BIOGRAPHICAL SKETCH (2023)

NAME: **Marée Raphaël**

POSITION TITLE: Senior Researcher in Machine Learning, Collaborative Software
Development, Human-Centered Computing
(Montefiore Institute, University of Liège)

EDUCATION/TRAINING:

INSTITUTION AND LOCATION	DEGREE	Completion Date	FIELD OF STUDY
University of Liège, Belgium	M.Sc	06/2000	Computer Science
University of Liège, Belgium	Ph.D.	02/2005	Computer Science (Machine Learning for Image Analysis)
Pasteur Institute, Paris, France	Postdoctoral	10/2015	Computer Science (Digital Pathology)

A. Personal Statement

I have a broad background in computer science including **machine learning**, bioimage analysis, distributed and **web software development**, and bioinformatics. Between 2005 and 2014, after getting a PhD degree in computer science, I worked as the manager of a bioinformatics core facility in a newly created research center in applied geno-proteomics (GIGA) at the University of Liège (ULiège). This challenging position gave me the opportunity to work closely with biomedical researchers from both academic and industrial environments. During that period, I developed several specific workflows to analyze proteomics and imaging datasets generated by biomedical researchers, which helped me to identify the crucial need for new bioimage analysis **collaborative tools**. Although this experience as core facility manager was very rich, I decided to reorient my career in 2014 to fully concentrate on research and development in bioimage informatics to advance both biomedical and computer science research by following open science principles. Since then, I have been very successful at obtaining research grants at the regional and international levels. As scientific coordinator or workpackage leader on these grants, I laid the groundwork for advanced computer science research by initiating and then supervising the development of two collaborative, open-source, web software platforms, **Cytomine** and **Biaflows**, and by designing generic machine learning algorithms for large-scale, high-resolution, bioimaging data. I have established strong ties with the bioimage analysis community (notably through workpackage co-leadership of two European-funded COST Actions, namely NEUBIAS "Network of European BioImage Analysts" and COMULIS "Correlated Multimodal Imaging in Life Sciences"; and workpackage co-leadership of an European-funded IMI project, namely BigPigcture). We also widely disseminated our results (more than 50 scientific presentations, open-source code distribution, …), which are now used worldwide in diverse research and education settings.
Since 2021, I am also widening my research interests into **human-centered computing, Solidarity HCI,** and computer-supported cooperative work, by iniating and coordinating the development of the open-source web software platform **Shareish** to foster mutual aid and solidarity in civil society communities, and by starting collaborative outdoor digital mapping activites.

Overall, I successfully administered projects of various sizes (incl. staffing, budget, outreach), collaborated with interdisciplinary research teams (incl. biomedical researchers, doctors, computer scientists, imaging scientists), and produced several peer-reviewed journal and conference publications from each project. As a result of these previous experiences, I am aware of the importance of frequent scientific and public communication, online data sharing among project members, open science, and of constructing a realistic research plan, timeline, and budget. I have also strong experience with supervision of MSc and PhD students, and with the organization of successful scientific events and hackathons.

B. Positions and Professional Experience

Positions and Employment
2005-2014   Bioinformatics Core Facility Manager, GIGA Research Center, ULiege, Belgium
2014-2015   Postdoctoral research fellow at Pasteur Institute (Bioimage Analysis Unit), Paris, France
2010-   Senior researcher in machine learning, collaborative software development, human-centered computing ; Head of Cytomine Research & Development, Montefiore Institute, ULiège

Other Professional Experience

Memberships and Steering
2015-19   Member of the Management Committee and Co-Lead of Workpackage 5 on Benchmarking for EU COST Action NEUBIAS (CA15124; https://neubias.org/ ; 36 member countries)
2018-22   Member of the Management Committee and Co-Lead of Workpackage 4 on Correlation Software for EU COST Action COMULIS (CA17121; https://comulis.eu/ ; 36 member countries)
2021-27   Deputy Lead of EU-funded IMI BigPicture Project Workpackage 4 on the development of open-source software tools for accessing, annotating, and mining digital pathology slides.

