BioImage-IT

Sylvain Prigent, Charles Kervrann, Jean Salamero

BioImage-IT

Sylvain Prigent, Charles Kervrann, Jean Salamero

France-BioImaging , France;

Inria, Centre Rennes-Bretagne Atlantique, France; Institut Curie, France

sylvain.prigent@inria.fr

New image acquisition systems generate large number of images and large volume images. Such data sets are hard to store, to process and to analyze for one user in a workstation. Many solutions exist for data management (Omero, OpenImadis…), image analysis (Fiji, Icy, CellProfiler, Python libraries…) and statistics (R…). Each of them has it specificities and several bridges has been developed between pieces of software. Nevertheless, in many use-cases, we need to perform analysis using tools that are available in different pieces of software and different languages. It is then tedious to create a workflow that bring the data from one tool to another. It needs programing skills and most of the time we develop a dedicated script using a dedicated file system for processed data management.

The aim of the BioImage-IT project it to create a "bandmaster" application that allow any scientist to annotate data, process data and analyze data using only one single high level application. This BioImage-IT application is based on 3 components:

- an image annotation method based on a *json* file system,
- an image processing and analysis tools integration method based on Docker and XML commands description,
- an application with a graphical interface to easily annotate data, run processing tools, and visualize data and results.

This software architecture has three main goals. First, data are annotated using a file system. This means that data are not dependent on any software like a SQL database, and each experiment can then be stored in a different directory and be moved from one server to another or to any drive with a simple copy pasting operation. Second, the processing tools are used as binary packages managed by Docker. Docker make it easy to deal with the dependencies and allows to use several versions of the same tool. Any existing tool can then be integrated as it is without re-inventing the wheel. Third, using a single "bandmaster" application allows to automatically generate metadata for any processed data, making available the trackability and repeatability of any result.

BioImage-IT is a starting open-source project looking for it community. It has been designed for bio-image analysis, but it architecture make it adaptable to different scientific data analysis. More information are available on the BioImageIT website: https://project.inria.fr/bioimageit