

Functional analysis



artmAnalysisQuantifications()

artmsEvidenceToSAINTq()

artmsEvidenceToSaintExpress()

artmsPhosphateOutput()

artmsPhotonOutput()

etc

Inputifies

keys.txt



evidence.txt

contrast.txt

config.yaml

artMS

**Analytical R Tools
for Mass Spectrometry**


<http://artms.org>



Console

Terminal ×



~/ 




> |


```
> artmsAnalysisQuantifications(  
  log2fc_file = "quant-phglobal-pre/phglobal-results.txt",  
  modelqc_file = "quant-phglobal-pre/phglobal-results_ModelQC.txt",  
  species = "human")
```


artMS

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Input Files

- evidence.txt
- keys.txt
- contrast.txt
- config.yaml

Functional analysis

Miscellaneous

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Console Terminal

~/


```
> 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
```

artMS

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Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

Input Files

evidence.txt

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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()



Miscellaneous

artmsEvidenceToSAINTq()
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EXCEL

-results-summary.xlsx

TXT FILES

-results-abundance-long.txt
-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

PDF FILES

-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