Scientific meetings co-organization or Program committee memberships (last eight years)
2015   14th International Congress for Stereology and Image Analysis
2016, 2018   1st and 2nd Computational Pathology workshop at European Conference on Computational Biology (ECCB)
2019   PC Member at MICCAI Computational Pathology Workshop
2020   Training school on Image processing for correlated and multimodal imaging techniques (with VIB, COMULIS)
2021   Special Session on Holistic approach to correlative microscopies: From sample preparation to data integration at IEEE International Symposium on Biomedical Imaging (ISBI) https://biomedicalimaging.org/2021/special-sessions/
2021-...   PC Member at CVPR Workshop on Computer Vision for Microscopy Image Analysis (CVMI)

Reviewing functions
- International journals (last 5 years): IEEE Pattern Analysis and Machine Intelligence, Nature Methods, Bioinformatics, Cancer Research, Medical Image Analysis, Nature Scientific Reports, Nature Scientific Data, IEEE Transactions on Biomedical Engineering, IEEE Signal Processing Magazine, Medical Image Analysis, Journal of Microscopy, PLOS Computational Biology, …
- International funding agencies: Marie Skłodowska-Curie Actions COFUND and Barcelona Institute of Science and Technology, UK Medical Research Council, European Research Council.

Mentoring and supervisory duties:
- Supervision of M.Sc. theses: > 25
- Co-supervision of Ph.D. theses: 5
- Ph.D. thesis jury committee member: > 5

Industry relations and valorization
2002-   Co-founder of PEPITe company specialized in data mining for industrial processes
2009-13   Development of the AI algorithm for BestCyte® cell sorter (CellSolutions LLC)
2017-25   Co-founder of Cytomine SCES (cooperative company with social economy goals and open-source promotion) and Member of its Board of Directors
2021-   Public-private partnership with members of the European Federation of Pharmaceutical Industries and Associations

C. Contribution to Science

I have published over 50 peer-reviewed papers (h-index 31 on Google Scholar):
http://orbi.ulg.ac.be/simple-search?query=%28%28uid%3Au188001%29%29&title=+&sort_by=1&order=DESC
https://scholar.google.com/citations?user=qG66mF8AAAAJ&hl=nl

1. In my early methodological research, I proposed a **generic framework for image analysis** based on tree-based ensemble machine learning. At that time (early 2000s) where deep learning methods were not popular, there was a lack of generic methods as many existing works targeted specific image types or were not evaluated thoroughly. Our methodology relied on raw pixel values without any explicit feature extraction but random-sized patches, somewhat similar to end-to-end deep learning methods. Originally designed for image classification (or object recognition), we have successively extended the approach for semantic segmentation, content-based image retrieval, and landmark detection. Our studies include extensive empirical evaluations (on tens of datasets) that proved the approach to be effective in many settings and this has been demonstrated further on real-world applications (see next section).

    a. "*Random Subwindows for Robust Image Classification*". Raphaël Marée, Pierre Geurts, Justus Piater, Louis Wehenkel. In Proceedings of the IEEE International Conference on Computer Vision and Pattern Recognition (CVPR), Volume 1, page 34–40, June 2005, San Diego, USA.
    b. "*Content-based Image Retrieval by Indexing Random Subwindows with Randomized Trees*". Raphaël Marée, Pierre Geurts, Louis Wehenkel. IPSJ Transactions on Computer Vision and Applications, Volume 1, Number 1, page 46-57 - jan 2009
    c. "*Extremely randomized trees and random subwindows for image classification, annotation, and retrieval*". Raphaël Marée, Louis Wehenkel, Pierre Geurts. Invited chapter in Book "Decision Forests for Computer Vision and Medical Image Analysis", Eds. A. Criminisi, J. Shotton, and E. Konukoglu. Springer, Advances in Computer Vision and Pattern Recognition series, pp. 125-141, 2013.
    d. "*Towards Generic Image Classification using Tree-based Learning: an Extensive Empirical Study*". Raphaël Marée, Pierre Geurts, and Louis Wehenkel. Pattern Recognition Letters, 2016.
    e. "*Landmark detection in 2D bioimages for geometric morphometrics: a multi-resolution tree-based approach*". Rémy Vandaele, Jessica Aceto, Marc Muller, Frédérique Peronnet, Vincent Debat, Ching-Wei Wang, Cheng-Ta Huang, Sébastien Jodogne, Philippe Martinive, Pierre Geurts, and Raphaël Marée. Nature Scientific Reports, 8:5, 38 (2018).

