

Galaxy

dev1.ab.wurnet.nl:8088

Galaxy

Analyze DataWorkflowShared DataVisualizationAdminHelpUser

Using 33.7 GB

Tools

search tools

START

Upload File from your computer

POST-GENOMICS

Proteomics MS tools

QC AND VALIDATION

Fasta Validator

Basic FASTA file validation

MS/MS DATABASE SEARCH STEPS

XITandem

MS/MS DB search

DB search converter

POST-PROCESSING, QUANTIFICATION AND IDENTIFICATION

Csv2Apm

Converts MS/MS data in CSV format to APML format

ProgenesisConverter

Converts Progenesis aligned feature lists in CSV format to APML

IsoFix

Identifies in-source decay peptides and corrects protein assignments

SedMat

Matches MS and MS/MS results

Quantiline

Labeled ms/ms data pre-processing for Protein Quantification (and Inference) pipelines

MsFilt

Filters annotations based MS/MS peptide identification and annotation quality measures

Quantifere

Protein Inference by Peptide Quantification patterns

VISUALIZATION

NapQ

[[experimental]]'no alignment'(alignment-free) peptide quantification

CytoExport

Exports CSV files to visually rich

Quantifere (version 1.0.1)

Peptide (filtered) quantification files (APML)s

The APML contents as aligned, annotated and scored feature lists, as produced by MsFilt tool. Select one or more files. For 2D-LC-MS we expect one file per fraction.

Add new Peptide (filtered) quantification files (APML)

Peptide (filtered) identification files (MS/MS identifications)s

Full set of MS/MS peptide identification files, including peptides that could not be quantified. This set of identifications is ideally filtered on some quality and statistical measures (e.g. as is done by MsFilt). Tip: to base the inference only on the selected peptide quantification files, you can select the same quantification files here as well. Select one or more files.

Add new Peptide (filtered) identification files (MS/MS identifications)

Data is from 2D LC-MS:

Data acquisition was done in multiple fractions.

Peptide identification files are not filtered by MsFilt:

Check this option if your identification files are either NOT filtered by MsFilt or are filtered but by some other tool

Quantification data to use:

auto

Quantification data to use for the pattern clustering and inference steps. NB: check if the chosen data is also present in your file, or choose 'auto' to let Quantifere check which quantification type is present in most peptides.

Minimum correlation in a cluster:

0.88

Features will be grouped by their protein annotation and sample intensity values correlation. Set here the minimum correlation expected between grouped members. This is used to guide the clustering algorithm.

Minimum protein coverage (%):

3.0

This will remove proteins that have a too small portion of their sequence covered by peptide matches.

Minimum number of different peptide matches with a score above average:

1

This will remove proteins that do not have enough reasonable peptides hits.

Minimum number of peptide identifications for inference peptides:

1

Minimum number of peptide identifications a peptide needs to be used as inference peptide for secondary proteins.

(Functional)annotation mapping file (csv or tsv format):

Selection is Optional

Optional file that maps protein accessions to a network, pathway or other higher level annotations. In this file a header line is expected with these 2 columns (names and lower case is important): accession,annotation

Refine matches model:

☒

This will let the algorithm search for a reduced set of secondary protein matches that still explains the variation in the peptide quantification patterns

Generate summary report:

☒

Execute

History

data 120, data 119, and data 3: Inference log (CSV)

125: Quantifere on data 120, data 119, and data 3: Proteins list (CSV)

124: MsFilt on data 1, data 117, and data 10 - HTML report

123: label x - MsFilt on data 1, data 117, and data 10: Protein coverage details (CSV)

122: label x - MsFilt on data 1, data 117, and data 10: Ranking table (CSV)

121: label x - MsFilt on data 1, data 117, and data 10: Full CSV

120: label x - MsFilt on data 1, data 117, and data 10: identifications (filtered APML)

119: label x - MsFilt on data 1, data 117, and data 10: quantifications (filtered APML)

117: Quantiline on data 10 and data 1: Peptides quantification (APML)

10: DB search converter on data 5

6: XITandem on data 2 and data 1 - HTML report

5: XITandem on data 2 and data 1 - Results XML

3: clusters_annotation.csv

2: MGI UniProtMouse 20071203 iPRG2008 fixed.fasta

1: mzML format_peaklists.zip