Cytomine for digital humanities: remote visualization, sharing, annotation and analysis of large-scale imaging datasets with web technologies and machine/deep learning

Authors: Ulysse Rubens, Matthia Sabatelli, Pierre Geurts, Raphaël Marée
Affiliation: Montefiore Institute, University of Liège, Belgium

The Cytomine project was initiated in 2010 at ULiège (http://uliege.cytomine.org) to build a rich web tool for the computer-assisted analysis of multi-gigapixel imaging data.

This software platform has been designed with the following objectives in mind: provide remote and collaborative principles, rely on data models that allow to easily organize and semantically annotate imaging datasets in a standardized way, efficiently support high-resolution multi-gigapixel images, and provide mechanisms to readily proofread and share image quantifications produced by computer vision or machine/deep learning-based algorithms. By emphasizing collaborative principles, our aim is to accelerate scientific progress and to significantly promote image data and algorithm accessibility and reusability. We want to break common practices in the research field where imaging datasets, quantification results, and associated knowledge are still often stored and analyzed within the restricted circle of a specific laboratory.

While originally motivated by tissue analysis in biomedical research applications (Marée et al., Bioinformatics 2016), the software was designed to be fully open and extensible. It has subsequently be used in various application domains where large images have to be analyzed (geology, earth observation,...).

In this demonstration we will present the main features of Cytomine and illustrate its use for computer vision in digital humanities. We will first show how it is currently used to explore high-resolution multispectral images of paintings. Secondly, we will illustrate how it is currently used to build ground-truth datasets for computer vision and deep learning for object detection in large painting databases (collected in the context of the INSIGHT project http://uahost.uantwerpen.be/insight/).

Cytomine software is web-based, free, and open-source. It can be installed on Linux-based systems (servers or personal computers) using Docker. Relevant documentation and publications, user guide, API description, and additional details can be found on http://uliege.cytomine.org and http://doc.cytomine.org/