

## Peaks Documentation

**Description:** Determine peaks in the spectrum using a series of digital filters.  
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**Summary:** Performs peak detection using digital convolution (moving-window) filters. The input spectrum is subjected to the following filters (in sequence): smoothing (low-pass) filter, adaptive background correction (unsharp masking) filter, and high-pass filter. The function returns a table with the original spectrum and the result of applying the filters.

### References:

- D. R. Mani & Michael Gillette. 2005. *Proteomic Data Analysis: Pattern Recognition for Medical Diagnosis and Biomarker Discovery*. In Mehmed Kantardzic and Jozef Zurada (Eds.) *New Generation of Data Mining Applications*, IEEE Press.

### Parameters:

Name	Description
spectrum.filename	spectrum data file - .csv
low.Da	Minimum M/Z to include
high.Da	Maximum M/Z to include
percentile	After applying filters, threshold above which peaks are located (default=0.65)
smoothing.size	Size of the smoothing filter (default=21)
adaptive.background.correction.strength	Strength of the adaptive background correction filter (default=0.75)
adaptive.background.correction.size	Size of the adaptive background correction filter (default=21)
high.pass.filter.strength	Strength of the high pass filter (default=10)
high.pass.filter.factor	Filter factor for the high pass filter (default=5)
output.file	output file name

### Output File:

1. odf file containing original spectrum and filtered (peak detected) spectrum.

### Platform dependencies:

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