R Basics

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CSAMA – 23^{th} June 2014

Plan

Introduction

Data types and structures
- Basic data types
- Higher order objects

Manipulating data
- Subsetting

Useful functions

Plotting

Programming

Packages

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

```r
ls()
```

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

```r
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"
```

```r
typeof(1)
```

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

```r
mode(1L)
```

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

```r
typeof(1L)
```

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

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

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

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

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

```r
mode(TRUE)
```

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

```r
typeof(FALSE)
```

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

```r
## 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?

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

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

## 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
```

```r
x <- 1:12
class(x)
```

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

```r
dim(x)
```

```
## NULL
```

```r
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
```

```r
class(x)
```

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

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
```

Lists

are ordered collections of elements that can be arbitrary R objects.

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

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

ll[1] ## a list of length 1

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

ll[[1]] ## or ll$a - first element

## [1] 1 2 3
```

```
ll

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

ll$f(ll)

## [1] 2
```

Data.frames

are 2-dimensional `lists` (with elements of same length!).

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

##   type    time
## 1 case  0.7838
## 2 case -0.6804
## 3 ctrl -0.6088
## 4 ctrl  2.2822
```

```r
dfr[1,]
```

```
##   type   time
## 1 case 0.7838
```

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

```
## [1] 0.7838
```

```r
dfr$time
```

```
## [1]  0.7838 -0.6804 -0.6088  2.2822
```

Environments

are unordered sets 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"
```

```r
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
```

Factors

for categorical data

```
sample.ExpressionSet$type

##  [1] Control Case    Control Case    Case
##  [6] Control Case    Case    Case    Control
## [11] Case    Control Case    Case    Case
## [16] Control Case    Control Case    Case
## [21] Control Control Control Control Case
## [26] Case
## Levels: Case Control
```

Data types summary

	1 dim	2 dims	n dims
same type	`vector`	`matrix`	`array`
diff types	`list`	`data.frame`*	`list`

(*elements of same length)

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"
## [3] "phenoData"         "featureData"
## [5] "annotation"        "protocolData"
## [7] ".__classVersion__"
```

```
?ExpressionSet
```

assayData expression values in identical sized matrices.

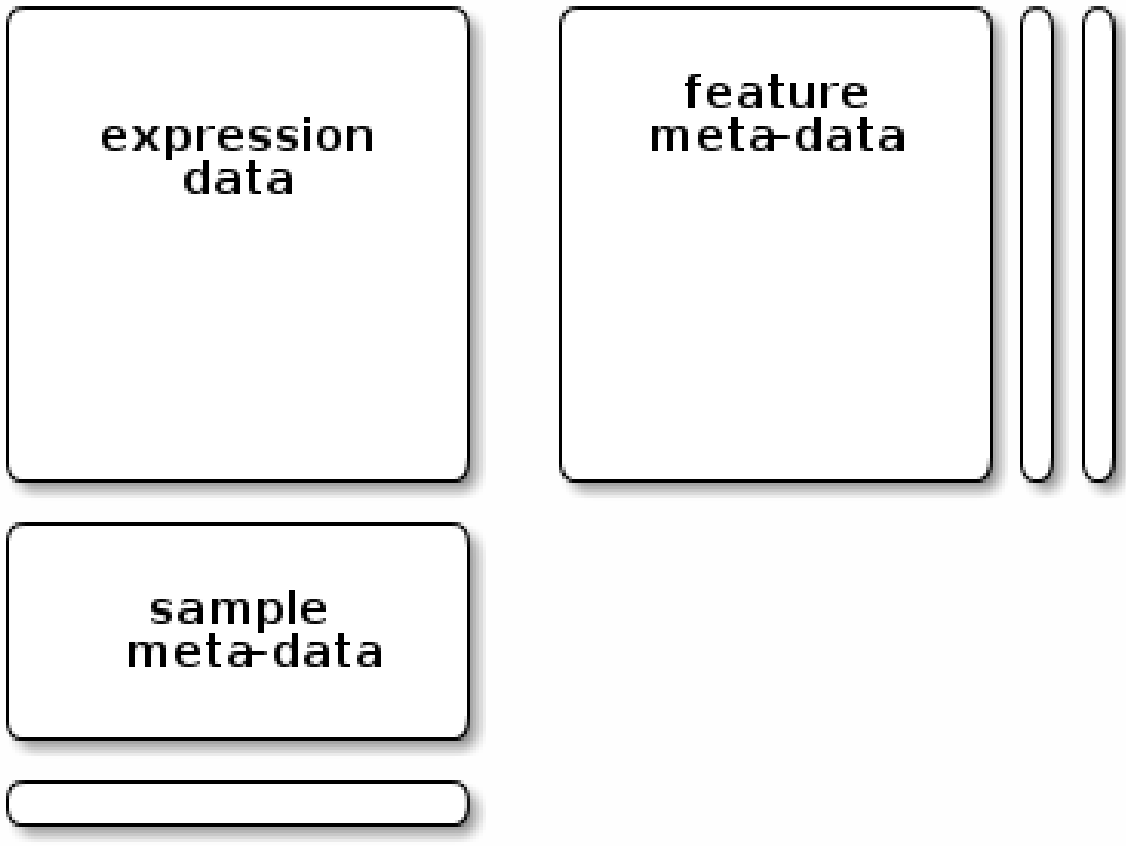
phenoData sample annotation in `AnnotatedDataFrame`.

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
## 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
```

