

Taller 3A

Estadística genómica

Juan David Henao Sánchez

28 de septiembre de 2015

Sobre unos datos del GEO (una sola medición en el tiempo) que comparen dos condiciones, identifique los genes diferencialmente expresados usando acde:

- Cargando las librerías

```
> library(acde)
> library("DESeq")
```

- Cargando los datos

```
> data <- read.table("GSE58972_REL6_6h_processed_data.txt", h=T)
> dim(data)
```

```
[1] 23284      8
```

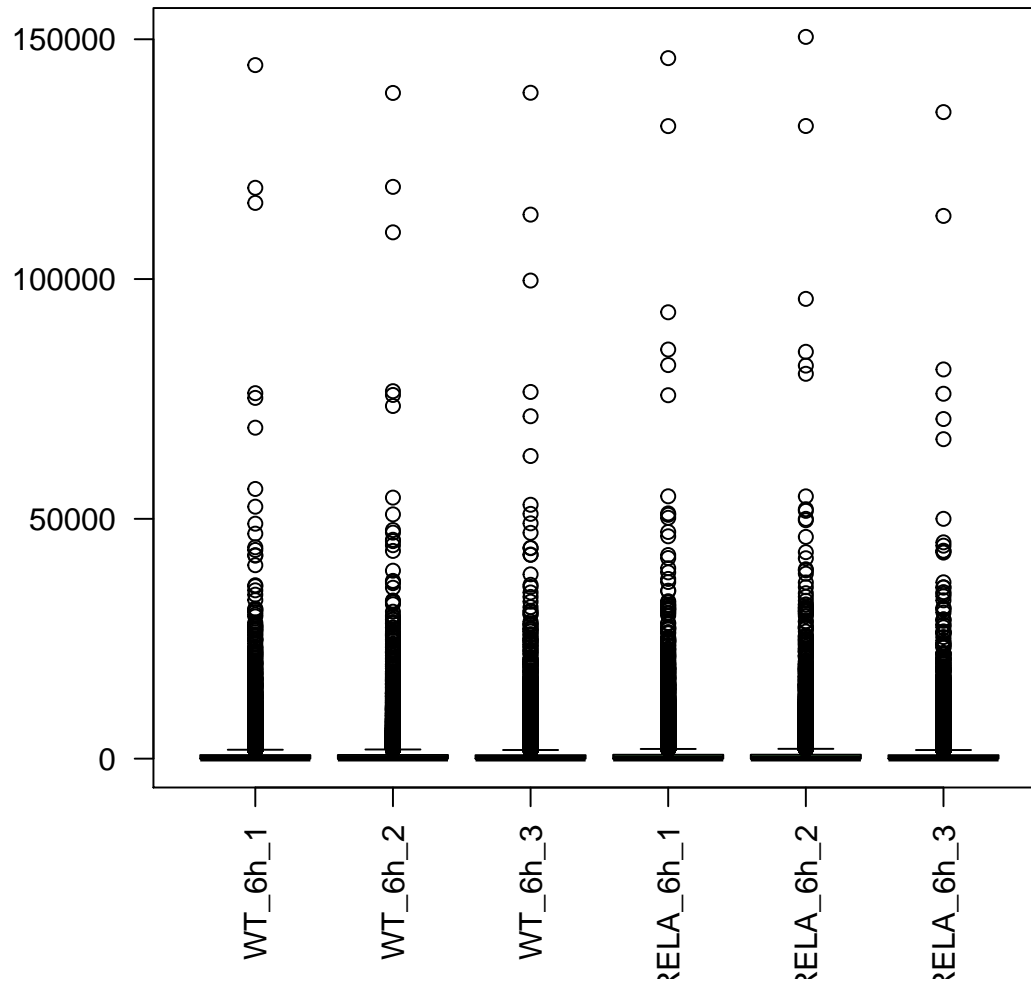
```
> head(data)
```

	gene description	WT_6h_1	WT_6h_2	WT_6h_3	RELA_6h_1	RELA_6h_2
1	0610005C13Rik	na	9	12	11	16
2	0610007C21Rik	na	534	581	512	537
3	0610007L01Rik	na	2124	2197	2168	2811
4	0610007N19Rik	na	17	26	21	18
5	0610007P08Rik	na	1410	1504	1543	1546
6	0610007P14Rik	na	2049	2008	2074	2192
	RELA_6h_3					
1			10			
2			501			
3			2265			
4			15			
5			1353			
6			1968			

