

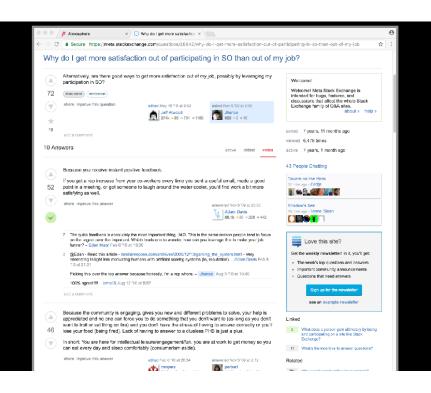
Recap From Last Time:

- UNIX pipes and redirects: How UNIX commands can be combined to generate flexible solutions to data manipulation tasks.
- UNIX commands: Further exploration of the 22 key UNIX commands that you will use during ~95% of your future UNIX work
- Jetstream: Starting up instances; ssh access from your Terminal application; Demoed installing and running bioinformatics software for a genome scale annotation.
- Cloud computing: Many bioinformatic tasks require large amounts of computing power and can't realistically be run on your own machine. These tasks are best performed using remote computers or cloud computing, which can only be accessed through a shell.

Today's Learning Goals

- Familiarity with R's basic syntax.
- Familiarity with major R data structures.
- Understand the basics of using functions.
- Be able to use R to read and parse comma-separated (.csv) formatted files ready for subsequent analysis.
- Appreciate how you can use R scripts to aid with reproducibility.

Side-Note: StackOverflow is your friend! x / g retudio - Error when installing " x @ Secure https://stackgyerflow.com/guestions/26445815/error-when-installing-devtocis-package Stackoverflow Questions Developer Jobs Tags Users Search Could someone help me to find out a solution to this error? > * installing *source* package 'RCurl' ... > \Rightarrow package 'RCurl' successfully unpacked and MD5 sums checked checking for curl. > failed for package 'RCurl' > removing 'fhome/puanch/R/XB5_64-pc-linux-gnu-library/3.9/RCurl' Warning in > non-zero exit status DRROM: dependency 'RCurl' is not available for merkage 'htte' r resoving '/home/juanch//8/366_64-pc-limx-guu-library/3.0/htte' Warning in l non-zere eart status ERGNE dependencies 'htte', 'RCurt' are not weaklable for package 'cevotos' r resoving '/home/juanch/%/366_64-pc-limx-guu-library/3.0/devtoels' Maraing non-zere eait status > The downloaded source packages are in mbipanel google-analytics print(sessionInfo(), locale=EALSE) R version 3.8.2 (2013-09-25) Platform: x86_64-pc-linux-gnu (64-bit) CleanSpark Inc. 9 San Diego, CA attached base packages: [1] stats graphics grDevices utils datasets method .net azure Dempusorp ♀ No office lessafor: 220K - £30K ♥ REMOTE ubuntu ratudio devtocia php phpunit Director, Data Science & Insights





What is R?

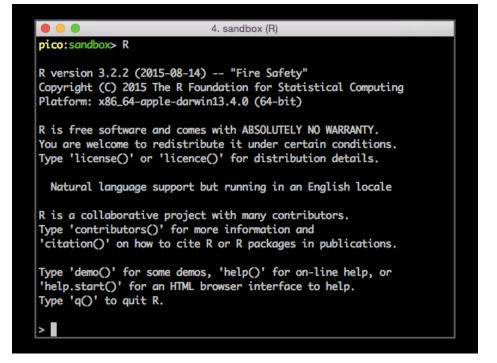
R is a freely distributed and widely used programing language and environment for statistical computing, data analysis and graphics.

