> a<-c(1,1); b <-c(4,5)

> sqrt(sum((a-b)^2)

+ (sum((a-b)^2)

+ a<-c(1,1); b <-c(4,5)

Error: unexpected symbol in:

"(sum((a-b)^2)

a"

> (sum((a-b)^2)

+ a<-c(1,1); b <-c(4,5)

Error: unexpected symbol in:

"(sum((a-b)^2)

a"

> (sum((a-b)^2)

+ sum((a-b)^2)

Error: unexpected symbol in:

"(sum((a-b)^2)

sum"

> sum((a-b)^2)

[1] 25

> sqrt(sum((a-b)^2))

[1] 5

> a<-c(1,1,6); b <-c(4,5,1)

> sqrt(sum((a-b)^2))

[1] 7.071068

> source("http://www.bioconductor.org/biocLite.R")

probando la URL 'https://bioconductor.org/packages/3.5/bioc/bin/macosx/el-capitan/contrib/3.4/BiocInstaller\_1.26.1.tgz'

Content type 'application/x-gzip' length 57409 bytes (56 KB)

==================================================

downloaded 56 KB

The downloaded binary packages are in

/var/folders/y0/mlwc6mk545b3r42y8x0cbz380000gn/T//Rtmpf9oqky/downloaded\_packages

Bioconductor version 3.5 (BiocInstaller 1.26.1), ?biocLite for help

> biocLite()

BioC\_mirror: https://bioconductor.org

Using Bioconductor 3.5 (BiocInstaller 1.26.1), R 3.4.1 (2017-06-30).

Installing package(s) ‘Biobase’, ‘IRanges’, ‘AnnotationDbi’

also installing the dependencies ‘bit’, ‘bit64’, ‘blob’, ‘memoise’, ‘BiocGenerics’, ‘S4Vectors’, ‘DBI’, ‘RSQLite’

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/bit\_1.1-12.tgz'

Content type 'application/x-gzip' length 240695 bytes (235 KB)

==================================================

downloaded 235 KB

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/bit64\_0.9-7.tgz'

Content type 'application/x-gzip' length 534016 bytes (521 KB)

==================================================

downloaded 521 KB

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/blob\_1.1.0.tgz'

Content type 'application/x-gzip' length 12359 bytes (12 KB)

==================================================

downloaded 12 KB

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/memoise\_1.1.0.tgz'

Content type 'application/x-gzip' length 27154 bytes (26 KB)

==================================================

downloaded 26 KB

probando la URL 'https://bioconductor.org/packages/3.5/bioc/bin/macosx/el-capitan/contrib/3.4/BiocGenerics\_0.22.1.tgz'

Content type 'application/x-gzip' length 570057 bytes (556 KB)

==================================================

downloaded 556 KB

probando la URL 'https://bioconductor.org/packages/3.5/bioc/bin/macosx/el-capitan/contrib/3.4/S4Vectors\_0.14.7.tgz'

Content type 'application/x-gzip' length 1201150 bytes (1.1 MB)

==================================================

downloaded 1.1 MB

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/DBI\_0.7.tgz'

Content type 'application/x-gzip' length 744832 bytes (727 KB)

==================================================

downloaded 727 KB

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/RSQLite\_2.0.tgz'

Content type 'application/x-gzip' length 3241881 bytes (3.1 MB)

==================================================

downloaded 3.1 MB

probando la URL 'https://bioconductor.org/packages/3.5/bioc/bin/macosx/el-capitan/contrib/3.4/Biobase\_2.36.2.tgz'

Content type 'application/x-gzip' length 2159398 bytes (2.1 MB)

==================================================

downloaded 2.1 MB

probando la URL 'https://bioconductor.org/packages/3.5/bioc/bin/macosx/el-capitan/contrib/3.4/IRanges\_2.10.5.tgz'

Content type 'application/x-gzip' length 1475605 bytes (1.4 MB)

==================================================

downloaded 1.4 MB

probando la URL 'https://bioconductor.org/packages/3.5/bioc/bin/macosx/el-capitan/contrib/3.4/AnnotationDbi\_1.38.2.tgz'

Content type 'application/x-gzip' length 4701596 bytes (4.5 MB)

