

Available for FREE with MassHunter and/or Mass Profiler Professional licenses

A Novel Batch Feature Extraction Software Tool for Differential Profiling of Mass Spectrometric Data

Profinder is the latest member of the MassHunter software family, built specifically to optimize chemometric profiling workflows. The recursive batch processing capability facilitates rapid and robust re-mining of raw data files, significantly reducing missing values.

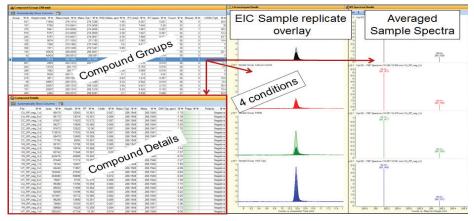
Higher quality results

Processing the mass spectrometric data generated from complex biological samples can be a noisy, challenging task for any feature-finding program. MassHunter Profinder greatly reduces the noise associated with profiling data sets by using a recursive feature extraction workflow. The software facilitates manual editing tasks such as overlaying, adding, and deleting peaks, and its user-defined peak re-integration capabilities can significantly reduce the false positives/false negatives that critically impact subsequent statistical analyses such as PCA.

Key Benefits

- Processes multiple highresolution MS data files
- Novel batch molecular feature extraction algorithms minimize false positives and false negatives
- A new isotope grouper for improved extraction of true biological compounds
- Multi-threading results in a major reduction in processing time
- Improve visualization of results through multiple chromatogram overlay and coloring by group
- Simple file format for exporting results and differential analysis in Mass Profiler Professional





MassHunter Profinder organizes batch extracted data into a few easy-to-manage windows, with powerful editing and chromatographic visualization capabilities.

Ordering information:

MassHunter Profinder is included at no additional cost as part of the MassHunter Qualitative Analysis and Mass Profiler Professional software package.

For more information: www.agilent.com/chem/profinder

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