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Cytomine: An Open-Source Software For Collaborative Analysis Of Whole-Slide Images

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Introduction/ Background

Major software for whole-slide image analysis and digital pathology are proprietary / closed-source which is not in line with current trends in open science and reproducible research. While some open-source software libraries exist for digital pathology (e.g. OpenSlide or NDPITools for reading and converting slide formats), to the best of our knowledge no open-source software exists that combines remote visualization, collaborative and semantic annotation, and semi-automated analysis of digital slides.

Aims

Our Cytomine project started in 2010 to build a rich web environment for multi-gigapixel imaging data. This tool 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 (using user-defined ontologies), efficiently support high-resolution multi-gigapixel images (incl. major scanner image formats), and provide mechanisms to readily proofread and share image quantifications produced by any image recognition algorithms. By emphasizing collaborative principles, our aim with Cytomine is to accelerate scientific progress and to significantly promote image data accessibility and reusability. We want to break common practices in this domain where imaging datasets, quantification results, and associated knowledge are still often stored and analyzed within the restricted circle of a specific laboratory.

Methods

Since the start of our project, we collaborated with biomedical researchers, pathologists, and computer scientists to shape the software and meet user and researcher needs. During development, we combined recent web, database, software development, and machine learning methodologies using open-source libraries. We also adopted modern practices (such as continuous integration and code quality testing) to build an industrial-grade software. In order to enable software extensibility and interoperability, we used a RESTful architecture so that e.g. other computer scientists can import/export data with their own algorithms and share their quantification results.

Results

The Cytomine software (http://www.cytomine.be/) has been released under an open-source licence since January 2016. In terms of code, Cytomine is composed of roughly 70K lines of code decomposed into its four main modules: Cytomine-Core (web server and database), Cytomine-WebUI (web user interface), Cytomine-IMS (image server), and Cytomine-DataMining (image recognition algorithms). Cytomine has now been used on various bio(medical) imaging datasets that involved various types of images and experts in different collaborative operating modes to perform various quantification tasks (in renal pathology, toxicology, developmental studies, lung and breast cancer research,...). By providing detailed documentation, installation instructions and source code, we hope that Cytomine will be used and extended for many purposes in digital pathology. Overall, we believe Cytomine is an important new tool of broad interest to foster active

communication and distributed collaboration between pathologists, life scientists, computer scientists, teachers and students working with digital slides.

Related paper:

"Collaborative analysis of multi-gigapixel imaging data using Cytomine". Bioinformatics, 2016. DOI: 10.1093/bioinformatics/btw013, 2016.