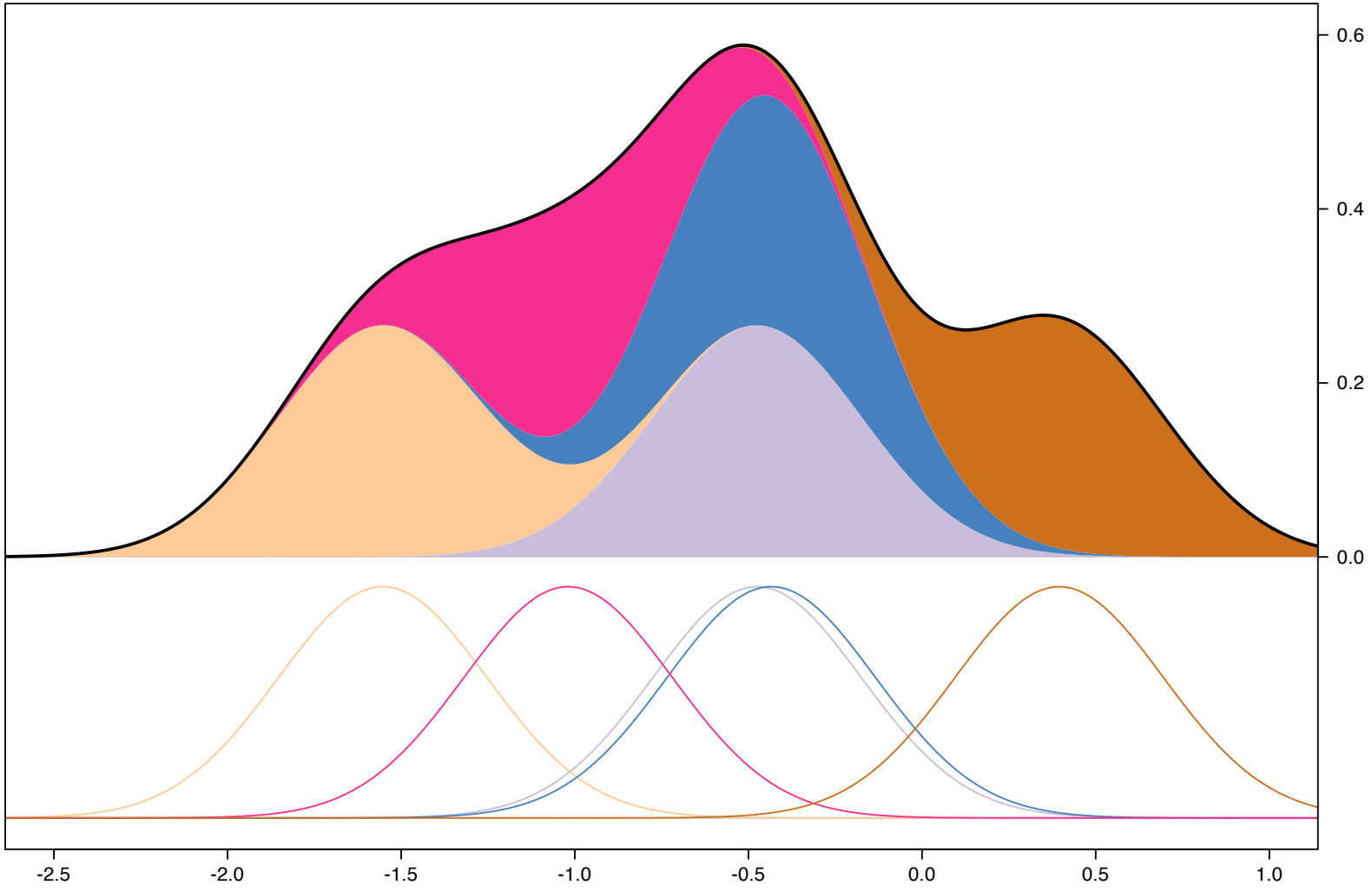
Even more graphics

- Taken from a collection of R demonstrations and graphics
  - http://addictedtor.free.fr/graphiques/

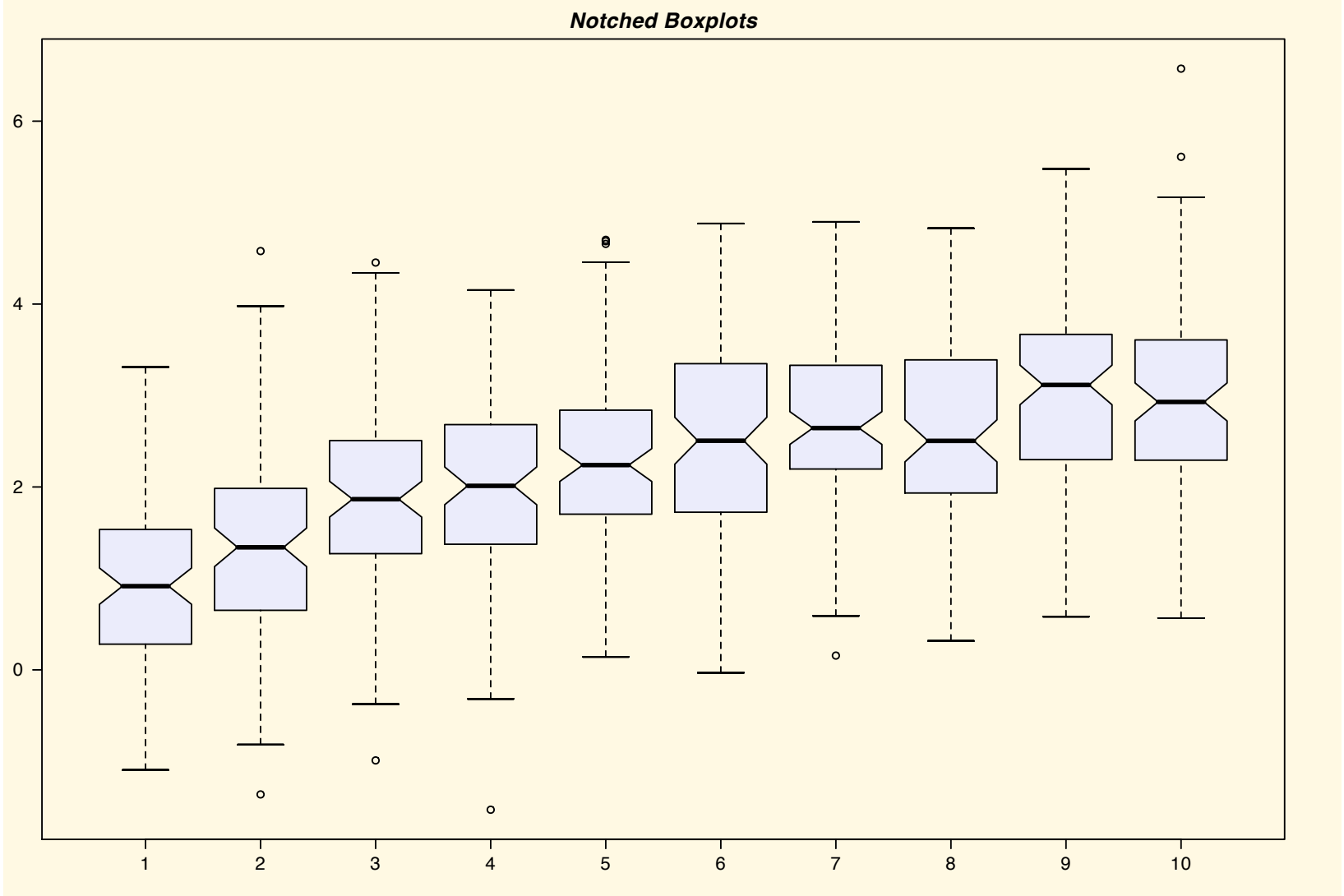
Principal components and clustering of sources of variance in USA arrest data



