

# Tarea

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Oligo permite la lectura de los archivos ".CEL".

```
library(oligo)

## Warning: package 'oligo' was built under R version 3.4.2
## Loading required package: BiocGenerics
## Warning: package 'BiocGenerics' was built under R version 3.4.2
## 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: oligoClasses
## Warning: package 'oligoClasses' was built under R version 3.4.2
## Welcome to oligoClasses version 1.40.0
## Loading required package: Biobase
## Warning: package 'Biobase' was built under R version 3.4.2
## Welcome to Bioconductor
##
## Vignettes contain introductory material; view with
```

```

##      'browseVignettes()'. To cite Bioconductor, see
##      'citation("Biobase)"', and for packages 'citation("pkgname)"'.
## Loading required package: Biostrings
## Warning: package 'Biostrings' was built under R version 3.4.2
## Loading required package: S4Vectors
## Warning: package 'S4Vectors' was built under R version 3.4.2
## Loading required package: stats4
##
## Attaching package: 'S4Vectors'
## The following object is masked from 'package:base':
##
##      expand.grid
## Loading required package: IRanges
## Warning: package 'IRanges' was built under R version 3.4.2
## Loading required package: XVector
## Warning: package 'XVector' was built under R version 3.4.2
##
## Attaching package: 'Biostrings'
## The following object is masked from 'package:base':
##
##      strsplit
## =====
## Welcome to oligo version 1.42.0
## =====

files=c("TAC_1.CEL","TAC_2.CEL","TAC_3.CEL","TAT_1.CEL","TAT_2.CEL","TAT_3.CEL")
hipo=read.celfiles(files)

## Loading required package: pd.ragene.2.0.st
## Loading required package: RSQLite
## Warning: package 'RSQLite' was built under R version 3.4.4
## Loading required package: DBI
## Warning: package 'DBI' was built under R version 3.4.4
## Platform design info loaded.

```

Normaliza los datos. El algoritmo realizar? la esta de fondo, la cuantificaci?n y la normalizaci?n de cuantiles

```
hip.rma.probe=rma(hipo, target="core")

## Background correcting
## Normalizing
## Calculating Expression

expresion<-exprs(hip.rma.probe)
```

Lima es un paquete que ofrece analisis multivariados. Se aplica para datos de secuenciación y datos de microarreglos, aplica estadística frecuentista y bayesiana. Este paquete me ofrece la posibilidad de contrastar la expresión génica de 2 o más grupos.

```
library(limma)

## Warning: package 'limma' was built under R version 3.4.3
##
## Attaching package: 'limma'
## The following object is masked from 'package:oligo':
##
## backgroundCorrect
## The following object is masked from 'package:BiocGenerics':
##
## plotMA

design=matrix(0,6,2)
  design[1:3,1]=1
  design[4:6,2]=1
  colnames(design)=c("Control", "SM")
contraste="SM-Control"
cont.matrix=makeContrasts(contraste, levels=design)
fit=lmFit(hip.rma.probe, design)
fitC=contrasts.fit(fit, cont.matrix)
fitCB=eBayes(fitC)
TT=topTable(fitCB, coef=1, adjust="fdr", sort.by="logFC", number=nrow(hip.rma.probe),
  genelist=fit$genes)
head(TT)

##           logFC AveExpr      t      P.Value adj.P.Val      B
## 17793757  3.743832 9.661380  5.209972 0.0013407956 0.9470858 -4.018840
## 17773733 -2.928610 7.073799 -2.694275 0.0316388165 0.9470858 -4.277625
## 17832387 -2.767796 4.531822 -4.354804 0.0035400517 0.9470858 -4.078485
## 17818150  2.673396 8.828497  7.618612 0.0001412634 0.9470858 -3.927514
## 17860610 -2.657330 9.725544 -3.091691 0.0180911464 0.9470858 -4.217123
## 17745928  2.624731 9.731650  3.635173 0.0087109317 0.9470858 -4.148389
```