==================================================

downloaded 4.5 MB

The downloaded binary packages are in

/var/folders/y0/mlwc6mk545b3r42y8x0cbz380000gn/T//Rtmpf9oqky/downloaded\_packages

Old packages: 'boot', 'data.table', 'FactoMineR', 'Matrix', 'mgcv', 'Rcpp', 'tidyselect'

Update all/some/none? [a/s/n]:

a

There is a binary version available but the source version is later:

binary source needs\_compilation

data.table 1.10.4-1 1.10.4-2 TRUE

Do you want to install from sources the package which needs compilation?

y/n: y

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/boot\_1.3-20.tgz'

Content type 'application/x-gzip' length 623781 bytes (609 KB)

==================================================

downloaded 609 KB

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/FactoMineR\_1.38.tgz'

Content type 'application/x-gzip' length 2968724 bytes (2.8 MB)

==================================================

downloaded 2.8 MB

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/Matrix\_1.2-11.tgz'

Content type 'application/x-gzip' length 2981428 bytes (2.8 MB)

==================================================

downloaded 2.8 MB

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/mgcv\_1.8-22.tgz'

Content type 'application/x-gzip' length 2880046 bytes (2.7 MB)

==================================================

downloaded 2.7 MB

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/Rcpp\_0.12.13.tgz'

Content type 'application/x-gzip' length 4336927 bytes (4.1 MB)

==================================================

downloaded 4.1 MB

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/tidyselect\_0.2.2.tgz'

Content type 'application/x-gzip' length 290159 bytes (283 KB)

==================================================

downloaded 283 KB

The downloaded binary packages are in

/var/folders/y0/mlwc6mk545b3r42y8x0cbz380000gn/T//Rtmpf9oqky/downloaded\_packages

installing the source package ‘data.table’

probando la URL 'https://cran.rstudio.com/src/contrib/data.table\_1.10.4-2.tar.gz'

Content type 'application/x-gzip' length 3071579 bytes (2.9 MB)

==================================================

downloaded 2.9 MB

\* installing \*source\* package ‘data.table’ ...

\*\* package ‘data.table’ successfully unpacked and MD5 sums checked

\*\* libs

Agreeing to the Xcode/iOS license requires admin privileges, please run “sudo xcodebuild -license” and then retry this command.

ERROR: compilation failed for package ‘data.table’

\* removing ‘/Library/Frameworks/R.framework/Versions/3.4/Resources/library/data.table’

\* restoring previous ‘/Library/Frameworks/R.framework/Versions/3.4/Resources/library/data.table’

The downloaded source packages are in

‘/private/var/folders/y0/mlwc6mk545b3r42y8x0cbz380000gn/T/Rtmpf9oqky/downloaded\_packages’

Warning message:

In install.packages(update[instlib == l, "Package"], l, repos = repos, :

installation of package ‘data.table’ had non-zero exit status

> biocLite("multtest")

BioC\_mirror: https://bioconductor.org

Using Bioconductor 3.5 (BiocInstaller 1.26.1), R 3.4.1 (2017-06-30).

Installing package(s) ‘multtest’

probando la URL 'https://bioconductor.org/packages/3.5/bioc/bin/macosx/el-capitan/contrib/3.4/multtest\_2.32.0.tgz'

Content type 'application/x-gzip' length 659647 bytes (644 KB)

==================================================

downloaded 644 KB

The downloaded binary packages are in

/var/folders/y0/mlwc6mk545b3r42y8x0cbz380000gn/T//Rtmpf9oqky/downloaded\_packages

Old packages: 'data.table'

Update all/some/none? [a/s/n]:

a

There is a binary version available but the source version is later:

binary source needs\_compilation

data.table 1.10.4-1 1.10.4-2 TRUE

Do you want to install from sources the package which needs compilation?

y/n: y

installing the source package ‘data.table’

probando la URL 'https://cran.rstudio.com/src/contrib/data.table\_1.10.4-2.tar.gz'

Content type 'application/x-gzip' length 3071579 bytes (2.9 MB)

==================================================

downloaded 2.9 MB

\* installing \*source\* package ‘data.table’ ...

\*\* package ‘data.table’ successfully unpacked and MD5 sums checked

\*\* libs

Agreeing to the Xcode/iOS license requires admin privileges, please run “sudo xcodebuild -license” and then retry this command.