`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] ?
```

Assignments with positive indices

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

```
x[1:6]
```

```
## [1]   1  20   3 400 500   6
```

Subsetting with negative indices

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

Subsetting with negative indices

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

```
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
##  [8]  TRUE  TRUE  TRUE

x[x > 5]

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

Subsetting with logical predicates

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

Subsetting with logical predicates

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

```
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[1, ] ## row -> vector (or drop = FALSE)

## [1]  1  4  7 10

M[, 1] ## column -> vector (or drop = FALSE)

## [1] 1 2 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, but of length 1

## $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`, HTS data, MS data, ...)

```
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)

```
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
##  [8] FALSE FALSE FALSE FALSE 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"
```

String manipulation (4)

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

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

```
strsplit(c("abc-def", "ghi-jkl"), "-")

## [[1]]
## [1] "abc" "def"
##
## [[2]]
## [1] "ghi" "jkl"
```

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
## 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
## z
## 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"
```

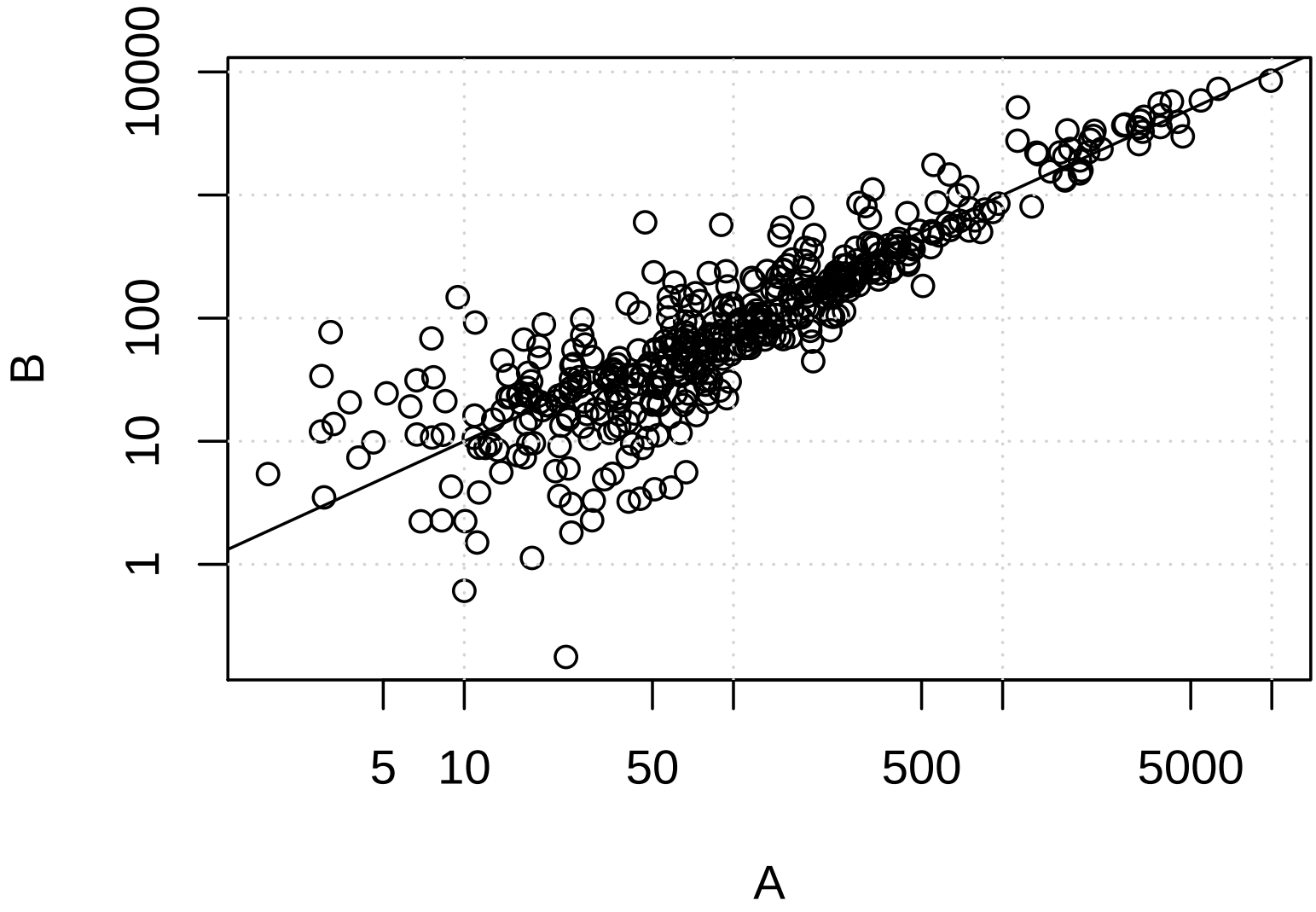
```r
M <- matrix(rnorm(1000), ncol=4)
head(M)
```

