Differential Expression with Diagnostic Plots using sam2counts and DESeq

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sam2counts and DESeq

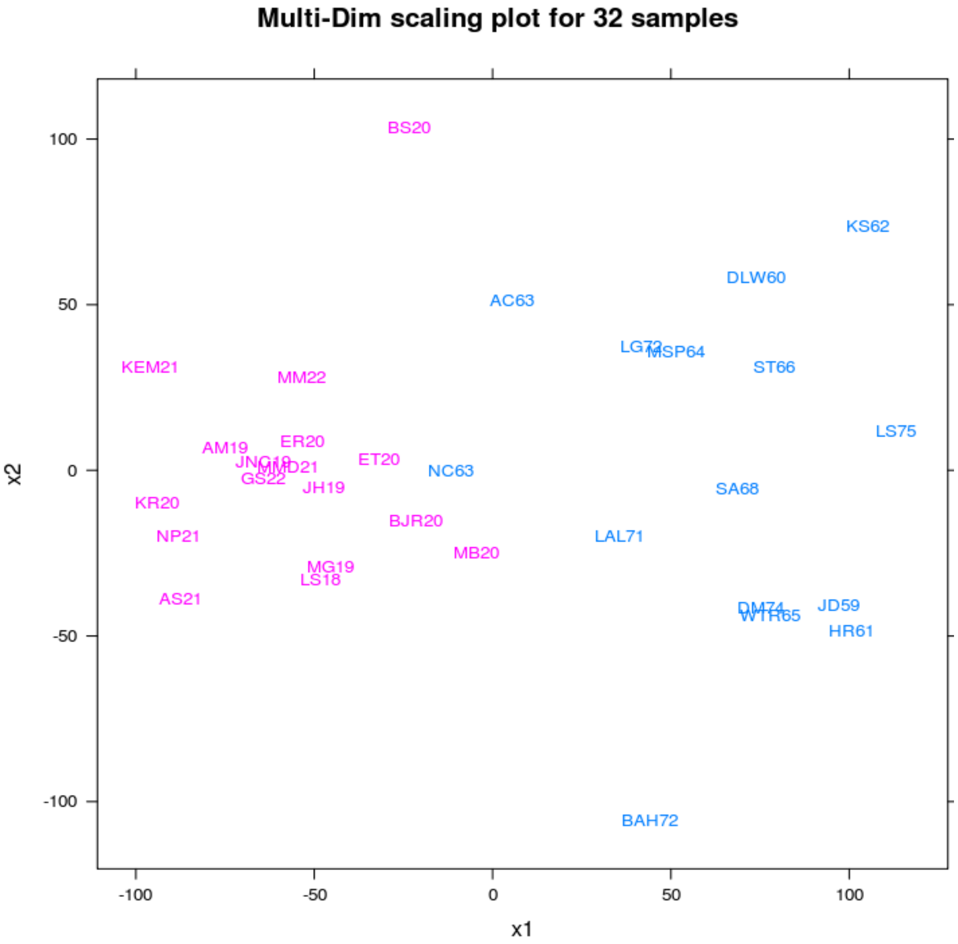
- Sam2counts
  - Python script that creates a counts table from reads aligned to transcripts.
  - Input in Galaxy
    - SAM files of sample read alignments to a transcriptome
    - Sample names
  - Output in Galaxy
    - Counts table of counts for each transcript per sample

