
COMPREHENSIVE COUPLED HIGHER DIMENSIONAL CHROMATOGRAPHIC AND MASS SPECTROMETRIC TOOLS FOR HIGH THROUGHPUT METABOLIC FINGERPRINTING

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The detection of early biomarkers for widespread diseases like diabetes type II is a challenging task. Potential biomarkers can be hidden within the genome, proteome or metabolome of a biological individual. Because of the biological variability large numbers of individuals have to be probed to get statistical significant results.

The focus of the present paper will be on metabolic fingerprinting based on different comprehensive coupled gas chromatographic/mass spectrometric tools and on a concerted data analysis technique as part of an integrative system biological concept for biomarker discovery.

Higher dimensional gas chromatographic devices are realized by comprehensive coupling of two or more preferable orthogonal devices. In case of GCxGC two gas chromatographic columns are coupled by a modulator device. Similar separation characteristics can be achieved by coupling only one gas chromatographic dimension with mass spectrometry (GCxMS). Here, mass spectrometry is used as independent separation dimension. However, this is only possible if the mass spectrometer allows a bijective relation between mass signal and chemical analyte. This relation can be achieved with soft ionization like photo ionization techniques. Both techniques can also be coupled to build a comprehensive three dimensional gas chromatographic/mass spectrometric separation.

While GCxMS results in a two dimensional separation plane, GCxGC-MS and GCxGCxMS give three dimensional separation spaces. An additional dimension can be added for the quantitative information. Along with the dimensionality also the amount of information increases dramatically. The bottleneck here is a fast and preferentially automatic data analysis routine combined with a profound statistical evaluation of the data.

We will present the concept for xMS based chromatographic techniques and compare them to conventional xGC techniques. In addition also a concept for data handling and data analysis will be presented. Both will be optimized for the special case of metabolic fingerprinting with the need for high throughput.