R Installed

Ape OUCH Geiger Laser

Flashdrive: R quicstart folder has simpleR.pdf

Tonight: Getting Started in R for Biologists

Tomorrow: R for Comparative Analysis

part of the "Phylogenetics for Dummies" series

Marguerite Butler, Mike Alfaro, and Samantha Price University of Hawaii UCLA NESCENT

Sponsored by: SICB, DSEB, and NESCENT Thanks!

An integrated suite of software facilities:

A fancy calculator

Data Management Handling and storage

Matrix Math: Manipulating matrices, vectors, and arrays

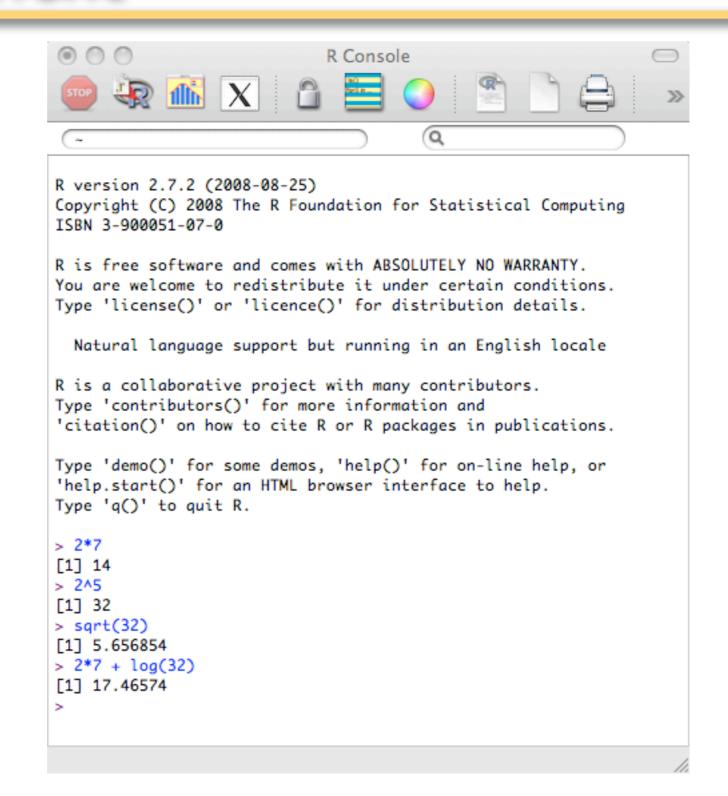
Statistics: A large, integrated set of tools for data analysis

Graphics: Graphical facilities for data analysis and display

Programming: Powerful programming language ('S')

Open-Source Development Platform

A fancy calculator



an integrated suite of software facilities:

Data Handling and Storage

```
> morph <- data.frame(species=LETTERS[1:5], size = rnorm(5, mean=15))</pre>
> morph
  species
        A 13.38846
        D 12.42916
> eco <- data.frame(species=LETTERS[5:1], ecology = sample(c("a", "b", "c"), 5,
replace=TRUE))
> eco
  species ecology
> merge(morph, eco)
  species
              size ecology
        A 13.38846
        B 14.83139
        D 12.42916
        E 17.32852
```

R has facilities for basic database functions: merging, matching, string matching, file access

an integrated suite of software facilities:

Data Handling and Storage

Matrix Math

```
matrix
> x <- matrix( data= 1:6, nrow=2)
[1,]
[2,]
> t(x)
                                        matrix transpose
    [,1] [,2]
[2,]
> y <- matrix( data = rnorm(9), nrow=3)
> y
[1,] 0.07969564 -0.04395246 -0.11727169
[2,] -0.01708504 -0.15159683 0.13944474
[3,] 0.56229980 0.25573414 -0.05902727
                                       matrix multiplication
                [,2]
        [,1]
[1,] 2.839940 0.7799277 0.005926158
[2,] 3.464850 0.8401126 -0.030928068
                                          matrix inverse
> solve(y)
         [,1]
                   [,2]
[1,] 1.779046 2.170144 1.5922018
[2,] -5.154919 -4.078422 0.6066952
[3,] -5.386179 3.003348 0.8546460
```

an integrated suite of software facilities:

