

Exercise for GRN Network Analysis

1. Read the gene expression profiles from the file "ExpMatAra.txt".
2. Read the table Annotations_for_genes_of_interest.txt, this file includes the genes of interest and their corresponding localization.
3. Write your own function to calculate the correlation between the genes. Compare it with rcorr function from Hmisc package in R.
4. Plot heatmap for genes which are significantly co-expressed with alpha set to 0.05 after fdr correction.
5. Create co-expression network for highly (abs correlation more than 0.5) and significantly (corrected p-values with fdr less than 0.05) co-expressed genes.
6. Perform hierarchical clustering and compare it with the implemented function in R hclust.

Homework

Hint: The homework assignment is DUE IN TWO WEEKS. Help for completion will be provided during the exercise.

7. Perform enrichment analysis for each cluster and find out enriched compartments for each cluster using hypergeometric test (localization, using localization data in file Annotations_for_genes_of_interest.txt). Predict localization for the genes for which the localization is assigned to "others".
8. Perform GO enrichment analysis for each cluster using the following packages:
 - a. library(GOstats)
 - b. library(org.At.tair.db)
9. Build co-expression network for highly and significantly correlated genes as mentioned above (use igraph). Find communities for the network, calculate corresponding modularity and perform GO enrichment analysis for each community.