2. As manager of a bioinformatics core facility (2005-2014) and through subsequent **interdisciplinary collaborations**, I contributed to **biomedical research** and to medicine. This translational impact was proven by the successful application of variants of aforementioned machine learning methodologies for cancer cells detection in whole-slide diagnostic cytology, tumor tissue segmentation in whole-slide imaging experimental histology to highlight unknown biological processes, and various proteomic data and image analyses e.g. in Zebrafish development research or cancer and inflammatory research (see full publication list).
    a. "*Discovery and biochemical characterisation of four novel biomarkers for osteoarthritis*". Dominique de Seny, Mohammed Sharif, Marianne Fillet, Gaël Cobraiville, Marie-Alice Meuwis, Raphaël Marée, Jean-Philippe Hauzeur, Louis Wehenkel, Edouard Louis, Marie-Paule Merville, John Kirwan, Clio Ribbens, Michel Malaise. Annals of the Rheumatic Diseases, 2011.
    b. "*Evaluation of CellSolutions' BestPrep Automated Thin-Layer Liquid Based Cytology Pap Slide Preparation and BestCyte Cell Sorter Imaging System*". Agnès Delga, Frédéric Goffin, Frédéric Kridelka, Raphaël Marée, Chantal Lambert, Philippe Delvenne . Acta Cytologica, Vol. 58, No. 5, 469-477, 2014.
    c. "*A hybrid human-computer approach for large-scale image-based measurements using web services and machine learning*". Raphaël Marée, Loïc Rollus, Benjamin Stevens, Gilles Louppe, Olivier Caubo, Natacha Rocks, Sandrine Bekaert, Didier Cataldo, Louis Wehenkel. Proc. IEEE International Symposium on Biomedical Imaging (ISBI), 2014.
    d. "*Phenotype Classification of Zebrafish Embryos by Supervised Learning*". Nathalie Jeanray, Raphaël Marée, Benoist Pruvost, Olivier Stern, Pierre Geurts, Louis Wehenkel, Marc Muller. PLoS One, 2015 Jan 9;10(1).
    e. "*Ozone-primed neutrophils promote early steps of tumor cell metastasis to lungs by enhancing their NET production*". Natacha Rocks, Céline Vanwinge, Coraline Radermecker, Silvia Blacher, Christine

Gilles, <u>Raphaël Marée</u>, Alison Gillard, Brigitte Evrard, Christel Pequeux, Thomas Marichal, Agnès Noel, Didier Cataldo. Thorax, 2019.