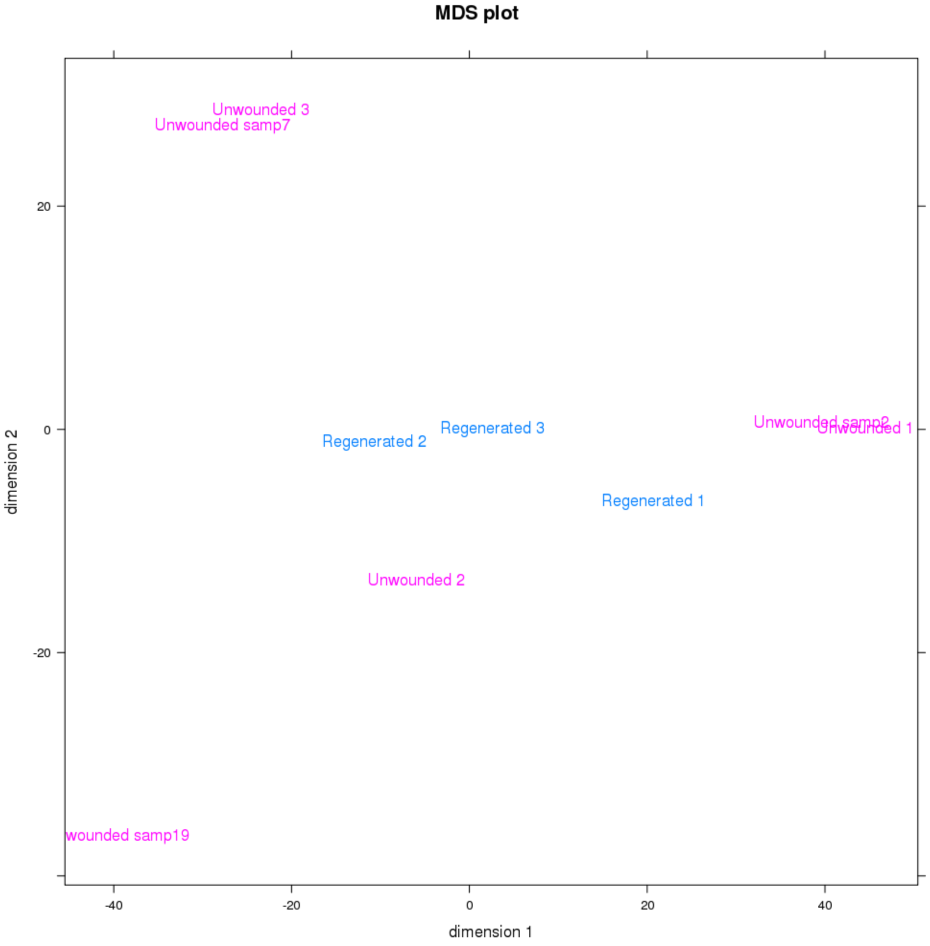
sam2counts and DESeq

- DESeq
  - Bioconductor package in R that is used to analyze differential expression data
  - Input in Galaxy
    - Counts file from sam2counts from reads aligned to a transcriptome
    - Column types and comparison types
  - Output in Galaxy
    - Toptable sorted by adjusted p-value
    - Page of diagnostic plots

