GenePattern

LocatePeaks Documentation

Module name:	LocatePeaks
Description:	Locates detected peaks in a spectrum.
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Release:	1.0

Summary: This function, when used in conjunction with the Peaks module, locates peaks in spectra. The output of the Peaks module contains the result of applying digital filters. This output can be visualized using the PlotPeaks module, and converted to peak lists using LocatePeaks. LocatePeaks identifies the location of a peak based on maximum of the filtered signal, or center of area.

References:

- None.

Parameters:

Name	Description
peaks.output.filename	The output from the Peaks module - .odf
output.file	output file name
locate.peaks.as	max-location of maximum filtered value, area-center of area of the peak

Return Value:

1. odf file containing original spectrum, filtered (peak detected) signal and located peaks (m/z values that contain a peak are marked with peak intensity; other m/z values contain 0).

Platform dependencies:

Task type:	Proteomics
CPU type:	any
OS:	any
Language:	R
Support files:	mclust_2.1-6.tgz, mclust_2.1-7.tar.gz, mclust_2.1-7.zip, pipeline.wrapper.R , process.r, util.r

Native command line: <R> <libdir>pipeline.wrapper.R peaks.locate.wrapper <peaks.output.filename> <output.file> <locate.peaks.as> <libdir>