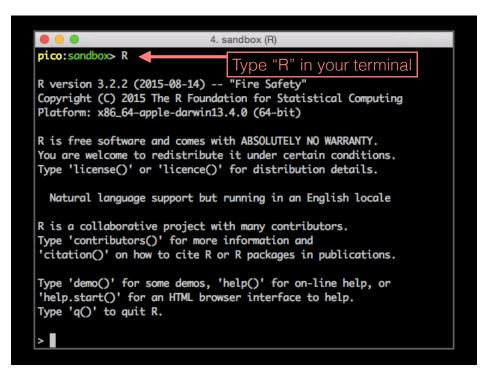


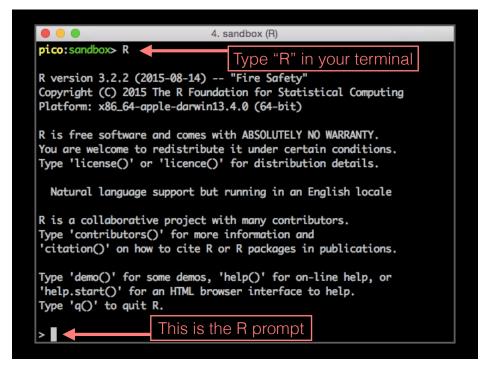
R provides an unparalleled interactive environment for data analysis.

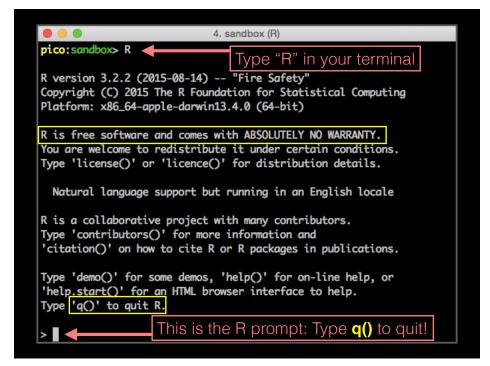
It is script-based (*i.e.* driven by computer code) and not GUI-based (point and click with menus).











What R is **NOT**

A performance optimized software library for incorporation into your own C/C++ etc. programs.

A molecular graphics program with a slick GUI.

Backed by a commercial guarantee or license.

Microsoft Excel!

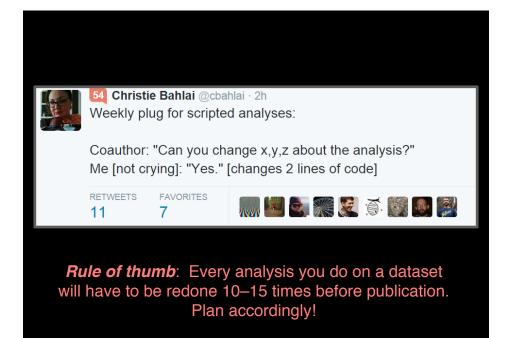
What about Excel?

- Data manipulation is easy
- · Can see what is happening
- But: graphics are poor
- Looping is hard
- Limited statistical capabilities
- Inflexible and irreproducible



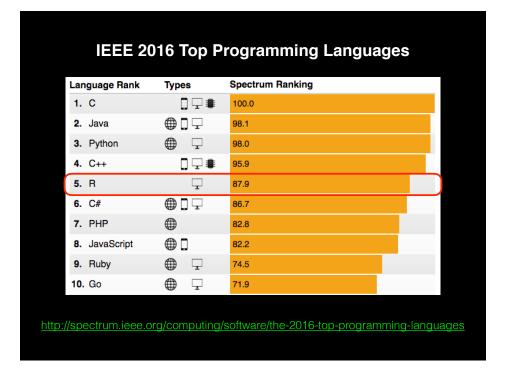
Use the right tool!

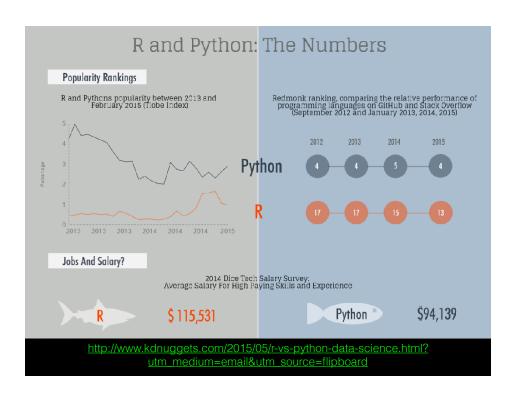
• There are many many things Excel just cannot do!



