

R Biological Analysis

Usage of bioinformatic resources to understand gene expression in colon cancer

File with the capture and study of the dataset

```
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```

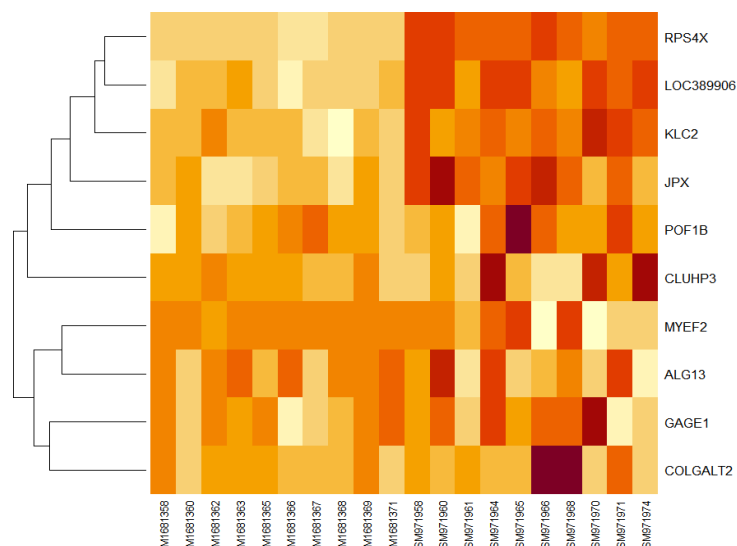
```
gset <- getGEO("GSE40967", GSEMatrix = TRUE, AnnotGPL = TRUE)
if (length(gset) > 1) idx <- grep("GPL570", attr(gset, "names")) else idx <- 1
gset <- gset[[idx]]
ex <- exprs(gset)
ex <- as.data.frame(ex)
probes <- getEAWP(gset)$probes
```

```
muestras_cancer_hombres <- exprs(gset[, gset$`Sex:ch1`=="Male"])
muestras_cancer_mujeres <- exprs(gset[, gset$`Sex:ch1`=="Female"])
```

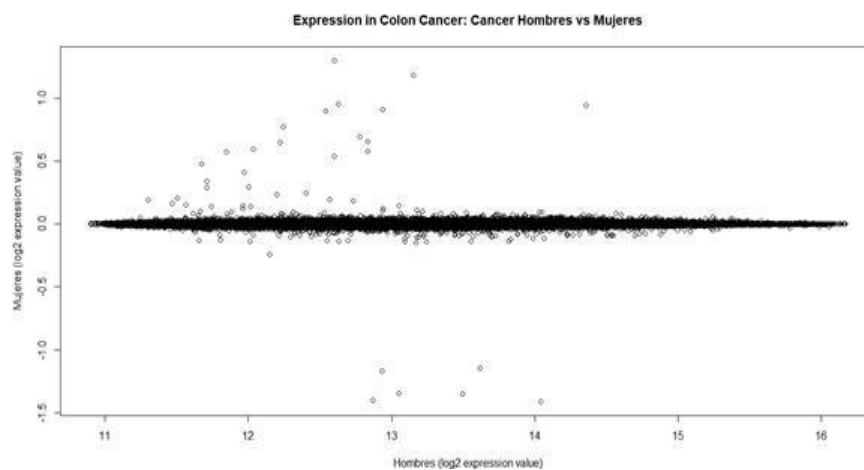
```
# Gráfica de dispersión
plot(microarray_means$means_cancer_hombres,
     microarray_means$means_cancer_mujeres,
     xlim = c(0,16), ylim = c(0,16),
     xaxt="n", yaxt="n",
     main = "Expression in Colon Cancer: Cancer Hombres vs Mujeres",
     xlab = "Hombres (log2 expression value)",
     ylab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

Graphs

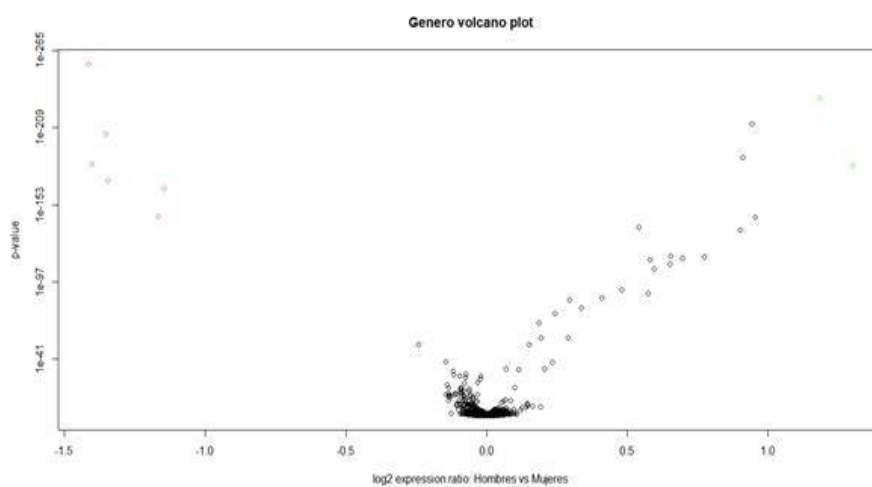
Heat map and dendrogram



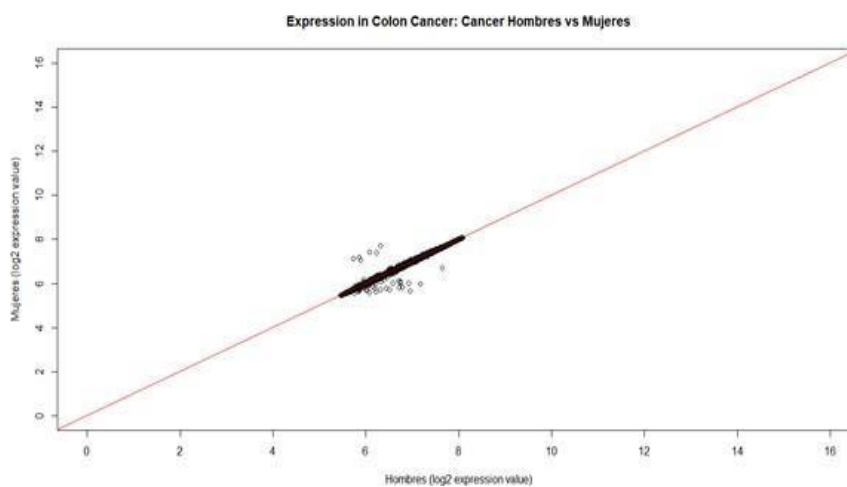
R-I



Volcano



Dispersion



José Luis Madrigal

Acknowledgments

To my friend who helped me better understand some concepts, Alan (with the usage of the GEO Dataset).