

Bio 311: Group Literature Synthesis HW

Due date: April 18, 2017

Instructions: Answer the following questions according to your analysis of the data and how it fits in with the literature. Choose a representative from your group and submit your group's answers to the representative's Sakai dropbox by the *beginning of class* on the due date. Email Drs. Magwene and Schmid to inform them whose dropbox is being used for your group.

- Carry out Gene Ontology (GO) analysis on clusters that you identified based on your gene expression and/or TF network analyses. What Gene Ontology terms are enriched in the different clusters? Make sure to consider all three GO categories – biological process, molecular function, and cellular component.
- For *each* of the biological process gene ontology terms of your three largest clusters, find at least one paper in the literature that discusses the biological process of interest. Provide full citations for those papers here. If your major clusters have many GO terms associated, use your best judgement for which few terms to look up (e.g. which terms have the lowest p-value? Are there terms that occur in more than one cluster? etc).
- Do your analyses shed light on how the specific biological processes of interest (identified by GO analysis above) might be regulated or changed by the stress conditions that your data sets represent?
- Summarize the biological results, insights, or conclusions from your gene expression and TF analyses in three to four bullet points. How do these results compare to the findings of your focal paper? These results and conclusions may be preliminary at this point.