MDS Plot

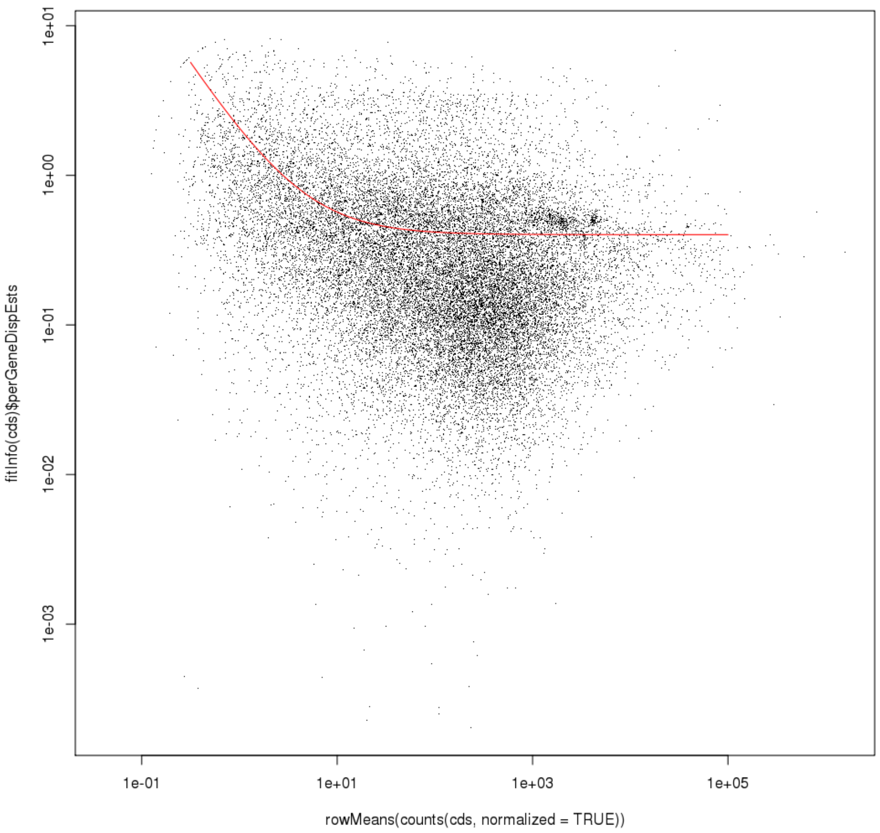
Represent distances in k-dimensional space in 2 dims

