Analyzing HTseq Data Using GenePattern

Phenotype Labels
BRCA_40_samples.cls

HTSeq Raw Counts
BRCA_40_samples.gct

Load a file to be easily accessible
RenameFile

Filter out uninformative genes
PreprocessDataset

Phenotype Labels
workshop_BRCA_labels.cls

Filtered HTSeq Counts
workshop_BRCA_filtered.gct

+

Perform diff. expression assuming negative binomial distribution
DESeq2

Perform diff. expression assuming normal distribution
ComparativeMarkerSelection

Transform counts to fit a normal distribution
PreprocessReadCounts

Ranked Gene List
negative_binomial_results

Ranked Gene List
naive_normal_results

Transformed HTSeq Counts
work[…].preprocessed.gct

Compare ranked gene lists
Lists Overlap %, Lists Similarity

Perform diff. expression assuming normal distribution
ComparativeMarkerSelection

Follow instructions from the notebook named
2017-11-02_11_CCMI_Workshop_Project.ipynb

Ranked Gene List
transformed_normal_results