ERROR: compilation failed for package ‘data.table’

\* removing ‘/Library/Frameworks/R.framework/Versions/3.4/Resources/library/data.table’

\* restoring previous ‘/Library/Frameworks/R.framework/Versions/3.4/Resources/library/data.table’

The downloaded source packages are in

‘/private/var/folders/y0/mlwc6mk545b3r42y8x0cbz380000gn/T/Rtmpf9oqky/downloaded\_packages’

Warning message:

In install.packages(update[instlib == l, "Package"], l, repos = repos, :

installation of package ‘data.table’ had non-zero exit status

> library(multtest);

Loading required package: BiocGenerics

Loading required package: parallel

Attaching package: ‘BiocGenerics’

The following objects are masked from ‘package:parallel’:

clusterApply, clusterApplyLB, clusterCall, clusterEvalQ, clusterExport, clusterMap, parApply, parCapply,

parLapply, parLapplyLB, parRapply, parSapply, parSapplyLB

The following objects are masked from ‘package:stats’:

IQR, mad, sd, var, xtabs

The following objects are masked from ‘package:base’:

anyDuplicated, append, as.data.frame, cbind, colMeans, colnames, colSums, do.call, duplicated, eval, evalq,

Filter, Find, get, grep, grepl, intersect, is.unsorted, lapply, lengths, Map, mapply, match, mget, order, paste,

pmax, pmax.int, pmin, pmin.int, Position, rank, rbind, Reduce, rowMeans, rownames, rowSums, sapply, setdiff,

sort, table, tapply, union, unique, unsplit, which, which.max, which.min

Loading required package: Biobase

Welcome to Bioconductor

Vignettes contain introductory material; view with 'browseVignettes()'. To cite Bioconductor, see

'citation("Biobase")', and for packages 'citation("pkgname")'.

> data(golub)

> golub.gnames[1042,]

[1] "2354" "CCND3 Cyclin D3" "M92287\_at"

> View(golub)

> View(golub.gnames)

> index <- grep("Cyclin",golub.gnames[,2])

> index

[1] 85 962 1042 1195 1212 1354 1421 1553 1597 1937 2027 2240

> golub.gnames[index,2]

[1] "CCND2 Cyclin D2" "CDK2 Cyclin-dependent kinase 2"

[3] "CCND3 Cyclin D3" "CDKN1A Cyclin-dependent kinase inhibitor 1A (p21, Cip1)"

[5] "CCNH Cyclin H" "Cyclin-dependent kinase 4 (CDK4) gene"

[7] "Cyclin G2 mRNA" "Cyclin A1 mRNA"

[9] "Cyclin-selective ubiquitin carrier protein mRNA" "CDK6 Cyclin-dependent kinase 6"

[11] "Cyclin G1 mRNA" "CCNF Cyclin F"

> View(golub)

> View(golub.gnames)

> View(golub)

> View(golub.gnames)

> View(golub)

> dist.cyclin <- dist(golub[index,],method="euclidian")

> diam <- as.matrix(dist.cyclin)

> colnames(diam) <- golub.gnames[index,3]

> rownames(diam) <- colnames(diam)

> diam[1:5,1:5]

D13639\_at M68520\_at M92287\_at U09579\_at U11791\_at

D13639\_at 0.000000 8.821806 11.55349 10.056814 8.669112

M68520\_at 8.821806 0.000000 11.70156 5.931260 2.934802

M92287\_at 11.553494 11.701562 0.00000 11.991333 11.900558

U09579\_at 10.056814 5.931260 11.99133 0.000000 5.698232

U11791\_at 8.669112 2.934802 11.90056 5.698232 0.000000

> library("genefilter")

Error in library("genefilter") : there is no package called ‘genefilter’

> library("genfilter")

Error in library("genfilter") : there is no package called ‘genfilter’

> library(genefilter)

Error in library(genefilter) : there is no package called ‘genefilter’

> source("http://www.bioconductor.org/biocLite.R")

Bioconductor version 3.5 (BiocInstaller 1.26.1), ?biocLite for help

> biocLite()

BioC\_mirror: https://bioconductor.org

Using Bioconductor 3.5 (BiocInstaller 1.26.1), R 3.4.1 (2017-06-30).