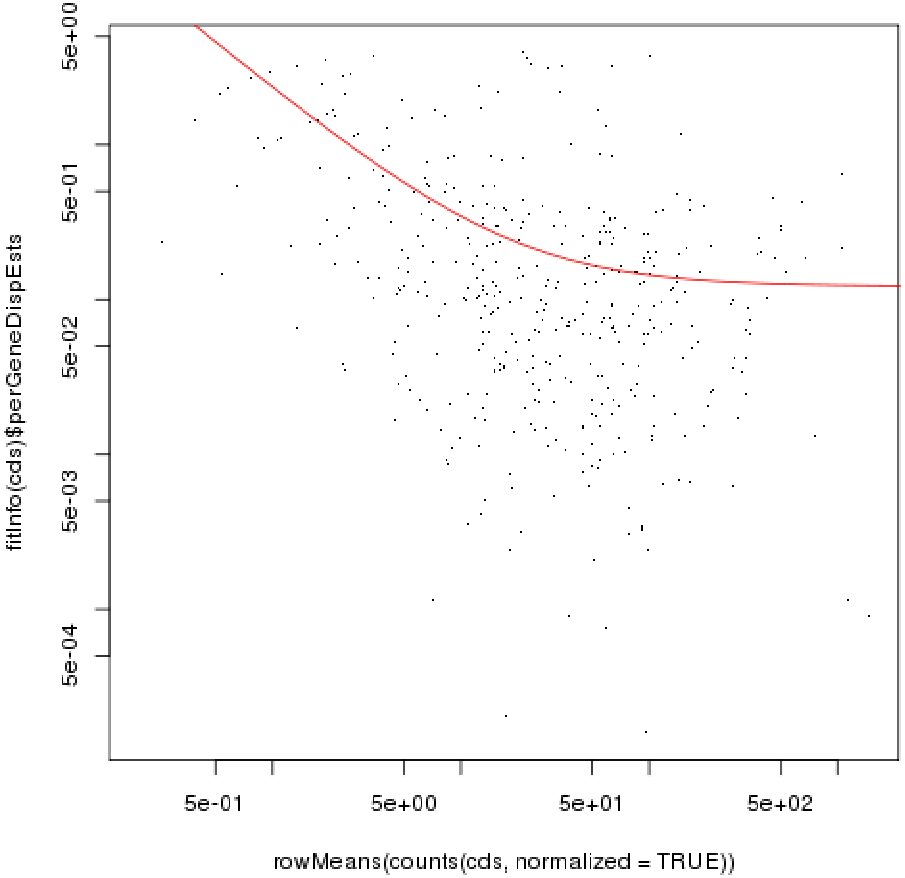




Dispersion Estimates

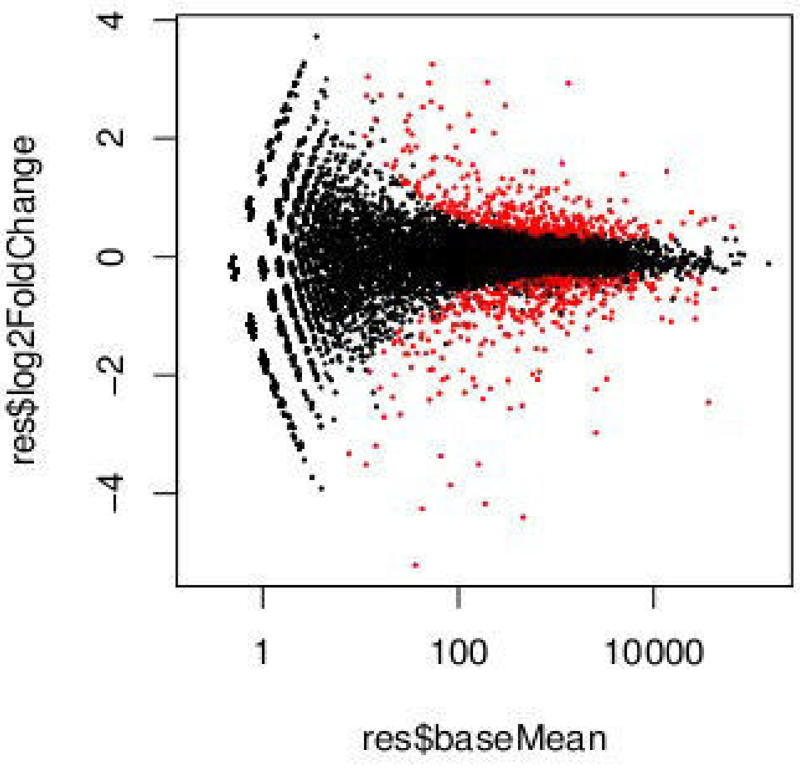
rowMeans vs. Gene Disp. Est.

