Exercise 2: Microarrays

Two colour microarray

2.1.1 Load microarray result files (.gpr-files) from 2 time points (0h vs reference, 7d vs reference) of a time series experiment during a fat cell differentiation process (*MM-1-29_0h-Ref.gpr, MM-1-35_Ref-0h.gpr, MM-1-45_7d-Ref.gpr, MM-1-46_Ref-7d.gpr*). Sample information: *3T3L1Sample.txt*, and chip information: *Chip11.gal*

2.1.2 Use `marray` Bioconductor package for background correction (normexp), normalization (loess), MA-plots and boxplots before and after normalization. Describe the differences caused by the normalization.

2.1.3 Show xy plots for the log2-ratios (M values) of the dye swap pairs and do a dye swap normalization. How would the xy plots look if the technical replicates were done without dye swap?

2.1.4 Provide a list of genes which where at least two-fold up or down-regulated in each and in both conditions.

Clustering

2.2.1 Download the expression profiles from a time series experiment with 519 genes and 8 timepoints (*genelist.txt*).

2.2.2 Perform a hierarchical clustering, show the heatmap and the dendrogram. Which clustering level would you choose?

2.2.3 Perform k-means clustering, plot the mean expression profile of each cluster and show the corresponding heatmap.

2.2.4 What are the advantages and disadvantages of the performed clustering methods? Which one would you choose? Why?

2.2.5 Calculate the correlation matrix of the genes and show the corresponding heatmap.