Data Handling and Storage

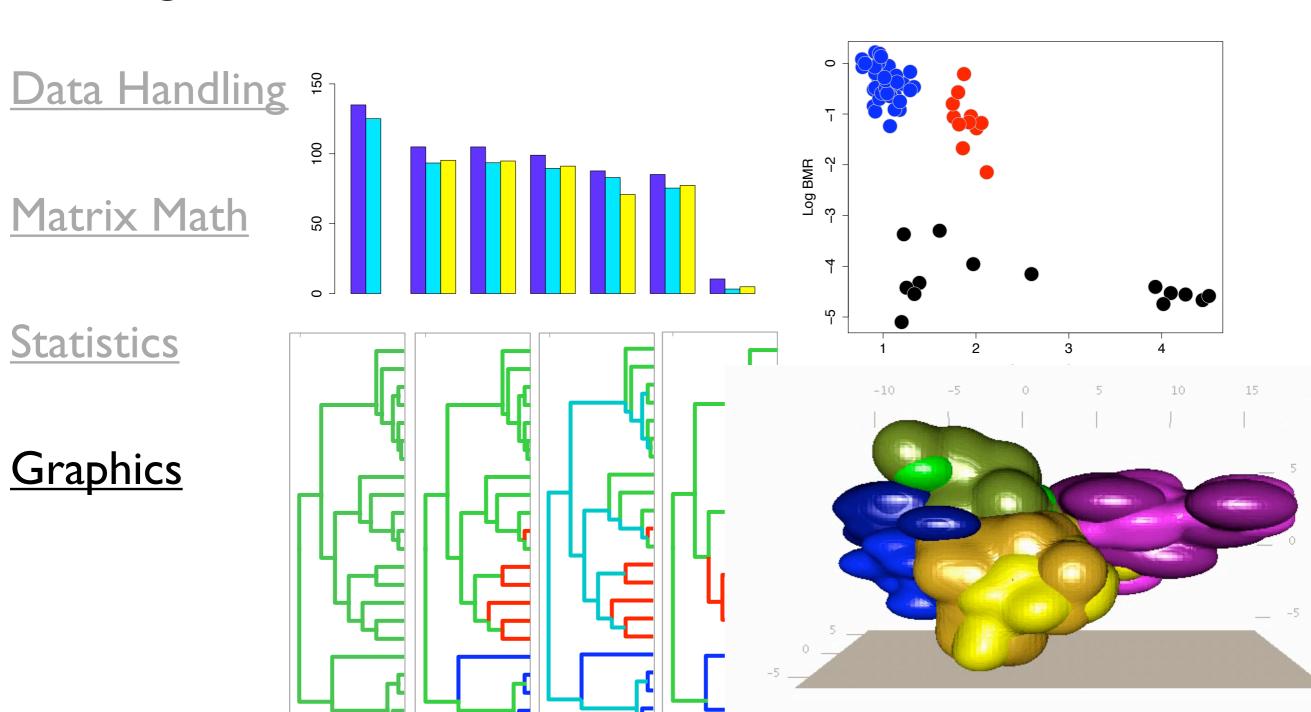
Matrix Math

Statistics

Linear Models
ANOVA

Non-parametric Statistics
Multivariate Statistics
Time Series
Numerical Methods
Optimization
etc. etc.

an integrated suite of software facilities:



an integrated suite of software facilities:

```
Data Handling and Storage
               (semi) Object-Oriented Design
                  Conditional Expressions
Matrix Math
                           (Loops)
                         (Recursion)
Statistics
                   Vectorized Calculations
                          Functions
Graphics
                          Packages
                         Extensibility
Programming
```

an integrated suite of software facilities:

R Homepage

Data Handling and Storage

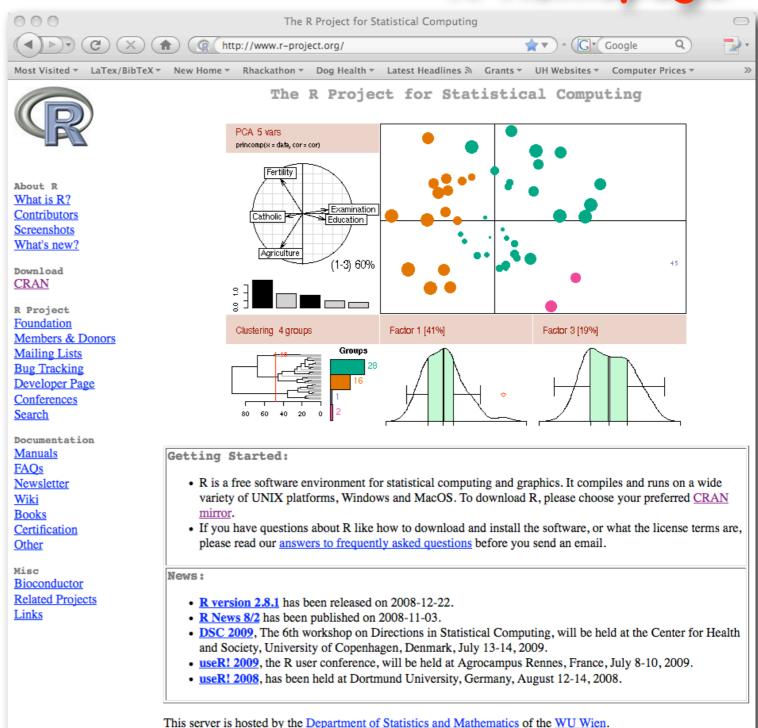
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Statistics

Graphics

Programming

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CRAN (Comprenensive R Archive Network)

an integrated suite

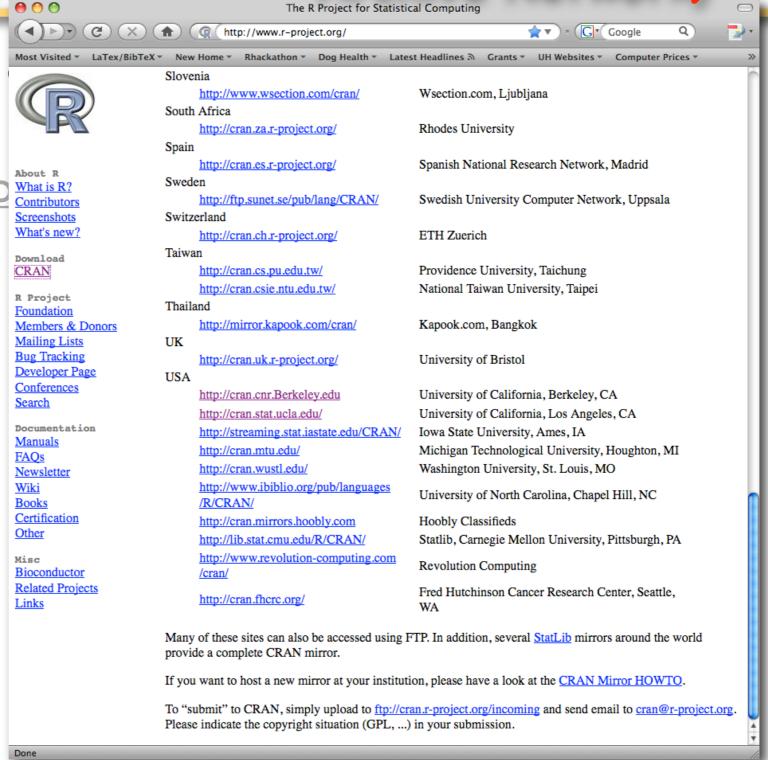
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Graphics

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Open-Source Community

the R environment support for all Major Platforms



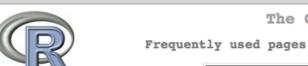
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Matrix Math

Statistics

Graphics

Programming



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The Comprehensive R Archive Network

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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

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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
- · 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.