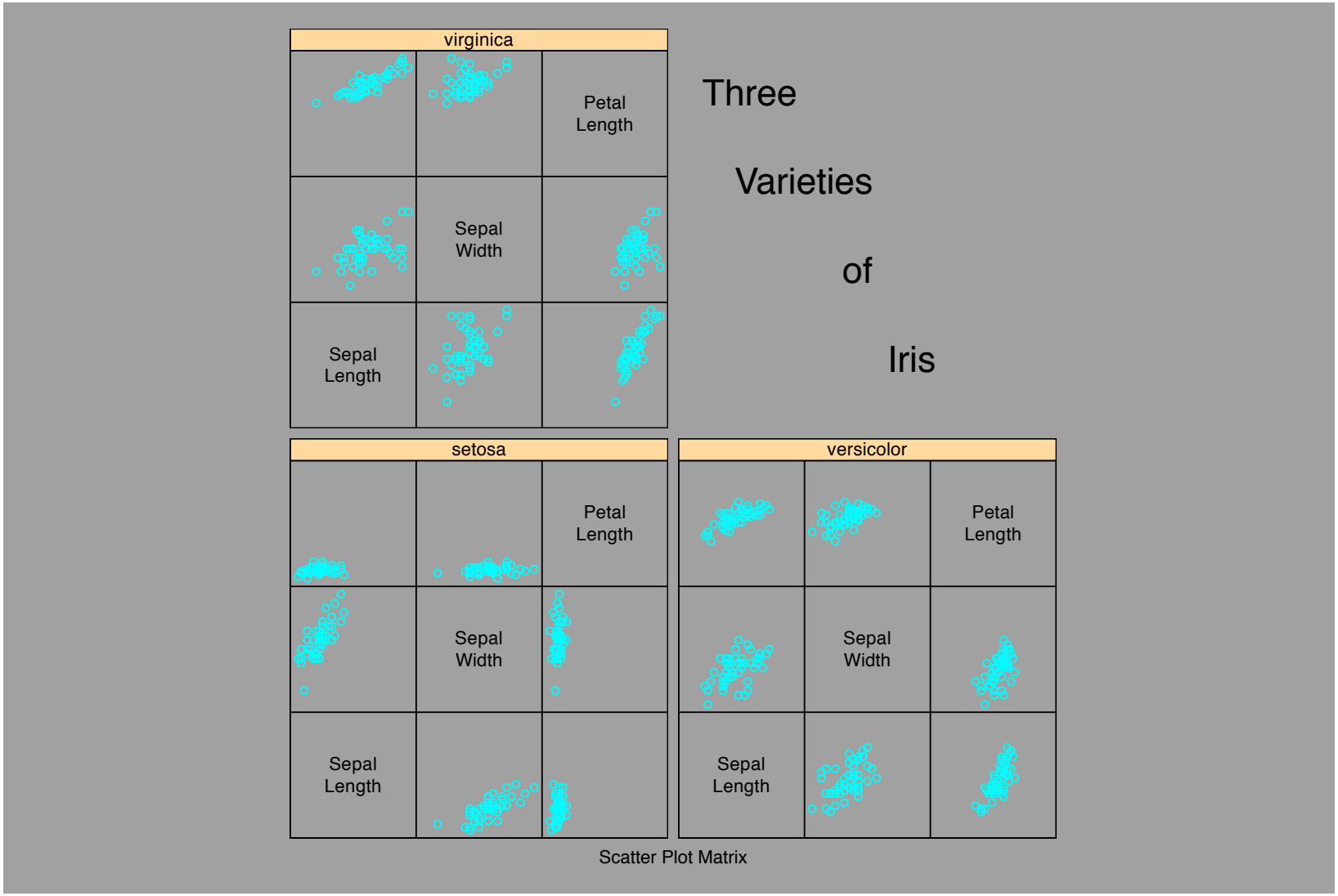
Mixture models



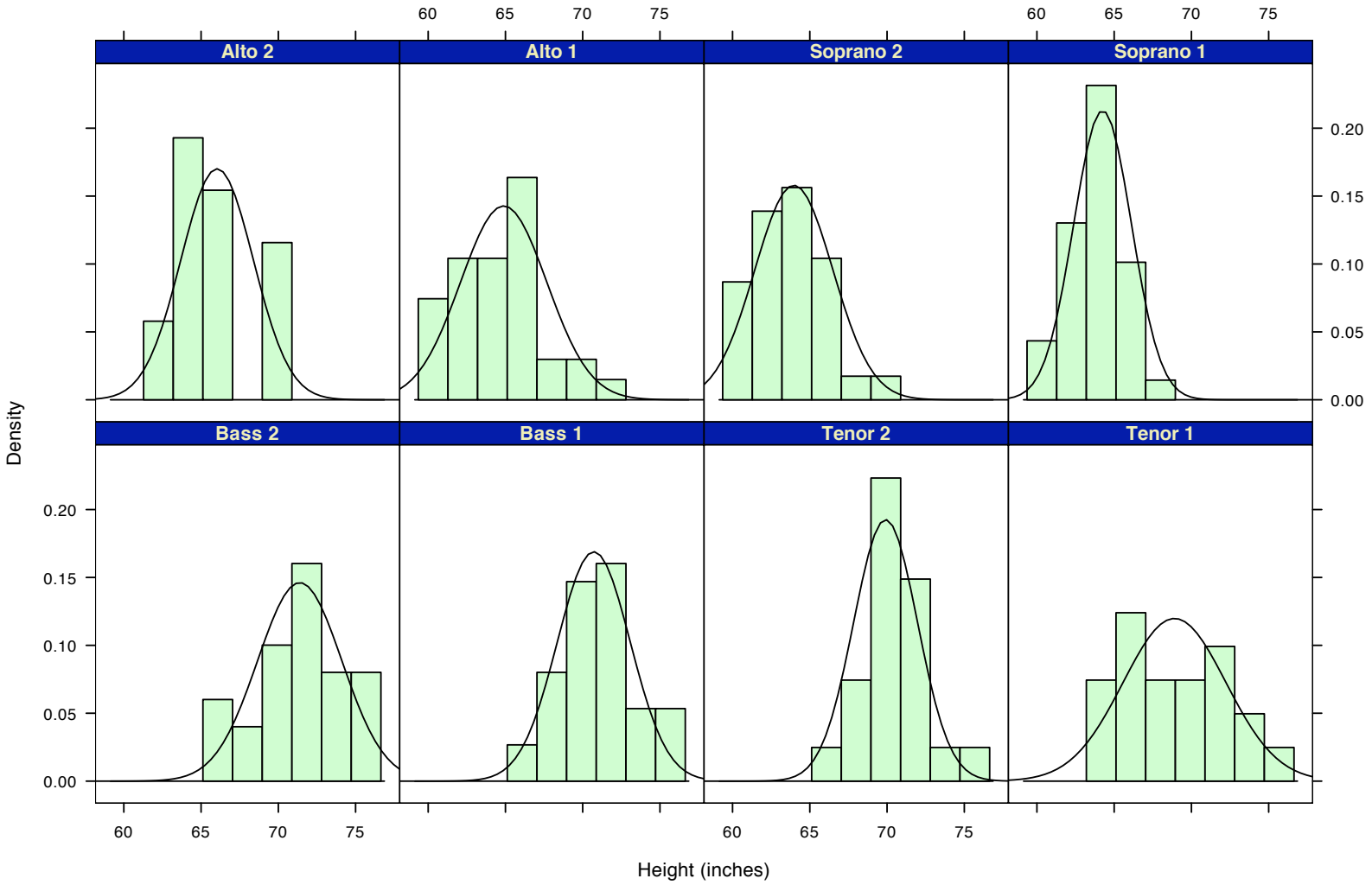
Notched Boxplots show confidence regions



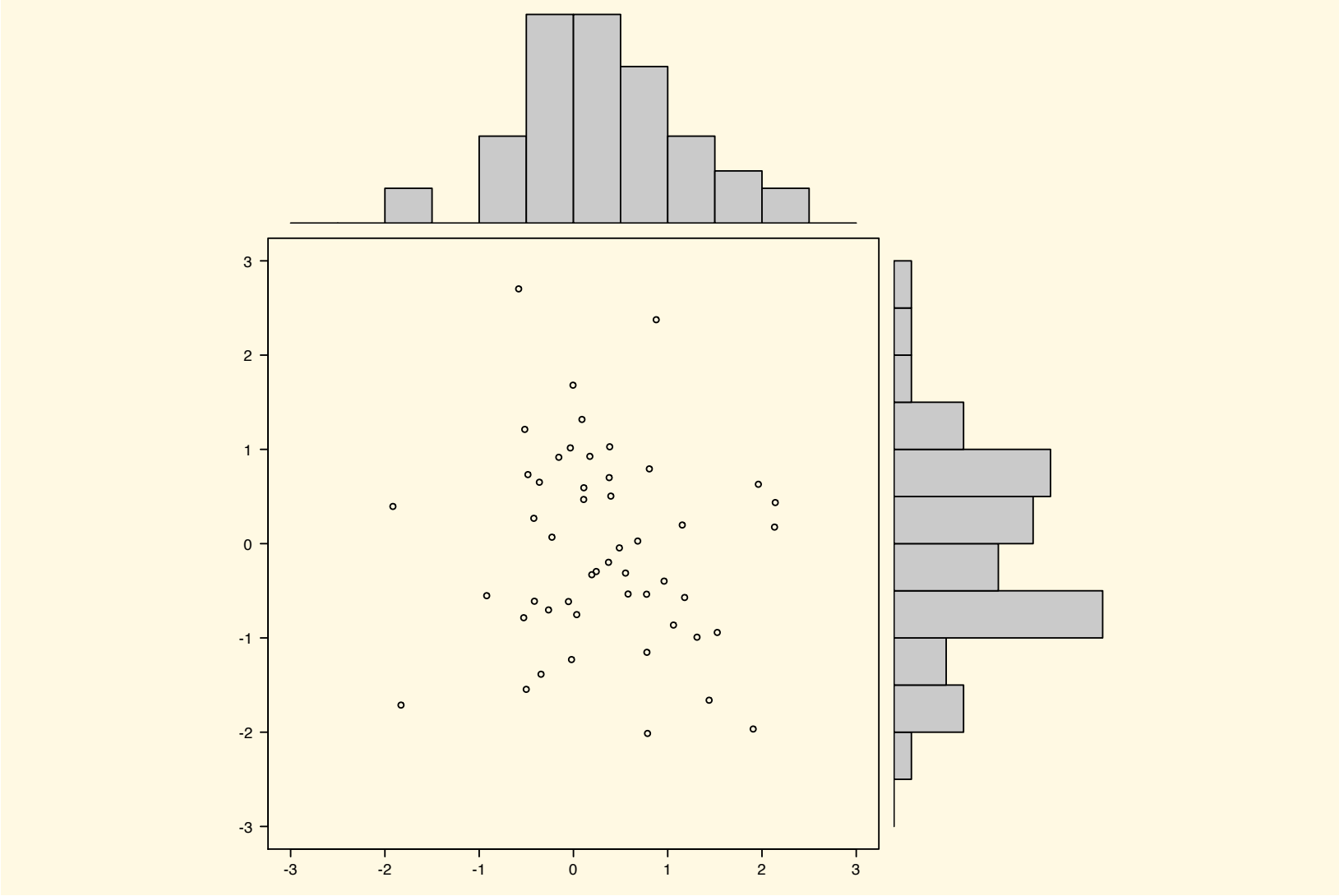
Multipanel graphs



Histograms and fitted distributions



Combine scatter plot with histograms



Why R?

I. Data manipulation including statistics as data

   A. the output of any function may be input for any other

II. Graphics for data exploration and interpretation

III. Statistical analysis

   A. Standard univariate and multivariate generalizations of the linear model

   B. Multivariate-structural extensions

Data Manipulation: Data Structures

I. Data types: integer, real, logical, character, string

II. Vectors of any data type

III. Matrices of any data type

IV. Data Frames (similar to matrix of mixed type)

V. Lists of any mixture of types

VI. All operations are functions and the returned values may be used in any data structure (e.g., as an element of a data frame or of a list)

Data structures

I. Elements (integers, reals, logicals, strings)

II. Vectors (ordered sets of similar elements)

III. Matrices (ordered sets of vectors of the same length)

IV. Data Frames (ordered sets of vectors where the vectors can be different, but all the same length)

V. Lists (ordered sets of anything, can be different lengths)

Structure examples

```
> x <- c(1,2,4)
> y <- c(letters[1:6],LETTERS[1:4])
> z <- seq(10,28,2)
> X <- matrix(1:20,ncol=4)
> Y <- matrix(c(11,22,44,4,15,42),ncol=3,byrow=TRUE)
> yz.df <-data.frame(A = y,b=z)
> L <- list(a=x,b=y,c=z,d=X,e=Y,f =yz.df)
> x
[1] 1 2 4
> y
 [1] "a" "b" "c" "d" "e" "f" "A" "B" "C" "D"
> z
 [1] 10 12 14 16 18 20 22 24 26 28
> X
     [,1] [,2] [,3] [,4]
[1,]    1    6   11   16
[2,]    2    7   12   17
[3,]    3    8   13   18
[4,]    4    9   14   19
[5,]    5   10   15   20
```

```
> Y
     [,1] [,2] [,3]
[1,]   11   22   44
[2,]    4   15   42
> yz.df
   A  b
1  a 10
2  b 12
3  c 14
4  d 16
5  e 18
6  f 20
7  A 22
8  B 24
9  C 26
10 D 28
```

Structure list

```
> L
$a
[1] 1 2 4

$b
 [1] "a" "b" "c" "d" "e" "f" "A" "B" "C" "D"

$c
 [1] 10 12 14 16 18 20 22 24 26 28

$d
     [,1] [,2] [,3] [,4]
[1,]    1    6   11   16
[2,]    2    7   12   17
[3,]    3    8   13   18
[4,]    4    9   14   19
[5,]    5   10   15   20
```

```
$e
     [,1] [,2] [,3]
[1,]   11   22   44
[2,]    4   15   42
$f
   A  b
1  a 10
2  b 12
3  c 14
4  d 16
5  e 18
6  f 20
7  A 22
8  B 24
9  C 26
10 D 28
```

Structure of lists

```
> str(L)
List of 6
 $ a: num [1:3] 1 2 4
 $ b: chr [1:10] "a" "b" "c" "d" ...
 $ c: num [1:10] 10 12 14 16 18 20 22 24 26 28
 $ d: int [1:5, 1:4] 1 2 3 4 5 6 7 8 9 10 ...
 $ e: num [1:2, 1:3] 11 4 22 15 44 42
 $ f:'data.frame': 10 obs. of  2 variables:
  ..$ A: Factor w/ 10 levels "a","A","b","B",..: 1 3 5 7 9 10 2 4
6 8
  ..$ b: num [1:10] 10 12 14 16 18 20 22 24 26 28
```

Accessing elements

```
> L$d
     [,1] [,2] [,3] [,4]
[1,]    1    6   11   16
[2,]    2    7   12   17
[3,]    3    8   13   18
[4,]    4    9   14   19
[5,]    5   10   15   20
> L[[4]]
     [,1] [,2] [,3] [,4]
[1,]    1    6   11   16
[2,]    2    7   12   17
[3,]    3    8   13   18
[4,]    4    9   14   19
[5,]    5   10   15   20
```

Manipulating data

I. Consider scoring a multiple choice test

   A. 10 items, 100 subjects

   B. create the scoring key

   C. score it

Scoring a multiple score test

```
> set.seed(42)
> my.items <- matrix(sample(5,500,replace=TRUE),ncol=5)
> my.key <- c(1,2,3,2,4)
> my.scores <- t(t(my.items)==my.key[])  #these are TRUE or FALSE
> my.scores <- t(t(my.items)==my.key[]) +0 #these are 1s or 0s
> my.total <- rowSums(my.scores)            #total score
> describe(my.total)
  var   n mean   sd median trimmed  mad min max range skew kurtosis   se
1   1 100 0.92 0.82      1    0.84 1.48   0   3     3 0.68    -0.03 0.08
> describe(my.scores)
  var   n mean   sd median trimmed mad min max range skew kurtosis   se
1   1 100 0.19 0.39      0    0.11   0   0   1     1 1.56     0.43 0.04
2   2 100 0.14 0.35      0    0.05   0   0   1     1 2.04     2.20 0.03
3   3 100 0.25 0.44      0    0.19   0   0   1     1 1.14    -0.71 0.04
4   4 100 0.22 0.42      0    0.15   0   0   1     1 1.33    -0.23 0.04
5   5 100 0.12 0.33      0    0.02   0   0   1     1 2.30     3.34 0.03
```

How does that work

```
> my.key
[1] 1 2 3 2 4
> dim(my.items)
[1] 100   5
> dim(t(my.items))
[1]   5 100
> t(my.items)[,1:10]
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
[1,]    5    5    2    5    4    3    4    1    4     4
[2,]    4    2    2    2    5    5    4    4    3     1
[3,]    5    3    5    3    1    3    5    3    2     2
[4,]    3    3    1    2    5    5    2    1    2     2
[5,]    1    3    4    3    5    1    5    2    1     2
> x <- t(my.items) == my.key
> x[,1:10]
      [,1]  [,2]  [,3]  [,4]  [,5]  [,6]  [,7]  [,8]  [,9] [,10]
[1,] FALSE FALSE FALSE FALSE FALSE FALSE FALSE  TRUE FALSE FALSE
[2,] FALSE  TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE
[3,] FALSE  TRUE FALSE  TRUE FALSE  TRUE FALSE  TRUE FALSE FALSE
[4,] FALSE FALSE FALSE  TRUE FALSE FALSE  TRUE FALSE  TRUE  TRUE
[5,] FALSE FALSE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE

> x0 <- x+0
> x0[,1:10]
     [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
[1,]    0    0    0    0    0    0    0    1    0     0
[2,]    0    1    1    1    0    0    0    0    0     0
[3,]    0    1    0    1    0    1    0    1    0     0
[4,]    0    0    0    1    0    0    1    0    1     1
[5,]    0    0    1    0    0    0    0    0    0     0
```

More on multiple choice

```
> my.scores <- t(t(my.items)==my.key[])  #these are TRUE or FALSE
> head(my.scores)
      [,1]  [,2]  [,3]  [,4]  [,5]
[1,] FALSE FALSE FALSE FALSE FALSE
[2,] FALSE  TRUE  TRUE FALSE FALSE
[3,] FALSE  TRUE FALSE FALSE  TRUE
[4,] FALSE  TRUE  TRUE  TRUE FALSE
[5,] FALSE FALSE FALSE FALSE FALSE
[6,] FALSE FALSE  TRUE FALSE FALSE
> my.scores <- t(t(my.items)==my.key[]) +0  #these are 1s or 0s
> my.scores
      [,1] [,2] [,3] [,4] [,5]
  [1,]    0    0    0    0    0
  [2,]    0    1    1    0    0
  [3,]    0    1    0    0    1
  [4,]    0    1    1    1    0
  [5,]    0    0    0    0    0
  [6,]    0    0    1    0    0
...
> my.total <- rowSums(my.scores)
> head(my.total)
[1] 0 2 2 3 0 1
```

