

MISA++: A standardized interface for automated bioimage analysis.

Gerst R, Medyukhina A, Figge MT (2020) MISA++: A standardized interface for automated bioimage analysis. *SoftwareX* 11, 100405.

[Details](#)



Abstract

Modern imaging techniques, such as lightsheet fluorescence microscopy (LSFM), allow the capture of whole organs in three spatial dimensions. The analysis of these big volume image data requires a combination of user-friendly and highly efficient tools. We here present *MISA++*, an image analysis framework that allows easy integration of custom high-performance *C++* tools into third-party applications via standardized components for parallelization, data and parameter handling, command line interface, and communication with third-party applications. We demonstrate its capabilities by implementing a plugin for *ImageJ* that provides a graphical user interface for any application built with our framework, and a high-performance re-implementation of our *Python*-based algorithm to segment glomeruli in LSFM images of whole murine kidneys.

Beteiligte Forschungseinheiten

[Angewandte Systembiologie](#) [Marc Thilo Figge](#) [Mehr erfahren](#)

Leibniz-HKI-Autor*innen



Marc Thilo Figge

[Details](#)



Ruman Gerst

[Details](#)



Anna Medyukhina

[Details](#)

Identifier

doi: 10.1016/j.softx.2020.100405