R Basics

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Plan

Plan

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"
```

Plan

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

```r
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

```r
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.

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

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

ll[[1]]

## [1] 1 2 3

ll$c(ll)

## [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 -0.15620
## 2 case -0.04061
## 3 ctrl  1.11508
## 4 ctrl  0.28386
```

```
dfr[1, ]

##   type    time
## 1 case -0.1562

dfr[1, "time"]

## [1] -0.1562

dfr$time

## [1] -0.15620 -0.04061  1.11508  0.28386
```

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"        "protocolDat
## [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`.

The assayData slot

Stored the expression data of the assay.

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

##                          A       B      C
## AFFX-MurIL2_at  192.74  85.753 176.76
## AFFX-MurIL10_at  97.14 126.196  77.92
## AFFX-MurIL4_at   45.82   8.831  33.06
## AFFX-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 feautres.

```
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
```

Plan

- 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  T

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
```

Plan

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
```

```r
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
```

```r
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)

```r
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 FAI
## [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

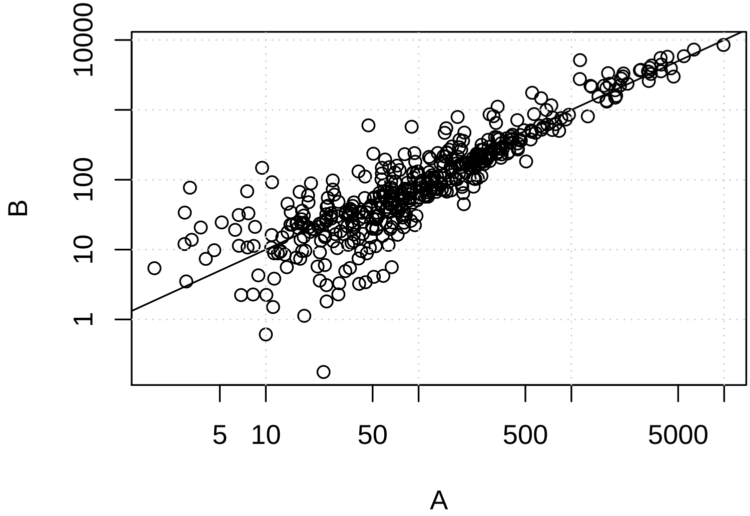
```
table(sample(letters, 100, replace = TRUE))

##
## 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
```

Plan

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

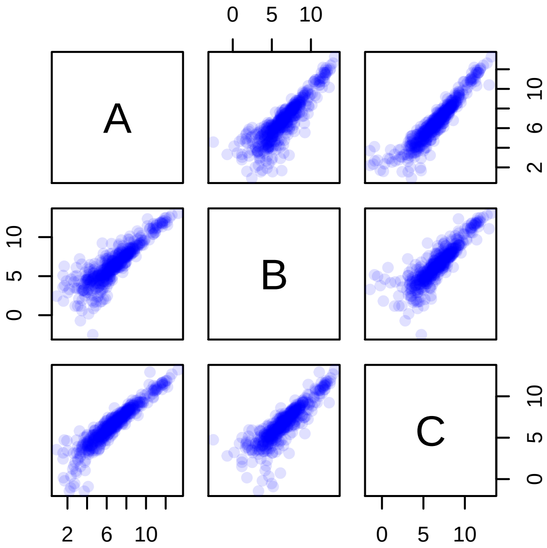
```r
plot(exprs(sample.ExpressionSet[, 1]),
     exprs(sample.ExpressionSet[, 2]),
     log = "xy",
     xlab = sampleNames(sample.ExpressionSet)[1],
     ylab = sampleNames(sample.ExpressionSet)[2])
abline(0, 1)
grid()
```