Or, just use a function

```
> data(iqitems)
> iq.keys <- c(4,4,3,1,4,3,2,3,1,4,1,3,4,3)
> score.multiple.choice(iq.keys,iqitems)
$item.stats
      key    0    1    2    3    4    5    6    r    n mean   sd  skew kurtosis   se
iq1     4 0.04 0.01 0.03 0.09 0.80 0.02 0.01 0.59 1000 0.80 0.40 -1.51     0.27 0.01
iq8     4 0.03 0.10 0.01 0.02 0.80 0.01 0.04 0.39 1000 0.80 0.40 -1.49     0.22 0.01
iq10    3 0.10 0.22 0.09 0.37 0.04 0.13 0.04 0.35 1000 0.37 0.48  0.53    -1.72 0.02
iq15    1 0.03 0.65 0.16 0.15 0.00 0.00 0.00 0.35 1000 0.65 0.48 -0.63    -1.60 0.02
iq20    4 0.03 0.02 0.03 0.03 0.85 0.02 0.01 0.42 1000 0.85 0.35 -2.00     2.01 0.01
iq44    3 0.03 0.10 0.06 0.64 0.02 0.14 0.01 0.42 1000 0.64 0.48 -0.61    -1.64 0.02
iq47    2 0.04 0.08 0.59 0.06 0.11 0.07 0.05 0.51 1000 0.59 0.49 -0.35    -1.88 0.02
iq2     3 0.07 0.08 0.31 0.32 0.15 0.05 0.02 0.26 1000 0.32 0.46  0.80    -1.37 0.01
iq11    1 0.04 0.87 0.03 0.01 0.01 0.01 0.04 0.54 1000 0.87 0.34 -2.15     2.61 0.01
iq16    4 0.05 0.05 0.08 0.07 0.74 0.01 0.00 0.56 1000 0.74 0.44 -1.11    -0.77 0.01
iq32    1 0.04 0.54 0.02 0.14 0.10 0.04 0.12 0.50 1000 0.54 0.50 -0.17    -1.97 0.02
iq37    3 0.07 0.10 0.09 0.26 0.13 0.02 0.34 0.23 1000 0.26 0.44  1.12    -0.74 0.01
iq43    4 0.04 0.07 0.04 0.02 0.78 0.03 0.00 0.50 1000 0.78 0.41 -1.35    -0.18 0.01
iq49    3 0.06 0.27 0.09 0.32 0.14 0.08 0.05 0.28 1000 0.32 0.47  0.79    -1.38 0.01

$alpha
         Averages
Averages     0.63

$av.r
         Averages
Averages     0.11
```

Examine the structure

```
> iq.scores <- score.multiple.choice(iq.keys,iqitems,short=FALSE)
> str(iq.scores)
List of 4
 $ scores    : num [1:1000, 1] 0.429 0.357 0.571 0.571 0.571 ...
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr [1:1000] "72" "95" "100" "136" ...
  .. ..$ : chr "Averages"
 $ item.stats:'data.frame':   14 obs. of  15 variables:
  ..$ key     : num [1:14] 4 4 3 1 4 3 2 3 1 4 ...
  ..$ 0       : num [1:14] 0.035 0.028 0.1 0.032 0.028 0.029 0.045 0.071 0.036 0.047 ...
  ..$ 1       : num [1:14] 0.01 0.104 0.223 0.651 0.024 0.097 0.08 0.078 0.866 0.054 ...
  ..$ 2       : num [1:14] 0.034 0.006 0.088 0.163 0.027 0.055 0.586 0.308 0.027 0.079 ...
  ..$ 3       : num [1:14] 0.088 0.016 0.371 0.153 0.034 0.645 0.063 0.315 0.011 0.07 ...
  ..$ 4       : num [1:14] 0.801 0.799 0.044 0.001 0.854 0.019 0.106 0.154 0.009 0.743 ...
  ..$ 5       : num [1:14] 0.024 0.009 0.133 0 0.019 0.145 0.067 0.053 0.008 0.007 ...
  ..$ 6       : num [1:14] 0.008 0.038 0.041 0 0.014 0.01 0.053 0.021 0.043 0 ...
  ..$ r       : num [1:14] 0.591 0.395 0.346 0.35 0.418 ...
  ..$ n       : num [1:14] 1000 1000 1000 1000 1000 1000 1000 1000 1000 1000 ...
  ..$ mean    : num [1:14] 0.801 0.799 0.371 0.651 0.854 0.645 0.586 0.315 0.866 0.743 ...
  ..$ sd      : num [1:14] 0.399 0.401 0.483 0.477 0.353 ...
  ..$ skew    : num [1:14] -1.506 -1.49 0.533 -0.633 -2.002 ...
  ..$ kurtosis: num [1:14] 0.267 0.22 -1.717 -1.601 2.01 ...
  ..$ se      : num [1:14] 0.0126 0.0127 0.0153 0.0151 0.0112 ...
 $ alpha     : num [1, 1] 0.63
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr "Averages"
  .. ..$ : chr "Averages"
 $ av.r      : num [1, 1] 0.11
  ..- attr(*, "dimnames")=List of 2
  .. ..$ : chr "Averages"
  .. ..$ : chr "Averages"
```

Use the relevant part of a list

```
> dim(iq.scores)
NULL
> length(iq.scores)
[1] 4
> dim(iq.scores$scores)
[1] 1000    1
> describe(iq.scores$scores)
         var    n mean   sd median trimmed  mad min  max range  skew kurtosis   se
Averages   1 1000 0.61 0.18   0.64    0.63 0.11   0 0.93  0.93 -1.07     1.44 0.01
```

Data Manipulation

I. standard arithmetic and logical operations

II. matrix operations including transpose, inner product, outer product, diagonal, trace, invert

III. searching, sorting, merging

IV. data cleaning by logical commands

Basic data description

```
summary(My.data)
      epiE            epiS           epiImp          epilie         epiNeur         bfagree          bfcon      
 Min.   : 1.00   Min.   : 0.000   Min.   : 0.000   Min.   :0.000   Min.   : 0.00   Min.   : 74.0   Min.   : 53.0  
 1st Qu.:11.00   1st Qu.: 6.000   1st Qu.: 3.000   1st Qu.:1.000   1st Qu.: 7.00   1st Qu.:112.0   1st Qu.: 99.0  
 Median :14.00   Median : 8.000   Median : 4.000   Median :2.000   Median :10.00   Median :126.0   Median :114.0  
 Mean   :13.68   Mean   : 7.978   Mean   : 4.784   Mean   :2.377   Mean   :10.41   Mean   :125.0   Mean   :113.3  
 3rd Qu.:16.00   3rd Qu.:10.000   3rd Qu.: 6.000   3rd Qu.:3.000   3rd Qu.:14.00   3rd Qu.:136.5   3rd Qu.:128.5  
 Max.   :99.00   Max.   :99.000   Max.   :99.000   Max.   :7.000   Max.   :23.00   Max.   :167.0   Max.   :178.0  
      bfext           bfneur           bfopen           bdi            traitanx        stateanx     
 Min.   :  8.0   Min.   : 34.00   Min.   : 73.0   Min.   : 0.000   Min.   :22.00   Min.   :21.00  
 1st Qu.: 87.5   1st Qu.: 70.00   1st Qu.:110.0   1st Qu.: 3.000   1st Qu.:32.00   1st Qu.:32.00  
 Median :104.0   Median : 90.00   Median :125.0   Median : 6.000   Median :38.00   Median :38.00  
 Mean   :102.2   Mean   : 87.97   Mean   :123.4   Mean   : 6.779   Mean   :39.01   Mean   :39.85  
 3rd Qu.:118.0   3rd Qu.:104.00   3rd Qu.:136.5   3rd Qu.: 9.000   3rd Qu.:44.00   3rd Qu.:46.50  
 Max.   :168.0   Max.   :152.00   Max.   :173.0   Max.   :27.000   Max.   :71.00   Max.   :79.00  

> describe(My.data)
          var   n   mean    sd median trimmed   mad min max range  skew kurtosis   se
epiE        1 231  13.33  4.14     14   13.49  4.45   1  22    21 -0.33    -0.06 0.27
epiS        2 231   7.58  2.69      8    7.77  2.97   0  13    13 -0.57    -0.02 0.18
epiImp      3 231   4.37  1.88      4    4.36  1.48   0   9     9  0.06    -0.62 0.12
epilie      4 231   2.38  1.50      2    2.27  1.48   0   7     7  0.66     0.24 0.10
epiNeur     5 231  10.41  4.90     10   10.39  4.45   0  23    23  0.06    -0.50 0.32
bfagree     6 231 125.00 18.14    126  125.26 17.79  74 167    93 -0.21    -0.27 1.19
bfcon       7 231 113.25 21.88    114  113.42 22.24  53 178   125 -0.02     0.23 1.44
bfext       8 231 102.18 26.45    104  102.99 22.24   8 168   160 -0.41     0.51 1.74
bfneur      9 231  87.97 23.34     90   87.70 23.72  34 152   118  0.07    -0.55 1.54
bfopen     10 231 123.43 20.51    125  123.78 20.76  73 173   100 -0.16    -0.16 1.35
bdi        11 231   6.78  5.78      6    5.97  4.45   0  27    27  1.29     1.50 0.38
traitanx   12 231  39.01  9.52     38   38.36  8.90  22  71    49  0.67     0.47 0.63
stateanx   13 231  39.85 11.48     38   38.92 10.38  21  79    58  0.72    -0.01 0.76
```

R graphics (base)

