Semi-automated image segmentation of Multi Isotope Imaging Mass Spectrometry data in the ImageJ plugin "OpenMIMS"

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Abstract

Multi-isotope imaging mass spectrometry (MIMS) is a technique for creating high quality image data with nanometer resolution that can be applied to many areas of biological research. Its ability to trace changes in the cell with non toxic markers and monitor dynamic states (e.g. protein turnover rate) is of great value for biomedical research[1][2][3]. In mouse models of disease, such as the trait anxiety model, the MIMS technology can be exploited to gain important protein turnover information in brain regions of interest for the anxiety phenotype. The analysis of the high resolution images generated by the MIMS technology involves a great deal of manual work. The ImageJ analysis module OpenMIMS[4] provides many tools for statistical analysis and visualization of MIMS data. Recently, the plugin has been extended to allow for fast and robust image segmentation. An SVM based segmentation algorithm has been developed to enable semi-automated image segmentation. The user is able to select features and classes to train a model which can later be used for quick prediction of regions of interest for images measured under similar conditions. Moreover the implemented segmentation framework allows developers an easy extension for other algorithms capable to segment MIMS images.

References

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