Old packages: 'data.table'

Update all/some/none? [a/s/n]:

biocLite("genefilter")

Update all/some/none? [a/s/n]:

library("genefilter")

Update all/some/none? [a/s/n]:

a

There is a binary version available but the source version is later:

binary source needs\_compilation

data.table 1.10.4-1 1.10.4-2 TRUE

Do you want to install from sources the package which needs compilation?

y/n: y

installing the source package ‘data.table’

probando la URL 'https://cran.rstudio.com/src/contrib/data.table\_1.10.4-2.tar.gz'

Content type 'application/x-gzip' length 3071579 bytes (2.9 MB)

==================================================

downloaded 2.9 MB

\* installing \*source\* package ‘data.table’ ...

\*\* package ‘data.table’ successfully unpacked and MD5 sums checked

\*\* libs

Agreeing to the Xcode/iOS license requires admin privileges, please run “sudo xcodebuild -license” and then retry this command.

ERROR: compilation failed for package ‘data.table’

\* removing ‘/Library/Frameworks/R.framework/Versions/3.4/Resources/library/data.table’

\* restoring previous ‘/Library/Frameworks/R.framework/Versions/3.4/Resources/library/data.table’

The downloaded source packages are in

‘/private/var/folders/y0/mlwc6mk545b3r42y8x0cbz380000gn/T/Rtmpf9oqky/downloaded\_packages’

Warning message:

In install.packages(update[instlib == l, "Package"], l, repos = repos, :

installation of package ‘data.table’ had non-zero exit status

> library("genefilter")

Error in library("genefilter") : there is no package called ‘genefilter’

> source("http://www.bioconductor.org/biocLite.R")

Bioconductor version 3.5 (BiocInstaller 1.26.1), ?biocLite for help

> library("genefilter")

Error in library("genefilter") : there is no package called ‘genefilter’

> source("http://www.bioconductor.org/biocLite.R")

Bioconductor version 3.5 (BiocInstaller 1.26.1), ?biocLite for help

> biocLite()

BioC\_mirror: https://bioconductor.org

Using Bioconductor 3.5 (BiocInstaller 1.26.1), R 3.4.1 (2017-06-30).

Old packages: 'data.table'

Update all/some/none? [a/s/n]:

a

There is a binary version available but the source version is later:

binary source needs\_compilation

data.table 1.10.4-1 1.10.4-2 TRUE

Do you want to install from sources the package which needs compilation?

y/n: y

installing the source package ‘data.table’

probando la URL 'https://cran.rstudio.com/src/contrib/data.table\_1.10.4-2.tar.gz'

Content type 'application/x-gzip' length 3071579 bytes (2.9 MB)

==================================================

downloaded 2.9 MB

\* installing \*source\* package ‘data.table’ ...

\*\* package ‘data.table’ successfully unpacked and MD5 sums checked

\*\* libs

Agreeing to the Xcode/iOS license requires admin privileges, please run “sudo xcodebuild -license” and then retry this command.

ERROR: compilation failed for package ‘data.table’

\* removing ‘/Library/Frameworks/R.framework/Versions/3.4/Resources/library/data.table’

\* restoring previous ‘/Library/Frameworks/R.framework/Versions/3.4/Resources/library/data.table’

The downloaded source packages are in

‘/private/var/folders/y0/mlwc6mk545b3r42y8x0cbz380000gn/T/Rtmpf9oqky/downloaded\_packages’

Warning message:

In install.packages(update[instlib == l, "Package"], l, repos = repos, :

installation of package ‘data.table’ had non-zero exit status

> biocLite("genefilter")

BioC\_mirror: https://bioconductor.org

Using Bioconductor 3.5 (BiocInstaller 1.26.1), R 3.4.1 (2017-06-30).

