

R Basics

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Computational Statistics for Genome Biology

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Plan

Introduction

Data types and structures

- Basic data types

- Higher order objects

Manipulating data

- Subsetting

Useful functions

Plotting

Programming

Packages

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Hello world

```
x <- 1  ## a variable
```

```
x
```

```
## [1] 1
```

```
x = 2  ## overwrite the value x
```

```
x
```

```
## [1] 2
```

```
y <- length(x)  ## calling a function
```

```
y
```

```
## [1] 1
```

Getting help

- ▶ Just ask!
- ▶ `help.start()` and the HTML help button in the Windows GUI.
- ▶ `help` and `?`: `help("data.frame")` or `?help`.
- ▶ `help.search`, `apropos`
- ▶ Online manuals and mailing lists
- ▶ Local R user groups

```
ls()
```

```
## [1] "x" "y"
```

```
rm(y)
```

```
ls()
```

```
## [1] "x"
```

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```
c(1, 3, 9, -1)
```

```
## [1] 1 3 9 -1
```

A vector contains an indexed set of values

- ▶ index starts at 1;
- ▶ all items are of the same storage mode;
- ▶ one of logical, numeric, complex or character,

numeric can further be broken into integer, single and double types (only important when passing these to C or Fortran code, though).


```
mode(1)
```

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

```
typeof(1)
```

```
## [1] "double"
```

```
mode(1L)
```

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

```
typeof(1L)
```

```
## [1] "integer"
```

```
mode("1")
```

```
## [1] "character"
```

```
typeof("1")
```

```
## [1] "character"
```

```
mode(TRUE)
```

```
## [1] "logical"
```

```
typeof(FALSE)
```

```
## [1] "logical"
```

```
## as we are talking about booleans...
```

```
TRUE & TRUE
```

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

The different modes an types can be retrieved and coerced with the `is.*` and `as.*` functions.

```
x <- 1
typeof(x)

## [1] "double"

y <- as.integer(x)
typeof(y)

## [1] "integer"

is.integer(y)

## [1] TRUE
```

Special values

NULL

NA

NaN

Inf

-Inf

`is.null()`

`is.na()`

`is.infinite()`

What are the mode and types of these?

All these are objects with a certain class.

```
class(x)
```

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

```
class("a character")
```

```
## [1] "character"
```

Creating vectors with functions

```
vector(mode = "character", length = 3)
```

```
## [1] "" "" ""
```

```
vector(mode = "numeric", length = 4)
```

```
## [1] 0 0 0 0
```

```
numeric(4)
```

```
## [1] 0 0 0 0
```

Creating vectors with functions (2)

```
x <- c(1, 4, 7, 10) ## concatenate
```

```
x
```

```
## [1] 1 4 7 10
```

```
y <- 1:5 ## integer sequence
```

```
y
```

```
## [1] 1 2 3 4 5
```

```
z <- seq(from = 1, to = 10, by = 2)
```

```
z
```

```
## [1] 1 3 5 7 9
```

Arguments by position or name

```
z1 <- seq(from = 1, to = 10, by = 2)
z2 <- seq(1, 10, 2)
z1 == z2
```

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

```
all(z1 == z2)
```

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

```
identical(z1, z2)
```

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


Vectorised arithmetic

```
x <- 1:5
```

```
y <- 5:1
```

```
x
```

```
## [1] 1 2 3 4 5
```

```
y
```

```
## [1] 5 4 3 2 1
```

```
x + y
```

```
## [1] 6 6 6 6 6
```

```
x^2
```

```
## [1] 1 4 9 16 25
```

Matrices

are 2-dimensional vectors

```
m <- matrix(1:12, nrow = 4, ncol = 3)
```

```
m
```

```
##      [,1] [,2] [,3]
## [1,]    1    5    9
## [2,]    2    6   10
## [3,]    3    7   11
## [4,]    4    8   12
```

```
dim(m)
```

```
## [1] 4 3
```

What if I don't get the data or dimensions right?