3. These collaborations highlighted the essential need for **software tools to collaborate more efficiently** (e.g. to build realistic ground-truth imaging datasets to train accurate recognition models). In 2010, I therefore initiated the development of the **Cytomine web software platform**. While most of the existing software tools at that time were desktop-based, we innovated by developing a rich internet application that relies on modern software technologies including efficient web user interfaces, geospatial databases, containers, computing clusters, and deep/machine learning. These disruptive methodological choices allow remote collaboration over the web between biomedical researchers and computer scientists, as well as between teachers and students. Consequently, this innovative tool has changed the way many individuals and institutions handle histology slides and microscopy imaging in general. In biomedical research, it allows multiple experts to manually annotate large image datasets to feed machine learning methods and to proofread results generated by trained models hence derive biologically-relevant knowledge, all these operations now being realized through web interfaces by geographically distant researchers. In education, many universities have decided to switch from training sessions using microscopes and physical slides to computer-aided sessions on virtual slides, and the first massive open online courses on histology (for French-speaking language) was organized. In other words, the increasing success of our approach is demonstrated by the regular use of Cytomine by **tens of thousands of users in various application settings**. The software is continuously developed by the team I supervise to further extend its functionalities and application domains.
   a. "*Collaborative analysis of multi-gigapixel images using Cytomine*". <u>Raphaël Marée</u>, Loïc Rollus, Benjamin Stévens, Renaud Hoyoux, Gilles Louppe, Rémy Vandaele, Jean-Michel Begon, Philipp Kainz, Pierre Geurts, and Louis Wehenkel. Bioinformatics, 1;32(9):1395-401, 2016. Project Documentation: https://uliege.cytomine.org ; Source code: https://github.com/cytomine-uliege/ ;
   b. "*The need for careful data collection for pattern recognition in digital pathology*". <u>Raphaël Marée</u>. Journal of Pathology Informatics, 8:19, 2017.
   c. "*A Massive Open Online Course (MOOC) on pratical histology: A goal, a tool, a large public ! Return on a first experience*". Sylvie Multon, Laurence Pesesse, Alodie Weatherspoon, Sandra Florquin, Jean-François Van de Poel, Pierre Martin, Grégoire Vincke, Renaud Hoyoux, <u>Raphaël Marée</u>, Dominique Verpoorten, Pierre Bonnet, Pascale Quatresooz, Valérie Defaweux. Annales de Pathologie, 2018.
   d. "*Cytomine: towards an open and collaborative software platform for digital pathology bridged to molecular investigations*". Ulysse Rubens, Renaud Hoyoux, Laurent Vanosmael, Mehdy Ouras, Maxime Tasset, Christopher Hamilton, Rémi Longuespée, <u>Raphaël Marée</u>. Proteomics Clinical Applications, Special Issue on Proteomics in Pathology, 2019.

4. Then, I further advocated **open science principles** and contributed to it through new software technology developments and evaluation protocols to ensure reproducibility and careful benchmarking of image analysis algorithms. In collaboration with international researchers (algorithm developers, bioimage analysts and imaging scientists), we setup the **BIAFLOWS** web platform (build upon Cytomine) for reproducible bioimage analysis. Through collaborative, remote, software development and the organization of tutorials and physical hackathons, we successfully integrated online and documented about 50 image analysis workflows from a large variety of software for a diversity of bioimage analysis tasks. I co-supervised this development as co-leader of the Benchmarking Software workpackage of the NEUBIAS European network. We believe this new approach can revolutionize how image analysis methodologies are published and benchmarked, with benefits for the whole scientific community. Notably, Cytomine and Biaflows developments are at the heart of the EU-funded BigPicture platform which brings together the main European research centers, hospitals and the pharmaceutical industry to develop the biggest database of digital pathology slides in which AI algorithms (including ours on transfer learning) will be benchmarked. I will serve as the co-investigator of these developments as BigPicture project's Workpackage 4 deputy co-lead.
   a. "*Comparison of deep transfer learning strategies for digital pathology*". Romain Mormont, Pierre Geurts, <u>Raphaël Marée</u>. Proc. IEEE CVPR Workshop on Computer Vision for Microscopy Image Analysis (CVMI), 2018.

