Prueba_Actividad_1

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Resolución de la actividad 1.1

Resolución de la actividad 1.2

```r
# Si no se dispone del paquete "GEOquery"
if (!require("GEOquery")){
  # Instala el paquete "GEOquery"
  BiocManager::install("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, sort,
##     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)

# Carga el paquete "GEOquery"
library("GEOquery")
# Crea un objetos GDS que albergue el DataSet sugerido en el ejercicio
GDS2294<-getGEO(GEO="GDS2294", destdir=getwd(), AnnotGPL=TRUE)
```

```
## Warning in grep(pattern, bfr, value = TRUE): unable to translate ' El n<a3>mero
## de serie del volumen es: 486F-DD03' to a wide string
```

```
## Warning in grep(pattern, bfr, value = TRUE): input string 2 is invalid
```

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## Warning in grep(pattern, bfr, value = TRUE): unable to translate ' El n<a3>mero
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```

```
## Warning in grep(pattern, bfr, value = TRUE): input string 2 is invalid
```

```
# Número total de muestras consideradas en el DataSet
Meta(GDS2294)$sample_count
```

```
## [1] "6"
```

```
# Muestras consideradas dentro de este DataSet
Meta(GDS2294)$sample_id
```

```
## [1] "GSM130365,GSM130366,GSM130367" "GSM130368,GSM130369,GSM130370"
```

```
# Plataforma utilizada para el análisis de las siguientes muestras
Meta(GDS2294)$platform
```

```
## [1] "GPL81"
```

```
# Nombres de las variables consideradas en la tabla de
names(Columns(GDS2294))
```

```
## [1] "sample"            "genotype/variation" "description"
```

```
# Cabecera de la tabla de datos fenotípicos asociada a este DataSet
head(Columns(GDS2294))
```

```
##      sample genotype/variation
## 1 GSM130365           wild type
## 2 GSM130366           wild type
## 3 GSM130367           wild type
## 4 GSM130368      HDAC1 knockout
## 5 GSM130369      HDAC1 knockout
## 6 GSM130370      HDAC1 knockout
##
## 1            Value for GSM130365: wild_type_embryonic_stem cells_biological_rep1; src: Mus musculus
## 2            Value for GSM130366: wild_type_embryonic_stem cells_biological_rep2; src: Mus musculus
## 3            Value for GSM130367: wild_type_embryonic_stem cells_biological_rep3; src: Mus musculus
## 4 Value for GSM130368: HDAC1_knock_out_embryonic_stem_cells_biological_rep1; src: Mus musculus embry
## 5 Value for GSM130369: HDAC1_knock_out_embryonic_stem_cells_biological_rep2; src: Mus musculus embry
## 6 Value for GSM130370: HDAC1_knock_out_embryonic_stem_cells_biological_rep3; src: Mus musculus embry
```

```r
# Muestras de cada tipo incluidas en el estudio
table(Columns(GDS2294)$"genotype/variation")
```

```
##
## HDAC1 knockout      wild type
##              3              3
```

```r
# Diagrama de barras de la variable "genotype/variation"
barplot(table(Columns(GDS2294)$"genotype/variation"), col=palette.colors(n=2, palette="Pastel 1"), cex.a
```
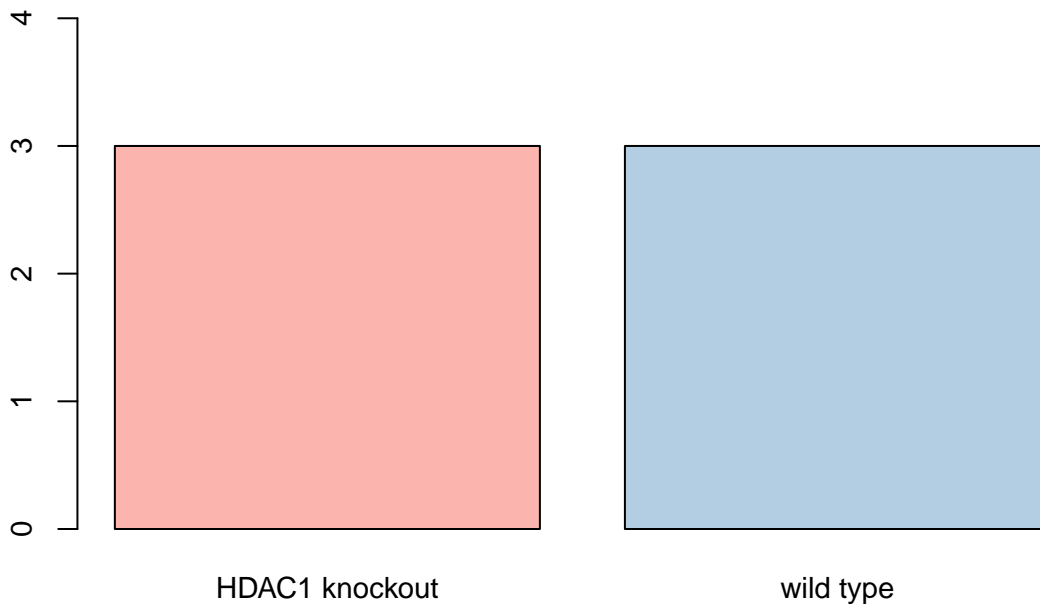
```
# Convierte el objeto GDS a un objeto de tipo ExpressionSet
expr_GDS2294<-GDS2eSet(GDS2294)
```

```
## Warning in grep(pattern, bfr, value = TRUE): unable to translate ' El n<a3>mero
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```