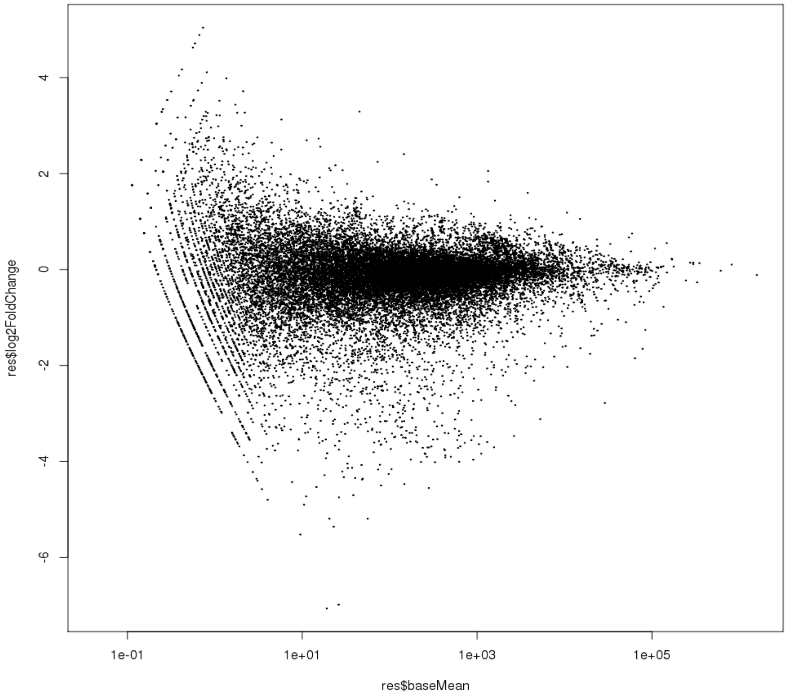




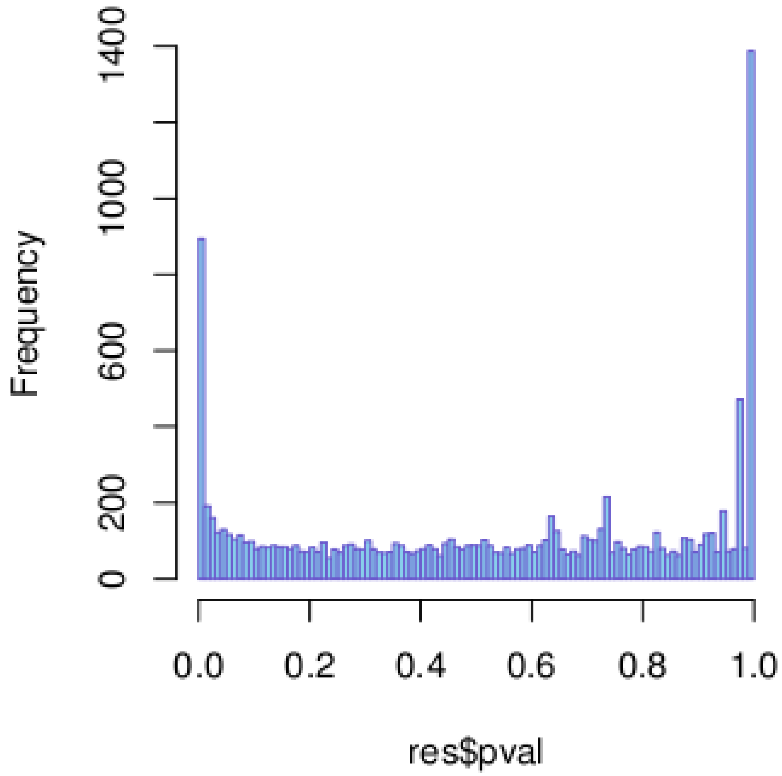
MA-Plot

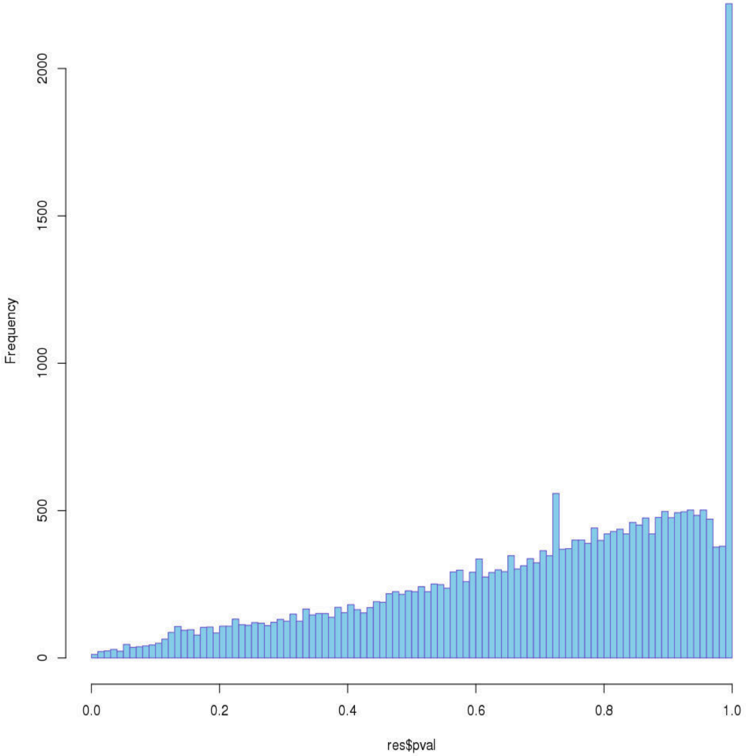
baseMean vs. log2foldChange





Histogram of p-values





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