I. Multiple graphics packages

   A. base graphics

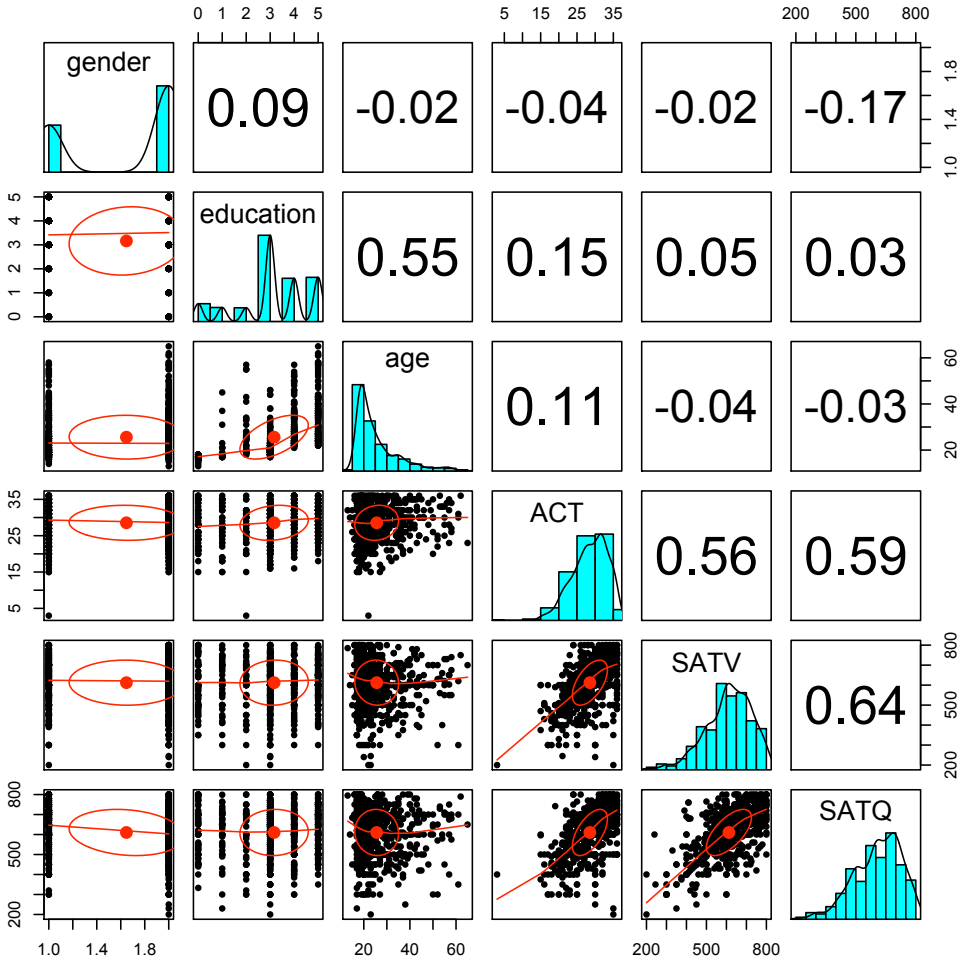
   B. lattice

   C. ggobi

II. Following examples from base graphics

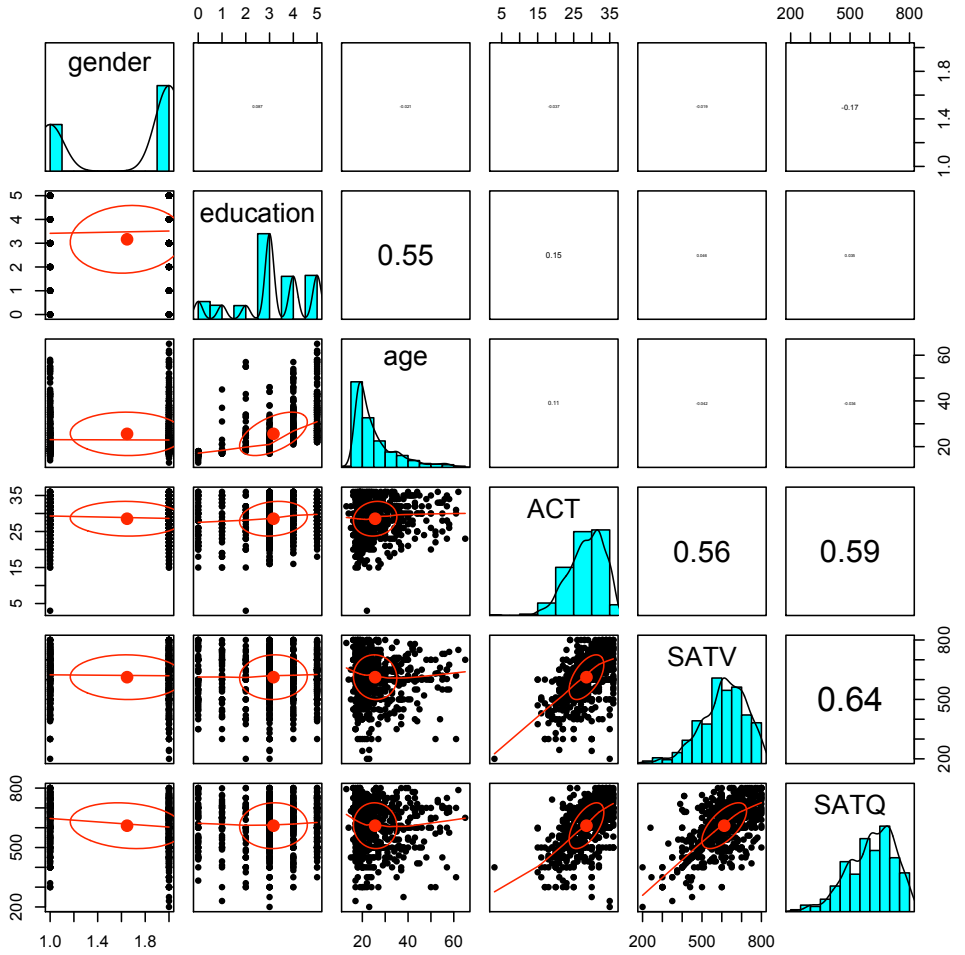
pairs.panels

```
> data(sat.act)
> pairs.panels(sat.act)
```

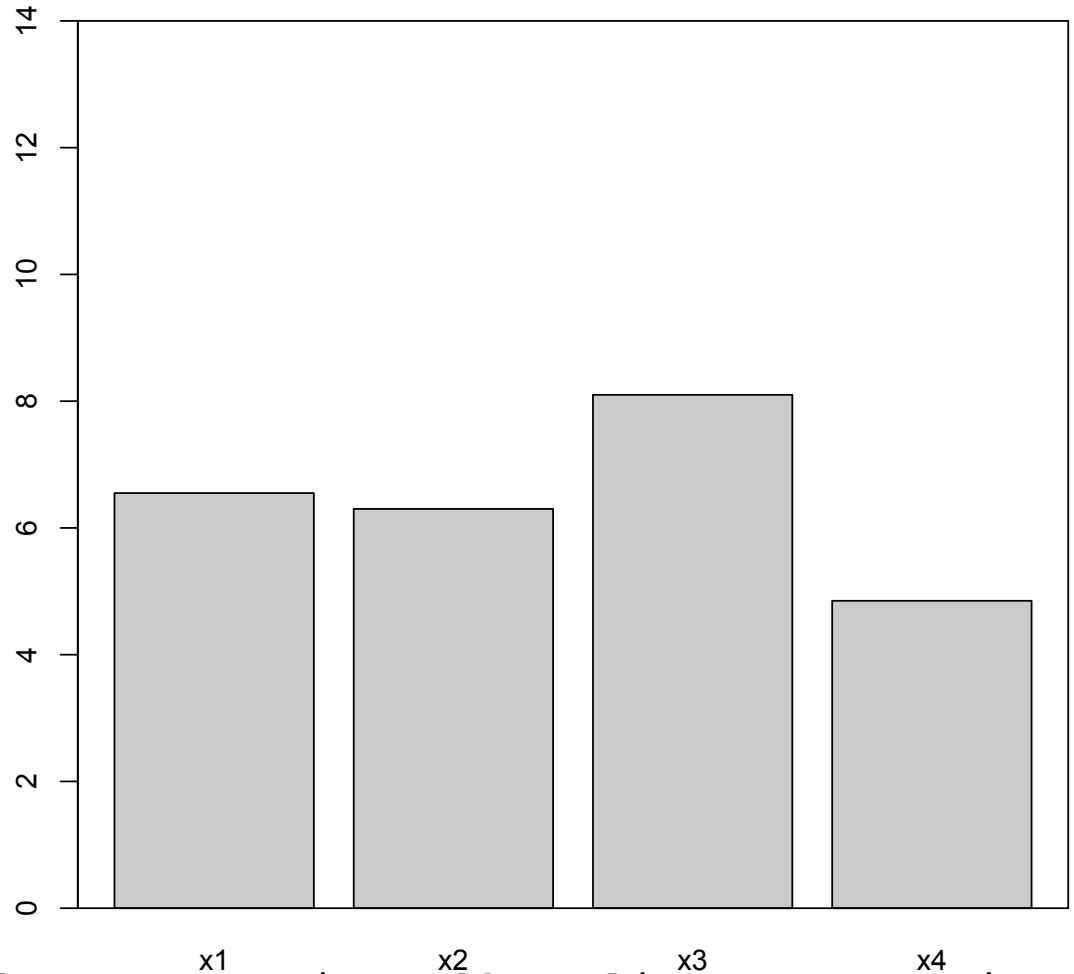


pairs.panels

```
pairs.panels(sat.act,scale=TRUE)
```

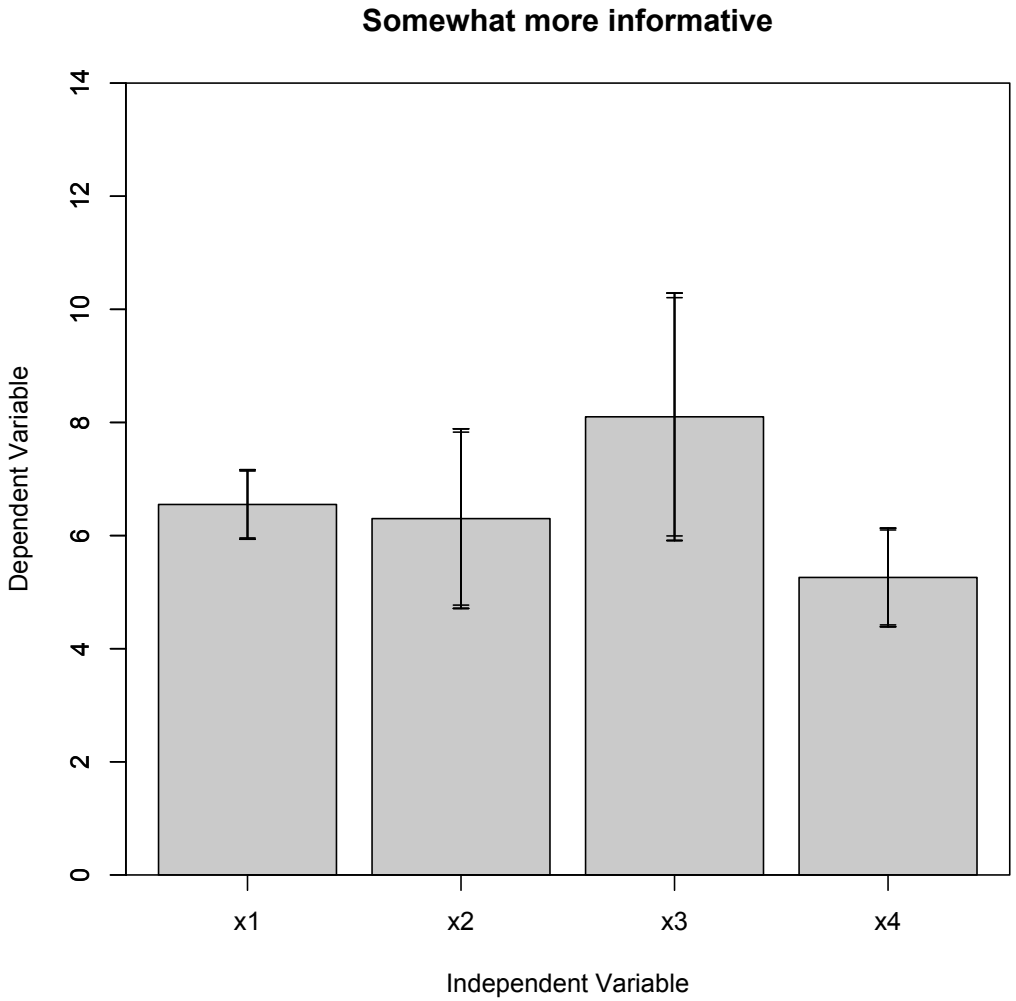


Do not draw bar graphs



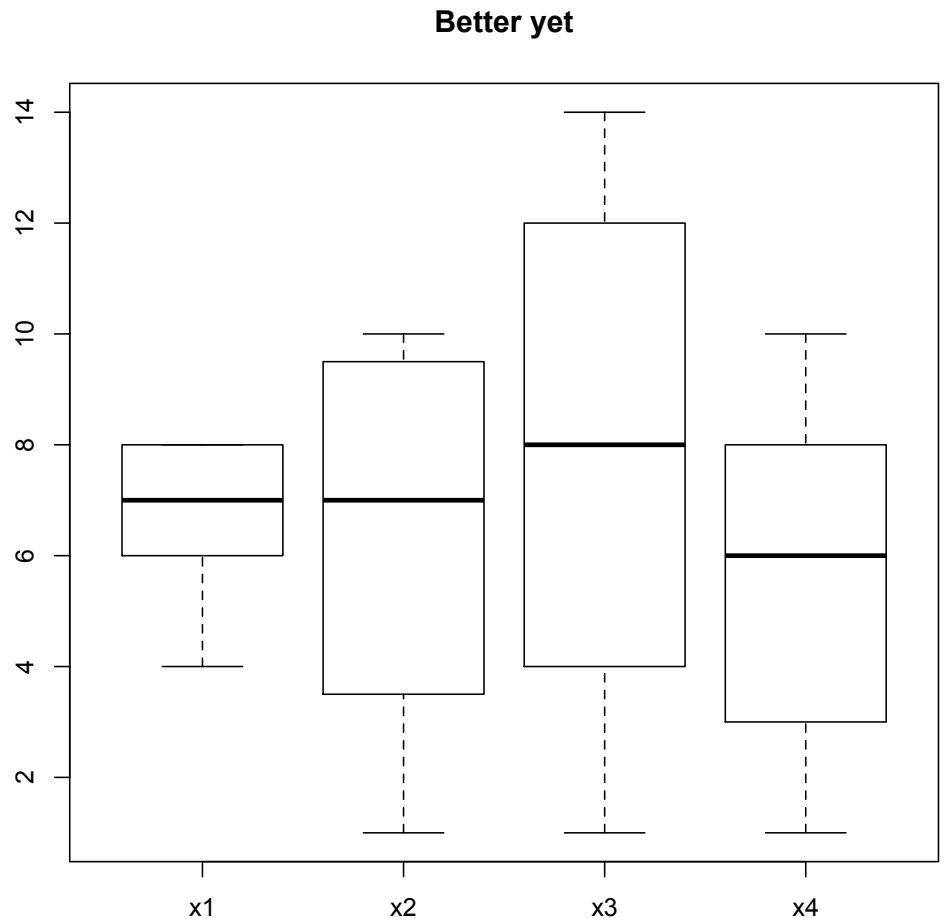

```
> barplot(colMeans(na.omit(X.df)),ylim=c(0,14),main="A particularly
uninformative graph")
> box()
```