```
##          [,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

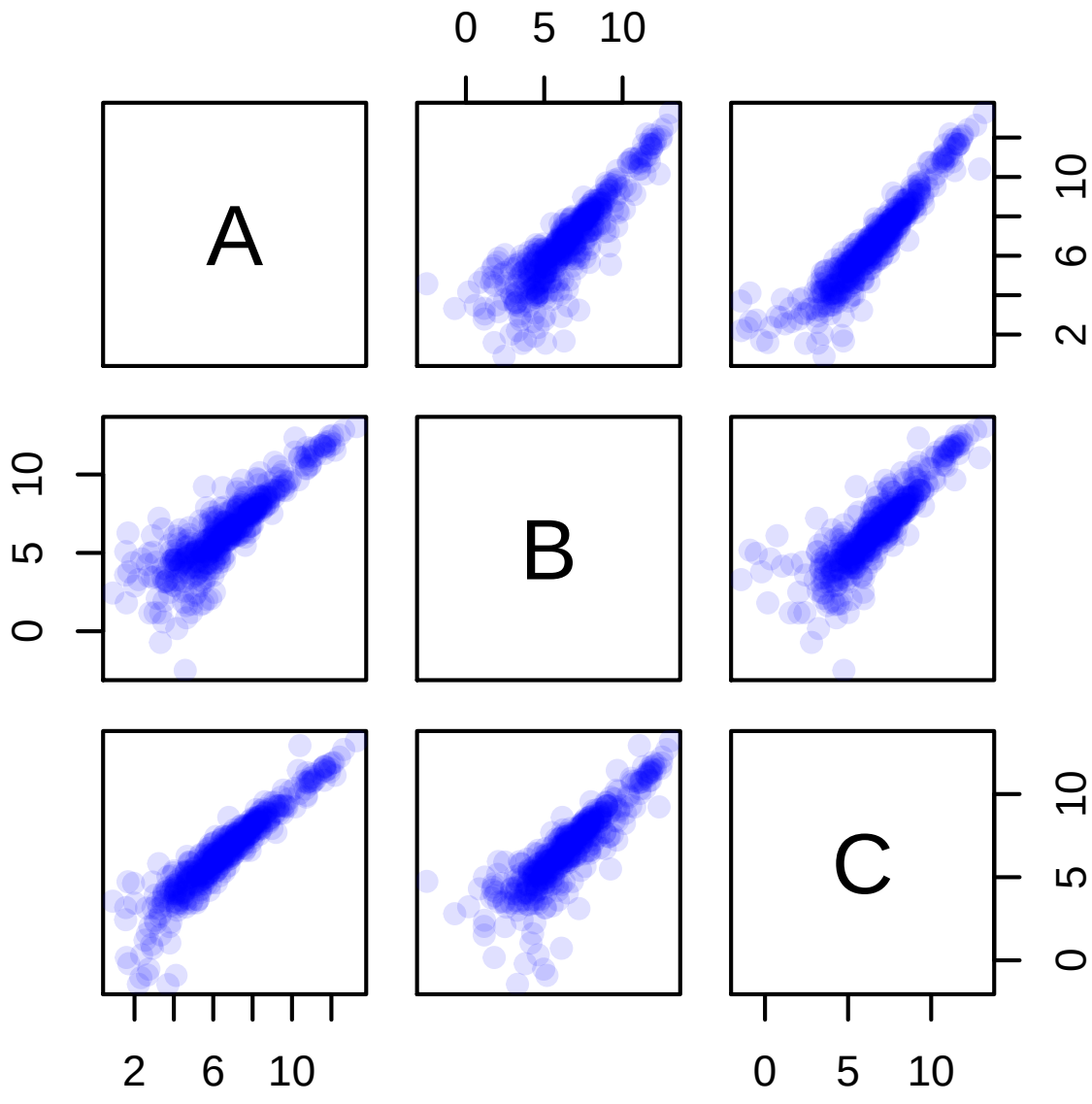
- Scatterplots with `plot`
- Boxplots with `boxplot`
- Barplots with `barplot`
- Histograms with `hist`
- `smoothScatter`

```
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()
```