```
matrix(1:11, 4, 3)
```

```
## Warning: data length [11] is not a sub-multiple  
or multiple of the number of rows [4]
```

```
##      [,1] [,2] [,3]  
## [1,]    1    5    9  
## [2,]    2    6   10  
## [3,]    3    7   11  
## [4,]    4    8    1
```

```
matrix(1:12, 3, 3)
```

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

```
x <- 1:12
```

```
class(x)
```

```
## [1] "integer"
```

```
dim(x)
```

```
## NULL
```

```
dim(x) <- c(4, 3)
```

```
x
```

```
##      [,1] [,2] [,3]  
## [1,]    1    5    9  
## [2,]    2    6   10  
## [3,]    3    7   11  
## [4,]    4    8   12
```

```
class(x)
```

Arrays

are n-dimensional vectors

```
array(1:16, dim = c(2, 4, 2))
```

```
## , , 1
```

```
##
```

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

```
## [1,]     1     3     5     7
```

```
## [2,]     2     4     6     8
```

```
##
```

```
## , , 2
```

```
##
```

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

```
## [1,]     9    11    13    15
```

```
## [2,]    10    12    14    16
```

list

is an ordered set of elements that can be arbitrary R objects.

```
l1 <- list(a = 1:3, c = length)
l1

## $a
## [1] 1 2 3
##
## $c
## function (x) .Primitive("length")

l1[[1]]

## [1] 1 2 3

l1$c(l1)

## [1] 2
```

data.frame

is a 2-dimensional list.

```
dfr <- data.frame(type = c(
  rep("case", 2),
  rep("ctrl", 2)),
  time = rnorm(4))
```

dfr

```
##   type    time
## 1 case  0.1577
## 2 case -0.8179
## 3 ctrl -0.7268
## 4 ctrl  0.9423
```

```
dfr[1, ]
```

```
##    type    time  
## 1 case 0.1577
```

```
dfr[1, "time"]
```

```
## [1] 0.1577
```

```
dfr$time
```

```
## [1] 0.1577 -0.8179 -0.7268 0.9423
```


environment

is an unordered collection of objects.

```
e <- new.env()  
e[["a"]] <- 1:3  
assign("b", "CSAMA", envir = e)  
ls(e)
```

```
## [1] "a" "b"
```

```
e$a
```

```
## [1] 1 2 3
```

```
get("b", e)
```

```
## [1] "CSAMA"
```

Names

We have seen that function arguments have names, and named our `data.frame` columns. We can also name `matrix`/`data.frame` columns and rows, dimensions, and vector items.

```
x <- c(a = 1, b = 2)
```

```
x
```

```
## a b
```

```
## 1 2
```

```
names(x)
```

```
## [1] "a" "b"
```

```
M <- matrix(c(4, 8, 5, 6, 4, 2, 1, 5, 7), nrow=3)
dimnames(M) <- list(year =
                     c(2005, 2006, 2007),
                     "mode of transport" =
                     c("plane", "bus", "boat"))
```

M

```
##           mode of transport
## year    plane bus boat
##  2005         4   6   1
##  2006         8   4   5
##  2007         5   2   7
```

factor

for categorical data

```
sample.ExpressionSet$type
```

```
## [1] Control Case Control Case Case Control Cas
## [9] Case Control Case Control Case Case Cas
## [17] Case Control Case Case Control Control Con
## [25] Case Case
## Levels: Case Control
```

Higher order objects

When the data to be stored is more complex, special objects are created to store and handle it in a specialised manner. These higher order objects are constructed using the data types we have seen so far as building blocks.

Let's look at how microarray data is handled in Bioconductor. The eSet model has been re-used for other technologies.

