Dr. Matthieu Foll

Curriculum Vitæ

Date of birth: 15th February 1982
Nationality: French
ORCID: 0000-0001-9006-8436
NIH BioSketch
Github organization: github.com/IARCbioinfo
Website: www.rarecancersgenomics.com

Computational Cancers Genomics Team
Genomic Epidemiology Branch
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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 turmours 6th 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).

Recent Research Support

2024–2027 **Understanding the spatiotemporal eco-evolutionary interactions in malignant pleural mesothelioma**.
Worldwide Cancer Research, 252,246 GBP. Alcala N (PI), Fernandez-Cuesta L, Foll M (co-Investigator), Jaehee Kim.
Award: www.worldwidecancerresearch.org

2023–2025 **Reconciling lung carcinoids histopathological and molecular classifications**.
Investigator Award, Neuroendocrine Tumor Research Foundation, 270,000 USD. Foll M (PI).
Award: netrf.org/research/reconciling-lung-carcinoids-histopathological-and-molecular-classifications/

2022–2024 **Intra-Tumour Heterogeneity of Pleural Mesothelioma at the Single-Cell Level**.
Concept Award, Congressionally Directed Medical Research Programs, 100,000 USD. Foll M (PI), Fernandez-Cuesta L (co-PI).
Award: app.dimensions.ai/details/grant/grant.13055977

Selected Open Science Projects

I have been advocating for open science since the beginning of my career, with a focus on open-source software and open data sharing.

2023 **HaloAE software** | GitHub: IARCbioinfo/HaloAE
A local transformer Auto-Encoder for anomaly detection and localization.
Role: Project co-founder, developer supervision.

2020 **Needlestack bioinformatics pipeline** | GitHub: IARCbioinfo/needlestack
An ultra-sensitive variant caller for multi-sample next generation sequencing data.
Role: Project founder, lead developer and supervision.

2019 **Medical Genomics Open Educational Resource** | GitHub: IARCbioinfo/medica_genomics_course
Medical Genomics course held annually at IARC and part of the INSA Lyon engineering school Master curriculum (French National Institute of Applied Sciences of Lyon). Includes all lecture slides and practicals for self-paced learning.
Role: Project co-founder, lecturer and supervision.

2014 **Cancer Genomics bioinformatics pipelines** | rarecancersgenomics.com/tools & github.com/IARCbioinfo
Best-practices pipelines for WGS, RNA-seq, and methylation data analysis and integration, mostly based on Nextflow.
Role: Project founder, developers supervision.

2014 **Rare Cancers Genomics data** | rarecancersgenomics.com/datasets
WGS, RNA-seq, and methylation data for rare cancers.
Role: Project co-founder.

2008 **BayeScan software** | GitHub: mfoll/BayeScan & GitHub: mfoll/BayeScanHierachical
Software to identify candidate loci under natural selection from genetic data. Publication cited >2,000 times, one of the most widely used method in the field.
Role: Project founder, developer.

Selected Oral Presentations

2025 **Reconciling molecular and morphological lung NET classifications using AI**.
Invited speaker, European Neuroendocrine Tumor Society (ENETS) annual conference, Krakow (Poland).

2024 **Understanding cancer biology through multi- omics genotype-phenotype tumour maps**.
Keynote speaker, BioSyl Computational Biology of Cancer 2024, Grenoble (France).

2024 **The Rare Cancers EPIC database: a gateway to rare cancer epidemiological research**.
Proffered Paper, ESMO Sarcoma and Rare Cancers Congress 2024, Lugano (Switzerland).
DOI: 10.1016/j.esmoop.2024.102440

2023 **Understanding cancer biology through multi-omics genotype-phenotype tumour maps: applications in rare cancers**.
Invited Speaker, EMBL conference Cancer Genomics, Heidelberg (Germany).

2023 **Malignant pleural mesothelioma: from inter- to intra-tumor heterogeneity**.
Young Investigator Award, 16th International Conference of the International Mesothelioma interest group (iMig), Lille (France).

2023 **Multi-omics characterization of rare heterogeneous tumors**.
Invited Presentation, 31st Annual Intelligent Systems For Molecular Biology (ISMB) / 22nd Annual European Conference on Computational Biology (ECCB), Lyon (France).
Video: youtu.be/BoeBCkxckLw

2023 **Biocomputational approaches for the study of rare endocrine cancers**.
Invited Speaker, European Congress of Endocrinology (ECE), Istambul (Turkey).