- Gráficoando los datos cargados

```
> boxplot(data[, 3:8], main="Boxplot Mus musculus", col="lightgreen", cex.names=0.2, las=2)
```

Boxplot Mus musculus



■ Creando el CountDataSet

```
> rownames(data) <- data$gene
> countsTable <- data[,3:8]
> head(countsTable)
```

	WT_6h_1	WT_6h_2	WT_6h_3	RELA_6h_1	RELA_6h_2	RELA_6h_3
0610005C13Rik	9	12	12	11	16	10
0610007C21Rik	534	581	562	512	537	501
0610007L01Rik	2124	2197	2168	2811	2706	2265
0610007N19Rik	17	26	21	18	20	15
0610007P08Rik	1410	1504	1543	1546	1577	1353
0610007P14Rik	2049	2008	2074	2192	2192	1968

```
> conds <- factor( c( "WT", "WT", "WT", "treated","treated","treated"))
> cds <- newCountDataSet( countsTable, conds )
```

■ Estimando el tamaño de los datos

```
> cds <- estimateSizeFactors( cds )
> sizeFactors(cds)
```

WT_6h_1	WT_6h_2	WT_6h_3	RELA_6h_1	RELA_6h_2	RELA_6h_3
0.9731925	0.9971984	0.9465783	1.0701892	1.0843975	0.9475568

- Normalización

```
> head(counts(cds,normalized=TRUE))
```

	WT_6h_1	WT_6h_2	WT_6h_3	RELA_6h_1	RELA_6h_2
0610005C13Rik	9.247913	12.03371	12.67724	10.27856	14.75474
0610007C21Rik	548.709529	582.63232	593.71741	478.42006	495.20587
0610007L01Rik	2182.507565	2203.17247	2290.35471	2626.63826	2495.39494
0610007N19Rik	17.468281	26.07305	22.18517	16.81946	18.44342
0610007P08Rik	1448.839768	1508.22549	1630.08179	1444.60432	1454.26379
0610007P14Rik	2105.441620	2013.64148	2191.04967	2048.23588	2021.39901
	RELA_6h_3				
0610005C13Rik	10.55346				
0610007C21Rik	528.72820				
0610007L01Rik	2390.35804				
0610007N19Rik	15.83019				
0610007P08Rik	1427.88275				
0610007P14Rik	2076.92037				

