

Date of birth: 15<sup>th</sup> February 1982

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[NIH BioSketch](#)

Github organization: [github.com/IARCbioinfo](#)

Website: [www.rarecancersgenomics.com](#)

Computational Cancers Genomics Team

Genomic Epidemiology Branch

International Agency for Research on Cancer (IARC-WHO)

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Research Group: [www.iarc.who.int/teams-ccg/](#)

Professional Appointments

2021-on **Team Leader**, International Agency for Research on Cancer (IARC-WHO), Lyon, France

2014-2020 **Scientist**, International Agency for Research on Cancer (IARC-WHO), Lyon, France

2012-2014 **Staff Research Scientist**, Swiss Federal Institute of Technology, Lausanne, Switzerland

2007-2012 **Postdoctoral Researcher**, Institute of Ecology and Evolution, University of Berne, Switzerland

Honors and awards

2024-on **Member of the WHO classification of tumours 6<sup>th</sup> edition subcommittee on computational pathology**, International Agency for Research on Cancer (IARC-WHO), [tumourclassification.iarc.who.int/](#)

2023 **Young investigator award**, International Mesothelioma Interest Group (iMig), [imig.org](#)

2022-2024 **Chair of the of the Rare Cancers Working Group**, European Prospective Investigation into Cancer and Nutrition (EPIC), [epic.iarc.who.int](#)

2022-on **Chair of the Data Science Steering Committee**, International Agency for Research on Cancer (IARC-WHO)

2021-on **Chair of the Health Technologies Pillar**, Scientific Steering Committee of the Lyon Auvergne Rhône-Alpes Canceropole (CLARA), [www.canceropole-clara.com](#)

2021-on **lung NET task force member**, European NEuroendocrine Tumors Society (ENETS), [www.enets.org](#)

2016-on **Scientific Committee member**, French MESOBANK (virtual mesothelioma national biobank), [www.netmeso.fr/netmeso/mesopath-et-mesobank](#)

Education

2004-2007 **PhD in Population Genetics and Evolution**, University of Grenoble, France. [theses.hal.science/tel-00216192/](#)

2001-2004 **MSc Computer science and Applied Mathematics, specialization in Bioinformatics**, Grenoble Institute of Technology ENSIMAG, Grenoble, France.

Personal Statement

I am a computational biologist with extensive training in applied mathematics, computer science, bioinformatics, and statistical genetics. During my doctoral and postdoctoral training, I focused on developing new statistical and computational methods to analyze large genomic datasets, including approaches for Bayesian inference, population genetics, and variant detection. Over the past decade, I have led interdisciplinary teams integrating genomics, transcriptomics, and pathology imaging data to advance translational cancer research, with a particular focus on thoracic tumors. In addition to my role as Team Leader, I also coordinate the bioinformatics efforts at the International Agency for Research on Cancer (IARC-WHO). In 2015, I created the Rare Cancers Genomics initiative together with Dr. Lynnette Fernandez-Cuesta. As part of these efforts, I have developed and supervised multiple open-source software projects aimed at ultra-sensitive variant calling, integrative multi-omics pipelines, and deep-learning-based image analysis.

Publications

83 publications in international peer-reviewed scientific journals, including 9 publications as first/co-first author, and 16 publications as last/co-last/corresponding author. Full list available at [Google Scholar](#) and [My NCBI Bibliography](#). 14'683 total citations, h-index: 45 (source: [Google Scholar](#)), named a 2024 Top Scholar by [ScholarGPS](#) (top 0.5% of all scholars worldwide) in [Genomics](#) and [Genotyping](#), mean [NIH iCite](#) Relative Citation Ratio: 3.35 (RCR, indicating that my publications have received, on average, 3.35 times as many citations per year as the median NIH-funded papers in their fields).