

# Seminar III: R/Bioconductor

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**Note:** Questions through the forum please. Those who are not from the sixth LCG  
generation send us an email so we can register you on the forum.

## Abstract

The following exercise will make sure that you can use the RMySQL package.

## 1 RMySQL

1. Use RMySQL to access your own database from the Bioinformatics and Statistics I course.

```
> library(RMySQL)
> con <- dbConnect(MySQL(), user = "mnoe", password = "eonm", dbname = "prom
+   host = "mitla.lcg.unam.mx")
> dbListTables(con)
```

```
[1] "Gene"           "Promoter"       "TranscriptionUnit"  
[4] "gene"          "promoter"       "promotor"  
[7] "tu_gene_link"
```

2. Use a query to retrieve data and make a plot :)

```
> df <- dbGetQuery(con, "SELECT * FROM Promoter")  
> dim(df)  
> library(lattice)  
> densityplot(~pos_1 | as.factor(promoter_sigma), data = df)  
> dbDisconnect(con)
```

3. If you don't have your own database, let me know.

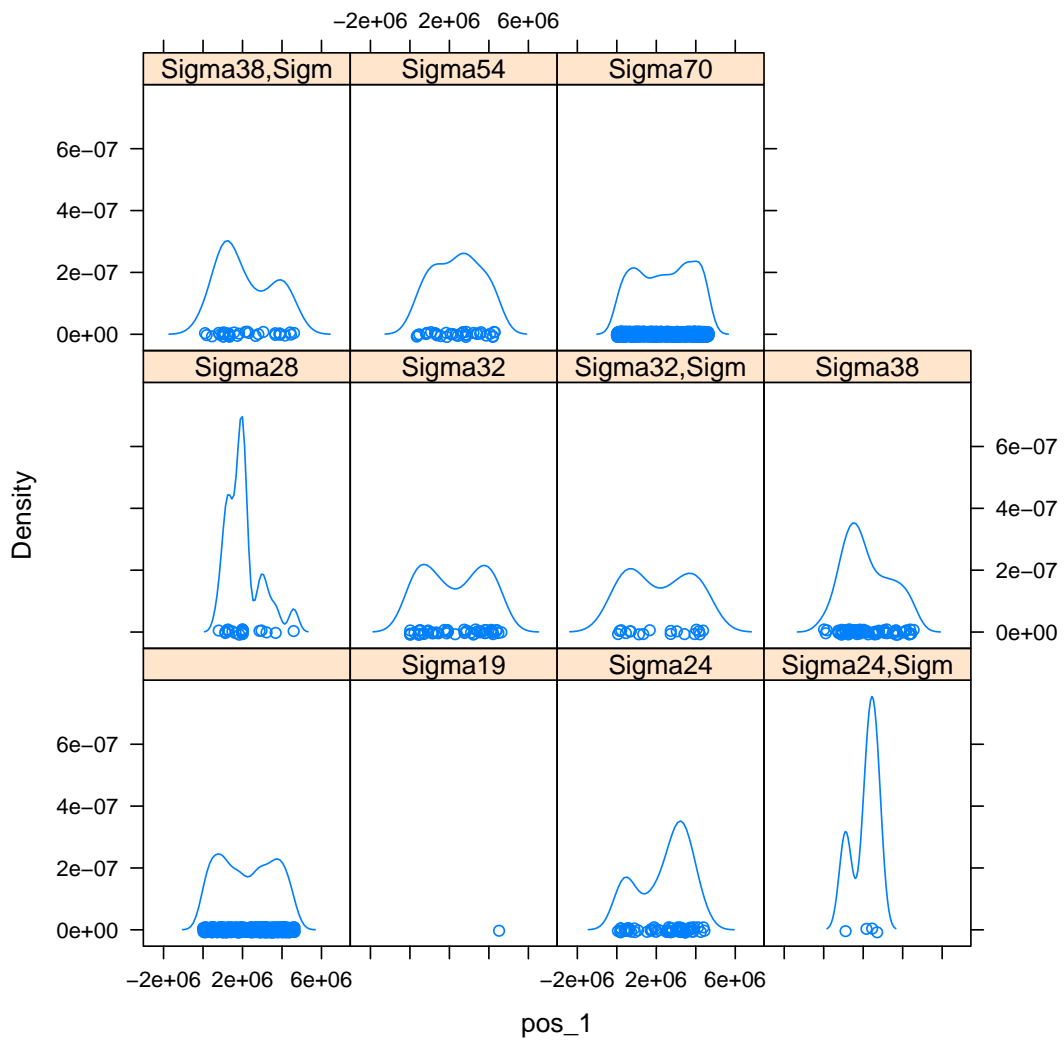


Figure 1: Densityplot for the pos\_1 by promoter\_sigma type