What are R and CRAN?

R is 'GNU S', a freely available language and environment for statistical computing and graphics which provides a wide variety of statistical and graphical techniques: linear and nonlinear modelling, statistical tests, time series analysis, classification, clustering, etc. Please consult the R project homepage for further information.

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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.

<u>CRAN Task Views</u> allow you to browse packages by topic and provide tools to automatically install all packages for special areas of interest. Currently, 22 views are available.

Daily Package Check Results

All packages are tested regularly on machines running <u>Debian GNU/Linux</u>. 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 <u>check summary</u> (some <u>timings</u> are also available). Additional details for Windows checking and building can be found in the <u>Windows check summary</u>.

Writing Your Own Packages

The manual <u>Writing R Extensions</u> (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 1630 objects including 1622 packages and 8 bundles containing 34 packages, for a total of 1656 available packages.

<u>ABCDEFGHIJKLMNOPQRSTUVWXYZ</u>

ADaCGH Analysis of data from aCGH experiments

AER Applied Econometrics with R

AIS Tools to look at the data ("Ad Inidicia Spectata")

ALS multivariate curve resolution alternating least squares (MCR-ALS)

AMORE flexible neural network package

ARES Allelic richness estimation, with extrapolation beyond the sample size

AcceptanceSampling Creation and evaluation of Acceptance Sampling Plans

AdMit Adaptive Mixture of Student-t distributions
AdaptFit Adaptive Semiparametic Regression

<u>AlgDesign</u> AlgDesign

Amelia II: A Program for Missing Data

AnalyzeFMRI Functions for analysis of fMRI datasets stored in the ANALYZE or NIFTI

format

Done

Open-Source Community

the R environment Package "home pages"

4) P) - (C)

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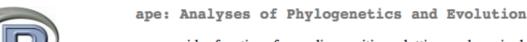
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ape provides functions for reading, writing, plotting, and manipulating phylogenetic trees, analyses of comparative data in a phylogenetic framework, analyses of diversification and macroevolution, computing distances from allelic and nucleotide data, reading nucleotide sequences, and several tools such as Mantel's test, computation of minimum spanning tree, the population parameter theta based on various approaches, nucleotide diversity, generalized skyline plots, estimation of absolute evolutionary rates and clock-like trees using mean path lengths, non-parametric rate smoothing and penalized likelihood, classifying genes in trees using the Klastorin-Misawa-Tajima approach. Phylogeny estimation can be done with the NJ, BIONJ, ME, and ML methods.

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The Comprehensive R Archive Network

Version: 2.2-2Depends: $R (\geq 2.6.0)$ gee, nlme, lattice Suggests:

2008-10-08 Date:

Author: Emmanuel Paradis, Ben Bolker, Julien Claude, Hoa Sien Cuong, Richard Desper, Benoit

Durand, Julien Dutheil, Olivier Gascuel, Gangolf Jobb, Christoph Heibl, Vincent Lefort, Jim Lemon, Yvonnick Noel, Johan Nylander, Rainer Opgen-Rhein, Korbinian Strimmer, Damien de

Vienne

Maintainer: Emmanuel Paradis < Emmanuel Paradis at ird.fr>

License: GPL (≥ 2)

URL: http://ape.mpl.ird.fr/

In views: Environmetrics, Genetics, Graphics

CRAN

ape results checks:

Downloads:

Package source: ape_2.2-2.tar.gz MacOS X binary: ape 2.2-2.tgz Windows binary: ape 2.2-2.zip Reference manual: ape.pdf Vignettes: Moran's I News/ChangeLog: ChangeLog Old sources: ape archive

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To automatically install these views, the ctv package needs to be installed, e.g., via install.packages("ctv")

Time Series Analysis

Analysis of Spatial Data

Survival Analysis

Psychometric Models and Methods

Statistics for the Social Sciences

Robust Statistical Methods

library("ctv")

Psychometrics

SocialSciences

Robust

Spatial

Survival

TimeSeries

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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")

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CRAN Task View: Statistical Genetics

Maintainer: Giovanni Montana

Contact: g.montana at imperial.ac.uk

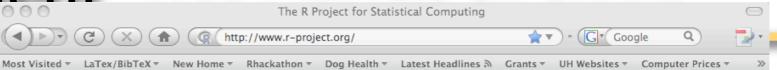
Version: 2008-12-08

Great advances have been made in the field of genetic analysis over the last years. The availability of millions of single nucleotide polymorphisms (SNPs) in widely available databases, coupled with major advances in SNP genotyping technology that reduce costs and increase throughput, are enabling a host of studies aimed at elucidating the genetic basis of complex disease. The focus in this task view is on R packages implementing statistical methods and algorithms for the analysis of genetic data and for related population genetics studies.

A number of R packages are already available and many more are most likely to be developed in the near future. Please send your comments and suggestions to the task view maintainer.

