PLAZA workshop

4B - Biological data analysis (co-expression analysis + DE + ChIP-Seq)

September 14-15, 2017

# CORNET Information

1. CORNET 3.0 <https://bioinformatics.psb.ugent.be/cornet/versions/cornet3.0/>

# Notes

1. When using CORNET in your internet browser, be sure that Pop-ups are NOT blocked and that Java is installed on your computer.

# Topics Covered

In this series of exercises you will learn how to use co-expression as a method to filter and prioritize experimental gene sets and to identify distinct biological processes being modulated in a specific experimental dataset.

# Exercises

## Part 1: Starting from the experiment “E2Fup\_chip” we will perform a co-expression analysis using CORNET and integrate experimental protein-protein interaction (PPI) data.

1. Using the PLAZA workbench where you created your experiment “E2Fup\_chip”, use the Export function to generate a list (text file) of the genes present [Export genes, annotations and sequences – Export Genes – Gene identifier]. Copy-paste the gene identifiers in a plain text document (Wordpad).
2. CORNET Co-expression analysis
	* Access CORNET3, select the Co-expression tool in the upper menu, and select Predefined sets of microarray expression data
	* Step1: Paste the exported gene identifiers in the box
	* Step2: Select Microarray data RNA-Seq compendium
	* Step3: Adjust Show to Pairwise correlations + Set Correlation Coefficient to 0.8
	* Select next to GO button: Also add: protein-protein interactions
	* Click GO to generate the Co-expression network
	* In the PPI menu, Step2, Select All databases + All experimental
	* Click GO (see Note 1 in case the Cytoscape application does not start)
3. To interpret the network shown in the Cytoscape application, please see the “Legend for Cytoscape visualization” shown in your web-browser.
	* Can you identify gene pairs which are showing co-expression and have a PPI interaction?
4. Analyze for gene AT3G24320 (MSH1) the network neighbors
	* Search for AT3G24320
	* Select – Nodes – First Neighbors of Selected Nodes
	* Create a new Network from these genes [File – New – Network – From Selected Nodes, All edges or push Ctrl-N]
	* Which genes in this network have a PPI? What experimental GO annotations are known for these genes, so in which process are these genes involved? [copy-paste the gene identifiers to look up GO data in PLAZA]

## Part 2: Identify putative signaling cascades which work downstream of the E2F TF.

1. In your experiment “E2Fup\_chipTF”, which gene families are represented by multiple copies? [View associated gene families – Sort using header #associated genes]
2. Write down the names of the two NAC TFs.
3. Starting from the PLAZA workbench experiment “E2Fup\_chipTF”, use the Export function to generate a list (text file) of the genes present [Export genes, annotations and sequences – Export Genes – Gene identifier]. Copy-paste the gene identifiers in a text document (Wordpad).
4. Start a new co-expression analysis using CORNET
	* Access CORNET3, select the Co-expression tool in the upper menu, and select Predefined sets of microarray expression data
	* Step1: Paste the exported gene identifiers from the previous step in the box
	* Step2: Select Microarray data: Biotic stress + Abiotic stress + Leaf + Root
	* Step3: Adjust Show to Pairwise correlations + Set Correlation Coefficient to **0.3**
	* Select next to GO button: Also add: protein-protein interactions
	* Click GO to generate the Co-expression network
	* In the PPI menu, Step2, Select All databases + All experimental
	* Click GO (see Note 1 in case the Cytoscape application does not start)
5. Which TFs share a PPI and what are the functions of these TFs?
6. Which other TF is showing co-expression with these two interacting TFs. Which GO annotations are available for this gene?
7. Do you find evidence that the NAC TFs identified in 2.6 are having working together? In which expression atlas do these TFs co-epxress? [Cytoscape – Data panel – Edge attribute browser – click Select All Attributes + select the edge between the two NAC TFs]