GSE1739 Dataset

Antonio Osamu Katagiri Tanaka - A01212611@itesm.mx

Dataset details

Title: Severe acute respiratory syndrome expression profile

Summary: Expression profiling of peripheral blood mononuclear cells (PBMC) from 10 adult patients with severe acute respiratory syndrome (SARS). Results provide insight into the host immune response to the SARS coronavirus.

Organism: Homo sapiens

Platform: GPL201: [HG-Focus] Affymetrix Human HG-Focus Target Array

Citation:
Reghunathan R, Jayapal M, Hsu LY, Chng HH et al. *Expression profile of immune response genes in patients with Severe Acute Respiratory Syndrome.* BMC Immunol 2005 Jan 18;6:2. PMID: 15655079

Reference Series: GSE1739

Sample count: 14

Value type: count

Series published: 2005/01/18

Dataset taken from: GDSbrowser, GSE1739 query, and GSE1739 geo2r

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The GSE1739 was selected for the Bioinformatics class assignments and activities. The reason behind this decision is the similarities that SARS shares with the novel coronavirus COVID-19. The purpose id to work with up-to-date data that is relecant to the current crisis.

```r
# Clear all objects (from the workspace)
rm(list = ls())

# Suppress Warning messages
options(warn = -1)

# Install packages from Bioconductor as they're not available in CRAN
# if (!requireNamespace("BiocManager", quietly=TRUE))
#     install.packages("BiocManager")
# BiocManager::install("GEOquery")
# BiocManager::install("Biobase")
# BiocManager::install("affy")
```

```r
library(GEOquery)
```

Load the Bioconductor libraries:

```
## Loading required package: Biobase

## 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, basename, cbind, colMeans,
##     colnames, colSums, dirname, 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

## 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)
```

```r
library(Biobase)
library(limma)
```

```
##
## Attaching package: 'limma'

## The following object is masked from 'package:BiocGenerics':
##
##     plotMA
```

```r
library(affy)
```

Command getGEO() and R lists   The command ´rgetGEO()´ is a function from the packages GEOquery (S. Davis and Meltzer 2007) that can download data directly from the GEO database.

The help command ?getGEO provides a description that stating that It directs the download (if no filename is specified) and parsing of a GEO SOFT format file into an R data structure[..]

However, the default command as specified in the Usage section is:

```r
# Enable Warning messages
options(warn = 0)
```