

Image Registration and Segmentation Paradigms in Fiji

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Abstract

Automatic image registration and segmentation tools are two of the most demanded features of any bio-imaging software. Image registration is understood as the alignment of multiple 2D or 3D images based on a simple (translation, rigid-body, affine) or not that simple (non-linear, elastic) transformation model. This search of a common coordinate system is vital in order to integrate or compare image data obtained from different measurements. Image segmentation involves the automatic labeling or detection of the structures of interest in our images — complete objects or often just their boundaries—, which simplifies the image representation and facilitates the posterior analysis. In that sense, Fiji has proven to be a very popular platform for bio-medical users and developers, with a very wide spectrum of state-of-the-art algorithms in both areas. The integration of such methods along with the need of a robust and straightforward workflow to deal with large data sets originated TrakEM2, one of the most powerful Fiji plugins. TrakEM2 allows the user to process the massive amount of image data (Tera byte scale) that modern microscopes produce nowadays in affordable personal desktop computers. Moreover, TrakEM2 integrates all the software pieces for volumetric reconstruction, visualization and analysis of objects from 2D sections in a very coherent and flexible way. The challenge now consists of progressively incorporating novel and more sophisticated methods and adapt them to function on such a large scale. A very representative example is the ongoing integration of machine learning based segmentation algorithms using the Weka and Knime toolboxes.

Biography



Ph.D. on Computer Science and Electrical Engineering for the Escuela Politécnica Superior (Universidad Autónoma de Madrid). Currently, working as a postdoctoral fellow at Sebastian Seung's lab (Massachusetts Institute of Technology, USA). Prior to that, I worked during my PhD at the Ortiz-de-Solorzano lab, at the Bioimaging Group (Lawrence Berkeley National Laboratory, California, USA), the Biocomputing Unit (National Centre for Biotechnology, Madrid, Spain), the Biomedical Signal Processing group in the Escuela Politécnica Superior (Universidad Autónoma de Madrid) and collaborated with the IRB Barcelona, in the Cell & Developmental Biology

group. Right after obtaining my PhD, I worked as a researcher in the Institute of Neuroinformatics (University and ETH, Zürich) and as a consultant at the Image Processing Facility in the Max Planck Institute of Molecular Cell Biology and Genetics (Dresden, Germany).

My research interests include image processing, graphics, biomedical image registration and segmentation, computer vision, machine learning and neuroscience. I am currently working on applying machine learning methods to improve the segmentation of neural structures in EM images. My specific focus centers on studying the performance of convolutional neural networks in contrast to more classical algorithms using pre-computed features.