Bioconductor

1. Retrieve a matrix containing the gene counts located in the chromosome 7 in the region 5Mb-12Mb of airway data using two R code: one using '[' and another using `GRanges` functionalities.

2. Find the gene symbol, chromosome position and GO pathway ID for '1003_s_at' (Affymetrix probe annotated in `hgu95av.db`)

3. Use what you have learned about `biomaRt` to find the gene symbol and name for the entrez gene IDs 1, 10 and 100.

4. Add the annotation of `pickrell.eset` having gene symbol, chromosome start and end and entrez id. NOTES: genes are encoded using ensembl ids. Use the 'Homo.sapiens' object to look up the chromosome start, chomosome end and entrez `columns()`.

5. Download GEO data set GSE85426 by executing:

```
library(GEOquery)
gds <- getGEO("GSE40732")[[1]]
gds
```

Answer the following questions using this object

- how many samples are analyzed?
- show the names of the variables (metadata) available in this study
- how many asthmatics are in the database (variable `characteristics_ch1`)?
- how many genes are analyzed?
- which is the name of the annotation?
- create a boxplot showing the gene expression of 'AB002294' (variable ID in the annoation - these are genebank numbers).