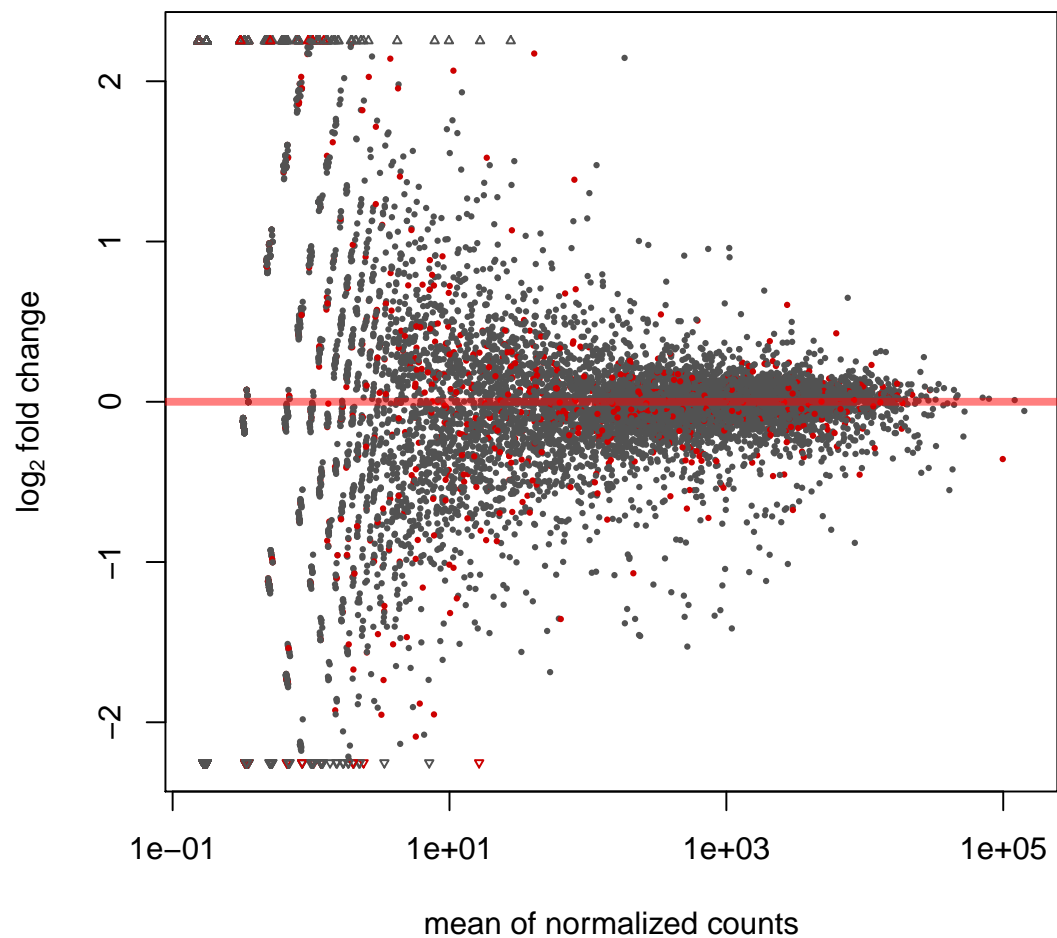
- Estimando las diferencias

```
> cds <- estimateDispersions( cds )
> res = nbinomTest(cds,"WT","treated")
> head(res)
```

	id	baseMean	baseMeanA	baseMeanB	foldChange	log2FoldChange
1	0610005C13Rik	11.59094	11.31962	11.86225	1.0479369	0.06755185
2	0610007C21Rik	537.90223	575.01975	500.78471	0.8709000	-0.19942100
3	0610007L01Rik	2364.73767	2225.34492	2504.13042	1.1252774	0.17028074
4	0610007N19Rik	19.46993	21.90883	17.03102	0.7773587	-0.36334771
5	0610007P08Rik	1485.64965	1529.04902	1442.25029	0.9432335	-0.08431310
6	0610007P14Rik	2076.11467	2103.37759	2048.85175	0.9740770	-0.03789226
	pval	padj				
1	0.9398718481	1.000000000				
2	0.0067509416	0.078064572				
3	0.0001904397	0.004043898				
4	0.3435939599	0.876773371				
5	0.1160588262	0.527125188				
6	0.4241029562	0.939431937				

- Gráficoando los resultados obtenidos

```
> plotMA(res)
```



■ Resultados finales

```
> resSig = res[ res$padj < 0.1, ]
> na.omit(dim(resSig))
```

```
[1] 8364      8
```

```
> na.omit(head(resSig))
```

	id	baseMean	baseMeanA	baseMeanB	foldChange	log2FoldChange
2	0610007C21Rik	537.9022	575.0198	500.7847	0.870900	-0.1994210
3	0610007L01Rik	2364.7377	2225.3449	2504.1304	1.125277	0.1702807
	pval	padj				
2	0.0067509416	0.078064572				
3	0.0001904397	0.004043898				