ProteoArray

Module name: ProteoArray
Description: LC-MS proteomic data processing module
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Release: 1 (Beta)

Summary: The ProteoArray module provides feature detection and sample alignment for liquid chromatography-mass spectrometry (LC-MS) based proteomic data. Given a series of LC-MS experiments in mzXML format, ProteoArray detects and aligns features across runs. For each LC-MS run, the module employs a mass/time binning approach, which sums the intensity of a peptide across sequential spectra during its elution profile. Peptides are then matched across all runs by mass and retention time, within 0.1 Da and 200 scans, respectively. The output array file (.gct) provides the peptide feature's mass as the name identifier, and retention time in each sample in the description column.

Notes:
- This package was developed and tested on LC-MS data produced on a Waters/Micromass LCT Premier, which is an electrospray time of flight mass spectrometer.

Parameters:

Name	Description
input.zip.filename	zip file of LC-MS runs in mzXML format.
output.file	output filename

Return Value:

1. gct file containing array of peptide features and their corresponding intensities.

Platform dependencies:

Task type:	Proteomics
CPU type:	any
OS:	any
Java JVM level:	1.4
Language:	Java