Installing package(s) ‘genefilter’

also installing the dependencies ‘XML’, ‘xtable’, ‘RCurl’, ‘annotate’

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/XML\_3.98-1.9.tgz'

Content type 'application/x-gzip' length 1923850 bytes (1.8 MB)

==================================================

downloaded 1.8 MB

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/xtable\_1.8-2.tgz'

Content type 'application/x-gzip' length 706898 bytes (690 KB)

==================================================

downloaded 690 KB

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/RCurl\_1.95-4.8.tgz'

Content type 'application/x-gzip' length 892550 bytes (871 KB)

==================================================

downloaded 871 KB

probando la URL 'https://bioconductor.org/packages/3.5/bioc/bin/macosx/el-capitan/contrib/3.4/annotate\_1.54.0.tgz'

Content type 'application/x-gzip' length 2013676 bytes (1.9 MB)

==================================================

downloaded 1.9 MB

probando la URL 'https://bioconductor.org/packages/3.5/bioc/bin/macosx/el-capitan/contrib/3.4/genefilter\_1.58.1.tgz'

Content type 'application/x-gzip' length 1960927 bytes (1.9 MB)

==================================================

downloaded 1.9 MB

The downloaded binary packages are in

/var/folders/y0/mlwc6mk545b3r42y8x0cbz380000gn/T//Rtmpf9oqky/downloaded\_packages

Old packages: 'data.table'

Update all/some/none? [a/s/n]:

a

There is a binary version available but the source version is later:

binary source needs\_compilation

data.table 1.10.4-1 1.10.4-2 TRUE

Do you want to install from sources the package which needs compilation?

y/n: y

installing the source package ‘data.table’

probando la URL 'https://cran.rstudio.com/src/contrib/data.table\_1.10.4-2.tar.gz'

Content type 'application/x-gzip' length 3071579 bytes (2.9 MB)

==================================================

downloaded 2.9 MB

\* installing \*source\* package ‘data.table’ ...

\*\* package ‘data.table’ successfully unpacked and MD5 sums checked

\*\* libs

Agreeing to the Xcode/iOS license requires admin privileges, please run “sudo xcodebuild -license” and then retry this command.

ERROR: compilation failed for package ‘data.table’

\* removing ‘/Library/Frameworks/R.framework/Versions/3.4/Resources/library/data.table’

\* restoring previous ‘/Library/Frameworks/R.framework/Versions/3.4/Resources/library/data.table’

The downloaded source packages are in

‘/private/var/folders/y0/mlwc6mk545b3r42y8x0cbz380000gn/T/Rtmpf9oqky/downloaded\_packages’

Warning message:

In install.packages(update[instlib == l, "Package"], l, repos = repos, :

installation of package ‘data.table’ had non-zero exit status

> library("genefilter")

> closeto1389\_at <- genefinder(ALL, "1389\_at", 10, method = "euc")

Error in genefinder(ALL, "1389\_at", 10, method = "euc") :

objeto 'ALL' no encontrado

> library("ALL");

Error in library("ALL") : there is no package called ‘ALL’

> library("genefilter"); library("ALL");data(ALL)

Error in library("ALL") : there is no package called ‘ALL’

> biocLite("genefilter")

BioC\_mirror: https://bioconductor.org

Using Bioconductor 3.5 (BiocInstaller 1.26.1), R 3.4.1 (2017-06-30).

Installing package(s) ‘genefilter’

probando la URL 'https://bioconductor.org/packages/3.5/bioc/bin/macosx/el-capitan/contrib/3.4/genefilter\_1.58.1.tgz'

Content type 'application/x-gzip' length 1960927 bytes (1.9 MB)

==================================================

downloaded 1.9 MB

The downloaded binary packages are in

/var/folders/y0/mlwc6mk545b3r42y8x0cbz380000gn/T//Rtmpf9oqky/downloaded\_packages

Old packages: 'data.table'

Update all/some/none? [a/s/n]:

a

There is a binary version available but the source version is later:

binary source needs\_compilation

data.table 1.10.4-1 1.10.4-2 TRUE

Do you want to install from sources the package which needs compilation?

y/n: y

installing the source package ‘data.table’

probando la URL 'https://cran.rstudio.com/src/contrib/data.table\_1.10.4-2.tar.gz'

Content type 'application/x-gzip' length 3071579 bytes (2.9 MB)

==================================================

downloaded 2.9 MB

\* installing \*source\* package ‘data.table’ ...

\*\* package ‘data.table’ successfully unpacked and MD5 sums checked

\*\* libs

Agreeing to the Xcode/iOS license requires admin privileges, please run “sudo xcodebuild -license” and then retry this command.