Somewhat better



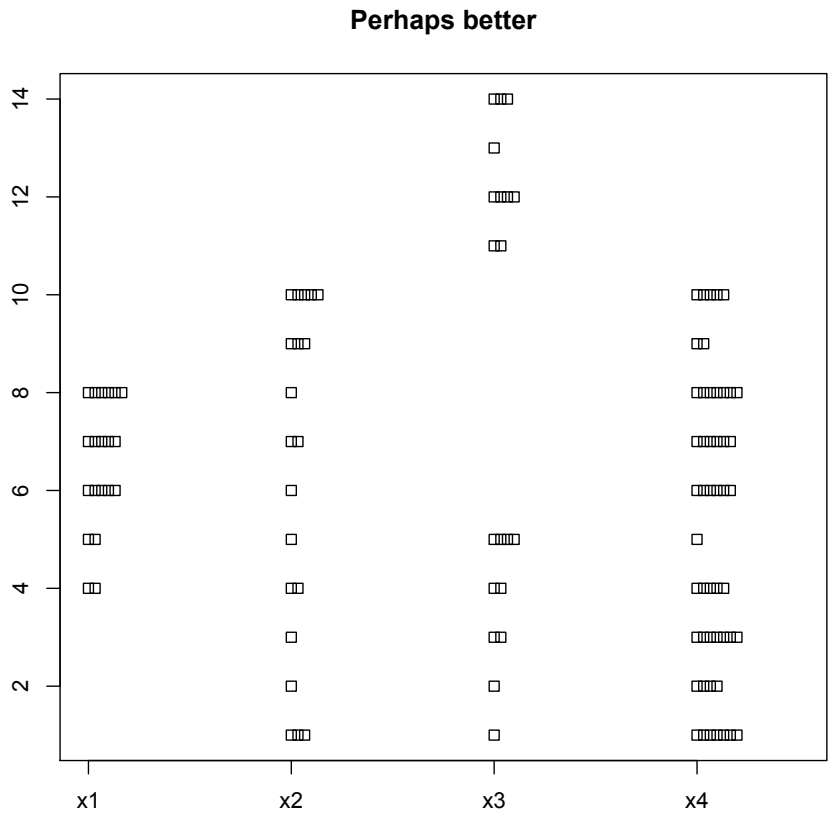

```
error.bars(X.df,bars=TRUE,ylim=c(0,14),
   main="Somewhat more informative")
```

box plot



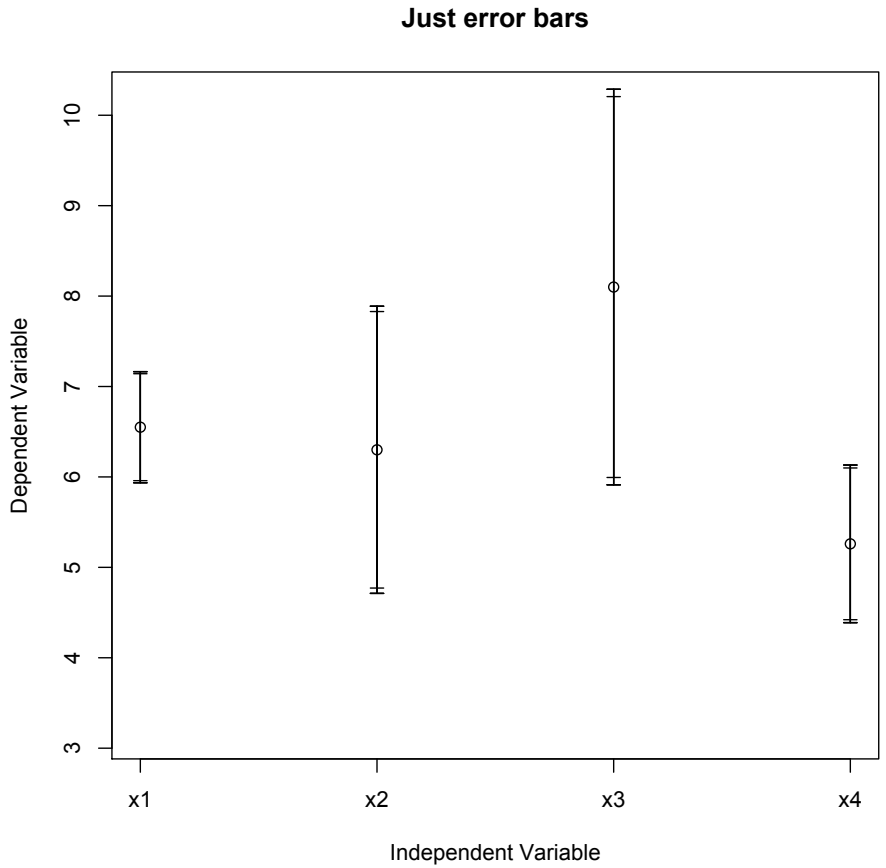

```
boxplot(X.df,main="Better yet")
```

stripchart



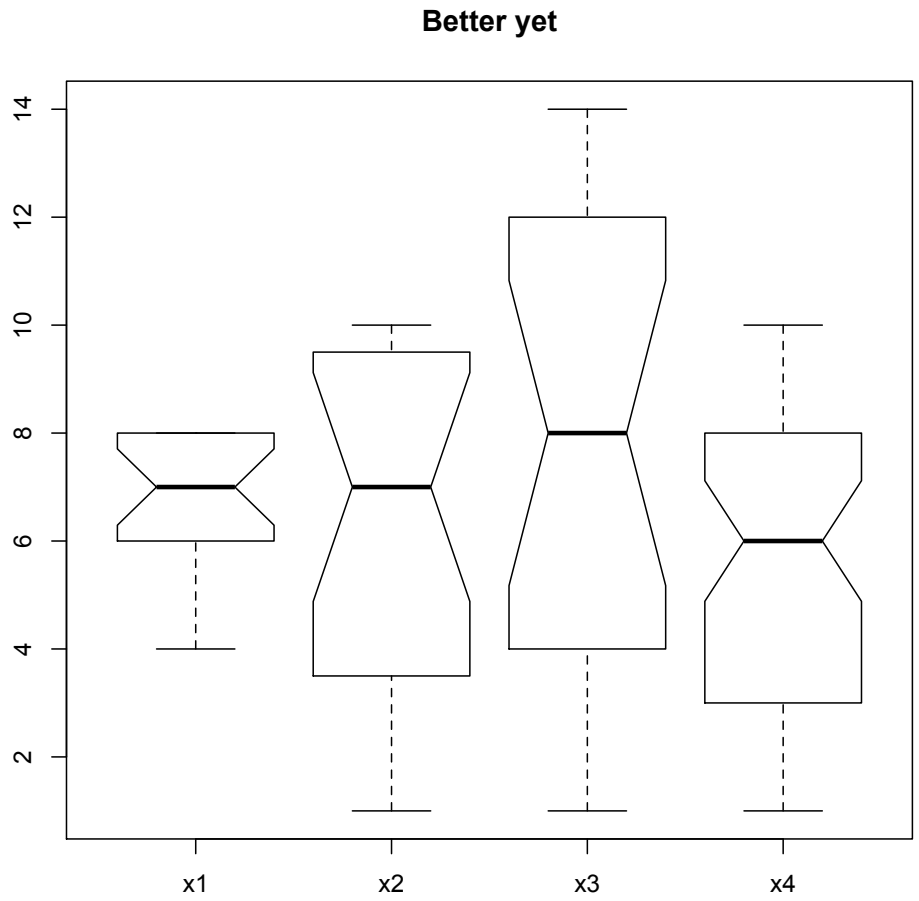

```
stripchart(X.df,method="stack",vertical=TRUE,main="Perhaps
better")
```

error.bars



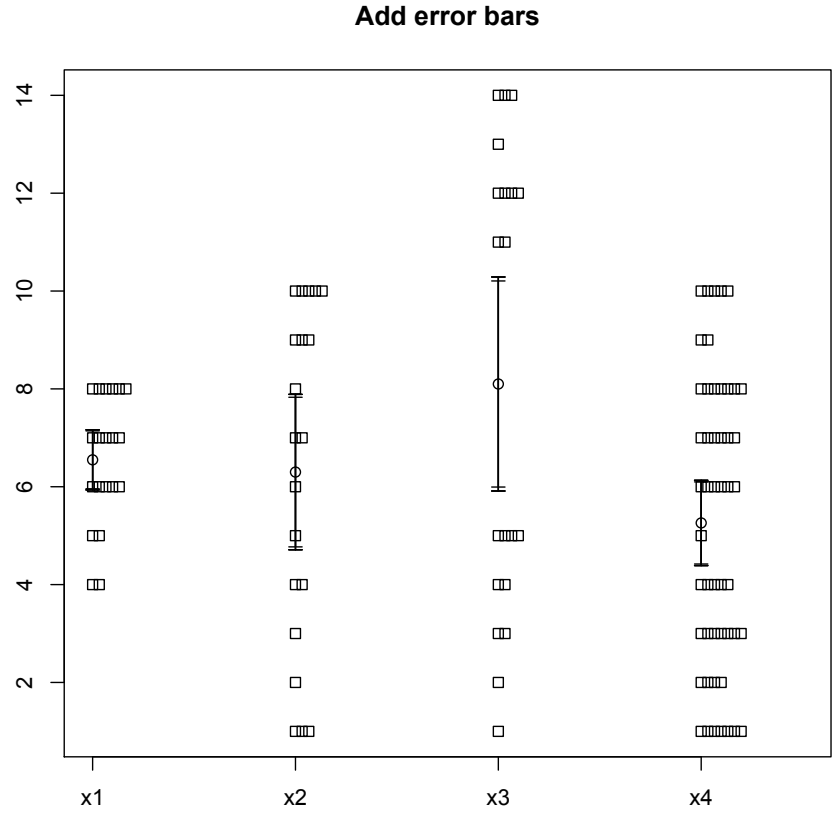

```
> error.bars(X.df,main="Just error bars")
```

notched boxplots




```
> boxplot(X.df,main="Better yet",notch=TRUE)
```

stripchart + error.bars



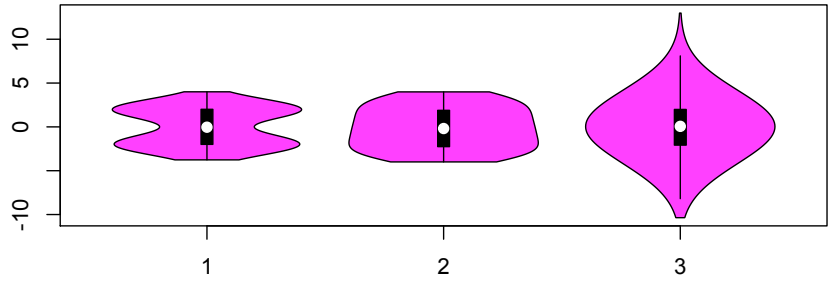

```
> stripchart(X.df,method="stack",vertical=TRUE,main="Add error bars")
> error.bars(X.df,add=TRUE)
```

