Transcriptomics Homework

Due Tuesday May, 3 2016

1. Use the gene count table in the class directory (/projects/academic/courses/bch519/spring16/transcriptome) to run differential gene analysis. Use edgeR to call all differentially expressed genes between the two groups. The file contains seven columns, one listing the gene names and six more showing the counts for each of the six samples (three in each replicate). Remember that you don’t need the gene name column for the edgeR analysis. Hint: use the cut command to remove that column. Submit the final table containing the fold change, concentration, p value and decision result. Save that table as Your\_last\_name.outputTable.txt
2. Draw a volcano plot of the fold change and p-value for all genes. Save the plot as Your\_last\_name.volcano.pdf
3. Draw a MA plot showing the concentration and fold change for all the genes. Save the plot as Your\_last\_name.maplot.pdf
4. Draw a heatmap of the log counts per million for all genes. Save the plot as Your\_last\_name.heatmap.pdf.
5. Perform GO term enrichment for your differentially expressed genes. You can run it as with either option (sorted ranked list or unsorted list with background). Remember, if you use the two list option, provide as the background only those genes on chr22. You can also just use the gene names that were in the original count table. Submit the excel spreadsheet and save it as Your\_last\_name.xls
6. Submit all commands and scripts that you used in the analysis
7. Submit via email to [evantarb@buffalo.edu](mailto:evantarb@buffalo.edu)

Files to submit:

edgeR Output table

Volcano Plot

MA Plot

Heatmap

GO term enrichment excel spreadsheet

All commands and scripts that you used. This can be submitted as a single txt file