Why use R?

Productivity
Flexibility
Designed for data analysis





- R is the "lingua franca" of data science in industry and academia.
- Large user and developer community.
 - As of Aug 1st 2016 there are 8811 add on R packages on <u>CRAN</u> and 1211 on Bioconductor - more on these later!
- Virtually every statistical technique is either already built into R, or available as a free package.
- Unparalleled exploratory data analysis environment.

Modularity	Core R functions are modular and work well with others
Interactivity	R offers an unparalleled exploratory data analysis environment
Infrastructure	Access to existing tools and cutting- edge statistical and graphical methods
Support	Extensive documentation and tutorials available online for R
R Philosophy	Encourages open standards and reproducibility

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Modularity

R was designed to allow users to interactively build complex workflows by interfacing smaller 'modular' functions together.



An alternative approach is to write a **single complex program** that takes raw data as input, and after hours of data processing, outputs publication figures and a final table of results.

All-in-one custom 'Monster' program

'Scripting' approach

Another common approach to bioinformatics data analysis is to write individual scripts in Perl/ Python/Awk/C etc. to carry out each subsequent step of an analysis



This can offer many advantages but can be challenging to make robustly modular and interactive.

Interactivity & exploratory data analysis

Learning R will give you the freedom to explore and experiment with your data.

"Data analysis, like experimentation, must be considered as a highly interactive, iterative process, whose actual steps are selected segments of a stubbily branching, tree-like pattern of possible actions". [J. W. Tukey]

Interactivity & exploratory data analysis

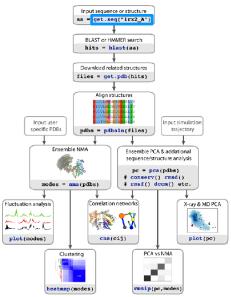
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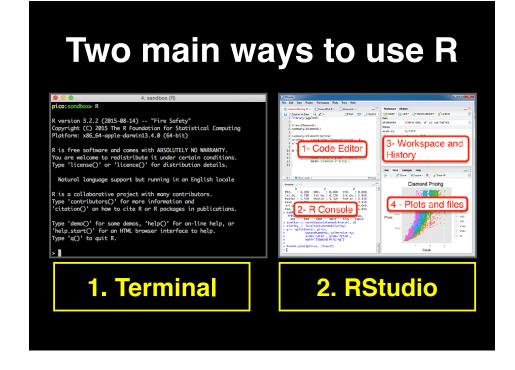
Bioinformatics data is intrinsically **high dimensional** and frequently 'messy' requiring **exploratory data analysis** to find patterns - both those that indicate interesting biological signals or suggest potential problems.

aa = get.seq("1rx2_A") BLAST or HMMER search hits = blast(aa) Download related structures Input simulation specific PDBs pdbs = pdbaln(files) trajectory Ensemble PCA & addational sequence/structure analysis pc = pca(pdbs) # conserv() rmsd() modes = nma(pdbs) # rmsf() dccm() etc. Fluctuation analysis Correlation netwo X-ray & MD PCA plot(modes) cna(cii) plot(pc) PCA vs NMA Clusterina rmsip(pc, modes heatmap (modes)

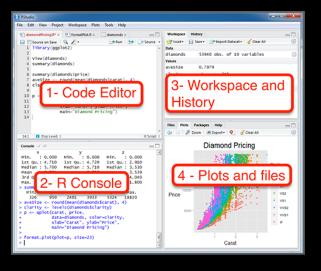
R Features = functions()

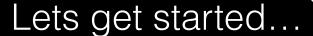


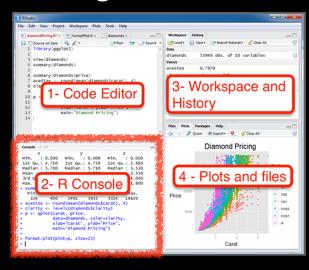




We will use RStudio today







Some simple R commands

R prompt!

