**Assignment #2: RNA-seq for Gene Expression Analyses P/BIO 381**

Your assignment for next week is to contrast differential expression between healthy (H) and sick (S) separately within each location, and then compare those results to running with location in the model as a control variable. Look at the degree that these two approaches converge, and then overall what we see in terms of number of significant differentially expressed genes going up vs. down.

Below are general guidelines that describe the elements of the assignment you should include in your short write-up. Please use 2 pages maximum to demonstrate your understanding of the conceptual background and technical details for using RNA sequencing for gene expression analyses. You should include relevant tables and figures (within the two-page limit) with legends. You may discuss the assignment with classmates, but the assignment should be prepared individually. Please provide your code for this assignment in your github lab notebook and note this in your assignment. Due Wednesday, March 8.

* Clear statement of objective (1 sentence).
* Conceptual background on what the analysis does (2-3 sentences).
* Verbal description of the mechanics of the pipeline (3-4 sentences).
* Present results (3-5 sentences).
* Tables and figures with legends.
* Interpretation (3-5 sentences).
* Critical thinking (2-3 sentences). What would you do differently? What would you do next?