Open and Collaborative Digital Pathology using Cytomine

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Abstract:

In this talk I'll present the past, present, and future of Cytomine.
Cytomine [1] (http://www.cytomine.org) is an open-source software, continuously developed since 2010. It is based on modern web and distributed software development methodologies and machine/deep learning. It provides remote and collaborative features so that users can readily and securely share their large-scale imaging data worldwide. It relies on data models that allow to easily organize and semantically annotate imaging datasets in a standardized way (e.g. to build pathology atlases for training courses or ground-truth datasets for machine learning). It efficiently supports digital slides produced by most scanner vendors. It provides mechanisms to proofread and share image quantifications produced by machine/deep learning-based algorithms. Cytomine can be used free of charge and it is distributed under a permissive license. It has been installed at various institutes worldwide and it is used by thousands of users in research and educational settings.

Recent research and developments will be presented such as our new web user interfaces and new modules for multimodal and multispectral data (Proteomics Clin Appl, 2019), object recognition in histology and cytology using deep transfer learning (CVMI 2018), user behavior analytics in educational settings (ECDP 2018), as well as our new reproducible architecture to benchmark bioimage analysis workflows.

Short bio:

Raphaël Marée received the PhD degree in computer science in 2005 from the University of Liège, Belgium, where he is now working at the Montefiore EE&CS Institute (http://www.montefiore.ulg.ac.be/~maree/). In 2010 he initiated the CYTOMINE research project (http://uliege.cytomine.org/), and since 2017 he is also co-founder of the not-for-profit Cytomine cooperative (http://cytomine.coop). His research interests are in the broad area of machine learning, computer vision techniques, and web-based software development, with specific focus on their applications on big imaging data such as in digital pathology and life science research, while following open science principles.

[1]   Raphaël Marée, Loïc Rollus, Benjamin Stévens, Renaud Hoyoux, Gilles Louppe, Rémy Vandaele, Jean-Michel Begon, Philipp Kainz, Pierre Geurts & Louis Wehenkel 2016. Collaborative analysis of multi-gigapixel imaging data using Cytomine. *Bioinformatics*, 32, (9), 1395-1401, doi:10.1093/bioinformatics/btw013.