2 > 3²

3 > sqrt(25)

[1] 5

4 > 2*(1+1)

[1] 4

 $\begin{array}{c} \mathbf{5} > 2 \times 1 + 1 \\ [1] 3 \end{array}$ Order of precedence

6 > exp(1) [1] 2.718282

7 > log(2.718282) [1] 1

9 > log(10

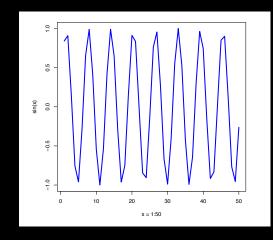
+ , base = 10)
[1] 1 Incomplete

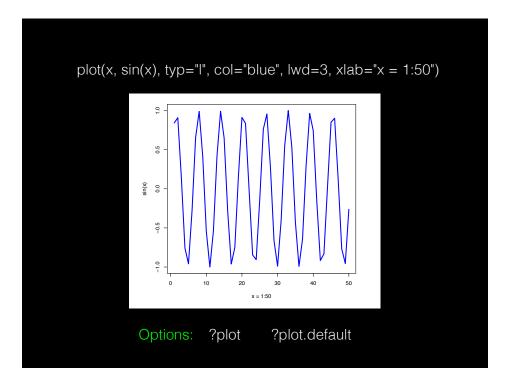
argument

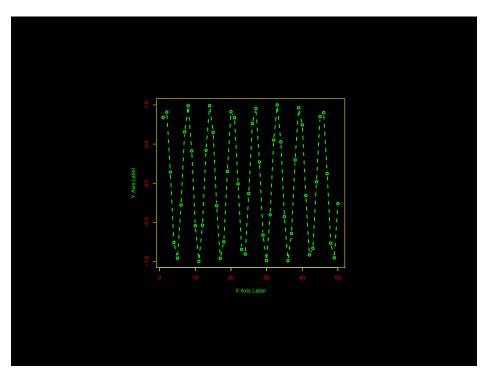
(10) > x=1:50 command

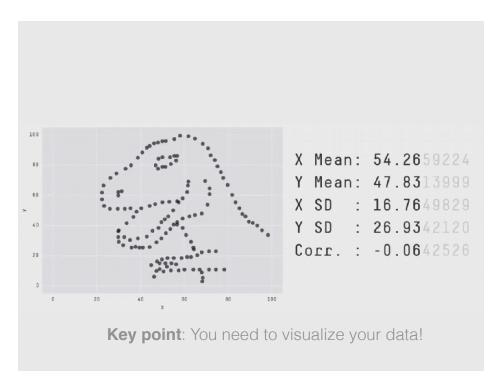
> plot(x, sin(x))

Does your plot look like this?











Error Messages

Sometimes the commands you enter will generate errors. Common beginner examples include:

• Incomplete brackets or quotes e.g.

```
((4+8)*20 <enter>
```

This eturns a + here, which means you need to enter the remaining bracket - R is waiting for you to finish your input.

Press <ESC> to abandon this line if you don't want to fix it.

• Not separating arguments by commas e.g.

```
plot(1:10 col="red")
```

• Typos including miss-spelling functions and using wrong type of brackets *e.a.*

 $exp{4}$

Your turn!

http://tinyurl.com/bggn213-rintro

If you have done the introductory DataCamp course then feel free to jump to section #3 Object Assignment

Topics Covered:

Calling Functions
Getting help in R
Vectors and vectorization
Workspace and working directory
RStudio projects

Topics Covered:

Calling Functions
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Vorkspace and working directory RStudio projects

Vectors

- Vectors are the most basic data structure in R
- All elements of a vector must be the same type

```
dbl_var <- c(1, 2.5, 4.5)
log_var <- c(TRUE, FALSE, T, F)
chr_var <- c("these are", "some", "strings")
```

• When you attempt to combine different types they will be <u>coerced</u> to the most flexible type.

```
var <- c(1, "G", "4", 0.05, TRUE)
```

Names

- You can name a vector in several ways:
 - When creating it: x <- c(a = 1, b = 2, c = 3)
 - By modifying an existing vector in place:

 You can then use the names to access (subset) vector elements:

Why is this useful?