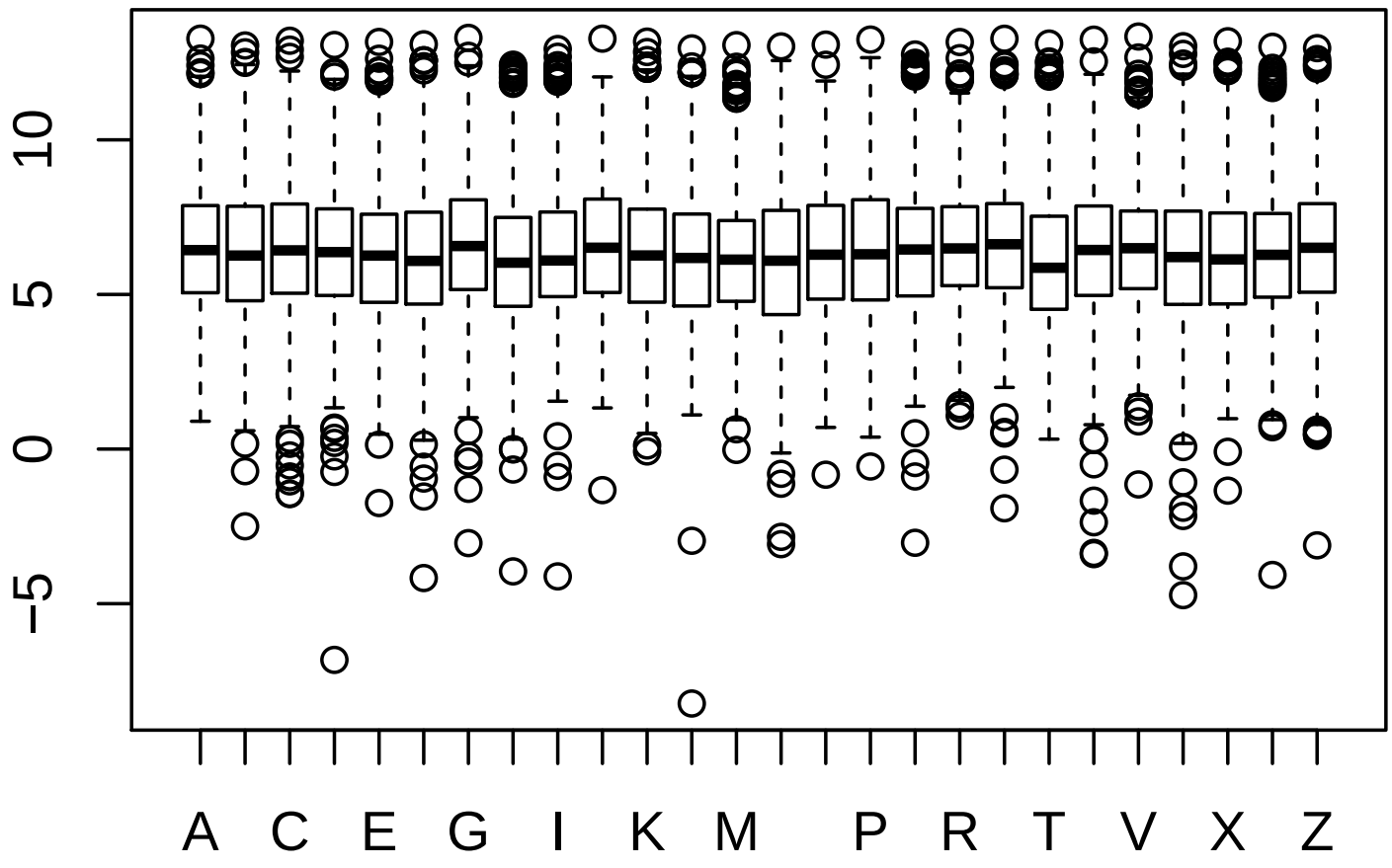

B
10000
100
10
1
5
10
50
500
5000
A

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