```
## Warning in grep(pattern, bfr, value = TRUE): input string 2 is invalid
```

```
# Dimensiones de la matriz de expresión
dim(exprs(expr_GDS2294))
```

```
## [1] 12488     6
```

```
# Cabecera de la matriz de expresión
head(exprs(expr_GDS2294))
```

```
##           GSM130365 GSM130366 GSM130367 GSM130368 GSM130369 GSM130370
## 100001_at      11.5       5.6      69.1      15.7      36.0      42.0
## 100002_at      20.5      32.4      93.3      31.8      14.4      22.9
## 100003_at      72.4      89.0      79.2      80.5     130.1      86.7
## 100004_at     261.0     226.2     365.1     432.0     447.3     288.1
## 100005_at    1086.2    1555.6    1487.1    1062.2    1365.9    1436.2
## 100006_at      49.7      52.9      15.0      25.8      48.8      54.8
```

```
# Dimensiones de la matriz de datos fenotípicos
dim(pData(expr_GDS2294))
```

```
## [1] 6 3
```

```
# Cabecera de la matriz de datos fenotípicos
head(pData(expr_GDS2294))
```

```
##              sample genotype/variation
## GSM130365 GSM130365          wild type
## GSM130366 GSM130366          wild type
## GSM130367 GSM130367          wild type
## GSM130368 GSM130368     HDAC1 knockout
## GSM130369 GSM130369     HDAC1 knockout
## GSM130370 GSM130370     HDAC1 knockout
```

```
##
## GSM130365                Value for GSM130365: wild_type_embryonic_stem cells_biological_rep1; src: Mus
## GSM130366                Value for GSM130366: wild_type_embryonic_stem cells_biological_rep2; src: Mus
## GSM130367                Value for GSM130367: wild_type_embryonic_stem cells_biological_rep3; src: Mus
## GSM130368 Value for GSM130368: HDAC1_knock_out_embryonic_stem_cells_biological_rep1; src: Mus muscul
## GSM130369 Value for GSM130369: HDAC1_knock_out_embryonic_stem_cells_biological_rep2; src: Mus muscul
## GSM130370 Value for GSM130370: HDAC1_knock_out_embryonic_stem_cells_biological_rep3; src: Mus muscul
```

```r
# Verifica que las filas de la matriz de datos fenotípicos se corresponden con las columnas de la matri
all(rownames(pData(expr_GDS2294))==colnames(exprs(expr_GDS2294)))
```

```
## [1] TRUE
```