2023 **The lungNENomics Project: a Comprehensive Multidisciplinary Characterisation of Pulmonary Carcinoids**.
Abstract presentation, European Neuroendocrine Tumor Society (ENETS) annual conference, Vienna (Austria).

2023 **Molecular features of lung neuroendocrine tumors**.
Invited Speaker, European Association of Nuclear Medicine (EANM) annual congress, Barcelona (Spain).

2022 **Multi-omics characterization of heterogeneous tumors**.
Invited Speaker, European Meeting on Molecular Diagnostics (EMMD), Noordwijk (Netherlands).

Selected Publications

2025# **The European Prospective Investigation into Cancer and Nutrition Cohort (EPIC): a gateway to rare cancer epidemiological research**.
ESMO Rare Cancers. DOI: https://doi.org/10.1016/j.esmorc.2025.100014
Fernandez-Cuesta L, Voegele C, Hemon B, Alcala K, Aune D, ..., Foll M.

2025# **Basic science and translational implications of current knowledge on neuroendocrine tumors**.
Journal of Clinical Investigation. DOI: https://doi.org/10.1172/jci186702; PMID: 40026252
Fernandez-Cuesta L, Alcala N, Mathian E, Derks J, Thirlwell C, Dayton T, Marinoni I, Perren A, Walter T, Foll M.

2024# **Assessment of the current and emerging criteria for the histopathological classification of lung neuroendocrine tumours in the lungNENomics project**.
ESMO Open. DOI: https://doi.org/10.1016/j.esmoop.2024.103591; PMID: 38878324
Mathian E, Drouet Y, Sexton-Oates A, Papotti MG, Pelosi G, ..., Foll M.
GitHub: https://github.com/IARCbioinfo/LNENBarlowTwins.

2024# **Multi-omic dataset of patient-derived tumor organoids of neuroendocrine neoplasms**.
Gigascience. DOI: 10.1093/gigascience/giae008; PMID: 38451475
Alcala N, Voegele C, Mangiante L, Sexton-Oates A, Clevers H, Fernandez-Cuesta L, Dayton TL, Foll M.
GitHub: IARCbioinfo/MS_panNEN_organoids.

2023 **Druggable growth dependencies and tumor evolution analysis in patient-derived organoids of neuroendocrine neoplasms from multiple body sites**.
Cancer Cell. DOI: 10.1016/j.ccell.2023.11.007; PMID: 38086335
Dayton TL, Alcala N, Moonen L, den Hartigh L, Geurts V, ..., Foll M, Fernández-Cuesta L, Clevers H.

2023# **Multiomic analysis of malignant pleural mesothelioma identifies molecular axes and specialized tumor profiles driving intertumor heterogeneity**. 24 citations
Nature Genetics. DOI: 10.1038/s41588-023-01321-1; PMID: 36928603
Mangiante L, Alcala N, Sexton-Oates A, Di Genova A, Gonzalez-Perez A, ..., Foll M#, Fernandez-Cuesta L#.

2023 **HaloAE: A Local Transformer Auto-Encoder for Anomaly Detection and Localization Based on HaloNet**.
Proceedings of the 18th International Joint Conference on Computer Vision, Imaging and Computer Graphics Theory and Applications (VISIGRAPP 2023). DOI: 10.5220/0011865900003417
Mathian E, Liu H, Fernandez-Cuesta L, Samaras D, Foll M, Chen L.
GitHub: IARCbioinfo/HaloAE.

2022# **A molecular phenotypic map of malignant pleural mesothelioma**.
Gigascience. DOI: 10.1093/gigascience/giac128; PMID: 36705549
Di Genova A, Mangiante L, Sexton-Oates A, Voegele C, Fernandez-Cuesta L, Alcala N, Foll M.
GitHub: IARCbioinfo/MESOMICS_data.

2021[#] **Challenges in lung and thoracic pathology: molecular advances in the classification of pleural mesotheliomas**.
Virchows Archiv. DOI: 10.1007/s00428-020-02980-9; PMID: 33411030
Fernandez-Cuesta L, Mangiante L, Alcala N, Foll M.

2020[#] **A molecular map of lung neuroendocrine neoplasms**.
Gigascience. DOI: 10.1093/gigascience/giaa112; PMID: 33124659
Gabriel AAG, Mathian E, Mangiante L, Voegele C, Cahais V, ..., Foll M.
GitHub: IARCbioinfo/DRMetrics.