- · Population Genetics: genetics implements classes and methods for representing genotype and haplotype data, and has several functions for population genetic analysis (e.g. functions for estimation and testing of Hardy-Weinberg and linkage disequilibria, etc.). Geneland has functions for detecting spatial structures from genetic data within a Bayesian framework via MCMC estimation, rmetasim provides an interface to the metasim engine for population genetics simulations. hapsim simulates haplotype data with pre-specified allele frequencies and LD patterns. A few population genetics functions are also implemeted in gap and popgen. popgen has functions for clustering SNP genotype data and SNP simulation from a Multinomial-Dirichlet model. hierfstat allows the estimation of hierarchical F-statistics from haploid or diploid genetic data. LDheatmap creates a heat map plot of measures of pairwise LD. mapLD measures linkage disequilibrium and constructs haplotype blocks. hwde fits models for genotypic disequilibria. Whilst HardyWeinberg provides graphical representation of disequilibria via ternary plots (also known as de Finetti diagrams). Biodem package provides functions for Biodemographical analysis, e.g. Fst() calculates the Fst from the conditional kinship matrix. Package kinship offers some functions for analysis on pedigrees. The adegenet implements a number of different methods for analysing population structure using multivariate statistics, graphics and spatial statistics.
- Phylogenetics: Phylogenetic and evolution analyses can be performed via ape and apTreeshape.
 Package ouch provides Ornstein-Uhlenbeck models for phylogenetic comparative hypotheses.
 PHYLOGR is a suite of functions for the analysis of phylogenetically simulated data sets and phylogenetically-based GLS model fitting. stepwise implements a method for stepwise detection of recombination breakpoints in sequence alignments. phangor estimates phylogenetic trees and networks using maximum likelihood, maximum parsimony, distance methods and Hadamard conjugation.
- Linkage: There are few native packages for performing parametric or non-parametric linkage analysis
 from within R itself, the calculations must be performed using external packages. However, there are a
 number of ancillary R packages that facilitate interface with these stand-alone programs and using the
 results for further analysis and presentation. ibdreg uses Identity By Descent (IBD) Non-Parametric
 Linkage (NPL) statistics for related pairs calculated externally to test for genetic linkage with
 covariates by regression modelling. multic also utilises IBD sharing statistics calculated externally for

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The R Manuals

edited by the R Development Core Team. Current Version: 2.8.1 (December 2008)

The following manuals for R were created on Debian Linux and may differ from the manuals for Mac or Windows on platform-specific pages, but most parts will be identical for all platforms. The correct version of the manuals for each platform are part of the respective R installations. Here they can be downloaded as PDF files or directly browsed as HTML:

- . An Introduction to R is based on the former "Notes on R", gives an introduction to the language and how to use R for doing statistical analysis and graphics. [browse HTML | download PDF]
- A draft of The R language definition documents the language per se. That is, the objects that it works on, and the details of the expression evaluation process, which are useful to know when programming R functions. [browse HTML | download PDF]
- . Writing R Extensions covers how to create your own packages, write R help files, and the foreign language (C, C++, Fortran, ...) interfaces. [browse HTML | download PDF]
- R Data Import/Export describes the import and export facilities available either in R itself or via packages which are available from CRAN. [browse HTML | download PDF]
- R Installation and Administration [browse HTML | download PDF]
- R Internals: a guide to the internal structures of R and coding standards for the core team working on R itself. [browse HTML | download PDF]
- The R Reference Index: contains all help files of the R standard and recommended packages in printable form. [download PDF, 14MB]

Translations of manuals into other languages than English are available from the contributed documentation section (only a few translations are available).

The latex or texinfo sources of the latest version of these documents are contained in every R source distribution (in the subdirectory doc/manual of the extracted archive). Older versions of the manual can be found in the respective archives of the R sources. The HTML versions of the manuals are also part of most R installations (accessible using function help.start()).

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Let's Play with !

R can save information in variables or objects

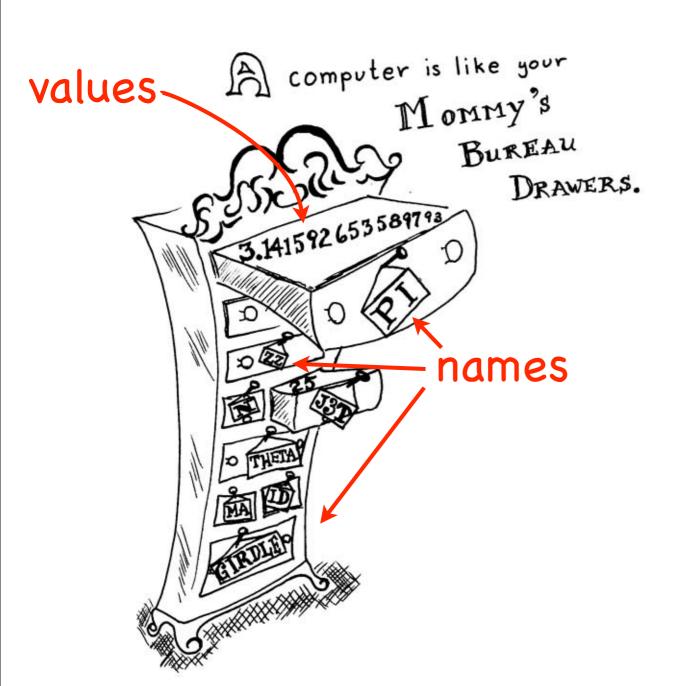
Assignment works by two types of operators:

Equal sign: right side stored in left side

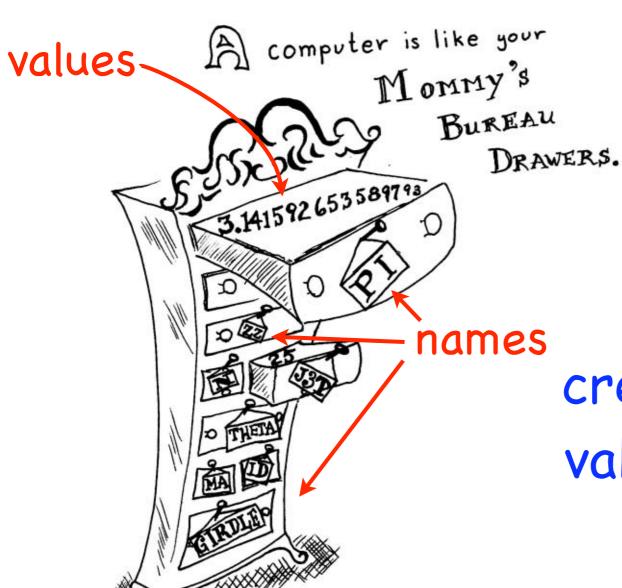
$$> x = 6$$
 (put 6 into x)