```
library(Biobase)
data(sample.ExpressionSet)
sample.ExpressionSet

## ExpressionSet (storageMode: lockedEnvironment)
## assayData: 500 features, 26 samples
##   element names: exprs, se.exprs
## protocolData: none
## phenoData
##   sampleNames: A B ... Z (26 total)
##   varLabels: sex type score
##   varMetadata: labelDescription
## featureData: none
## experimentData: use 'experimentData(object)'
## Annotation: hgu95av2
```

```
class(sample.ExpressionSet)
```

```
## [1] "ExpressionSet"
```

```
## attr(,"package")
```

```
## [1] "Biobase"
```

```
slotNames(sample.ExpressionSet)
```

```
## [1] "experimentData"      "assayData"           "phenoData"
```

```
## [4] "featureData"         "annotation"          "protocolData"
```

```
## [7] ".__classVersion__"
```

```
`?`(class, ExpressionSet)
```

assayData expression values in identical sized matrices.

phenoData sample annotation in `AnnotatedDataFrame`.

featureData feature annotation in `AnnotatedDataFrame`.

experimentData description of the experiment as a MIAME object
(see `?MIAME` for more details).

annotation type of chip as a character.

protocolData scan dates as a character.

**expression
data**

**feature
meta-data**

**sample
meta-data**

The assayData slot

Stored the expression data of the assay.

```
exprs(sample.ExpressionSet)[1:4, 1:3]
```

```
##           A           B           C
## AFX-MurIL2_at 192.74  85.753 176.76
## AFX-MurIL10_at 97.14 126.196  77.92
## AFX-MurIL4_at  45.82   8.831  33.06
## AFX-MurFAS_at  22.54   3.601  14.69
```

```
dim(sample.ExpressionSet)
```

```
## Features  Samples
##         500       26
```

The `phenoData` slot

stores the meta data about the samples.

```
phenoData(sample.ExpressionSet)

## An object of class 'AnnotatedDataFrame'
##   sampleNames: A B ... Z (26 total)
##   varLabels: sex type score
##   varMetadata: labelDescription
```

The `featureData` slot

stores the meta data about the features.

```
featureData(sample.ExpressionSet)
```

```
## An object of class 'AnnotatedDataFrame': none
```

```
## NULL
```

AnnotatedDataFrame

consists of a collection of samples and the values of variables measured on those samples. There is also a description of each variable measured. AnnotatedDataFrame associates a `data.frame` with its metadata.

```
head(pData(sample.ExpressionSet))
```

##	sex	type	score
## A	Female	Control	0.75
## B	Male	Case	0.40
## C	Male	Control	0.73
## D	Male	Case	0.42
## E	Female	Case	0.93
## F	Male	Control	0.22

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- ▶ One of the most powerful features of R is its ability to manipulate subsets of vectors and arrays.
- ▶ As seen, subsetting is done with, `[]`, `[,]`, ...

Subsetting with positive indices

```
x <- 1:10
```

```
x[3:7]
```

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

```
x[9:11]
```

```
## [1] 9 10 NA
```

```
x[0:1]
```

```
## [1] 1
```

```
x[c(1, 7, 2, NA)]
```

```
## [1] 1 7 2 NA
```


Assignments with positive indices

```
x[2] <- 20  
x[4:5] <- x[4:5] * 100  
x[1:6]  
  
## [1] 1 20 3 400 500 6
```

Subsetting with negative indices

```
x <- 1:10  
x[-c(3:7)]
```

```
## [1]  1  2  8  9 10
```

Subsetting with logical predicates

```
x[c(TRUE, TRUE, rep(FALSE, 8))]
```

```
## [1] 1 2
```

```
x > 5
```

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

```
x[x > 5]
```

```
## [1] 6 7 8 9 10
```

```
x[c(TRUE, FALSE)] ## recycled
```

```
## [1] 1 3 5 7 9
```

Subsetting by names

```
x <- c(a = 1, b = 2, c = 2)
```

```
x[c("a", "c")]
```

```
## a c
```

```
## 1 2
```

```
x[c("a", "d")]
```

```
##      a <NA>
```

```
##      1  NA
```

Subsetting matrices

```
M <- matrix(1:12, 3)
```

```
M[2, 3] <- 0
```

```
M
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    1    4    7   10
## [2,]    2    5    0   11
## [3,]    3    6    9   12
```

Subsetting matrices (2)

