Abstract: M²aia: Mass Spectrometry Imaging Applications for Interactive Analysis in MITK

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Mass spectrometry imaging (MSI) is a label-free analysis method for resolving biomolecules or pharmaceuticals in the spatial domain. It offers unique perspectives for the examination of entire organs or other tissue specimens. Owing to increasing capabilities of modern MSI devices, the use of 3D and multi-modal MSI becomes feasible in routine applications — resulting in hundreds of gigabytes of data. To fully leverage such MSI acquisitions, interactive tools for 3D image reconstruction, visualization, and analysis are required, which preferably should be open-source to allow scientists to develop custom extensions. We introduce M²aia (MSI applications for interactive analysis in MITK), a software tool providing interactive and memory-efficient data access and signal processing of multiple large MSI datasets stored in imzML format. M²aia extends MITK, a popular open-source tool in medical image processing. Besides the steps of a typical signal processing workflow, M²aia offers fast visual interaction, image segmentation, deformable 3D image reconstruction, and multi-modal registration. A unique feature is that fused data with individual mass axes can be visualized in a shared coordinate system. We demonstrate features of M²aia by reanalyzing an N-glycan mouse kidney dataset and 3D reconstruction and multi-modal image registration of a lipid and peptide dataset of a mouse brain, which we make publicly available. To our knowledge, M²aia is the first extensible open-source application that enables a fast, user-friendly, and interactive exploration of large datasets. M²aia is applicable to a wide range of MSI analysis tasks. The work was published in GigaScience 2021 [1].

References

1. Cordes J, Enzlein T, Marsching C, Hinze M, Engelhardt S, Hopf C et al. M²aia: interactive, fast, and memory-efficient analysis of 2D and 3D multi-modal mass spectrometry imaging data. GigaScience. 2021;10(7):giab049.