

Zelig for R Cheat Sheet

Launch R

GUI (Windows or RAqua) Double-click icon
ESS within XEmacs M-x R (Esc, then x, then R)
Terminal R
To quit, type `q()`.

Installing Zelig Within R, type:
`source("http://gking.harvard.edu/zelig/install.R")`

Loading Zelig Within R, type: `library(Zelig)`

Syntax *R is case-sensitive!*

Default R prompt `>`
Execute a command Press Return or Enter
Comment rest of line `#`
Store objects `<-`
Separate arguments for functions `,`

Saving objects to disk To the working directory:
Save objects `save(x1, x2, file = "object.RData")`
Save workspace `save.image()`
Save workspace to file `save.image(file = "May21.RData")`

Common commands

List objects in workspace `ls()`
Remove objects from workspaces `remove(x1, x2)`
Length of a vector `length(x)`
Dimensions of a matrix or array `dim(x)`
Names for lists or data frames `names(x)`
Type of object `class(x)`
Summary (for most things) `summary(x)`
Cross tab `tabular(x)`
Loading packages `library(PACKAGE)`
Quitting R `q()`
Batch mode `source("myfile.R")`

Logical operators

Exactly equals `==`
Not equal `!=`
Greater than `>`
Greater than or equal `>=`
Less than `<`
Less than or equal `<=`
And `&`
Or `|`

(Note: `=` is *not* a logical operator!)

Plots to screen by default. Let `x` and `y` be vectors of length n

Scatterplot `plot(x, y)`
Line plot `plot(x, y, type = "l")`
Add points `points(x, y)`
Add a line `lines(x, y)`
Histogram `hist(x)`
Kernel density plot `plot(density(x))`
Contour plot `contour(x, y)`

Plot options Separate options with commas:

Title `main = "My Title"`
X-axis label `xlab = "Independent Var"`
Y-axis label `ylab = "Dependent Var"`
X-axis limits `xlim = c(0, 10)`
Y-axis limits `ylim = c(0, 1)`
Colors `color = "red" or color = c("red", "blue")`

Saving plots Export plots as `.pdf` or `.eps` files

Call the file to which you will store the plot:

o For `.eps` files:
`ps.options(family = c("Times"), pointsize = 12)`
`postscript(file = "mygraph.eps", horizontal = FALSE,`
`paper = "special", width = 6.25, height = 4)`
o For `.pdf` files:
`pdf(file = "mygraph.pdf", width = 6.25, height = 4,`
`family = "Times", pointsize = 12)`

Draw your plot (it won't display to screen).

Close and save the file using `dev.off()`.

Math operations `+ - \ *`

For vectors or arrays of the same dimension, R performs math operations on each (i) or (i, j) or (i, j, \dots, n) element with its corresponding element in the other vector or array.

Matrix operations

Transpose `t(P)`
Inverse `solve(P)`
Matrix multiplication `P %*% Q`

Data structures (or R objects)

R stores all objects in the *workspace* (or RAM). You can store all types of objects – at the same time.

Scalars Store a scalar value using `<-` (e.g., `a <- 5`)

Numeric `1, 3.1416, NA, NaN, -Inf, Inf`
Logical `TRUE, FALSE`
Character `"Alpha", "beta"`

(Character values are always enclosed in quotes.)

Arrays

An array can have one dimension (a vector), two dimensions (a matrix), or $n > 2$ dimensions. Arrays hold one type of scalar value.

Vectors: 1D arrays with undefined length.

Vector (undefined type/length) `var <- array()`
Integer vector `var <- 10:20`
Numerical vector `var <- c(2, 13, 44)`
Numerical vector `var <- seq(5, 10, by = 0.5)`
Character vector `var <- rep("file", 15)`

Use `c()` and `rep()` with numeric, character, and logical values.

To generate a **logical vector** (TRUE/FALSE), use logical operators compare two vectors of the same length:

`var1 <- c(1, 3, 5, 7, 9); var2 <- c(1, 2, 3, 4, 5)`
`logical <- var1 == var2`

Use logical vectors to recode other vectors or matrices. Putting a logical statement in square brackets extracts only those elements for which the logical statement is TRUE:

`var3 <- var1[logical]` or `var3 <- var1[var1 == var2]`

A **factor vector** is a special vector that separates each unique value of the vector into either indicator variables (for unordered factors) or a Helmert contrast matrix (for ordered factors) in regression functions.

Matrices and arrays 2+D arrays have fixed dimensions.

