



CompareSpectra Documentation

Description: Compares two spectra to determine similarity
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Summary: Filters the two spectra to remove noise and matrix signal (by restricting spectra to between low.Da and high.Da), and determines similarity by computing the maximum of the cross correlation function.

Parameters:

Name	Description
spectrum1.filename	Spectrum file - .csv
spectrum2.filename	Spectrum file - .csv
output.file	Output file name - .odf
low.Da	Minimum M/Z to include
high.Da	Maximum M/Z to include

Output File:

1. odf file containing the maximum cross correlation

Platform dependencies:

Module type: Proteomics
CPU type: any
OS: any
Language: R 2.5

GenePattern Module Version Notes

Date	Version	Description
10/12/12	2	Fixed parsing of input files, changed default value of output file, and suppressed R package startup messages