Arrow: assignment direction follows arrow

- > x < 6 (put 6 into x)
- > 6 -> x (put 6 into x)
- > 6 = x (error! cannot put x into 6)



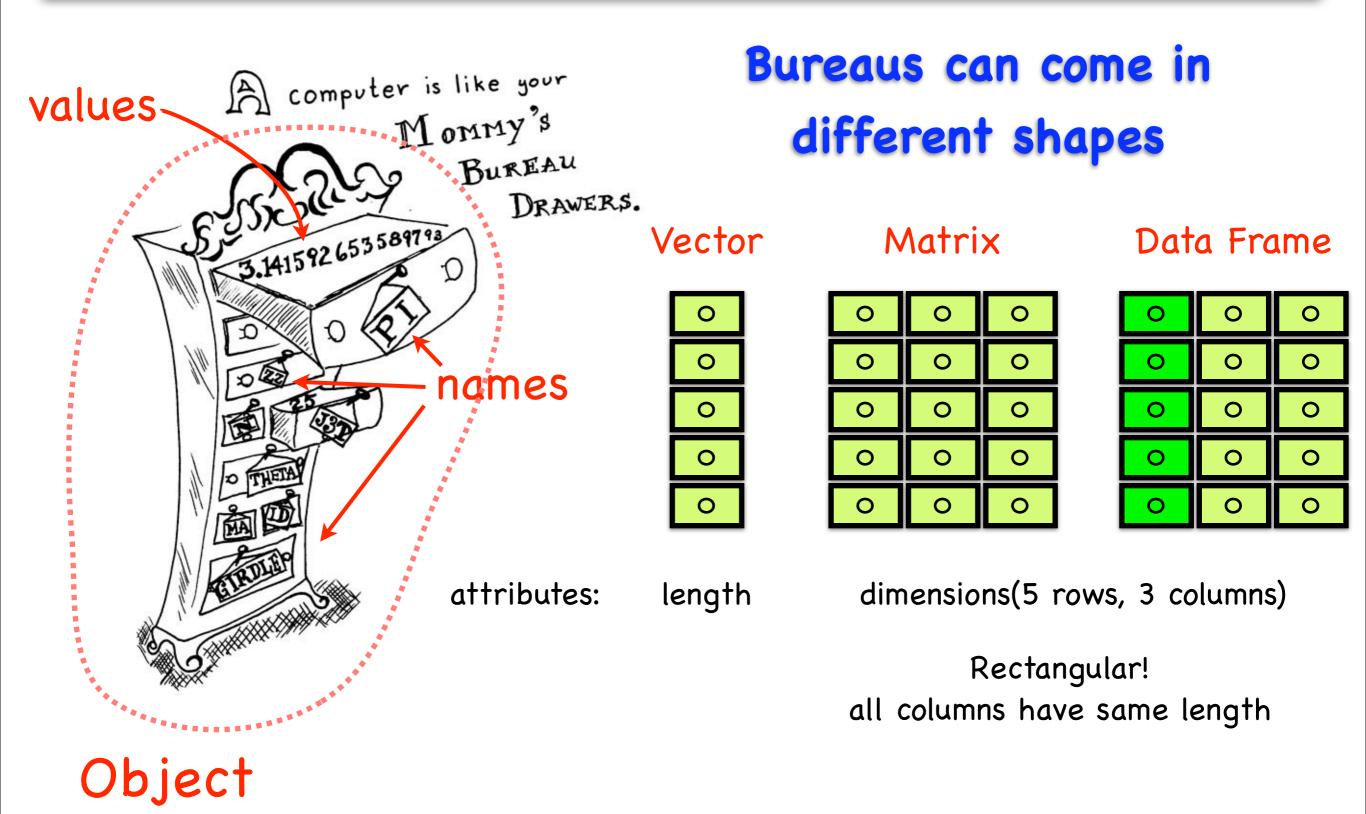
In R, there are drawers for:
Numbers
Characters (alphabetical strings)
Logical (TRUE or FALSE)
Complex Numbers (don't worry)

