Exercise 4: Biomolecular network analysis

4.1 Transcriptional regulatory network motifs

4.1.1 In a study of human hepatocytes (Odom T., et al. 2006) targets of 6 transcription factors were identified and their interactions were summarized into a file. 1 means there is a protein-DNA interaction detected and 0 means there is no protein-DNA interaction. Load the file into R.

4.1.2 Find transcription factor (TF) crosstalk and autoregulation of the TFs (see Fig. 1). Report the total number of TF crosstalk combinations and include a condensed table of them. Report all TFs which show autoregulation.

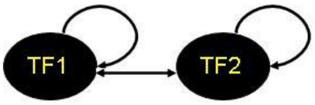

Figure 1: TF-Autoregulation and TF-Crosstalk.

4.1.3 Find feed forward loops (FFL) and create a table with the different TFs-genes combinations (see Fig. 2). Report the total number of FFLs found and include a table with the number of FFLs per TF.

4.1.4 List the different combinations of genes that are regulated by exactly 3 of the 6 transcription factors (see Fig. 3). Report the number of genes and include a table with the number of genes regulated by a certain combination of TFs.

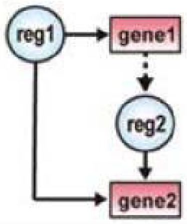

Figure 2: Feed forward loop

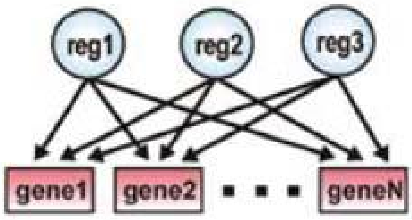

Figure 3: Genes regulated by 3 TFs

4.2 Gene co-expression network

4.2.1 Download the gene expression profiles (365 genes) from a time series experiment during adipocyte differentiation. Load the file into R.

4.2.2 Calculate correlation matrix and keep only statistically significant gene-gene interactions with p-value $p < 0.05$ and the absolute value of the Pearson correlation coefficient $|r| > 0.7$. Report the number of statistically significant genes and include the top 10 interactions (in terms of correlation) as a table with r, $|r|$, and p-value.

4.2.3 Use Cytoscape (download from the course web site) for visualizing the gene co-expression network. Provide a .sif file, which is a a text file, where in every line one interaction of the network is given.
Alternatively, you can create the co-expression network with the R package igraph (which would fit better with point 4.3 as everthing is created in one go.

4.3 Sweave Report

Create your report by creating a Sweave file which contains text, R commands and results in a single file.