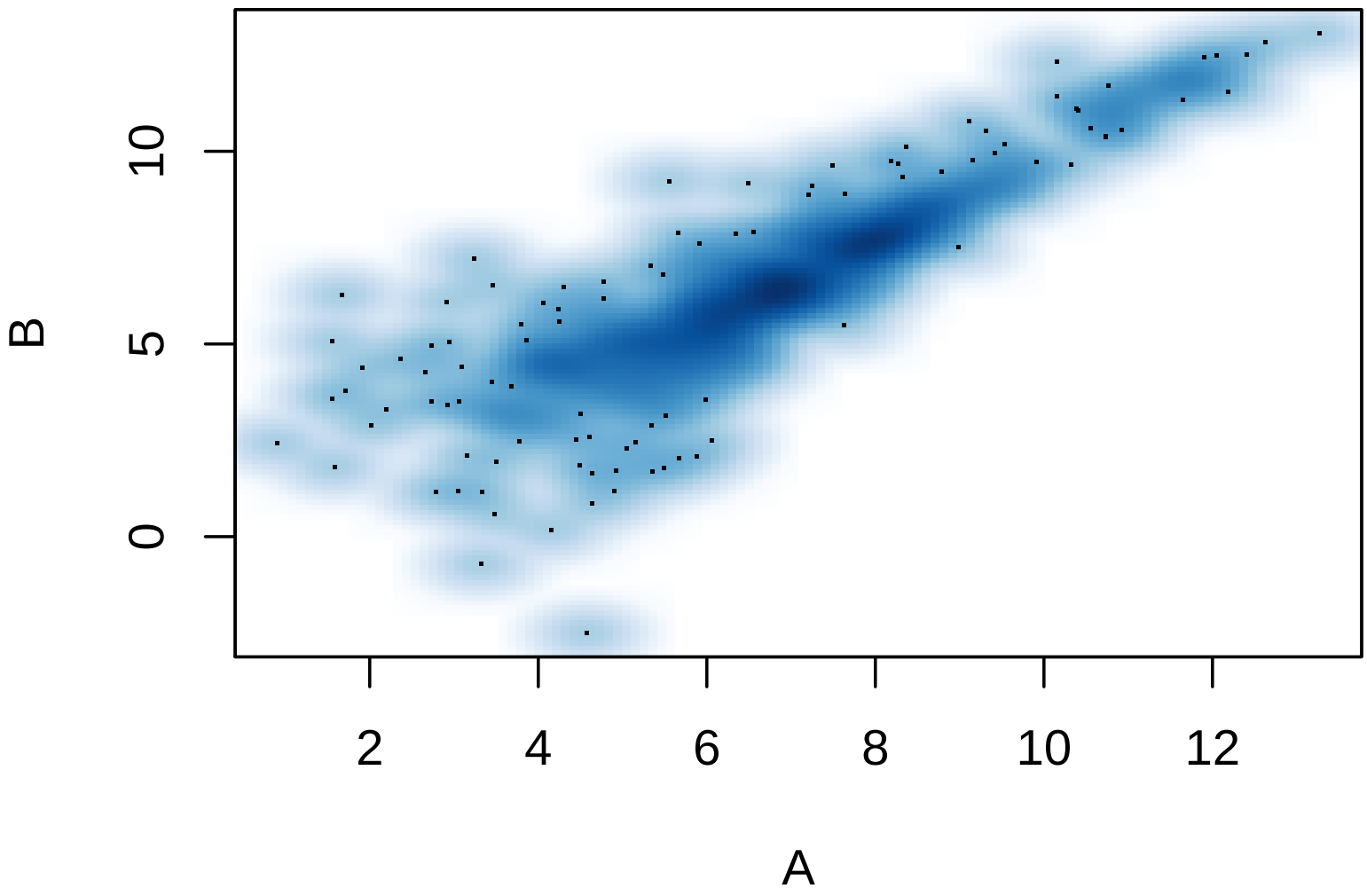
```
pairs(log2(exprs(sample.ExpressionSet)[, 1:4]),
      pch = 19,
      col = "#0000FF20")
```