 Because if you know the name (i.e. your label) then you don't have to remember which element of a vector the data you are after was stored in. Consider this fictional example:

What would happen?

- 1 > x <- 1:3; names(x) <- c("a", "b", "c", "d")
- **2** > x <-1:3; names(x) <- 3:1; x[3]
- **3** > x["3"]

R has many data structures

These include:

- vector
- data frame
- list
- matrix
- factors

data.frame

- data.frame is the *de facto* data structure for most tabular data and what we use for statistics and plotting with ggplot2 - more on this later!
- Arguably the most important R data structure
- Data frames can have additional attributes such as rownames() and colnames(), which can be useful for annotating data, with things like subject_id or sample_id

data.frame continued.

• Created with the function data.frame()

dat <- data.frame(id = letters[1:10], x = 1:10, y = 11:20)

 Or more commonly when reading delimited files (i.e. importing data) with the functions read.csv(), read.table(), read_xlsx() etc...

dep <- read.csv2("http://bio3d.uib.no/data/pdb_deposition2.csv")</pre>

R Studio can do this for you via:
 File > Import Dataset > From CSV...

Useful data.frame Functions

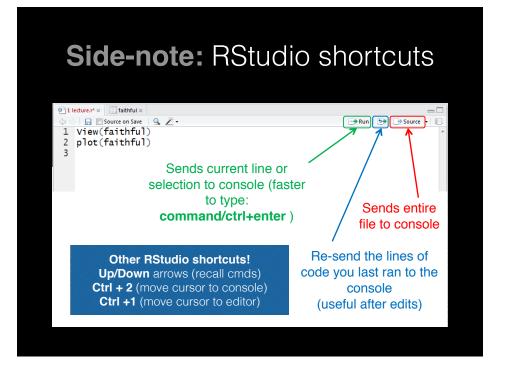
- head() -and tail() shows first 6 rows and last 6 rows respectively
- **dim()** returns the dimensions (i.e. number of rows and columns)
- **nrow()** and **ncol()** returns the number of rows and columns separately.
- rownames() and colnames()- shows the names attribute for rows and columns
- **str()** returns the structure including name, type and preview of data in each column

Key Points

- R's basic data types are **logical**, **character**, **numeric**, integer and complex.
- R's basic data structures include **vectors**, lists, **data frames**, matrices and factors.
- Objects may have attributes, such as **name**, **dim**ension, and **class**.

R scripts

- A simple text file with your R commands (e.g. lecture7.r) that contains your R code for one complete analysis
- Scientific method: complete record of your analysis
- Reproducible: rerunning your code is easy for you or someone else
- In RStudio, select code and type <ctrl+enter> to run the code in the R console
- Key point: Save your R script!



Rscript: Third way to use R







1. Terminal

2. RStudio

3. Rscript

From the command line!

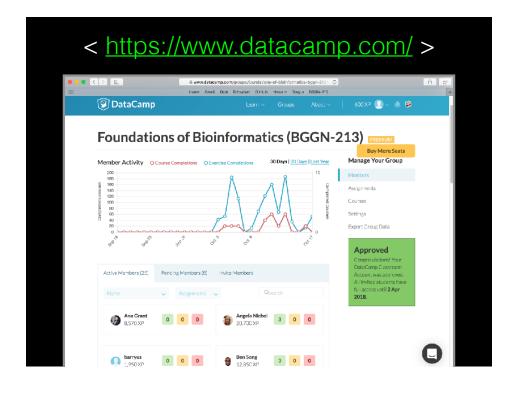
> Rscript --vanilla my_analysis.R # or within R: source(my_analysis.R)