ERROR: compilation failed for package ‘data.table’

\* removing ‘/Library/Frameworks/R.framework/Versions/3.4/Resources/library/data.table’

\* restoring previous ‘/Library/Frameworks/R.framework/Versions/3.4/Resources/library/data.table’

The downloaded source packages are in

‘/private/var/folders/y0/mlwc6mk545b3r42y8x0cbz380000gn/T/Rtmpf9oqky/downloaded\_packages’

Warning message:

In install.packages(update[instlib == l, "Package"], l, repos = repos, :

installation of package ‘data.table’ had non-zero exit status

> library("genefilter");

> biocLite("ALL")

BioC\_mirror: https://bioconductor.org

Using Bioconductor 3.5 (BiocInstaller 1.26.1), R 3.4.1 (2017-06-30).

Installing package(s) ‘ALL’

installing the source package ‘ALL’

probando la URL 'https://bioconductor.org/packages/3.5/data/experiment/src/contrib/ALL\_1.18.0.tar.gz'

Content type 'application/x-gzip' length 11401826 bytes (10.9 MB)

==================================================

downloaded 10.9 MB

\* installing \*source\* package ‘ALL’ ...

\*\* R

\*\* data

\*\* inst

\*\* preparing package for lazy loading

\*\* help

\*\*\* installing help indices

\*\* building package indices

\*\* installing vignettes

\*\* testing if installed package can be loaded

\* DONE (ALL)

The downloaded source packages are in

‘/private/var/folders/y0/mlwc6mk545b3r42y8x0cbz380000gn/T/Rtmpf9oqky/downloaded\_packages’

Old packages: 'data.table'

Update all/some/none? [a/s/n]:

a

There is a binary version available but the source version is later:

binary source needs\_compilation

data.table 1.10.4-1 1.10.4-2 TRUE

Do you want to install from sources the package which needs compilation?

y/n: y

installing the source package ‘data.table’

probando la URL 'https://cran.rstudio.com/src/contrib/data.table\_1.10.4-2.tar.gz'

Content type 'application/x-gzip' length 3071579 bytes (2.9 MB)

==================================================

downloaded 2.9 MB

\* installing \*source\* package ‘data.table’ ...

\*\* package ‘data.table’ successfully unpacked and MD5 sums checked

\*\* libs

Agreeing to the Xcode/iOS license requires admin privileges, please run “sudo xcodebuild -license” and then retry this command.

ERROR: compilation failed for package ‘data.table’

\* removing ‘/Library/Frameworks/R.framework/Versions/3.4/Resources/library/data.table’

\* restoring previous ‘/Library/Frameworks/R.framework/Versions/3.4/Resources/library/data.table’

The downloaded source packages are in

‘/private/var/folders/y0/mlwc6mk545b3r42y8x0cbz380000gn/T/Rtmpf9oqky/downloaded\_packages’

Warning message:

In install.packages(update[instlib == l, "Package"], l, repos = repos, :

installation of package ‘data.table’ had non-zero exit status

> library("ALL");

> closeto1389\_at <- genefinder(ALL, "1389\_at", 10, method = "euc")

Error in genefinder(ALL, "1389\_at", 10, method = "euc") :

objeto 'ALL' no encontrado

> data(ALL)

> closeto1389\_at <- genefinder(ALL, "1389\_at", 10, method = "euc")

> closeto1389\_at[[1]]$indices

[1] 2653 1096 6634 9255 6639 11402 9849 2274 8518 10736

> featureNames(ALL)[closeto1389\_at[[1]]$indices]

[1] "32629\_f\_at" "1988\_at" "36571\_at" "39168\_at" "36576\_at" "41295\_at" "39756\_g\_at" "32254\_at" "38438\_at"

[10] "40635\_at"

> str(closeto1389\_at)

List of 1

$ 1389\_at:List of 2

..$ indices: num [1:10] 2653 1096 6634 9255 6639 ...

..$ dists : num [1:10] 12.6 12.8 12.8 12.8 13 ...

