Collaborative analysis of gigapixel images using Cytomine

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Introduction

Many scientific studies heavily rely on imaging datasets. Indeed, in various scientific domains (biology, biomedecine, astronomy, botany, geology, paleobiology, marine research, materials science,...), projects leading to terabytes of imaging data are becoming usual e.g. in biology when experimental studies rely on whole-slide virtual microscopy, high-content screening, and automated volume electron microscopy. To foster collaborative and multidisciplinary large-scale image analysis, we developed Cytomine, a rich web environment to readily and securely organize, explore, analyze, and share gigapixel images as well as derived semantic and quantitative information.

Materials and Methods

Cytomine (http://www.cytomine.be/) is a web-based software environment for remote and collaborative analysis of gigapixel images. It is an extensible platform that we are continuously developing since 2010. It is based on modern web and distributed software development methodologies and semantic image analysis using machine learning algorithms [Marée et al., 2013a]. The software is decomposed into four main components communicating through web mechanisms: Cytomine core, Cytomine Image Management System, Cytomine web user interface, and Cytomine analysis modules, as illustrated by Figure 1.
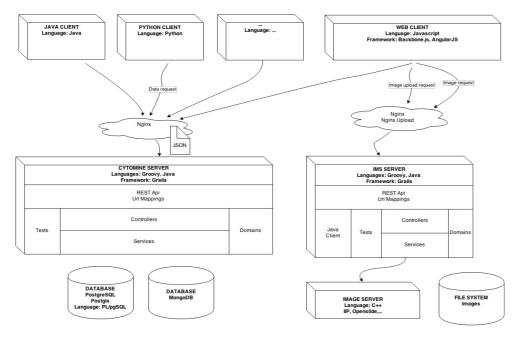

Figure 1. Architecture of the Cytomine software

Results and Discussion

While our first developments were primarily motivated by the analysis of brightfield cytology and histology images in lung cancer research [Marée et al., 2013b, 2014], our software is versatile and extensible, as shown by several usage examples in Figure 2 and as already demonstrated by the use of the whole software or some variants of its analysis modules on various bio(medical) imaging data including [Bertrand et al. 2014, Jeanray et al. 2015, Jouret et al., 2015]. More than 100 users have access to our software. They created more than 200 projects and uploaded more than 20000 images in which they created more than 10 millions of annotations (regions of interest) either manually or by using our machine learning algorithms.
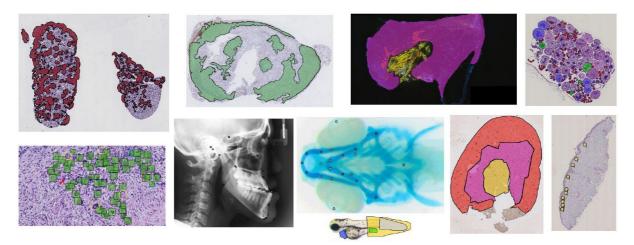

Figure 1. Examples of biomedical images analyzed with Cytomine.

Conclusion

To help the scientific community to integrate, optimize, and extend the Cytomine software for their own specific purposes, we will supply the full code and release it under an open-source software license.

Acknowledgments

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