

R Biological Analysis

Usage of bioinformatic resources to understand gene expression in colon cancer

File with dataset from GEO

```
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```

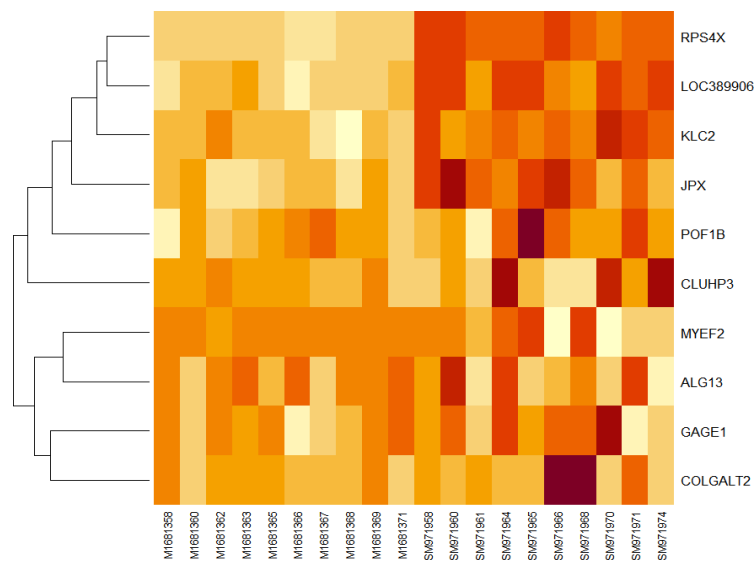
```
gset <- getGEO("GSE40967", GSEMatrix = TRUE, AnnotGPL = TRUE)  
if (length(gset) > 1) idx <- grep("GPL570", attr(gset, "names")) else idx <- 1  
gset <- gset[[idx]]  
ex <- exprs(gset)  
ex <- as.data.frame(ex)  
probes <- getEAWP(gset)$probes
```

```
muestras_cancer_hombres <- exprs(gset[, gset$`Sex:chl` == "Male"])  
muestras_cancer_mujeres <- exprs(gset[, gset$`Sex:chl` == "Female"])
```

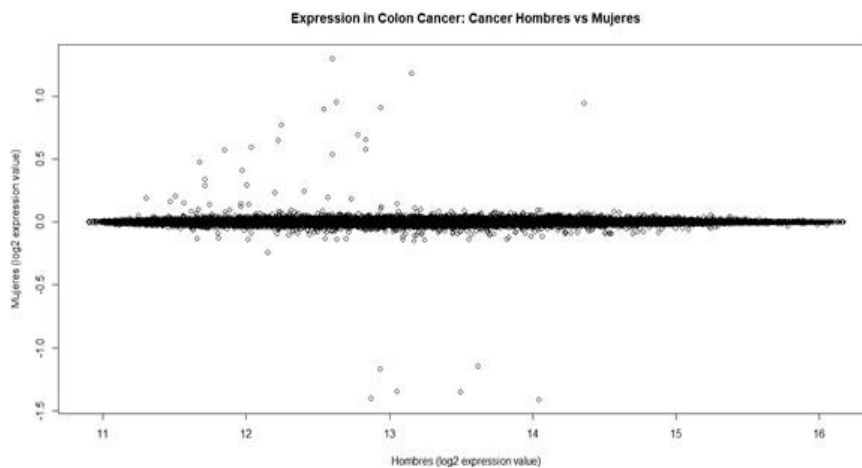
```
# Gráfica de dispersión  
plot(microarray_means$means_cancer_hombres,  
      microarray_means$means_cancer_mujeres,  
      xlim = c(0,16), ylim = c(0,16),  
      xaxt="n", yaxt="n",  
      main = "Expression in Colon Cancer: Cancer Hombres vs Mujeres",  
      xlab = "Hombres (log2 expression value)",  
      ylab = "Mujeres (log2 expression value)")  
axis(1, at=seq(0,16,2))  
axis(2, at=seq(0,16,2))
```

Graphs

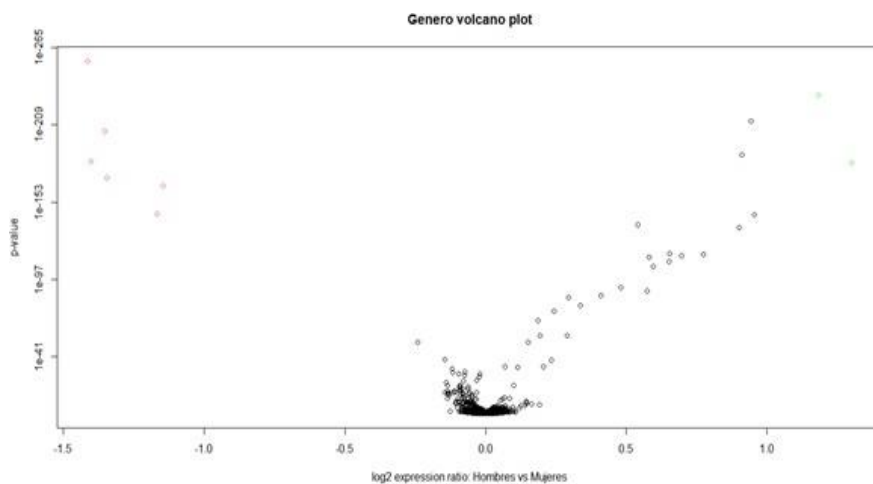
Heat map and dendrogram



R-I



Volcano



Dispersion