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

```
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)
- *ggplot2: Elegant Graphics for Data Analysis*, Hadley Wickham (2009)
- *Lattice: Multivariate Data Visualization with R*, Deepayan Sarkar (2008)

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.

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

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

```r
apply(M, 1, sum) ## better rowSums
```

```
## [1] 12 15 18
```

```r
apply(M, 2, sum) ## better colSums
```

```
## [1]  6 15 24
```

```r
2
```

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

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

```
## [1] -0.007927
```

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

```
## [1] -0.1797  0.1277 -0.1224
```

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

```
##         [,1]    [,2]
## [1,]  1.0899  0.2212
## [2,] -0.2316 -0.1071
## [3,] -1.0130  0.4857
```

Conditionals

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

```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 define your own `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.

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

## [1] 11

x

## [1] 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

```
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: 2.25.0
## 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, RUnit, golubEsets
## Depends: R (>= 2.10), BiocGenerics (>= 0.3.2), utils
## Imports: methods
## 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
## Packaged: 2014-04-12 03:49:35 UTC; biocbuild
## Built: R 3.2.0; x86_64-unknown-linux-gnu; 2014-04-15 00:32:48 UTC;
##        unix
##
## -- File: /home/lgatto/R/x86_64-unknown-linux-gnu-library/3.2/Biobase/Meta/pa
```

Package versions

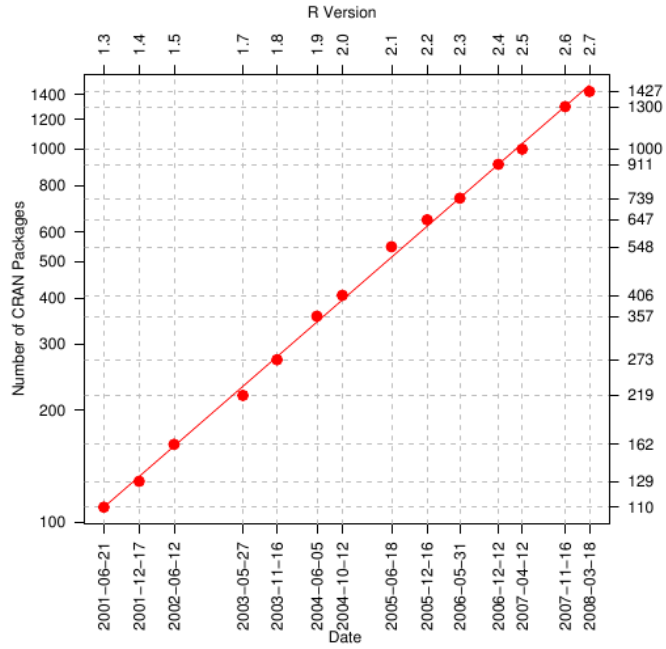
- New Bioconductor releases appear twice a year. Bioconductor versions are **tied** to `R` versions.
- Stable packages versions are `x.y.z` where `x` $>=$ 1 and `y` is even
- Devel packages have `y` odd.

Bioconductor 636 reviewed packages

CRAN 3889 packages

R-forge 1313 projects

(19^{th} 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.

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

- R Under development (unstable) (2014-04-10 r65396), 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=en_GB.UTF-8, 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 2.25.0, BiocGenerics 0.11.2, knitr 1.6
- Loaded via a namespace (and not attached): evaluate 0.5.5, formatR 0.10, stringr 0.6.2, tools 3.2.0

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

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

Thank you for your attention