

Pairwise_edgeR

This repository provides a set of scripts and templates for running the exact test provided by edgeR on one or more pairs of RNA Sequencing data to apply this workflow:

1. Clone this repository
2. Copy datafiles with readcounts for each sample into the ‘data’ folder.
 - HTSeq-count generates a two column table with feature ID’s in the first column and read counts in the second column
 - Stringtie import for edgeR analysis is not currently implemented; but will be implemented using the tximport package
3. Make updates to the script “Pairwise_edgeR_ExactTest.R”
 - update the variables “edb”, “groups”, and “contrasts” to reflect the desired sample assignment and contrasts
 - Update the call to function “createDEGSpreadSheet” to match the column configuration desired for output spreadsheets.
 - If needed, run the first 22 lines interactively to generate a sample manifest file. This file can be edited in a spreadsheet editor to add sample grouping information.
4. Run the script “Pairwise_edgeR_ExactTest.R” to generate spreadsheets with Differential expression statistics calculated by edgeR
 - Future versions will also generate a pdf report that has dispersion and MDS plots and summary DE statistics