Side-Note: R workspaces

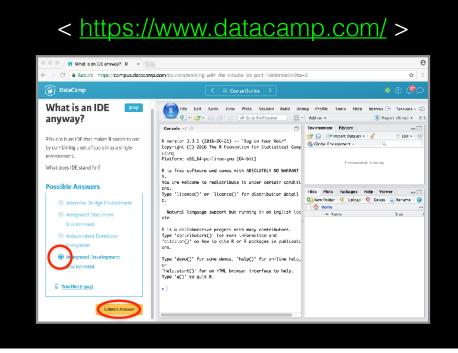
- When you close RStudio, SAVE YOUR .R SCRIPT
- You can also save data and variables in an R workspace, but this is generally not recommended
- Exception: working with an enormous dataset
- Better to start with a clean, empty workspace so that past analyses don't interfere with current analyses
- rm(list = ls()) clears out your workspace
- You should be able to reproduce everything from your R script, so save your R script, don't save your workspace!

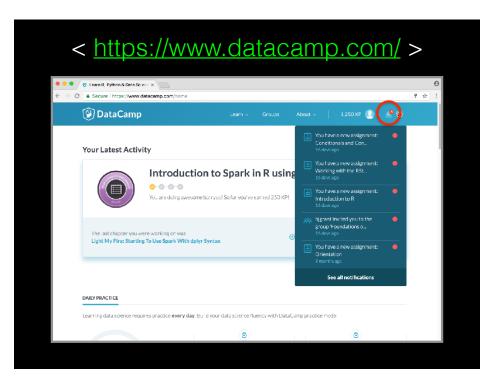
Learning Resources

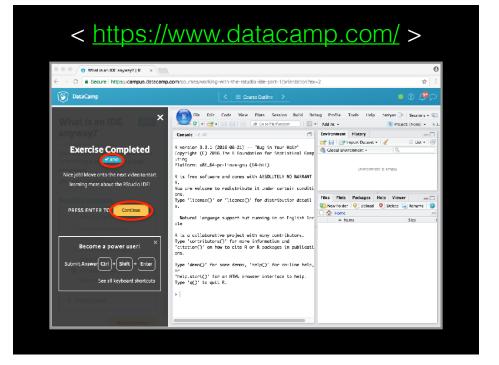
- TryR. An excellent interactive online R tutorial for beginners.
 - < http://tryr.codeschool.com/ >
- RStudio. A well designed reference card for RStudio.
 - < https://help.github.com/categories/bootcamp/ >
- DataCamp. Online tutorials using R in your browser.
 - < https://www.datacamp.com/ >
- R for Data Science. A new O'Reilly book that will teach you how to do data science with R, by Garrett Grolemund and Hadley Wickham.
 - < http://r4ds.had.co.nz/ >

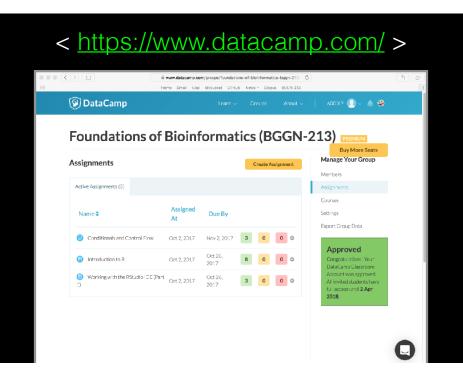


< https://www.datacamp.com/ > (P) DataCamp Foundations of Bioinformatics (BGGN-213) Buy More Seats Manage Your Group Assignments Create Assignment Members Export Group Data Conditionals and Control Flow Oct 2, 2017 Nov 2, 2017 3 0 0 © Approved Introduction to R. Oct 2, 2017 Congratulations: You DataCamp Classroom Working with the RStudio IDE (Part Oct 2, 2017) 3 0 0 0 All invited students hav ull access until 2 Apr 2018.