```
M < 9
```

```
##      [,1] [,2] [,3] [,4]
## [1,] TRUE TRUE  TRUE FALSE
## [2,] TRUE TRUE  TRUE FALSE
## [3,] TRUE TRUE FALSE FALSE
```

```
M[M < 9] <- -1
```

```
M
```

```
##      [,1] [,2] [,3] [,4]
## [1,]   -1   -1   -1   10
## [2,]   -1   -1   -1   11
## [3,]   -1   -1    9   12
```

Subsetting lists

```
ll <- list(a = 1:3, b = "CSAMA", c = length)
ll[1]    ## still a list

## $a
## [1] 1 2 3

ll[[1]]  ## first element of the list

## [1] 1 2 3
```

Subsetting ExpressionSet instances

It is reasonable to expect that subsetting operations work also for higher order objects.

```
sample.ExpressionSet[1:10, 1:2]

## ExpressionSet (storageMode: lockedEnvironment)
## assayData: 10 features, 2 samples
##   element names: exprs, se.exprs
## protocolData: none
## phenoData
##   sampleNames: A B
##   varLabels: sex type score
##   varMetadata: labelDescription
## featureData: none
## experimentData: use 'experimentData(object)'
## Annotation: hgu95av2
```


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Data IO

read.table creates a `data.frame` from a spreadsheet file.

write.table writes a `data.frame/matrix` to a spreadsheet (tsv, csv).

save writes an binary representation of R objects to a file (cross-platform).

load load a binary R file from disk.

Specialised data formats often have specific i/o functionality (microarray CEL files, XML, ...)

```
read.table("./Data/data.csv", sep = ",",  
           header = TRUE, row.names = 1)
```

```
##           A  B C  D  
## 1 -0.15330 10 x 10  
## 2 -0.13868  3 n  9  
## 3 -0.43323  2 f  8  
## 4  1.64569  4 o  7  
## 5  0.23381  6 b  6  
## 6  0.98770  9 m  5  
## 7 -0.25565  7 c  4  
## 8 -0.74719  1 l  3  
## 9 -0.02001  5 e  2  
## 10 -0.95000  8 v  1
```

```
read.csv("./Data/data.csv", row.names = 1)
```

```
##           A  B C  D
## 1  -0.15330 10 x 10
## 2  -0.13868  3 n  9
## 3  -0.43323  2 f  8
## 4   1.64569  4 o  7
## 5   0.23381  6 b  6
## 6   0.98770  9 m  5
## 7  -0.25565  7 c  4
## 8  -0.74719  1 l  3
## 9  -0.02001  5 e  2
## 10 -0.95000  8 v  1
```

```
x <- read.csv("../Data/data.csv", row.names = 1)
save(x, file = "../Data/data.rda")
rm(x)
load("../Data/data.rda")
x[1:3, ]
```

```
##           A  B C  D
## 1 -0.1533 10 x 10
## 2 -0.1387  3 n  9
## 3 -0.4332  2 f  8
```

String manipulation (1)

```
paste("abc", "def", sep = "-")
```

```
## [1] "abc-def"
```

```
paste0("abc", "def")
```

```
## [1] "abcdef"
```

String manipulation (2)

```
month.name[1:4]
```

```
## [1] "January" "February" "March"    "April"
```

```
grep("Feb", month.name)
```

```
## [1] 2
```

```
grep("Feb", month.name, value = TRUE)
```

```
## [1] "February"
```

```
grepl("Feb", month.name)
```

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

```
## [12] FALSE
```

String manipulation (3)

```
month.name[1]
```

```
## [1] "January"
```

```
length(month.name[1])
```

```
## [1] 1
```

```
nchar(month.name[1])
```

```
## [1] 7
```


String manipulation (4)

```
strsplit("abc-def", "-")
```

```
## [[1]]
```

```
## [1] "abc" "def"
```

Comparing and matching (1)