b. "*Open Practices and Resources for Collaborative Digital Pathology*", <u>Raphaël Marée</u>. Frontiers in Medecine, 2019.
c. "*Multi-task pre-training of deep neural networks for digital pathology*". Romain Mormont, Pierre Geurts, <u>Raphaël Marée</u>. IEEE Journal of Biomedical and Health Informatics, 2020.
d. "*BIAFLOWS: A collaborative framework to reproducibly deploy and benchmark bioimage analysis workflows*". Ulysse Rubens, Romain Mormont, Lassi Paavolainen, Volker Baecker, Benjamin Pavie, Leandro A. Scholz, Gino Michiels, Devrim Ünay, Graeme Ball, Renaud Hoyoux, Rémy Vandaele, Ofra Golani,Stefan G. Stanciu, Natasa Sladoje, Perrine Paul-Gilloteaux, <u>Raphaël Marée*</u>, Sébastien Tosi*. Cell Patterns, 2020. Demo server: https://biaflows.neubias.org/ ; Documentation: http://biaflows-doc.neubias.org/ ; Source code: https://github.com/neubias-wg5

5. In the recent years, I further applied similar web software development methodologies and machine learning to **foster mutual aid (solidarity) in the civic society** through the development of an open-source, map-based, web platform that enables generalized exchange (or indirect reciprocity). This work is at the intersection of human-centered computing, computer-supported cooperative work, social computing, and geographical information systems. While this may seem like a shift in my research interests, I see it as a logical extension of my focus on facilitating collaborative practices, from the scientific community to civil society communities.
   a. "*Shareish (Share & Cherish): an open-source, map-based, web platform to foster mutual aid*". Adrien Guilliams, Ulysse Rubens, Florent Banneux, Pierre Chapeau, <u>Raphaël Marée</u>. Proc. 11th International Conference on Communities and Technologies, 2023. Demo server: https://shareish.org ; Source code: https://github.com/shareish/
   b. "*On designing Shareish, an open-source, map-based, web platform to facilitate diverse solidarity practices*", Guilliams, Banneux, Rubens, … Marée. In Human Technology: An Interdisciplinary Journal on Humans in ICT Environments, 20 (2), p. 285–324.

D. Research Support

Ongoing Research Support:

2021-2027   BIGPICTURE (H2020 IMI, grant n°1017072)
             https://www.bigpicture.eu
             Amount of funding (total project): 69 641 907 €
             Role in project: Workpackage 4 "Software tools" co-lead

2024-2027   DigiPathConnect (Interreg Meuse-Rhine)
             https://www.interregmeuserhine.eu/en/projects/digipathconnect
             Amount of funding (total project): €4.229.830,54
             Role in project: "Software tools" development

2021-2025   ARIAC (DigitalWallonia4.ai)
             Role in project: co-supervising a PhD Thesis

Previous Research Support

2010-2016   CYTOMINE "Software platform for the exploration and automatic analysis of cyto-histological
             digital slides" (Wallonia, grant n°1017072, https://recherche-
              technologie.wallonie.be/projets/index.html?IDD=17115)
             Amount of funding (total project): 1 452 186 €
             Role in project: Principal Investigator (Head of Cytomine R&D team), scientific coordination.

2014-2017   HISTOWEB "Transforming the Cytomine software platform for practical histology courses"
             (Wallonia grant n°1318185, https://recherche-technologie.wallonie.be/projets/index.html?
             IDD=2427)
             Amount of funding (total project): 1 053 019 €

Role in project: Head of Cytomine R&D team

2014-2020   IDEES (https://www.cetic.be/IDEES) "The Internet of tomorrow to develop businesses, the economy and society " European Regional Development Fund
Amount of funding (total project): 8 713 493 € (Uliège: 170 000€)
Role in project: Research on "Technological foundations – data analysis"

2016-2020   NEUBIAS (https://www.cost.eu/actions/CA15124/) "A new Network of European BioImage Analysts to advance life science imaging" (Horizon 2020 COST ACTION)
Amount of funding (total project): 736 000 €
Role in project: Co-lead of WP5 Software development and Management Committee Member

2018-2022   COMULIS (https://www.cost.eu/actions/CA17121/) "Correlated Multimodal Imaging in Life Sciences" (Horizon 2020 COST ACTION)
Role in project: Co-lead of WP4 Software development and Management Committee Member