aescos_M0.157analisis_datos_omicos_actividad_1.1

2024-10-02

```
rm(list = ls())
```

1. Select a GEO (Gene Expression Omnibus) datasetfrom the list presented in the "GEOdatasets_enhanced.xls" document available in the resources of the activity.

He seleccionado el data set MyD88 deficient macrophage response to zymosan. Estudio realizado en mus musculus (ratón) dataset: GDS2686, Serie: GSE6376

2. Leer los datos desde GEO utilizando el paquete GEOquery. Esto os proporcionará un objeto clase expressionSet con los datos normalizados y una tabla adicional con información sobre el estudio.

```
require(GEOquery)
```

```
## Loading required package: GEOquery
```

```
## Loading required package: Biobase
```

```
## Loading required package: BiocGenerics
```

```
##
## Attaching package: 'BiocGenerics'
```

```
## The following objects are masked from 'package:stats':
##
##     IQR, mad, sd, var, xtabs
```

```
## The following objects are masked from 'package:base':
##
##     anyDuplicated, aperm, append, as.data.frame, basename, cbind,
##     colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,
##     get, grep, grepl, intersect, is.unsorted, lapply, Map, mapply,
##     match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,
##     Position, rank, rbind, Reduce, rownames, sapply, setdiff, table,
##     tapply, union, unique, unsplit, which.max, which.min
```

```
## Welcome to Bioconductor
##
##     Vignettes contain introductory material; view with
##     'browseVignettes()'. To cite Bioconductor, see
##     'citation("Biobase")', and for packages 'citation("pkgname")'.
```

```
## Setting options('download.file.method.GEOquery'='auto')
```

```
## Setting options('GEOquery.inmemory.gpl'=FALSE)
```

```
gds <- getGEO("GDS2686")
```

3. Determinar la estructura de los datos (filas, columnas)y el diseño del estudio (grupos de muestras o individuos, tratamientos si los hay, etc.) que los ha generado.

– La información del experimento podéis descargarla también de GEO, bien con GEOquery si proporcionáis el identificador de dataset GDSxxxx o accediendo a la página del estudio.

```
class(gds)
```

```
## [1] "GDS"
## attr(,"package")
## [1] "GEOquery"
```

```
slotNames(gds)
```

```
## [1] "gpl"       "dataTable" "header"
```

```
head(Meta(gds))
```

```
## $channel_count
## [1] "1"
##
## $dataset_id
## [1] "GDS2686" "GDS2686"
##
## $description
## [1] "Analysis of MyD88-deficient macrophages treated with fungal cell wall component zymosan. Zymosan-induced
Toll-like receptor (TLR) signaling is transduced via adaptor protein MyD88. Results provide insight into the role
of non-TLR innate immune signaling in response to zymosan and pathogenic fungi."
## [2] "control"
## [3] "zymosan"
##
## $email
## [1] "geo@ncbi.nlm.nih.gov"
##
## $feature_count
## [1] "45101"
##
## $institute
## [1] "NCBI NLM NIH"
```