



Contribution ID: 110

Type: Poster

P64 - A new ImageJ plugin for ion beam imaging and data processing at AIFIRA facility

Friday, 11 July 2014 13:00 (1 hour)

Quantification and imaging of chemical elements at cellular level require the combination of techniques such as micro-PIXE, micro-RBS, STIM, secondary electron imaging associated with optical and fluorescence microscopy techniques employed prior to irradiation [1]. Such a numerous set of methods generates an important amount of data per experiment. Typically, for any acquisition the following data has to be processed: chemical map for each element present with concentration above detection limit, density and backscattered maps, mean and local spectra corresponding to relevant region of interest such as whole cell, intracellular compartment, nanoparticles, etc... These operations are time consuming, repetitive and as such could be source of errors in data manipulation.

In order to optimize this first step in data processing, we developed a new tool for batch data processing and imaging. This tool has been developed as a plugin in imageJ [2], a versatile tool for image processing that is suitable for treatment of basic IBA data operation [3]. Because ImageJ is written in Java, the plugin can be used under Linux, Mas OS X, Windows in both 32-bits and 64-bits environments [2], which may interest scientists working on open-access ion beam facilities like AIFIRA. The main features of this plugin will be presented here: listfile processing, spectroscopic imaging, local information extraction, quantitative density maps and database management using OMERO [4].

References

- [1] See in this proceedings, Q. Letrequeesser et al.
- [2] Rasband, W.S., ImageJ, U. S. National Institutes of Health, Bethesda, Maryland, USA, <http://imagej.nih.gov/ij/>, 1997-2014.
- [3] C. Udalagama, X. Chen, A.A. Bettiol, F. Watt, "An ion beam analysis software based on ImageJ", Nucl. Instr. Meth. B 306, 59-63.
- [4] Goldberg, I., C. Allan, J.-M. Burel, D. Creager, A. Falconi, H. Hochheiser, J. Johnston, J. Mellen, P.K. Sorger, and J.R. Swedlow. (2005) The Open Microscopy Environment (OME) Data Model and XML File: Open Tools for Informatics and Quantitative Analysis in Biological Imaging. Genome Biol. 6:R47.

Primary author: Dr DEVES, guillaume (CNRS- CENBG/PCV University of Bordeaux, France)

Co-authors: Mr BESSY, Adrien (University of Bordeaux, France); Mr NAAR, Amir (University of Bordeaux, France); Dr MICHELET, Claire (Centre d'Etudes Nucléaires de Bordeaux Gradignan, Université de Bordeaux, France); Mr BUGA, Florian (University of Bordeaux, France); Dr SEZNEC, Hervé (CENBG - University of Bordeaux - CNRS/IN2P3, France); Mrs GHANTY, Jeveta (University of Bordeaux, France); Dr DAUDIN, Laurent (CENBG - University of Bordeaux - CNRS/IN2P3, France); Dr BARBERET, Philippe (CENBG - University of Bordeaux - CNRS/IN2P3, France); Mr SOMMARD, Vivien (University of Bordeaux, France)

Presenters: Dr BARBERET, Philippe (CENBG - University of Bordeaux - CNRS/IN2P3, France); Dr DEVES, guillaume (CNRS- CENBG/PCV University of Bordeaux, France)

Session Classification: Poster Session with Cheese and Wine