> names <- list(c("g1","g2","g3","g4","g5"),c("p1","p2"))

> sl.clus.dat<- matrix(c(1,1,1,1.1,3,2,3,2.3,5,5),ncol = 2,byrow = TRUE,dimnames = names)

> sl.clus.dat

p1 p2

g1 1 1.0

g2 1 1.1

g3 3 2.0

g4 3 2.3

g5 5 5.0

> plot(sl.clus.dat,type="n", xlim=c(0,6), ylim=c(0,6))

> text(sl.clus.dat,labels=row.names(sl.clus.dat))

> print(dist(sl.clus.dat,method="euclidian"),digits=3)

g1 g2 g3 g4

g2 0.10

g3 2.24 2.19

g4 2.39 2.33 0.30

g5 5.66 5.59 3.61 3.36

> sl.out<-hclust(dist(sl.clus.dat,method="euclidian"),method="single")

> plot(sl.out)

> sl.out<-hclust(dist(rnorm(20,0,1),method="euclidian"),method="single")

> plot(sl.out)

> x <- c(rnorm(10,0,0.1),rnorm(10,3,0.5),rnorm(10,10,1.0))

Warning messages:

1: In doTryCatch(return(expr), name, parentenv, handler) :

display list redraw incomplete

2: In doTryCatch(return(expr), name, parentenv, handler) :

invalid graphics state

3: In doTryCatch(return(expr), name, parentenv, handler) :

invalid graphics state

> plot(hclust(dist(x,method="euclidian"),method="single"))

> data(golub, package="multtest")

> clusdata <- data.frame(golub[1042,],golub[2124,])

> colnames(clusdata)<-c("CCND3 Cyclin D3","Zyxin")

> gol.fac <- factor(golub.cl,levels=0:1, labels= c("ALL","AML"))

> plot(clusdata, pch=as.numeric(gol.fac))

> legend("topright",legend=c("ALL","AML"),pch=1:2)

> plot(hclust(dist(clusdata,method="euclidian"),method="single"))

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> plot(clusdata, pch=as.numeric(gol.fac))

> legend("topright",legend=c("ALL","AML"),pch=1:2)

> data <- rbind(matrix(rnorm(100,0,0.5), ncol = 2), matrix(rnorm(100,2,0.5), ncol = 2))

> cl <- kmeans(data, 2)

> cl

K-means clustering with 2 clusters of sizes 50, 50

Cluster means:

[,1] [,2]

1 2.08856996 1.9671132

2 -0.02468619 0.1409407

Clustering vector:

[1] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1

[64] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

Within cluster sum of squares by cluster:

[1] 27.91031 22.91080

(between\_SS / total\_SS = 79.3 %)

Available components:

[1] "cluster" "centers" "totss" "withinss" "tot.withinss" "betweenss" "size" "iter"

[9] "ifault"

> cl <- kmeans(data, 3)

> cl

K-means clustering with 3 clusters of sizes 31, 19, 50

Cluster means:

[,1] [,2]

1 -0.04751409 -0.2050212

2 0.01255932 0.7054050

3 2.08856996 1.9671132

Clustering vector:

[1] 1 1 2 1 1 2 1 2 2 1 1 1 1 2 1 1 1 1 2 1 1 1 1 1 1 1 2 2 1 2 2 2 1 2 2 1 2 2 2 2 1 1 2 1 1 1 1 1 2 1 3 3 3 3 3 3 3 3 3 3 3 3 3

[64] 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3

Within cluster sum of squares by cluster:

[1] 9.004170 4.099959 27.910309

(between\_SS / total\_SS = 83.3 %)

Available components:

[1] "cluster" "centers" "totss" "withinss" "tot.withinss" "betweenss" "size" "iter"

[9] "ifault"

> cl <- kmeans(data, 50)

> cl

K-means clustering with 50 clusters of sizes 2, 2, 1, 1, 1, 2, 1, 2, 1, 1, 3, 3, 1, 3, 2, 1, 2, 3, 3, 3, 2, 2, 4, 2, 2, 2, 1, 3, 1, 3, 1, 3, 1, 1, 4, 1, 2, 2, 1, 1, 1, 1, 2, 2, 2, 4, 5, 1, 2, 3

Cluster means:

[,1] [,2]

