

# Taller 3A

## Estadística genómica

Juan David Henao Sánchez

23 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:**

```
> library(acde)
> library("DESeq")
> #####
> data <- read.table("GSE55477_GeneExpression_RPKMs.txt", h=T)
> dim(data)
```

[1] 13321 9

```
> head(data)
```

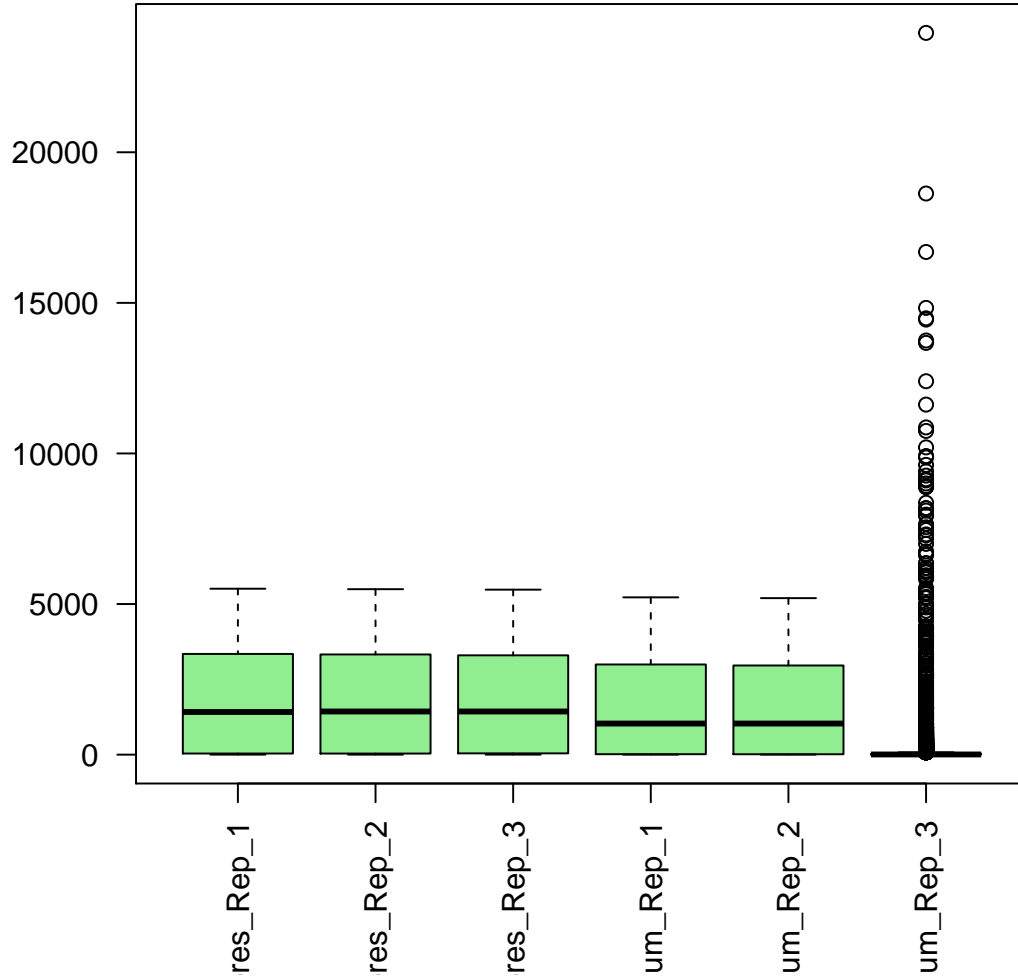
	GeneID	Chromosome	Gene_length	Spores_Rep_1	Spores_Rep_2	Spores_Rep_3
1	FGSG_11641	Fgchr1	666	0	0	0
2	FGSG_11605	Fgchr1	1134	0.11	0	0
3	FGSG_11642	Fgchr1	669	1.68	2.26	3.14
4	FGSG_11643	Fgchr1	396	0	0	0
5	FGSG_11600	Fgchr1	1305	0.96	0.62	0.54
6	FGSG_11601	Fgchr1	423	0.59	0.55	0.28

	Mycelium_Rep_1	Mycelium_Rep_2	Mycelium_Rep_3
1	0	0	0.00
2	0.25	0	0.16
3	0.64	1.56	3.47
4	0	0	0.00
5	0.22	0.11	0.41
6	0	0	0.00

```
> boxplot(data[, 4:9], main="Boxplot Fusarium graminearum", col="lightgreen", cex.names=0.2, las=2)
```

## Boxplot Fusarium graminearum



```
> rownames(data) <- data$GeneID
```