```
set.seed(1)
x <- sample(letters[1:10], 6)
y <- sample(letters[1:10], 6)
x

## [1] "c" "d" "e" "g" "b" "h"

y

## [1] "j" "f" "i" "a" "b" "g"
```

Comparing and matching (2)

```
intersect(x, y)
```

```
## [1] "g" "b"
```

```
setdiff(x, y)
```

```
## [1] "c" "d" "e" "h"
```

```
union(x, y)
```

```
## [1] "c" "d" "e" "g" "b" "h" "j" "f" "i" "a"
```

Comparing and matching (3)

```
x %in% y
```

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

```
x == y
```

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

```
match(x, y)
```

```
## [1] NA NA NA  6  5 NA
```

Generating data (1)

```
seq(1, 7, 3)
```

```
## [1] 1 4 7
```

```
rep(1:2, 2)
```

```
## [1] 1 2 1 2
```

```
rep(1:2, each = 2)
```

```
## [1] 1 1 2 2
```

Generating data (2)

```
runif(5)
```

```
## [1] 0.6870 0.3841 0.7698 0.4977 0.7176
```

```
rnorm(5)
```

```
## [1] 2.4047 0.7636 -0.7990 -1.1477 -0.2895
```

About the data

```
table(sample(letters, 100, replace = TRUE))
```

```
##
```

```
## 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  
## 2 2 4 4 2 2 4 2 6 4 5 7 9 3 1 3 5 3 5 5 6 4 5 2 2 3
```

```
summary(rnorm(100))
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.  
## -1.6800 -0.8280 -0.0081 -0.0089  0.6090  2.6600
```

```
head(x)
```

```
## [1] "c" "d" "e" "g" "b" "h"
```

```
tail(x)
```

```
## [1] "c" "d" "e" "g" "b" "h"
```

```
M <- matrix(rnorm(1000), ncol = 4)
head(M)
```

```
##           [,1]      [,2]      [,3]      [,4]
## [1,]  0.7796 -0.3399 -1.44689 -0.1658
## [2,]  0.7132  0.6063  1.01951  0.5571
## [3,] -0.5429  1.3411  1.17855  1.4443
## [4,]  0.8858  0.7673 -0.01026  0.9014
## [5,] -0.3486  0.1937  0.26862 -0.2220
## [6,] -1.0081  1.1406  1.34203  0.1062
```


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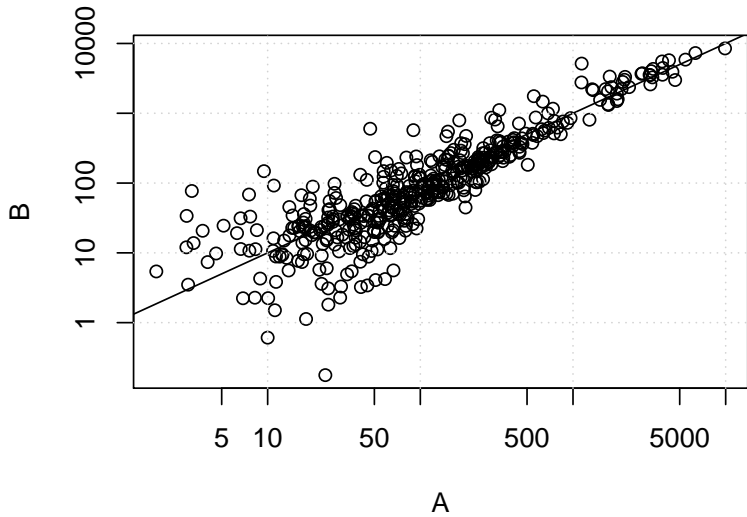
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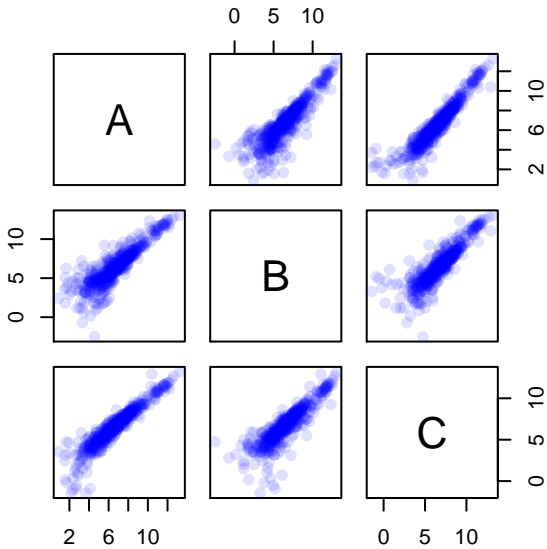
- ▶ Scatterplots with `plot`
- ▶ Boxplots with `boxplot`
- ▶ Barplots with `barplot`
- ▶ Histograms with `hist`
- ▶ `smoothScatter`