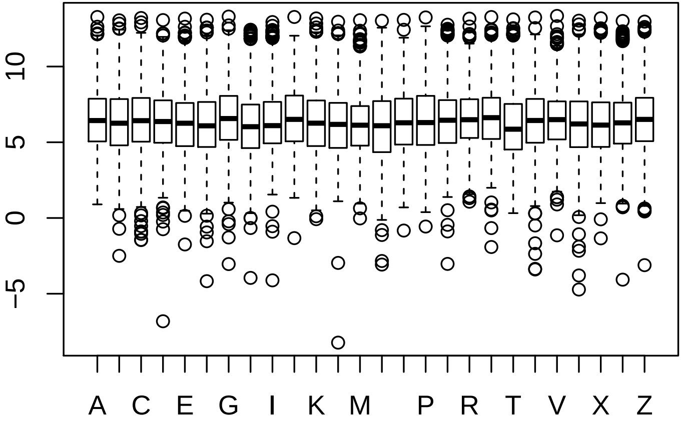
10000
100
10
1
B
5
10
50
500
5000
A

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

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

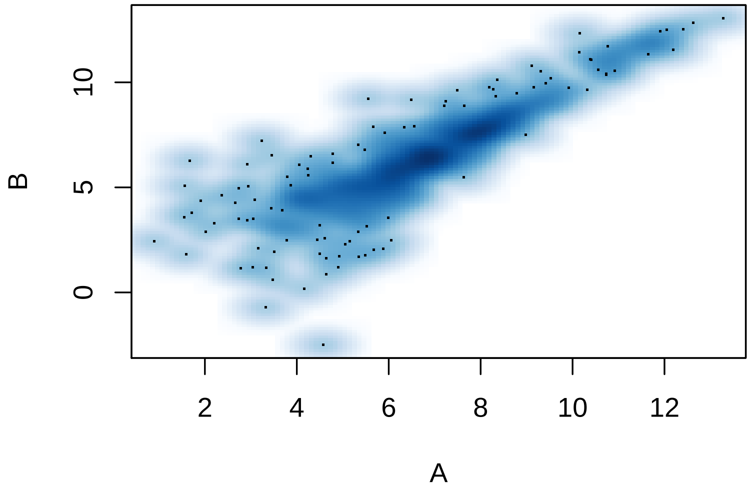

A
B
C
0
5
10
2
6
10
0
5
10
2
6
10
0
5
10
0
5
10

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



10
5
0
−5
A
C
E
G
I
K
M
P
R
T
V
X
Z

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



References

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)

Plan

Flow control

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

```r
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"
```

```r
mean(rnorm(100))

## [1] -0.1387

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

## [1]  0.02065 -0.05645 -0.04048

replicate(2, rnorm(3))

##         [,1]     [,2]
## [1,] 0.8121 -0.02083
## [2,] 1.1400 -0.66887
## [3,] 1.0946  0.96060
```

Conditionals

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

```r
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 any where 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.

```r
x <- 1
f <- function() {
    x <- x + 10
    x
}
f()
```

```
## [1] 11
```

```r
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 0 0 0 2 3 0 2 1 1

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

## [1] 1 4 2 2 1
```

Plan

- Primary mechanism to distribute `R` software is via packages.
- Packages are installed in libraries (directories) on your had 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

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

- Vignettes (mandatory for Bioconductor packages)

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

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

- Demos

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

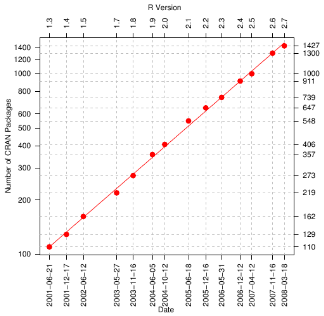
```
packageDescription("Biobase")

## Package: Biobase
## Title: Biobase: Base functions for Bioconductor
## Version: 2.21.0
## 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: 2013-04-04 04:26:03 UTC; biocbuild
## Built: R 3.1.0; x86_64-unknown-linux-gnu; 2013-04-11 01:21:26 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` >= 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 2.21.0, 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

Thank you for your attention