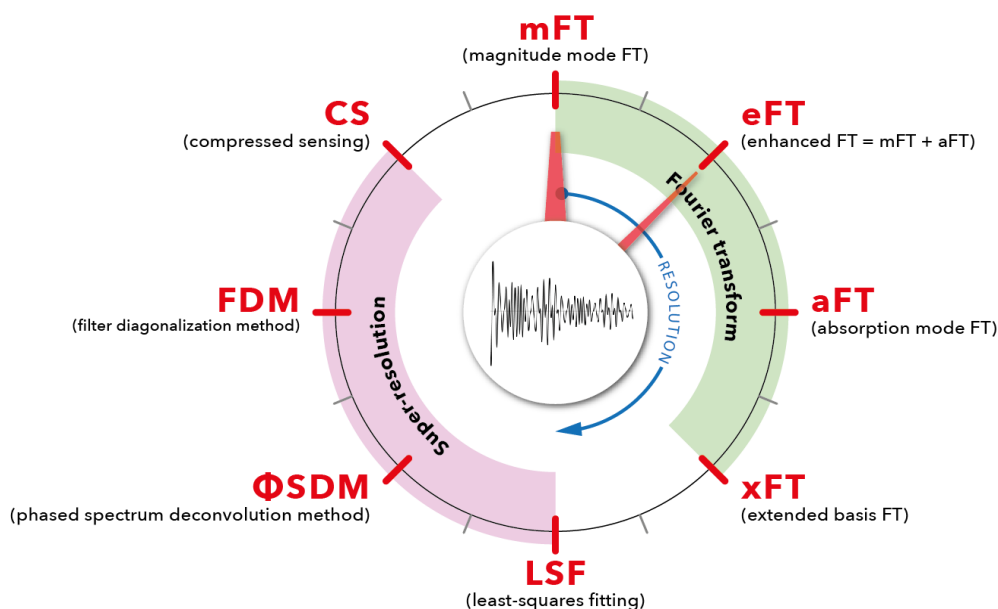## Super-Resolution Mass Spectrometry

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Resolution is one of the most important analytical characteristics in mass spectrometry. Fourier transform mass spectrometry (FTMS) offers the highest resolution performance among all mass spectrometers, Figure [1]. However, achieving high- and ultra-high-resolution in FTMS requires long ion detection times (time-domain transient length), up to 3-4 s and beyond [2]. Acquiring such long transients in FTMS is challenging and is not supported by the majority of FTMS instruments. In addition, the long transients are prohibitive for time-constraint experiments (omics and imaging).

Super-resolution mass spectrometry (SRMS) was thus introduced as an analytical technique to overcome the uncertainty principle in FT and provide a multiple-fold (2-10 times) increase in resolution compared to the conventional FT methods for the same length transients. To achieve this enhanced resolution performance, the SR algorithms are used, Figure [1]. Many SR algorithms, such as Filter Diagonalization Method (FDM), were initially developed and used in the NMR.

On a practical side, the SRMS implementation requires access to the time-domain transients. These are directly available from many NMR and FT-ICR MS instruments but not from the Orbitraps. To enable access to the Orbitrap transients, we developed an external high-performance data acquisition system (FTMS Booster) that acquires time-domain data in parallel to mass spectra [3].

We will introduce the basics of the SRMS and review the SRMS development and main methods from the early days to the most recent advances and applications [2]. Our group at EPFL and then at Spectroswiss has played a pioneering role in the SRMS development and coined the SRMS term.

[1] Y. O. Tsybin, *Chimia*, **2014**, *68*, 168-174.
[2] A. N. Kozhinov, A. Johnson, K. O. Nagornov *et al.*, DOI: 10.1021/acs.analchem.2c04742
[3] K. O. Nagornov, M. Zennegg, A. N. Kozhinov et al., *JASMS*, **2020**, *31*, 257-266