```
plot(exprs(sample.ExpressionSet[, 1]),  
      exprs(sample.ExpressionSet[, 2]),  
      log = "xy",  
      xlab = sampleNames(sample.ExpressionSet)[1],  
      ylab = sampleNames(sample.ExpressionSet)[2])  
abline(0, 1)  
grid()
```

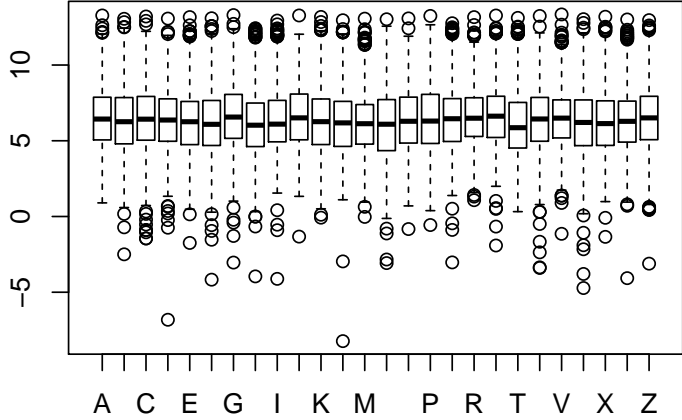


To create subplots, one can use `par(mfrow = c(2,2))`, `layout`, or (for scatterplots)

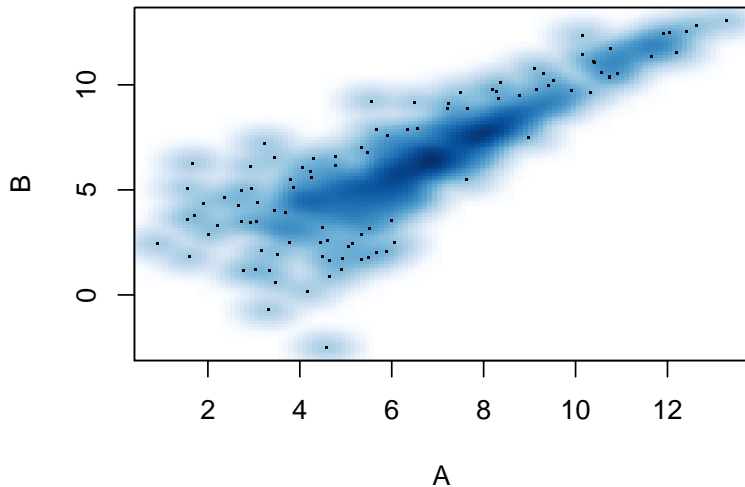
```
pairs(log2(exprs(sample.ExpressionSet)[, 1:4])),  
      pch = 19,  
      col = "#0000FF20")
```



```
boxplot(log2(exprs(sample.ExpressionSet)))
```




```
smoothScatter(log2(exprs(sample.ExpressionSet)[, 1:2]))
```



We have not covered lattice and ggplot2.

References

- ▶ <http://gallery.r-enthusiasts.com/allgraph.php>
- ▶ R Graphics manual:
http://rgm3.lab.nig.ac.jp/RGM/r_image_list
- ▶ <http://www.cookbook-r.com/Graphs/> (ggplot2)

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Useful functions

Plotting

Programming

Packages

Flow control