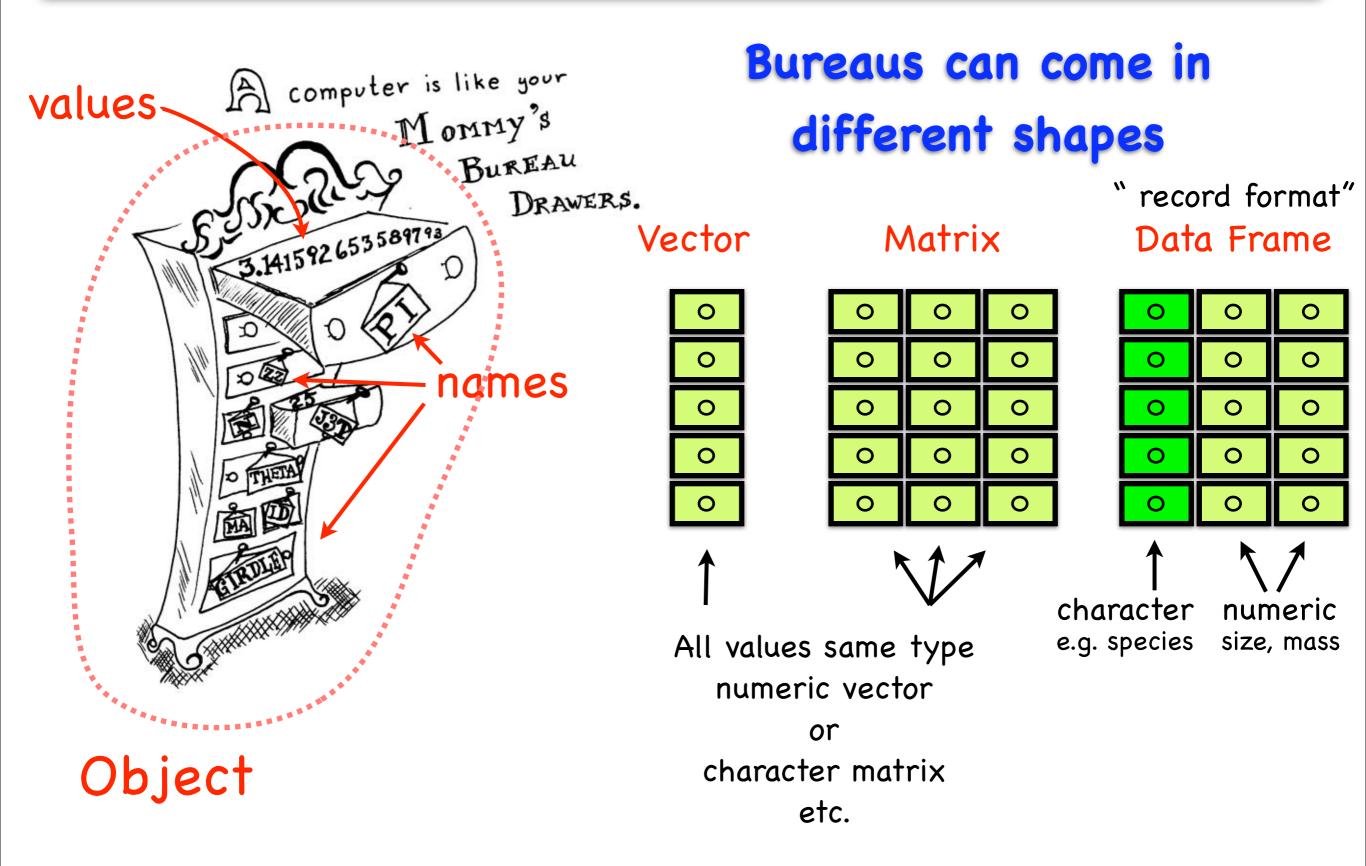


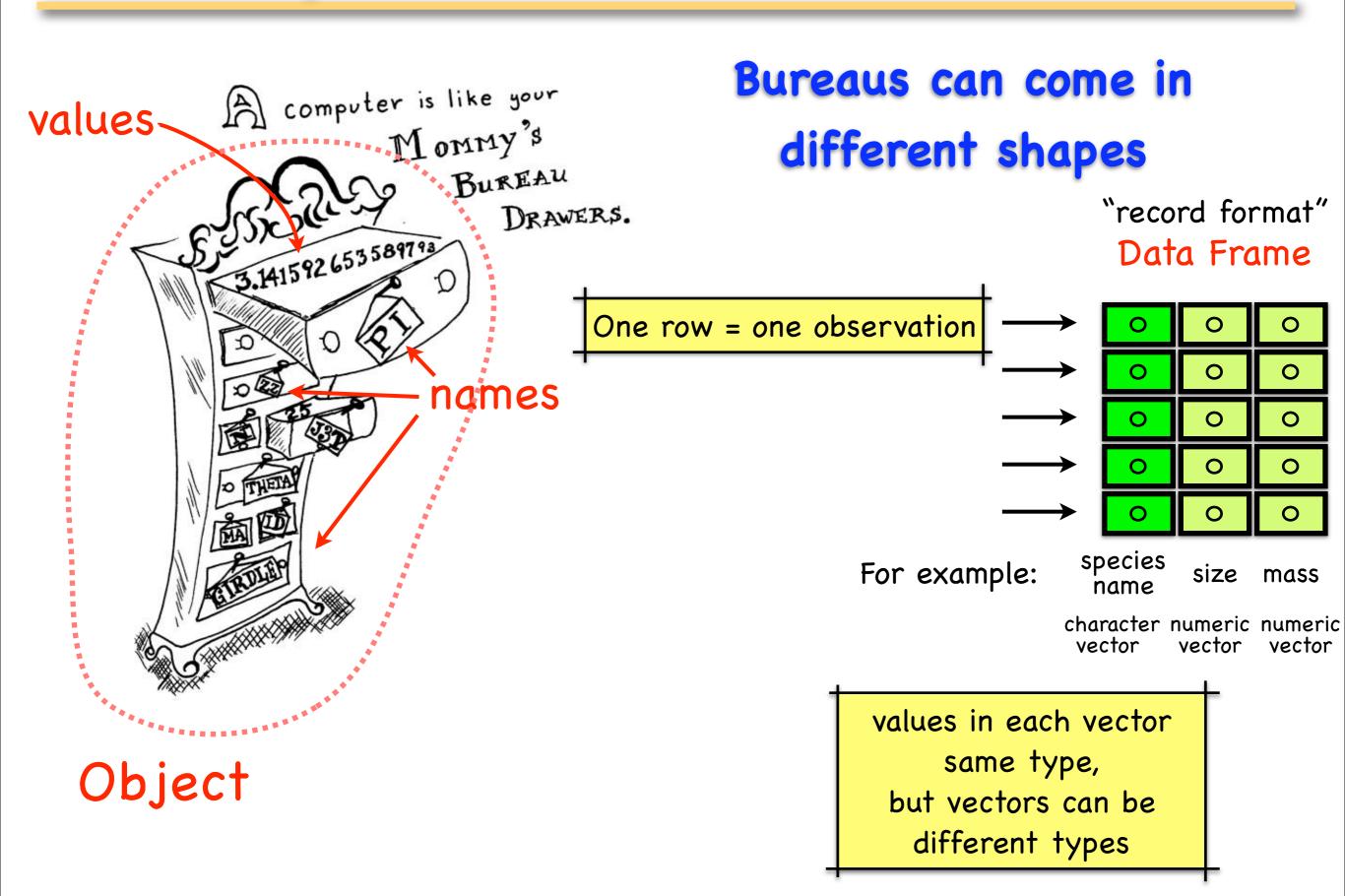
In R, there are drawers for:
Numbers
Characters (alphabetical strings)
Logical (TRUE or FALSE)
Complex Numbers (don't worry)