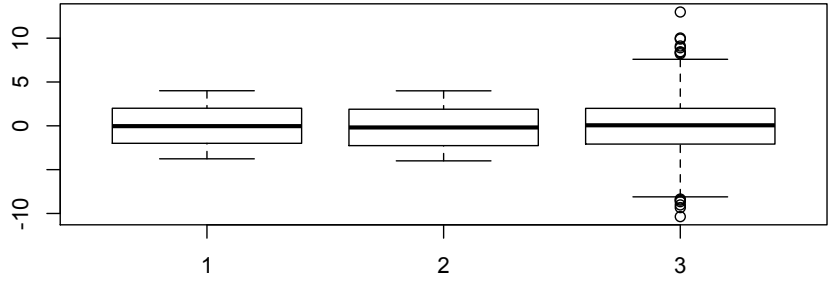
Alternatives with larger data sets

I. The violin plot shows density distributions

II. Available in the vioplot package

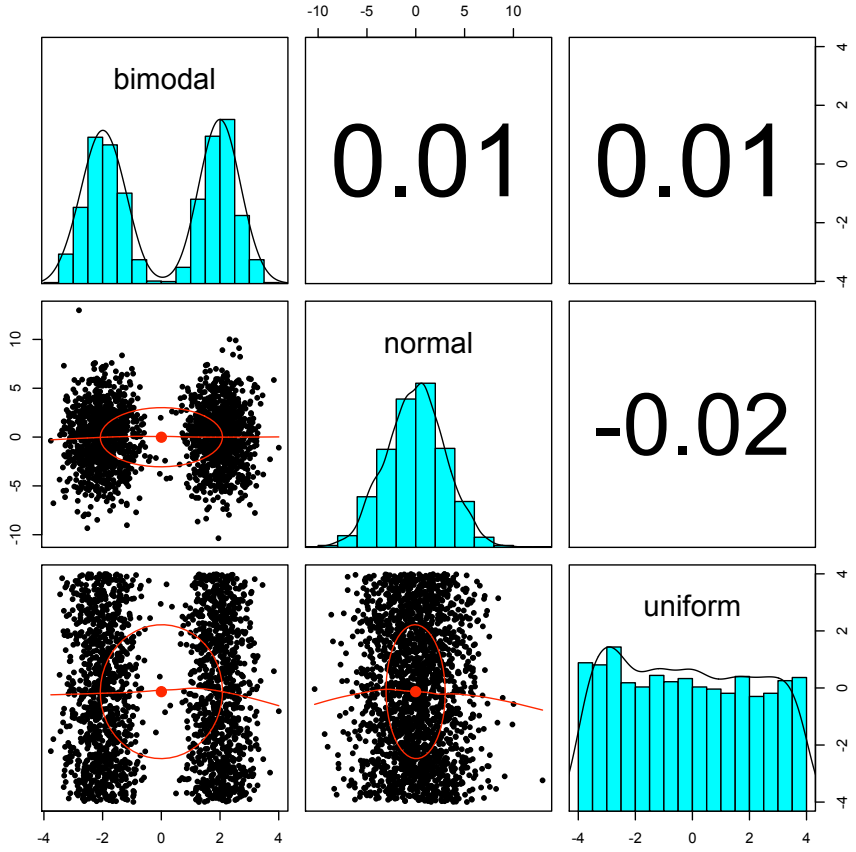
violin plots





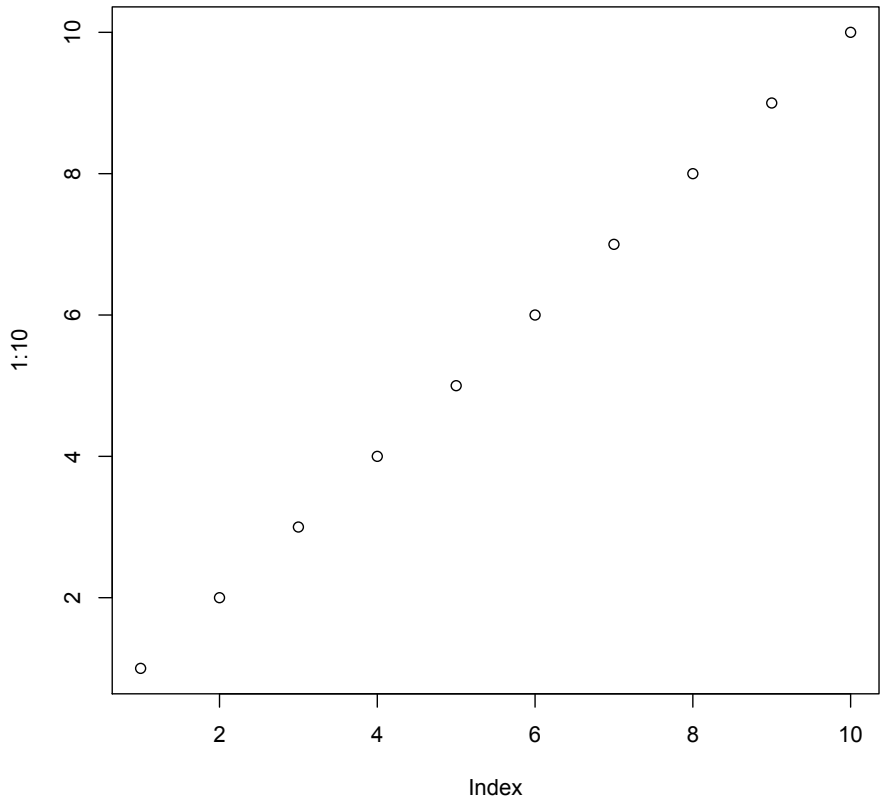

```
mu<-2
  si<-0.6
  bimodal<-c(rnorm(1000,-mu,si),rnorm(1000,mu,si))
  uniform<-runif(2000,-4,4)
  normal<-rnorm(2000,0,3)
  vioplot(bimodal,uniform,normal)
  boxplot(bimodal,uniform,normal)
```

An alternative



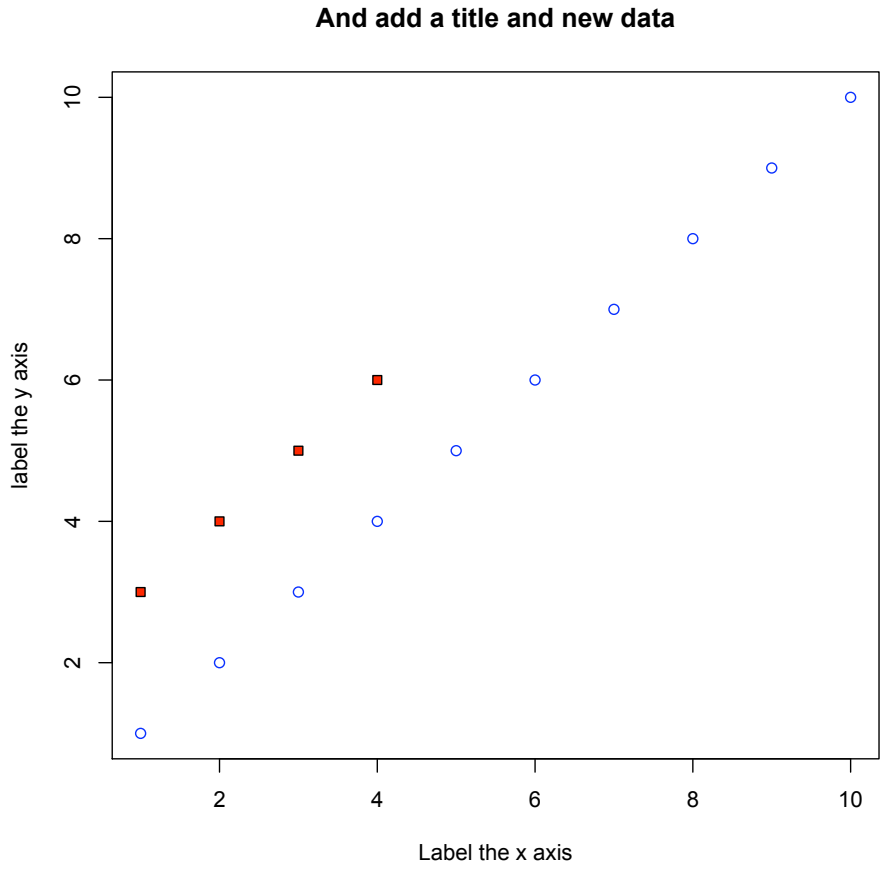

```
> bnu <-data.frame(bimodal,normal,uniform)
> pairs.panels(bnu)
```

Graphics 101



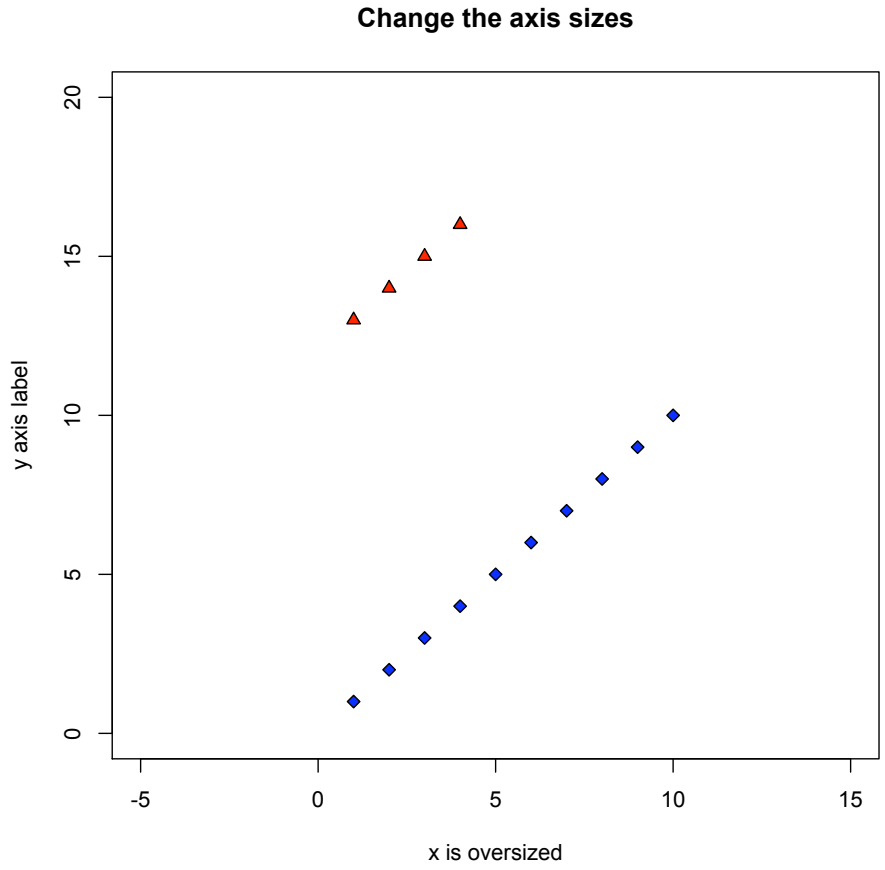

```
plot(1:10)
```

specify labels and title



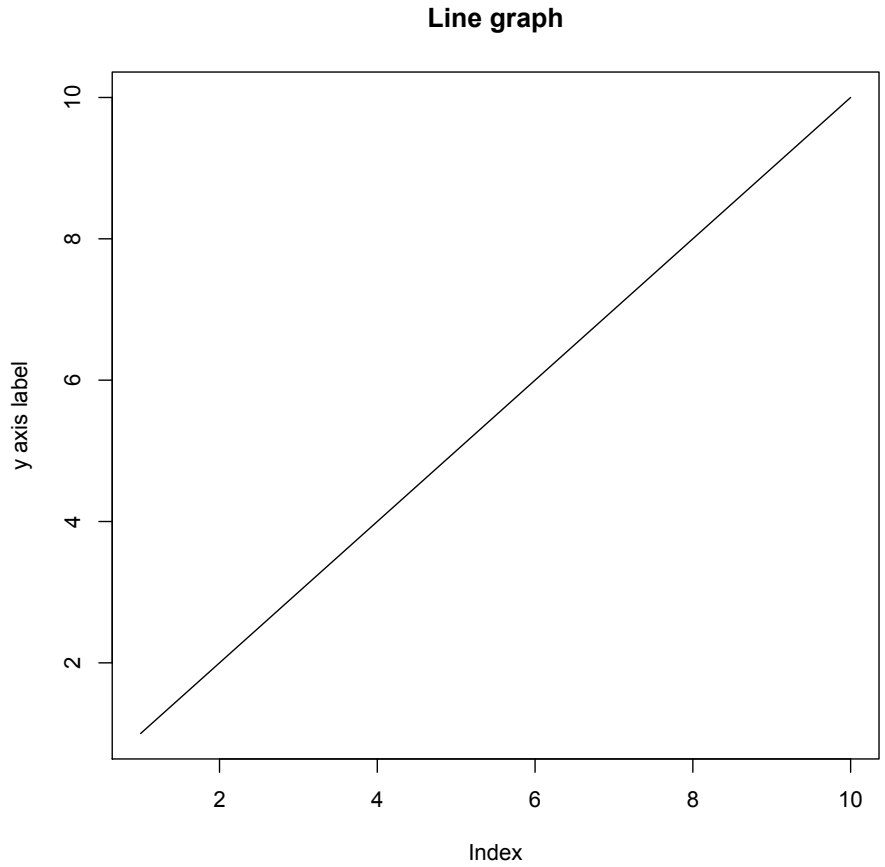

```
> plot(1:10,xlab ="Label the x axis",ylab="label the y axis",
+ main="And add a title and new data",pch=21,col="blue")
> points(1:4,3:6,bg="red",pch=22)
```

Change the ranges



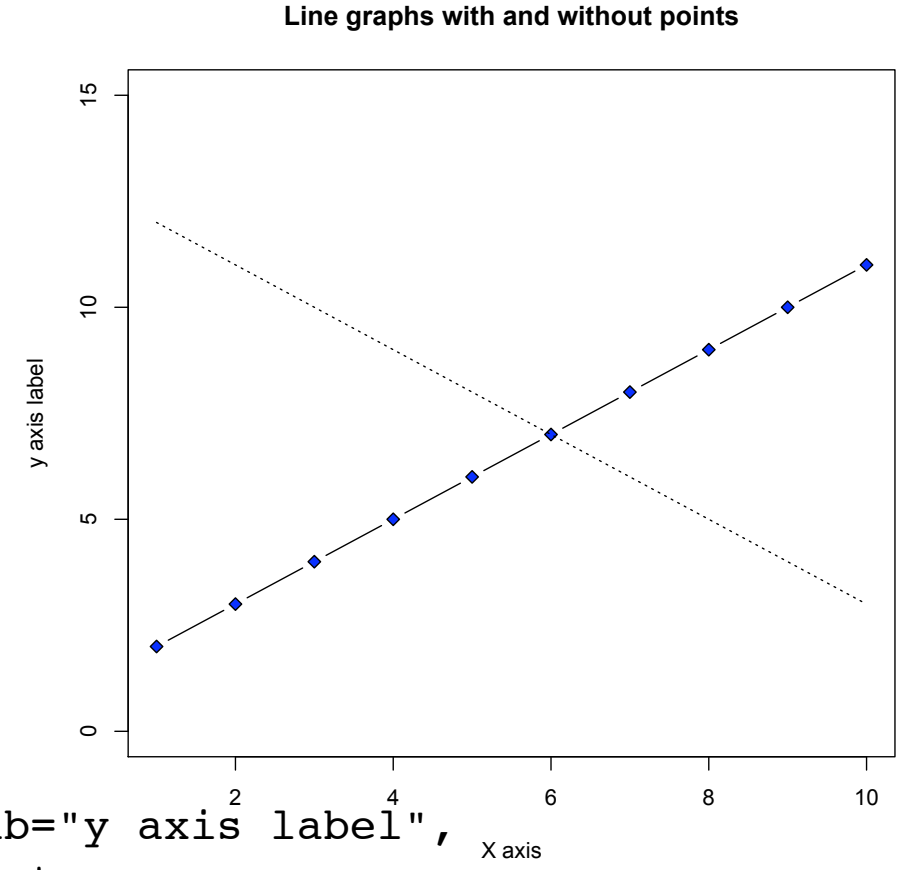

```
> plot(1:10,xlab ="x is oversized",ylab="y axis label",
+ main="Change the axis sizes",pch=23,bg="blue",xlim=c(-5,15),ylim=c
(0,20))
> points(1:4,13:16,bg="red",pch=24)
```

