

Functional analysis



Miscellaneous

artmsAnalysisQuantifications()

artmsEvidenceToSAINTq() artmsEvidenceToSaintExpress() artmsPhosfateOutput() artmsPhotonOutput() etc





Input Files

keys.txt





config.yaml

artMS

Analytical R Tools for Mass Spectrometry

http://artms.org



Console Terminal \times

--- Removing log2fc outliers (-15 < log2fc < +15) --- Number of +/- INF values: 324 --- Merging Changes with bioReplica Info ---+ Enrichment analysis using gProfiler...done! ---+ Corum Protein Complex Enrichment Analysis ---+ Enrichment analysis using gProfiler...done! ---+ Corum Protein Complex Enrichment Analysis 3) Enrichment of selected NEGATIVE significant changes ---+ Enrichment analysis using gProfiler...done! ---+ Corum Protein Complex Enrichment Analysis



http://artms.org



Input Files

evidence.txt

keys.txt

contrast.txt

config.yaml

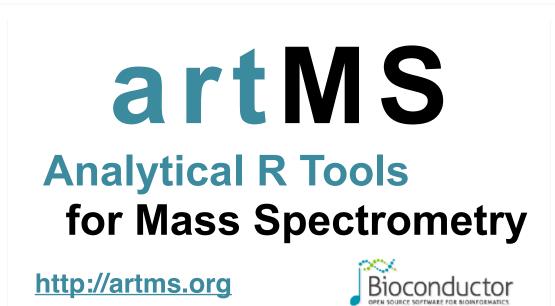
Functional analysis

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Terminal Console ~/ # > artmsAnalysisQuantifications(log2fc_file = "quant-phglobal-pre/phglobal-results.txt", modelqc_file = "quant-phglobal-pre/phglobal-results_ModelQC.txt", species = "human") artMS: ANALYSIS OF QUANTIFICATIONS --- No Pathogen extra in these samples >> LOADING QUANTIFICATIONS (-results.txt from MSstats) >> LOADING modelqc FILE (ABUNDANCE) --- Outliers kept (user selection) --- Total number of genes/proteins: 3526 --- Removing log2fc outliers (-15 < log2fc < +15) >> IMPUTING MISSING VALUES --- Number of +/- INF values: 324 --- Plotting distributions of log2fc and pvalues >> PLOTS: ABUNDANCE PLOTS >> PLOTS: REPRODUCIBILITY PLOTS >> PLOT: CORRELATION BETWEEN ALL COMPARISONS >> PLOT: CORRELATION BETWEEN QUANTIFICATIONS (based on log2fc values) --- Only one Comparison is available (correlation is not possible) >> PRINCIPAL COMPONENT ANALYSIS BASED ON ABUNDANCE >> ANNOTATIONS --- Abundance data --- Relative Quantifications (Log2fc) >> FILTERING CHANGES BEFORE PRINTING OUT --- Merging Changes with bioReplica Info --- Removing NA --- Add labeling of condition more abundant in the quantification --- Removing proteins not found in a minimal number (2) of biological replicates --- Filtering is done! >> GENERATING QC PLOTS ABOUT CHANGES (log2fc) --- Distribution of log2fc and pvalues --- Proportion imputed values >> HEATMAPS OF CHANGES (log2fc) --- All changes --- Only significant changes >> ENRICHMENT ANALYSIS OF SELECTED CHANGES USING GPROFILER 1) Enrichment of ALL significant Changes ---+ Enrichment analysis using gProfiler...done! --- No significant results from the enrichment analysis ---+ Corum Protein Complex Enrichment Analysis 2) Enrichment of selected POSITIVE significant changes ---+ Enrichment analysis using gProfiler...done! ---+ Corum Protein Complex Enrichment Analysis 3) Enrichment of selected NEGATIVE significant changes ---+ Enrichment analysis using gProfiler...done! ---+ Corum Protein Complex Enrichment Analysis --- Annotating species(s) in files >> GENERATING FINAL OUTPUT FILES >> PLOT OUT: TOTAL NUMBER OF PROTEINS/SITES QUANTIFIED >> CLUSTERING ANALYSIS OF QUANTIFICATIONS >> WRITING THE OUTPUT FILES Folder <artms_cs_ph-cancer/quant-phglobal-pre/analysis_quant_adjpvalue> - EXCEL: artms_cs_ph-cancer/quant-phglobal-pre/analysis_quant_adjpvalue/phglobal-results-summary.xlsx - Log2fc Wide: artms_cs_ph-cancer/quant-phglobal-pre/analysis_quant_adjpvalue/phglobal-results-log2fc-wide.txt - Log2fc Impute: artms_cs_ph-cancer/quant-phglobal-pre/analysis_quant_adjpvalue/phglobal-results-log2fc-wide.txt - ENRICHMENT files should also be out >> SUPER ANALYSIS COMPLETED



Input Files

we evidence.txt

keys.txt

contrast.txt

config.yaml

- Annotations
- Summary files in different format (xls, txt) and shapes
- Numerous summary plots
- Enrichment analysis using Gprofiler
- PCA of protein abundance
- PCA of quantifications
- Clustering analysis

Functional analysis

artmsAnalysisQuantifications()

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EXCEL

-results-summary.xlsx

-results-abundance-long.txt

TXT FILES

PDF FILES

-results-abundance-wide.txt
-results-enrich-MAC-allsignificants-corum.txt

-results-enrich-MAC-allsignificants.txt

-results-enrich-MAC-negatives-corum.txt

-results-enrich-MAC-negatives.txt

-results-enrich-MAC-positives-corum.txt

-results-enrich-MAC-positives.txt

-results-log2fc-long.txt

-results-log2fc-wide.txt

-results.log2fc-clusterheatmap-enriched.txt

-results.log2fc-clusterheatmap.txt

-results-enrich-MAC-allsignificants-corum.pdf

-results-enrich-MAC-negatives-corum.pdf

-results-enrich-MAC-positives-corum.pdf

-results-pca-correlations.pdf

-results-pca-pca01.pdf

-results-pca-pca02.pdf

-results-pca-pca03.pdf

-results.clustering.abundance.all-overview.pdf

-results.clustering.abundance.all-zoom.pdf

-results.clustering.log2fc.all-overview.pdf

-results.clustering.log2fc.all-zoom.pdf

-results.clustering.log2fcSign.all-overview.pdf

-results.clustering.log2fcSign.all-zoom.pdf

-results.distributions.pdf

-results.distributionsFil.pdf

-results.imputation.pdf

-results.log2fc-clusterheatmap.pdf

-results.log2fc-clusters.pdf

-results.log2fc-corr.pdf

-results.log2fc-dendro.pdf

-results.log2fc-individuals-pca.pdf

-results.TotalQuantifications.pdf

-results.correlationConditions.pdf

-results.correlationQuantifications.pdf

-results.relativeABUNDANCE.pdf

-results.reproducibilityAbundance.pdf