Tools and strategies for visualization of large image datasets in high-resolution imaging mass spectrometry

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Mass spectrometry based proteomics is one of the scientific domains in which experiments produce a large amount of data that need special environments to interpret the results. Without the use of suitable tools and strategies, the transformation of the large data sets into information is not easily achievable. Therefore, in the context of the virtual laboratory of enhanced science, software tools are developed to handle mass spectrometry data sets. Using different data processing strategies for visualization, it enables fast mass spectrometric imaging of large surfaces at high-spatial resolution and thus aids in the understanding of various diseases and disorders. This article describes how to optimize the handling and processing of the data sets, including the selection of the most optimal data formats and the use of parallel processing. It also describes the tools and solutions and their application in mass spectrometric imaging strategies, including new measurement principles, image enhancement, and image artifact suppression.

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