```
for (var in seq) expr  
while (cond) expr  
repeat expr break
```

```
for (i in 1:4) {  
  ## bad  
  print(i^2)  
}
```

```
## [1] 1  
## [1] 4  
## [1] 9  
## [1] 16
```

```
(1:4)^2  ## good
```

```
## [1] 1 4 9 16
```

The `apply` family and friends

- ▶ Applies a function to each element of an input, being a list or a vector (`sapply`, `lapply`), a matrix or a data frame (`apply`) or an environment (`eapply`).
- ▶ Same functionality than an explicit `for` loop, but often more elegant, function-centric, **not** faster.

```
M <- matrix(1:9, ncol = 3)
```

```
M
```

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

```
apply(M, 1, max)
```

```
## [1] 7 8 9
```

```
apply(M, 2, max)
```

```
## [1] 3 6 9
```

```
2
```

```
## [1] 2
```

```
sapply(month.name[1:2], paste0, "_2012")
```

```
##           January           February  
## "January_2012" "February_2012"
```

```
lapply(month.name[1:2], paste0, "_2012")
```

```
## [[1]]  
## [1] "January_2012"  
##  
## [[2]]  
## [1] "February_2012"
```



```
mean(rnorm(100))
```

```
## [1] 0.01442
```

```
replicate(3, mean(rnorm(100)))
```

```
## [1] 0.07269 0.05121 -0.18742
```

```
replicate(2, rnorm(3))
```

```
##           [,1]      [,2]
```

```
## [1,] -1.5004 -0.2154
```

```
## [2,] 1.0644 -1.3324
```

```
## [3,] 0.5066 1.6416
```

Conditionals

```
if (cond) expr1 else expr2  
ifelse(cond, expr1, expr2)  
switch
```

```
x <- 2
if (x > 0) {
  ## bad
  log2(x)
} else {
  log2(-x)
}

## [1] 1

log2(abs(x))  ## better

## [1] 1
```

Exception handling

`try(exprs)` will either return the value of the expression `expr`, or an object of class `try-error`.

`tryCatch` provides a more configurable mechanism for condition handling and error recovery.

Writing functions

```
myFun <- function(param1, param2, ...) {  
  ## function body  
  ## acting on copies of the params  
  ans <- param1 + param2  
  return(ans)  
}
```

Function facts

- ▶ Single return value.
- ▶ To return multiple items, use a list or a proper object (see OO programming).
- ▶ The return value is either the last statement, or explicit return using `return` (can be called from anywhere in a function)

Function facts (cont.)

- Functions act on a pass-by-copy semantic.

```
x <- 1
f <- function(x) {
  x <- x + 10
  x
}
f(x)
## [1] 11

x
## [1] 1
```

Function facts (cont.)

- Functions live/act in their own environment and have access to *global* variables.

```
x <- 1
f <- function() {
  x <- x + 10
  x
}
f()
## [1] 11

x
## [1] 1
```


Anonymous function

```
M <- matrix(rnorm(50), ncol = 5)
M[sample(50, 10)] <- NA
sum(is.na(M))

## [1] 10

apply(M, 1, function(x) sum(is.na(x)))

## [1] 1 2 2 0 1 1 1 1 0 1

apply(M, 2, function(x) sum(is.na(x)))

## [1] 3 1 0 3 3
```

Plan

Introduction

Data types and structures

- Basic data types

- Higher order objects

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Packages

- ▶ Primary mechanism to distribute R software is via packages.
- ▶ Packages are installed in libraries (directories) on your hard disk, and they are loaded with the `library` function.
- ▶ There are software, data and annotation packages.
- ▶ The Comprehensive R Archive Network (CRAN) is the main package repository. It provides an automatic build framework for package authors.
- ▶ The Bioconductor project manages its own CRAN-style repository.
- ▶ R-forge – <https://r-forge.r-project.org/>

Package installation

- ▶ From within R , using `install.packages` - takes care of dependencies.
- ▶ Update all installed packages with `update.packages`.
- ▶ For Bioconductor packages, use `biocLite`:

