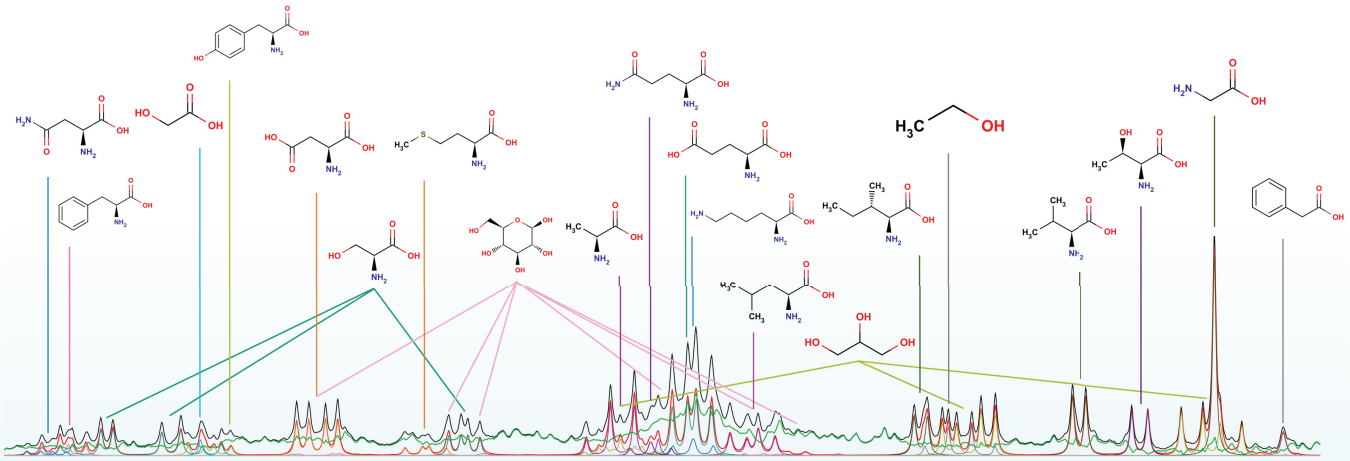
Ask for a TRIAL VERSION

CHENOMX

QUANTITATIVE METABOLITE MEASUREMENTS WITH NMR.



DISCOVER MORE

- Quantitative results with high-throughput experiments
- Deconvolve overlapping spectral regions
- Identify metabolites using detailed compound signatures
- NEW library from HMDB.ca source *(over 600 entries)*
- Automatic batch profiling
- Create useful figures for talks and publications

www.chenomx.com

About Us

CHENOMX offers a unique and patented method of simplifying the measurement of the concentration of biological mixture components as measured by NMR instruments. The method is based on software and an extensive spectral signature library of relevant metabolites. The signature library consists of both theoretical and empirical data within a model which adjusts to the NMR field strength and sample conditions to closely match that of the experiment spectrum. Then the software, through a combination of automated and supervised operation, uses the models to de-convolute the spectral signatures of the various components in the mixture being measured. Overlapping spectral areas are simplified by the subtraction of the identified peaks of known components from the spectrum as they are fitted into the spectrum and thus are made visible to be compared to other compounds that were previously hidden.

The result is that 1D H NMR spectra can be turned into tables of identified compounds and their concentration in a convenient and straightforward way.

The Technology Platform

Chenomx's patented NMR-based metabolomics platform provides a powerful, global analysis of small molecule metabolites within complex biological mixtures. A compound list of over 300 metabolite models is used as a reference database for the analysis. Users are able to add their own compounds to the library as needed.

Metabolomics

Metabolic profiling, or metabolomics, is the study of patterns in the complement of low molecular weight compounds found in biological fluid samples. Small molecule byproducts of metabolic processes vary in concentration and relative proportion in response to disruptions in the metabolism of an organism, providing insight into the health status of the organism. Genetic abnormalities, enzyme inhibition or activation, pathological conditions, and drug actions can create metabolic disruptions detectable in the metabolite content of biofluids.

Nuclear Magnetic Resonance

Nuclear Magnetic Resonance (NMR) spectroscopy is a powerful tool with a wide range of applications in academia, industry, and medicine. NMR has proven to be a versatile and productive technology for metabolomics.

Unlike other analysis platforms, NMR does not rely on separating mixtures before analysis. NMR can simultaneously scan for hundreds of metabolites in biological samples, and has been referred to as a "universal detector". NMR's non-destructive, global detection make it a strong choice for any metabolomics study.

Targeted Profiling

Chenomx's patented Targeted Profiling technique addresses two of the more challenging aspects of NMR-based metabolomics: identifying and quantifying metabolites.

Targeted Profiling identifies compounds in a complex biofluid mixture rapidly and accurately. This direct analysis approach differs from previously published methods, which depend on binned spectral areas. Targeted profiling relies instead on libraries of compound signatures modeled to behave like the pure spectra of the individual compounds under comparable experimental conditions. The underlying spectral libraries are collected at a variety of pH conditions to account for variations among sets of samples. Analysis of samples using target profiling directly yields both the identity and concentration of individual compounds in a single operation.

What You'll Need for the Software

- **Chenomx runs on multiple platforms including:** Windows, Mac OS X, Linux
- **The Chenomx library supports** 400 through 800 NMR spectrometers manufactured by Agilent/Varian, Bruker, JEOL and others supporting the JCAMP spectral data format. Other field strengths are supported by the software with user-created libraries**.**
- **Libraries available utilizing HMDB.ca spectral data.**

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