Key Points

- R's basic data types are **logical**, **character**, **numeric**, integer and complex.
- R's basic data structures include **vectors**, lists, **data frames**, matrices and factors.
- Objects may have attributes, such as name, dimension, and class.
- DataCamp, StackOverflow and help() are your friends.

Final Knowledge Check!

- What is R and why should we use it?
- Familiarity with R's basic syntax.
- Familiarity with major R data structures namely *vectors* and *data.frames* (with more on *lists* and *matrices* next day).
- Understand the basics of using functions (arguments, vectorizion and re-cycling).
- Be able to use R to read and parse comma-separated (.csv) formatted files ready for subsequent analysis.
- · Appreciate how you can use R scripts to aid with reproducibility.

Optionali

http://swcarpentry.github.io/r-novice-inflammation/

Sections: 1, 11 & 12 only!

Help from within R

- Getting help for a function
- > help("log")
- > ?log
- Searching across packages
- > help.search("logarithm")
- · Finding all functions of a particular type
- > apropos("log") [7] "SSlogis" "as.data.frame.logical" "as.logical" "as.logical.factor" "dlogis" "is.logical" [13] "log" "log10" "log1p" "log2" "logLik" "logb" [19] "logical" "loglin" "plogis" "print.logLik" "glogis" "rlogis"

Optional Exercise

Use R to do the following. Create a new script to save your work and code up the following four equations:

```
1 + 2(3 + 4)
ln(4^3+3^{2+1})
 \sqrt{(4+3)(2+1)}
```

log (base) R Documentation

Logarithms and Exponentials

Description What the function does in general terms Avector of the same length on a containing the transformed values. log (0) gives Inf., and

log computes legarithms, by default natural logarithms, leg10 computes common (i.e., base 10) logarithms, and leg2 computes binary (i.e., base 2) logarithms. The general form $\log (x)$ base) computes logarithms with base bas

logic (x) computes log(1+x) accurately also for |x| << 1 (and less accurately when x is

exp computes the exponential function

=x_1=1 (x) computes $\exp(x) - f$ accurately also for |x| << 1

Usage How to use the function

log(x, base = exp(1)) logb(x, base = exp(1) 10g2 (x)

logic(x)

Arguments What does the function need

x a numeric or complex vector.

base a positive or complex number: the base with respect to which locarithms are computed Dafaults to e=exp(1).

All except logic are generic functions; methods can be defined for them individually or via the Math group generic.

10210 and 1022 are only convenience wrappers, but logs to bases 10 and 2 (whether computed vio log or the wrappers) will be computed more efficiently and accurately where supported by the US. Methods can be set for them individually (and otherwise methods for log

Logic is a wrapper for Log for compatibility with S. If (S3 or S4) methods are set for Log they will be dispatched. Do not set \$4 methods on loab itself.

All except log are <u>primitive</u> functions

R: Logarithms and Exponentials =

Value What does the function return

log(x) for negative values of x is NaN. exp(-Inf) is 0.

For complex inputs to the log functions, the value is a complex number with imaginary part in the range [-pi, pi]: which end of the range is used might be platform-specific

exp, expm1, log, log10, log2 and log1p are SI generic and are members of the $\underline{\tt Math}$ group generic.

Note that this means that the S4 generic for tog has a signature with only one argument, \mathbf{x}_{c} but that base can be passed to methods (but will not be used for method selection). On the other hand, if you only set a method for the Math group generic then base argument of log will be ignored for your class.

logip and expm1 may be taken from the operating system, but if not available there are based on the Fortran subroutine dinect by W. Full often of Les Alames Scientific Leberatory (see http://www.nctib.org/slotec/finib/dinet.f and (for small x) a single Newton step for the solution of Logip(y) = x respectively.

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

Chambers, J. M. (1998) Programming with Data. A Guide to the S Language. Springer. (for

See Also Discover other related functions

[Examples] Sample code showing how it works

x <- 10^-(1+2*1:9)

 $\operatorname{chind}(x, \log(1+x), \log(x), \exp(x)-1, \exp(x))$

[Fackage base version 3.0.1 Index]