1 0.55290729 -0.15902746

2 -0.34926092 -0.02847177

3 -0.68678975 -0.36610213

4 1.99771243 0.88845338

5 -0.06738770 0.08944262

6 -0.19812229 -0.04146581

7 -0.66050548 -0.18599679

8 -0.64802381 0.61627144

9 2.65822952 1.75312336

10 0.29770181 -0.10382016

11 2.78898704 2.53889595

12 2.34031394 2.28330837

13 2.86115010 1.53770719

14 1.54450734 2.08243315

15 2.04229979 1.80179349

16 3.38373810 3.39268813

17 -0.02497814 -0.41914448

18 1.99062361 2.50558166

19 2.49876301 2.01528490

20 -0.32306768 0.12753965

21 -0.73376775 -0.79919149

22 2.22736884 1.13179810

23 0.31701022 1.02988455

24 0.29104541 0.10559250

25 2.44105259 1.54506493

26 1.12177765 1.68391513

27 1.55308545 1.32997622

28 0.26794580 0.62820251

29 1.67397203 0.89974463

30 1.59676930 1.61203312

31 0.69398596 0.03987502

32 -0.12841125 0.59412727

33 2.79463545 1.09165099

34 0.88477639 2.96803657

35 -0.24469391 0.41816743

36 0.81070847 0.07612875

37 2.24064655 1.53890950

38 2.31571352 2.68878044

39 0.74425362 0.24514605

40 -0.86200005 -0.05513882

41 0.11277311 -0.05453482

42 0.70856398 0.06280314

43 0.15986822 -0.59842464

44 -0.25165302 -0.63358436

45 -0.06440672 -0.21049611

46 2.20973243 1.72439748

47 1.52195121 2.45699459

48 0.38595180 -0.67250614

49 0.04127611 1.23290445

50 2.37163412 1.80619468

Clustering vector:

[1] 20 6 28 48 43 23 40 35 32 1 43 45 45 32 36 3 20 6 28 24 2 44 41 2 21 17 49 35 42 23 8 35 1 8 23 31 35 39 23 49 20 24

[43] 32 44 5 17 7 21 28 10 37 47 30 46 13 46 50 11 14 11 9 12 33 15 46 18 50 47 19 38 29 25 22 30 16 18 38 47 19 11 27 47 12 22

[85] 37 4 18 26 14 15 46 34 14 25 50 19 12 30 26 47

Within cluster sum of squares by cluster:

[1] 0.0145734110 0.0051958256 0.0000000000 0.0000000000 0.0000000000 0.0046432492 0.0000000000 0.0195006736 0.0000000000

[10] 0.0000000000 0.0437955449 0.0048397795 0.0000000000 0.0263643851 0.0302533362 0.0000000000 0.0262746618 0.1599640427

[19] 0.0183982790 0.0067587233 0.0132206797 0.0192706903 0.0264783621 0.0068167900 0.0181218023 0.0637963843 0.0000000000

[28] 0.0577817200 0.0000000000 0.0286571576 0.0000000000 0.0522842792 0.0000000000 0.0000000000 0.0403297373 0.0000000000

[37] 0.0003600565 0.0273230894 0.0000000000 0.0000000000 0.0000000000 0.0000000000 0.0046007913 0.0394949472 0.0080629722

[46] 0.0103209025 0.2017649669 0.0000000000 0.0126172617 0.0166084815

(between\_SS / total\_SS = 99.6 %)

Available components:

[1] "cluster" "centers" "totss" "withinss" "tot.withinss" "betweenss" "size" "iter"

[9] "ifault"

> plot(data,col=cl$cluster)

> points(cl$centers,col=1:2, pch=8,cex=2)

> library(teachingdemos)

Error in library(teachingdemos) :

there is no package called ‘teachingdemos’

> library(TeachingDemos)

Error in library(TeachingDemos) :

there is no package called ‘TeachingDemos’

> install.packages("TeachingDemos")

probando la URL 'https://cran.rstudio.com/bin/macosx/el-capitan/contrib/3.4/TeachingDemos\_2.10.tgz'

Content type 'application/x-gzip' length 1696058 bytes (1.6 MB)

==================================================

downloaded 1.6 MB

The downloaded binary packages are in

/var/folders/y0/mlwc6mk545b3r42y8x0cbz380000gn/T//Rtmpf9oqky/downloaded\_packages

> library(TeachingDemos)

> put.points.demo()

> sl.out<-hclust(dist(rnorm(20,0,1),method="euclidian"),method="single")

> plot(sl.out)

> eigen(cor(golub))$values[1:5]

[1] 25.4382629 2.0757158 1.2484411 1.0713373 0.7365232