```
source("http://www.bioconductor.org/biocLite.R")  
## or, if you have already done so in the past  
library("BiocInstaller")  
biocLite("packageName")
```

Getting information about packages

- ▶ CRAN/Bioconductor/R-forge web pages
- ▶ Documentation

```
help(package = "Biobase")
```

- ▶ Vignettes (mandatory for Bioconductor packages)

```
vignette(package = "Biobase")
```

```
vignette("Bioconductor", package = "Biobase")
```

- ▶ Demos

```
demo("lattice", package = "lattice")
```

```
packageDescription("Biobase")
```

```
## Package: Biobase
## Title: Biobase: Base functions for Bioconductor
## Version: 2.21.3
## Author: R. Gentleman, V. Carey, M. Morgan, S. Falcon
## Description: Functions that are needed by many other packages or
##             which replace R functions.
## Suggests: tools, tkWidgets, ALL
## Depends: R (>= 2.10), BiocGenerics (>= 0.3.2), utils
## Imports: methods, BiocGenerics
## Maintainer: Bioconductor Package Maintainer
##             <maintainer@bioconductor.org>
## License: Artistic-2.0
## Collate: tools.R strings.R environment.R vignettes.R packages.R
##             .....
## LazyLoad: yes
## biocViews: Infrastructure, Bioinformatics
## Packaged: 2013-05-30 02:26:59 UTC; biocbuild
## Built: R 3.1.0; x86_64-unknown-linux-gnu; 2013-06-04 17:08:04 UTC;
##             unix
##
## -- File: /home/lgatto/R/x86_64-unknown-linux-gnu-library/3.1/Biobase/Meta/pa
```

Package versions

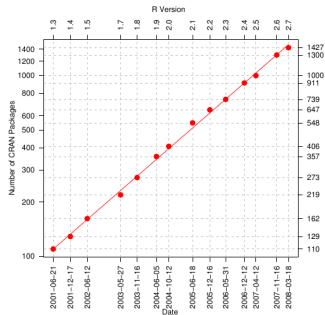
- ▶ New Bioconductor releases appear twice a year. Bioconductor versions are tied to R versions.
- ▶ Stable packages versions are $x.y.z$ where $x \geq 1$ and y is even
- ▶ Devel packages have z odd.
- ▶ New (devel) packages have $0.y.z$ (y odd); if $y == 99$, then the package will become $1.0.0$ in the next release.

Bioconductor 636 reviewed
packages

CRAN 3889 packages

R-forge 1313 projects

(19th June 2012)



Finding packages

- ▶ BiocViews – <http://bioconductor.org/packages/release/BiocViews.html>.
- ▶ CRAN Task Views – <http://cran.r-project.org/web/views/>.
- ▶ sos to search inside contributed R packages.

References

- ▶ W. N. Venables, D. M. Smith and the R Development Core Team, An Introduction to R (get it with `help.start()`)
- ▶ R. Gentleman, R Programming for Bioinformatics, CRC Press, 2008

```
toLatex(sessionInfo())
```

- ▶ R Under development (unstable) (2013-04-05 r62500), x86_64-unknown-linux-gnu
- ▶ Locale: LC_CTYPE=en_GB.UTF-8, LC_NUMERIC=C, LC_TIME=en_GB.UTF-8, LC_COLLATE=en_GB.UTF-8, LC_MONETARY=en_GB.UTF-8, LC_MESSAGES=en_GB.UTF-8, LC_PAPER=C, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_GB.UTF-8, LC_IDENTIFICATION=C
- ▶ Base packages: base, datasets, graphics, grDevices, methods, parallel, stats, utils
- ▶ Other packages: Biobase 2.21.3, BiocGenerics 0.7.2, knitr 1.2
- ▶ Loaded via a namespace (and not attached): digest 0.6.3, evaluate 0.4.3, formatR 0.7, stringr 0.6.2, tools 3.1.0

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- ▶ Course web page and more material:
<https://github.com/lgatto/TeachingMaterial>

Thank you for your attention