Create a new drawer by creating a name, and shoving a value into it - R will assign the "type" or "mode"

```
> x <- 25
name value
> mode(x)
[1] "numeric"
```

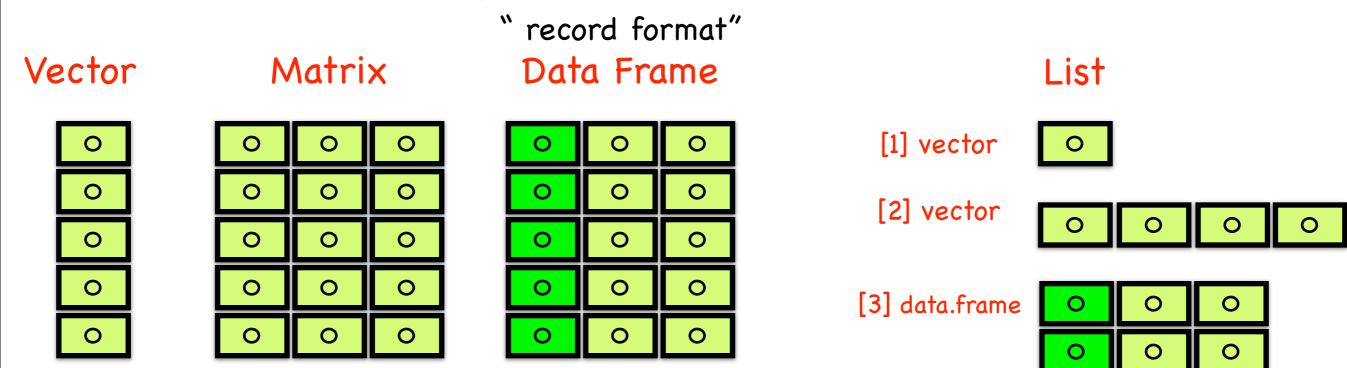




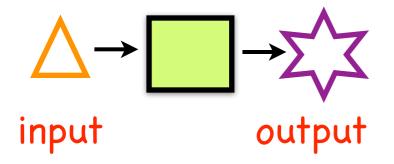


Bureaus can come in different shapes

All of these are classes of objects



Functions

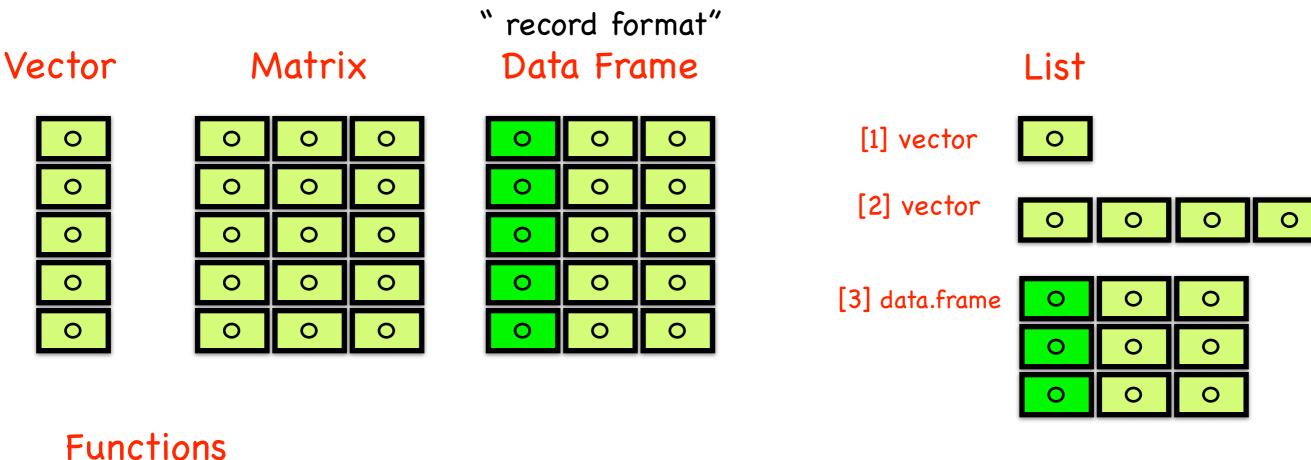


a "list" of objects

- offers more flexibility
- often used for model output
- R has many functions that operate on lists

Bureaus can come in different shapes

All of these are classes of objects



5 25

a "list" of objects - offers more flexibility - often used for model output - R has many functions that operate on lists

Common Sources of Error

1) Typos! Computers are very anal that way.

- > length = 6 # is not the same as
 > lengths = 6
- 2) R is case sensitive
 - > length != Length
- 3) Using () when should use [] and vice versa
 - > mean(x) # use () for functions
 - > mean[x] # error
 - > x[5] # select an element of a vector, matrix, data.frame, etc.
 - > x(5) # error
- 4) No comma or comma in the wrong place
 - > x[5,3] # fifth row, third column of x
 - > x[5 3] # error
 - > x[5,3,] # error

Common Sources of Error

- 5) Forgetting quotes for character strings (R will assume it's another named object or variable)
 - > treatment = c("a", "b", "c")
 - > treatment == a # error R thinks a is another object

What is it?

check using class() and attributes()

All objects have **class, mode** and **length** (the number of vector elements; everything is a vector in R)

names are optional

Derived objects can have **attributes** such as: **dim** (dimensions -- number of rows, columns) **row.names** (other programmer-defined attributes)