Plot the same data as a line graph



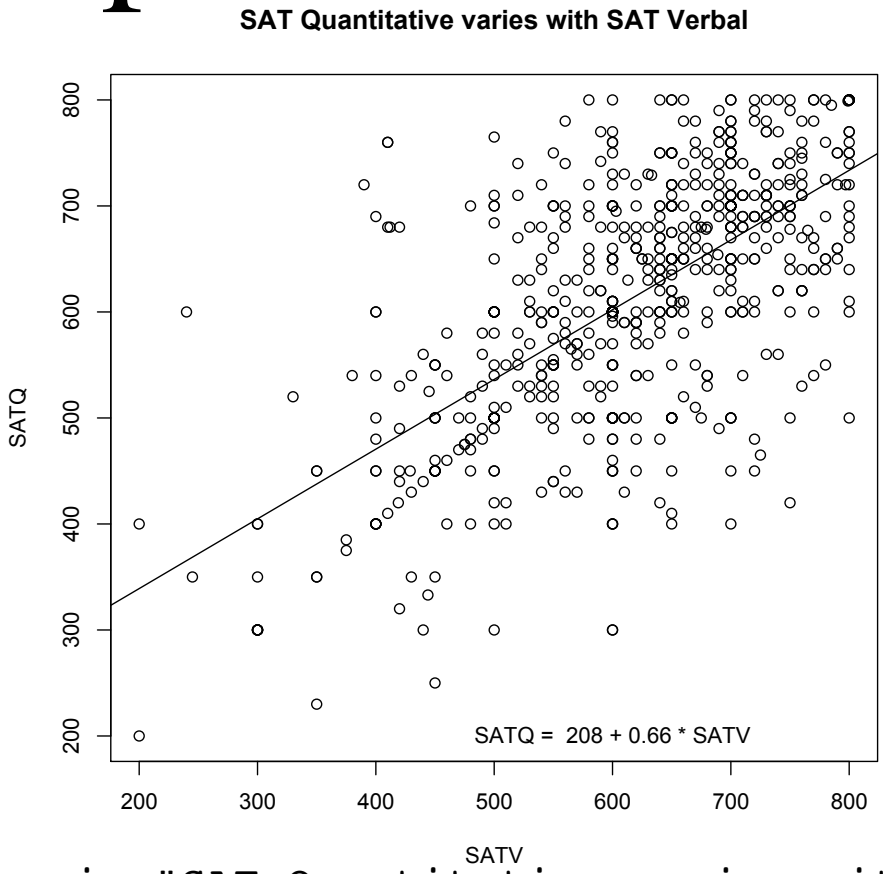

```
> plot(1:10,ylab="y axis label",main="Line
graph",pch=23,bg="blue",type="l")
```

Show the data points, add a line



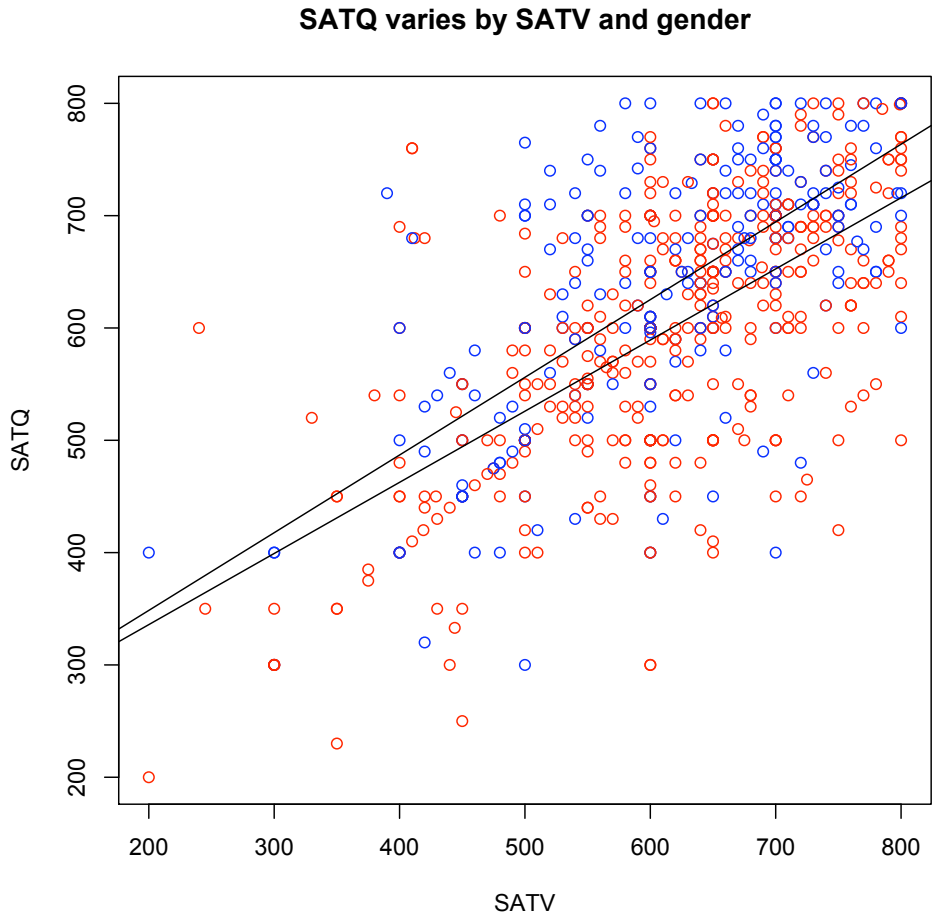

```
> plot(1:10,2:11,xlab="X axis",ylab="y axis label",
+ main="Line graphs with and without
points",pch=23,bg="blue",type="b",ylim=c(0,15))
> points(1:10,12:3,type="l",lty="dotted")
```

Regression plots




```
> data(sat.act)
> with(sat.act,plot(SATQ~SATV,main="SAT Quantitative varies with SAT
Verbal"))
> model = lm(SATQ~SATV,data=sat.act)
> abline(model)
> lab <- paste("SATQ = ",round(model$coef[1]),"+",round(model$coef[2],
2),"* SATV")
> text(600,200,lab)
```

Two groups




```
> data(sat.act)
> color <- c("blue","red")
> with(sat.act,plot(SATQ~SATV,col=color[gender],main="SATQ varies by
SATV and gender"))
> by(sat.act,sat.act$gender,function(x) abline(lm(SATQ~SATV,data=x)))
```

The actual regression

```
> by(sat.act,sat.act$gender, function(x) lm(SATQ~SATV,data=x))
sat.act$gender: 1

Call:
lm(formula = SATQ ~ SATV, data = x)

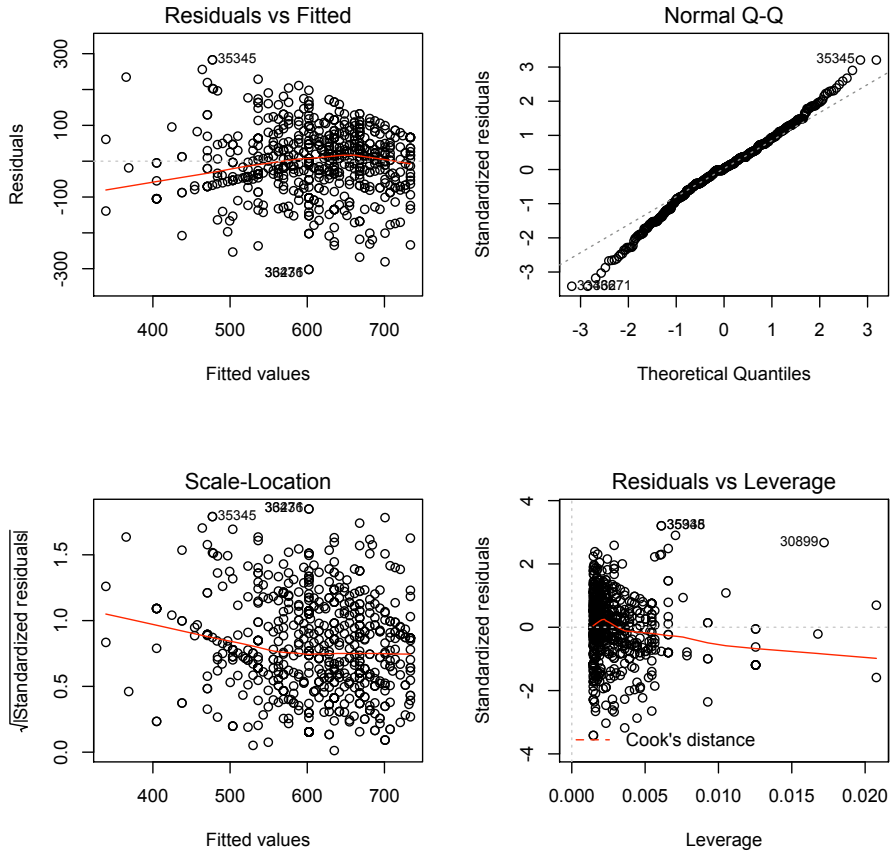
Coefficients:
(Intercept)         SATV
   210.2046       0.6917

------------------------------------------------------------
-
sat.act$gender: 2

Call:
lm(formula = SATQ ~ SATV, data = x)

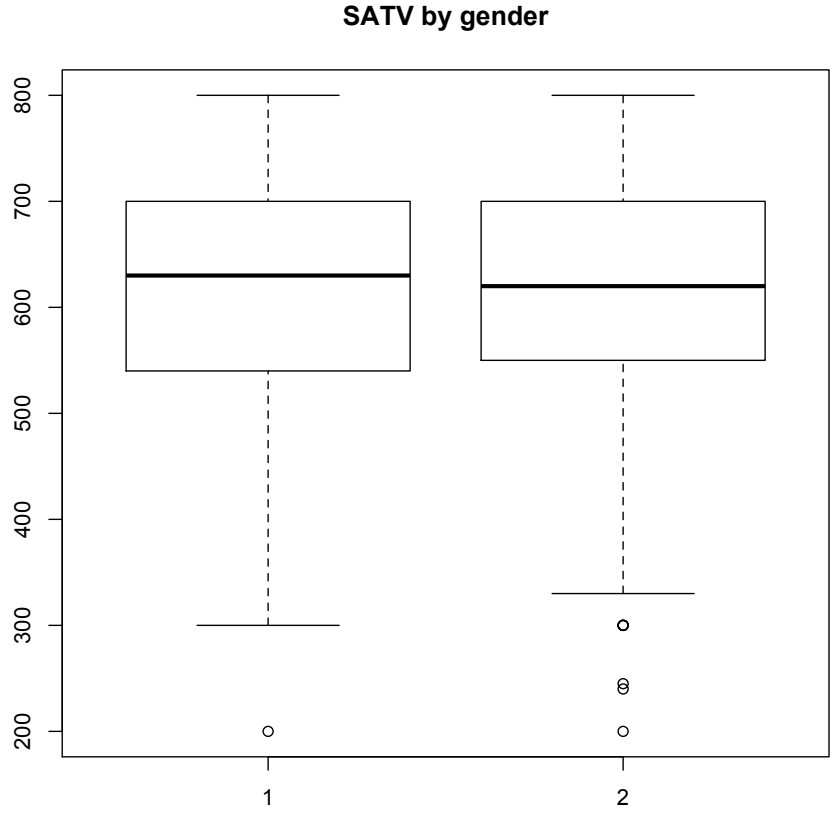
Coefficients:
(Intercept)         SATV
   209.2093       0.6334
```

Error diagnostics




```
> op <- par(mfrow=c(2,2))
> plot(lm(SATQ~SATV,data=sat.act))
> op <- par(mfrow=c(1,1))
```

Boxplots by group




```
boxplot(sat.act$SATV~sat.act$gender,main="SATV by gender")
```

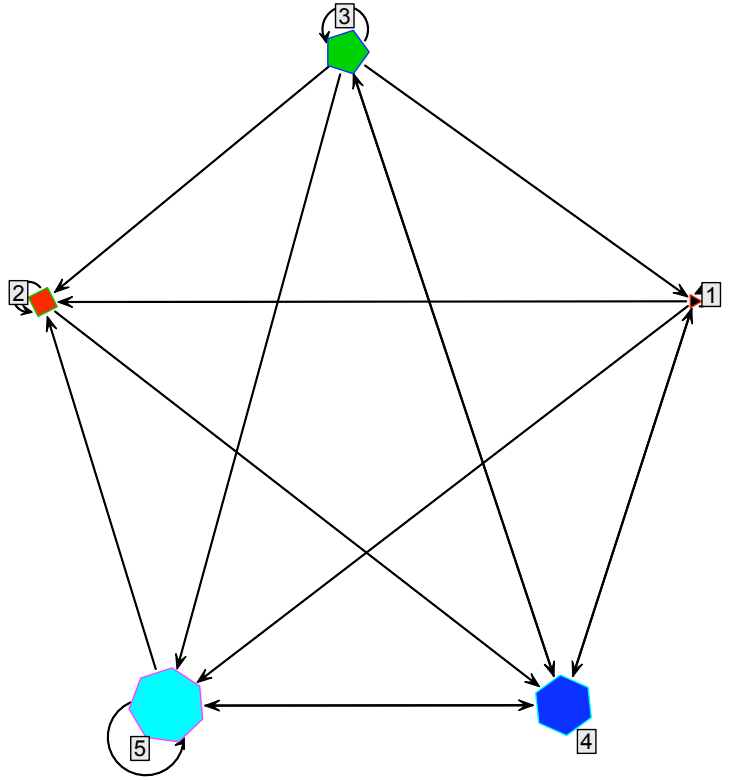
More complex graphs

I. Using the Rgraphviz package (installed from Bioconductor rather than CRAN)

   A. I have added the most important graphic functions for doing path/structure diagrams into psych so does not require Rgraphviz