Create a matrix `mat <- matrix(NA, nrow = 5, ncol = 5)`
`mat <- cbind(v1, v2)`
`mat <- rbind(v1, v2)`
Create an array `arr <- array(NA, dim = c(3, 2, 1),`
`dimnames = list(NULL, NULL, "x1"))`

Extracting or recoding elements in a matrix or array:

Row in a matrix `mat[5,]`
Column in a matrix `mat[, 5]`
3rd dimension in a 4D array `arr[, , 5,]`

Lists A list can contain scalars, matrices, and arrays of different types (numeric, logical, factor, and character) at the same time. Lists have a flexible number of elements and can be enlarged on the fly.

Create a list `ll <- list(a = 5, b = c("in", "out"))`
`ll <- list(); ll$a <- 5`
Extract list elements `ll[[6]]`
`ll$a`
Remove list elements `ll[[6]] <- NULL`
`ll$a <- NULL`

Data Frames A data frame is a list in which every list element has the same length or number of observations. Like a list, each element can be of a different class. Use list *or* matrix operations on a data frame. For a data frame `data`:

View the 5th row `data[5,]`
Extract the 7th variable `data[[7]]`
Extract the age variable `data$age`
Insert a new variable `data$new <- new.var`

Delimiters

Functions you use ()
Functions you write { }
N-dimensional arrays N = 1: []
N = 2: [,]
N = 3: [, ,]
Lists \$ or [[]]

Loading data

Change directories (using `setwd()`) to the directory that contains your data files *before* attempting to read data into R!

Space- or tab-delimited `data <- read.table("data.tab")`
Comma-separated values `data <- read.csv("data.csv")`
Stata .dta file `library(foreign)`
`data <- read.dta("data.dta")`
SPSS .sav file `library(foreign)`
`data <- read.spss("data.sav",`
`to.data.frame = TRUE)`

Options for loading data

- o First row = variable names:
`data <- read.table("data.tab", header = TRUE)`
- o Missing values = -9 (for example)
`data <- read.table("data.tab", na.strings = "-9")`
(Recodes missing values as R NA values.)

(You can combine both options.)

Verifying data integrity

The `data` object is an R `data.frame`, with special properties:

- o Each variable (column) has a name:
 - To view names: `names(data)`
 - If names are missing or incorrect, assign correct names
`names(data) <- c("Y", "X")`
- o Observations (rows) may have a name:
 - To view names: `rownames(data)`
 - If names are missing or incorrect, assign correct names
`rownames(data) <- 1:nrow(data)`
- o Display the 5th row: `data[5,]`
- o Display the variable Y: `data$Y`
- o Display a summary of the entire data frame: `summary(data)`

Distributions

For all distributions, let

`x`, `q` be vectors of quantiles
`p` be a vector of probabilities
`n` be a scalar (the number of random draws).

Uniform

CDF `dunif(x, min = 0, max = 1)`
PDF `punif(q, min = 0, max = 1)`
Quantiles `qunif(p, min = 0, max = 1)`
Random Draws `runif(n, min = 0, max = 1)`

Bernoulli

Same as Binomial with `size = 1`.

Binomial

CDF `dbinom(x, size, prob)`
PDF `pbinom(q, size, prob)`
Quantiles `qbinom(p, size, prob)`
Random Draws `rbinom(n, size, prob)`

Beta

CDF `dbeta(x, shape1, shape2)`
PDF `pbeta(q, shape1, shape2)`
Quantiles `qbeta(p, shape1, shape2)`
Random Draws `rbeta(n, shape1, shape2)`

Poisson

CDF `dpois(x, size, prob)`
PDF `ppois(q, size, prob)`
Quantiles `qpois(p, size, prob)`
Random Draws `rpois(n, size, prob)`

Gamma

CDF `dgamma(x, shape, rate = 1, scale = 1/rate)`
PDF `pgamma(q, shape, rate = 1, scale = 1/rate)`
Quantiles `qgamma(p, shape, rate = 1, scale = 1/rate)`
Random Draws `rgamma(n, shape, rate = 1, scale = 1/rate)`

Normal

CDF `dnorm(x, mean = 0, sd = 1)`
PDF `pnorm(q, mean = 0, sd = 1)`
Quantiles `qnorm(p, mean = 0, sd = 1)`
Random Draws `rnorm(n, mean = 0, sd = 1)`

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<http://www.people.fas.harvard.edu/~olau/computing/Rtips.pdf>