Functions and Operators perform actions

Functions

```
\triangle \rightarrow \bigcirc \rightarrow \bigcirc \bigcirc
input
output
```

- > mean(x) # mean of x [1] 2
- > ls()

Functions and Operators perform actions

Functions and Operators perform actions

Operators are used for symbolic math to fi

(otherwise very similar to functions)

- > 2*2 # * multiplication symbol
- > 2^2 # ^ power (2 squared)
- > x == 2 # x equals 2 (element by element)
- > x < 2 # x less than 2

R works on Objects

What is an object? An abstraction

- data vector, matrix, array, data frame, list, or function
- a definition for a type of data to be stored (object class)
- *ways of bundling parts of programs into small, manageable pieces (functions or methods)
- an object is a component of a program that knows how to perform certain actions and to interact with other pieces of the program.
- Functions can be described as "black boxes" that take an input and spit out an output. Objects can be thought of as "smart" black boxes. That is, objects can know how to do more than one specific task (method or behavior), and they can store their own set of data.

Objects should mimic behavior of real-world counterparts

All objects have class, mode and length

And possibly other attributes

When working with a new package, you want to know what kind of object you are dealing with:

A common source of error is putting the wrong class of object into a function

Huh?

"Atomic" datatypes basic types for the single element. (can't break it down any further).

mode: the atomic data type (**class** = **mode** if object is atomic)

class: classes can be derived (i.e., programmer defined) or atomic -- also refers to the classes that the object inherits (i.e., which methods used are determined by the class of object)

R object types

Vector: a one-dimensional array of arbitrary **length**.

Matrix: a two-dimensional array with an arbitrary number of rows and columns.

Array: as a matrix, but of **arbitrary dimension** (i.e., more than 2).

Data frame: a set of data organized similarly to a matrix. However each column of the data frame may contain its own type of data. Columns typically correspond to variables in a statistical study, while rows correspond to observations of these variables.

Function: a set of commands that are packaged into a unit with defined input and output (I/O is not necessary, though).

List: an arbitrary collection of other R objects (which may include other lists).

```
> x < - cbind(a=1:3, pi=pi) # simple
                    # matrix w/ dimnames
> x
     a
             рi
[1,] 1 3.141593
[2,] 2 3.141593
[3,] 3 3.141593
> class(x)
[1] "matrix"
> attributes(x)
$dim
[1] 3 2
$dimnames
$dimnames[[1]]
NULL
$dimnames[[2]]
[1] "a" "pi"
> attributes(x) <- NULL</pre>
> x # now just a vector of length 6
[1] 1.000000 2.000000 3.000000 3.141593
   3.141593 3.141593
                # vector is default mode
> class(x)
[1] "numeric"
```

the R environment: Session

SESSION: A "session" is a single use of the R language, the period between starting R up and shutting it down.

Within a session, you may load packages, create R objects, produce graphics, or write/run scripts.

WORKSPACE: The collection of objects currently stored.

```
> ls() # display the names of objects in workspace
```

```
> rm(list=ls()) # deletes all objects from workspace
```

the R environment: Session

At end of SESSION:

Save workspace image? [y/n/c]:

If you say "y", the objects are written to a file called ".RData" in the current directory, and the command lines used in the session are saved to a file called ".Rhistory".

NOTE: Generally, files that start with a "." are hidden in the directory.

IF you restart R from the same directory, it will reload the default (.Rhistory, .Rdata) history and workspace files.

use save(), save.image(), savehistory() to save these files with your own names specified within the parentheses.

the R environment: Packages

The R programming language is written in **modules** called **packages**, which are groups of related functions organized together in a bundle.

Packages are the means by which R is extended by the open-source community (user contributed packages)

Not all aspects of the R programming language are **loaded** every time you fire R up. -- you have to load optional packages with every new session.

the R environment: Packages

default packages at startup are base & a few others.

```
> search() # gives search path for R objects

[1] ".GlobalEnv" "tools:RGUI" "package:methods" "package:stats"
[5] "package:graphics" "package:grDevices" "package:utils"
"package:datasets"
[9] "Autoloads" "package:base"
```

When you type a command or object name in R, it "searches" through the "search path" for a match and then takes appropriate action (be it the name of a data object, function, operator, etc.).

NOTE: Don't create objects with the same name as R commands! (e.g., t, T, F, c all are special characters) Results are unpredictable

the R environment: Packages

INSTALLING Packages: saves the package source code to the appropriate place in your computer's file directory (usually a place that users don't mess with)

LOADING Packages: attaches the package from your computer's R library to your search path (adds it to your session).

```
> library("packagename")
```

the R environment: Working Directory

R program software is stored in a "safe" location on your computer. (usually you never want to touch this. In fact, you may not even know where this is – that's OK).

R working directory is the location where you keep your own R scripts, input files, and output files.

BEST PRACTICES: Keep your software directories pristine!
Keep data directories separate.

This simplifies maintenance, prevents corruption of important software, and simplifies backup.

References

- Jonathan Baron's R help Page http://finzi.psych.upenn.edu/page
- An Introduction to R http://cran.r-project.org/doc/manuals/R-intro.pdf
- "An Introduction to R: Software for Statistical Modelling & Computing" by Petra Kuhnert and Bill Venables http://cran.r-project.org/doc/contrib/Kuhnert+Venables-R_Course_Notes.zip
- Programming in R (a great web page!) by Vincent Zoonekynd http://zoonek2.free.fr/UNIX/48_R/02.html
- Programming in R (with R & BioConductor) by Thomas Girke http://faculty.ucr.edu/
 <u>~tgirke/Documents/R_BioCond/R_Programming.html</u>
- (Generally, see the R manuals at http://cran.r-project.org/manuals.html
- Online C++ tutorial:What is an object? http://www.intap.net/~drw/cpp/cpp06_01.htm
- The JAVA tutorials: What is an object? http://java.sun.com/docs/books/tutorial/java/concepts/
 object.html