II. Using the Social Network Analysis (sna) package.

sna example

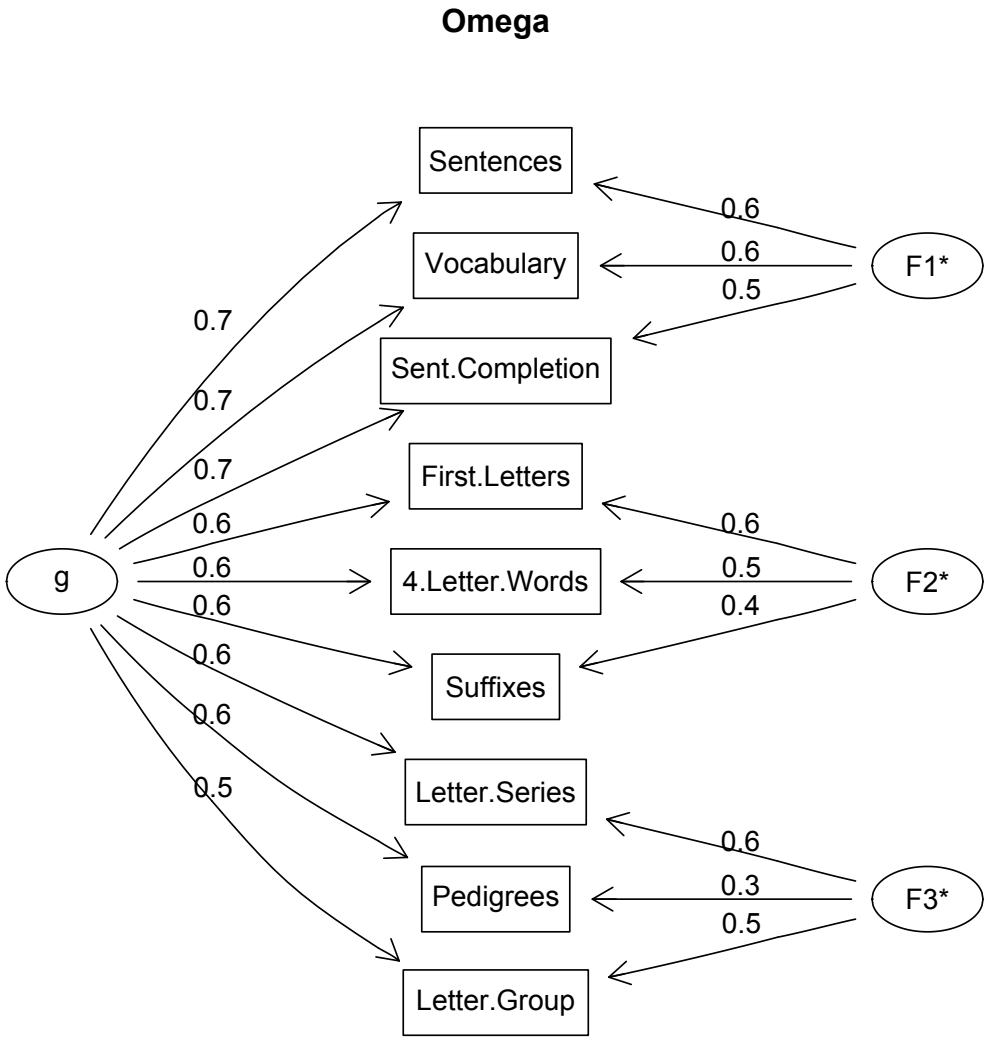



```
#A colorful demonstration...
gplot(rgraph(5,diag=TRUE),diag=TRUE,vertex.cex=1:5,vertex.sides=3:8,
    vertex.col=1:5,vertex.border=2:6,vertex.rot=(0:4)*72,
    displaylabels=TRUE,label.bg="gray90")
```

Cluster analysis with Rgraphviz output


```
> data(Harman74.cor)
> ic<- ICLUST(Harman74.cor$cov,title="The Holzinger-Harman 24 mental
measurement problem")
```

A bifactor solution



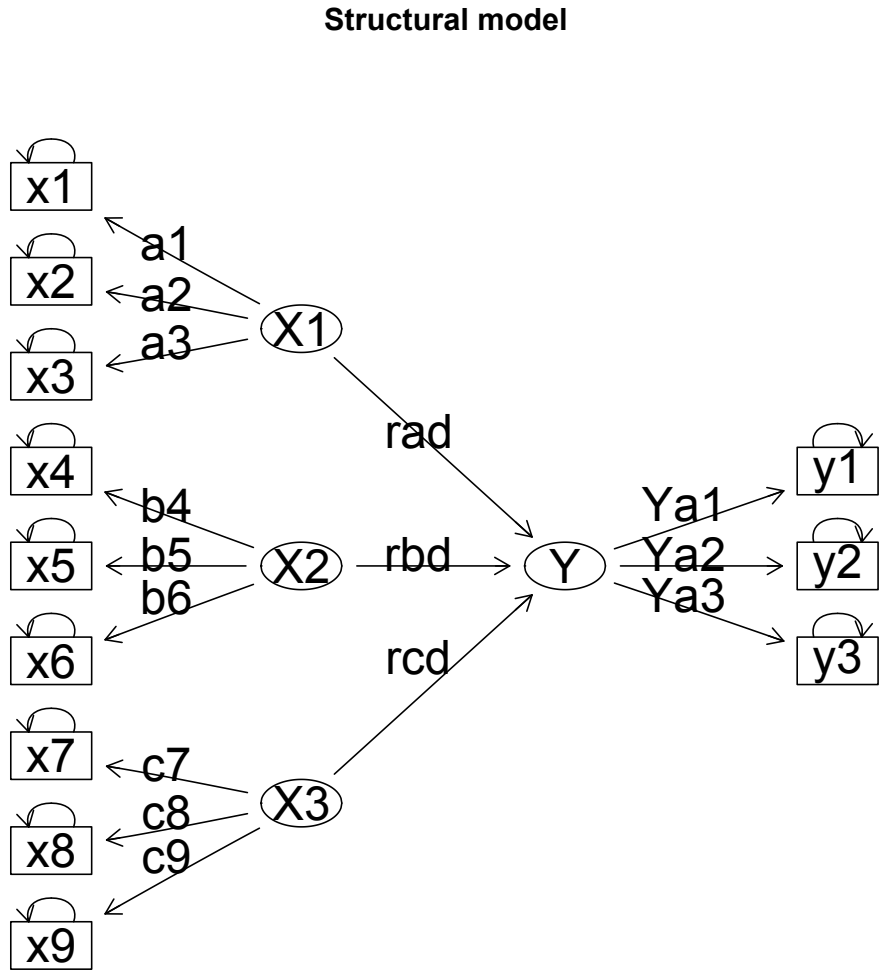

```
> data(bifactor)
> om <- omega(Thurstone,main="A bifactor solution to a Thurstone data
set")
```

Creating matrix input for a graph

```
> fxs <- structure.list(9,list(X1=c(1,2,3), X2 =c(4,5,6),X3 = c
(7,8,9)))
> phi <- phi.list(4,list(F1=c(4),F2=c(4),F3=c(4),F4=c(1,2,3)))
> fyx <- structure.list(3,list(Y=c(1,2,3)),"Y")
>
> fxs
      X1   X2   X3
 [1,] "a1" "0"  "0"
 [2,] "a2" "0"  "0"
 [3,] "a3" "0"  "0"
 [4,] "0"  "b4" "0"
 [5,] "0"  "b5" "0"
 [6,] "0"  "b6" "0"
 [7,] "0"  "0"  "c7"
 [8,] "0"  "0"  "c8"
 [9,] "0"  "0"  "c9"
```

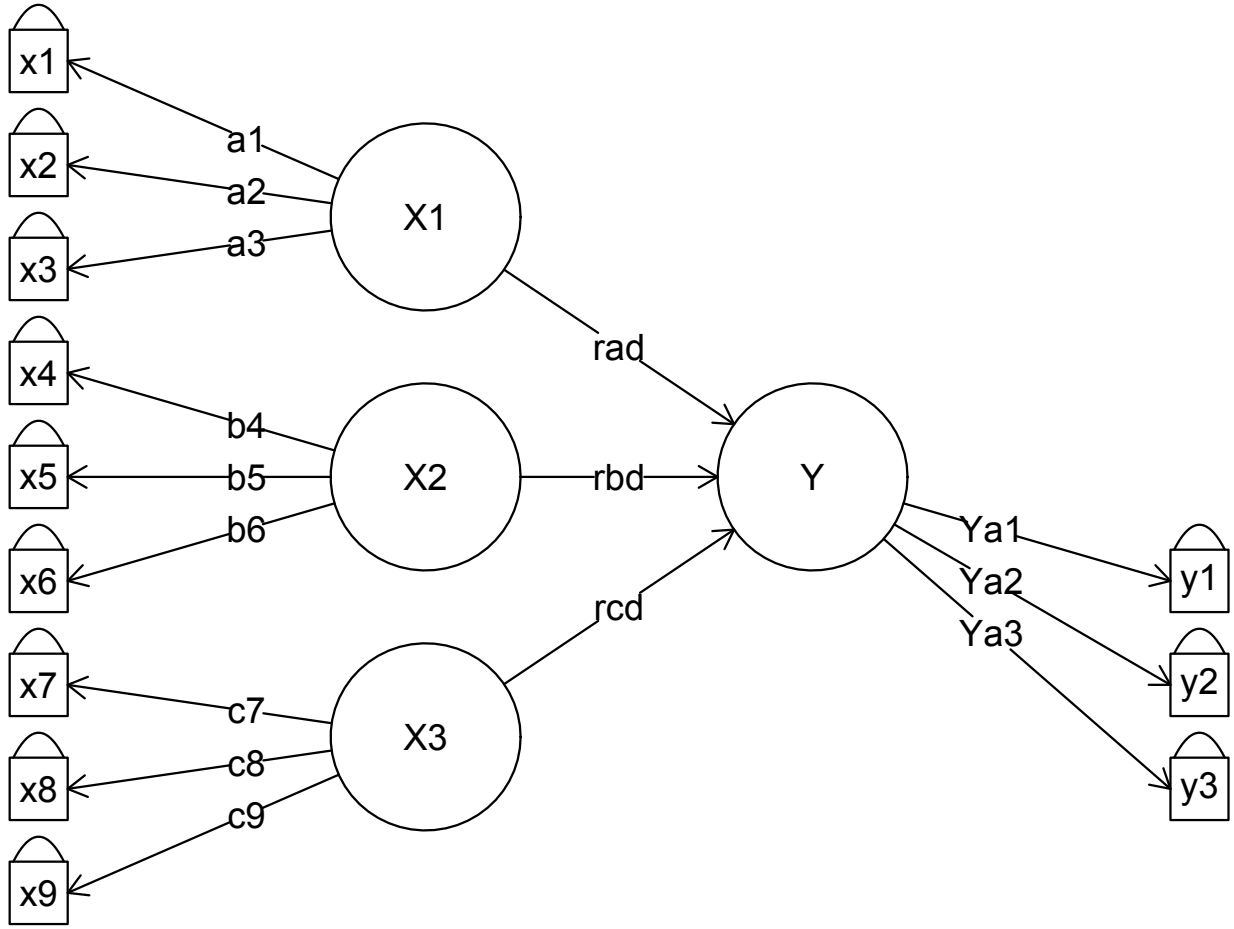
```
> phi
   F1    F2    F3    F4
F1 "1"   "0"   "0"   "rda"
F2 "0"   "1"   "0"   "rdb"
F3 "0"   "0"   "1"   "rdc"
F4 "rad" "rbd" "rcd" "1"
> fyx
     Y
[1,] "Ya1"
[2,] "Ya2"
[3,] "Ya3
```

Showing the matrices




```
> sg3 <- structure.graph(fxs,phi,fyx)
```

Using psych without Rgraphviz




```
> fxs <- structure.list(9,list(X1=c(1,2,3), X2 =c(4,5,6),X3 = c(7,8,9)))
> phi <- phi.list(4,list(F1=c(4),F2=c(4),F3=c(4),F4=c(1,2,3)))
> fyx <- structure.list(3,list(Y=c(1,2,3)),"Y")
> structure.diagram(fxs,phi,fyx)
```

graphics in psych

- Primitives:
  - dia.rect
  - dia.ellipse
  - dia.arrow
  - dia.curve
  - dia.self
- Applications
  - fa.diagram
  - iclust.diagram
  - omega.diagram
  - structure.diagram