

MASS SPECTROMETRIC IMAGING FOR FREE (ALMOST)

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MALDI mass spectrometric imaging (MSI) is a relatively new technique, which combines arrays of MALDI-TOF mass spectra with digital analysis to produce computer-generated images. Each spectrum corresponds to a single pixel in the final image, which in a typical application shows the distribution of compounds of a certain m/z value or in an m/z range. The abundance of those compounds is shown as a gradation of brightness or colour corresponding to their peak height. MSI is of particular interest in the analysis of biological materials, where it is used to visualise various compounds, from low molecular weight molecules to 50 or 100 kDa proteins.

In general, the limiting factor for the application of MSI can be the lack of software to mechanically and digitally prepare and drive the MSI and to process the results. Most major manufacturers either have software commercially available or are working on software solutions, while there is also third-party software for some instruments.

In our work on mammalian models for brain plasticity, we wanted to complement established imaging techniques (such as immunocytochemistry and *in situ* hybridisation) with MSI, because the latter does not require stains, labels, or advance knowledge of the molecules to be visualised. For this purpose, we had the Bruker Reflex IV MALDI-TOF at our disposal. In order to successfully implement MSI on this instrument, we have developed a low-cost solution for the application of matrix on tissue sections (using a flatbed plotter), and we have designed two new software programs, which enable MALDI mass spectrometric imaging on Bruker Reflex and Ultraflex instruments. The first program, *CreateTarget*, creates a high density raster with the dimensions of the tissue section, and converts these parameters to a virtual target plate file that can be imported in the normal Bruker mass spectrometer control software. Following automated spectrum acquisition, the second program, *Analyze This!*, converts the array of spectra to an Analyze 7.5 image format that can be read by the freely available BioMap image analysis software. These programs are sufficient to allow mass spectrometric imaging, and offer a valid and free alternative to commercially available software.