What statistic to use to measure variability?

diagnosticsVarPlot

Evaluate the relationship between candidate statistics - coefficient of variation (CV), median absolute deviation (MAD), standard deviation (SD) - and average expression for your dataset.

ONE SAMPLE ANALYSIS

pathVarOneSample

Identify pathways and gene sets that have a different distribution in expression variability than the global distribution (all genes).

Genes are first clustered into discrete classes of expression variability, i.e. low to high, depending on the structure of the data.

Gene counts in each variability class are compared between defined pathways and the global reference (all genes).

Assessment of statistical significance in the difference is based on either an exact result using the exact test, or an asymptotic approximation using the Chi-squared test.

TWO SAMPLE ANALYSIS

pathVarTwoSamplesCont

Identify pathways and gene sets that have a different distribution in expression variability between two user-defined groups, e.g. disease versus control.

Assessment of statistical significance in the difference is based on the Kolmogorov-Smirnov test (with bootstrapping).

pathVarTwoSamplesDisc

Identify pathways and gene sets that have a different distribution in expression variability between two user-defined groups, e.g. disease versus control.

Genes are first clustered into 3 discrete classes of expression variability,.

Gene counts in each variability class are compared between the two groups.

Assessment of statistical significance in the difference is based on either an exact result using the exact test, or an asymptotic approximation using the Chi-squared test.

Output

S4 class:
geneDistributionSet

S4 class:
geneDistributionSet2

S4 class:
geneDistributionSet3

Interpret Results: Visualization and Plotting

Plot results for specific pathways of interest.

plotPway
saveAsPDF

Extract genes from specific pathways of interest.

getGenes