2020[#] **Needlestack: an ultra-sensitive variant caller for multi-sample next generation sequencing data**.
NAR Genomics and Bioinformatics. DOI: 10.1093/gigascience/giac128; PMID: 36705549
Delhomme TM, Avogbe PH, Gabriel AAG, Alcala N, Leblay N, ..., Foll M.
GitHub: IARCbioinfo/needlestack.

2020 **EURACAN/IASLC Proposals for Updating the Histologic Classification of Pleural Mesothelioma: Towards a More Multidisciplinary Approach**. 147 citations
Journal of Thoracic Oncology. DOI: 10.1016/j.jtho.2019.08.2506; PMID: 31546041
Nicholson AG, Sauter JL, Nowak AK, Kindler HL, Gill RR, ..., Foll M, ..., Galateau-Salle F.

2019[#] **Molecular studies of lung neuroendocrine neoplasms uncover new concepts and entities**.
Translational Lung Cancer Research. DOI: 10.21037/tlcr.2019.11.08; PMID: 32038931
Fernandez-Cuesta L, Foll M.

2019[#] **Redefining malignant pleural mesothelioma types as a continuum uncovers immune-vascular interactions**.
EBioMedicine. DOI: 10.1016/j.ebiom.2019.09.003; PMID: 31648983
Alcala N, Mangiante L, Le-Stang N, Gustafson CE, Boyault S, ..., Foll M[#], Galateau-Salle F[#], Fernandez-Cuesta L[#].

2019[#] **Integrative and comparative genomic analyses identify clinically relevant pulmonary carcinoid groups and unveil the supra-carcinoids**. 141 citations
Nature communications. DOI: 10.1038/s41467-019-11276-9; PMID: 31431620
Alcala N, Leblay N, Gabriel AAG, Mangiante L, Hervas D, ..., Foll M[#], Fernandez-Cuesta L[#].

2019 **Linking a mutation to survival in wild mice**. 172 citations
Science. DOI: 10.1126/science.aav3824; PMID: 30705186
Barrett RDH, Laurent S, Mallarino R, Pfeifer SP, Xu CCY, Foll M, ..., Hoekstra HE.

2018 **Prediction of acute myeloid leukaemia risk in healthy individuals**. 778 citations
Nature. DOI: 10.1038/s41586-018-0317-6; PMID: 29988082
Abelson S, Collord G, Ng SWK, Weissbrod O, Mendelson Cohen N, ..., Foll M, ..., Shlush LI.

2017 **BAP1 Is Altered by Copy Number Loss, Mutation, and/or Loss of Protein Expression in More Than 70% of Malignant Peritoneal Mesotheliomas**.
Journal of Thoracic Oncology. DOI: 10.1016/j.jtho.2016.12.019; PMID: 28034829
Leblay N, Leprêtre F, Le Stang N, Gautier-Stein A, Villeneuve L, ..., Foll M, Fernandez-Cuesta L, Brevet M.

2015[*] **WFABC: a Wright-Fisher ABC-based approach for inferring effective population sizes and selection coefficients from time-sampled data**.
Molecular Ecology Resources. DOI: 10.1111/1755-0998.12280; PMID: 24834845
Foll M, Shim H, Jensen JD.
GitHub: mfoll/WFABC.

2014[*] **Widespread signals of convergent adaptation to high altitude in Asia and America**.
The American Journal of Human Genetics. DOI: 10.1016/j.ajhg.2014.09.002; PMID: 25262650
Foll M, Gaggiotti OE, Daub JT, Vatsiou A, Excoffier L.
GitHub: mfoll/BayeScanHierachical.

2014[*] **Adaptive, convergent origins of the pygmy phenotype in African rainforest hunter-gatherers**.
Proceedings of the National Academy of Sciences. DOI: 10.1073/pnas.1402875111; PMID: 25136101
Perry GH, Foll M, Grenier JC, Patin E, Nédélec Y, ..., Barreiro LB.

2014[*] **Influenza virus drug resistance: a time-sampled population genetics perspective**.
PLOS Genetics. DOI: 10.1371/journal.pgen.1004185; PMID: 24586206
Foll M, Poh YP, Renzette N, Ferrer-Admetlla A, Bank C, ..., Jensen JD.

2013[#] **Robust demographic inference from genomic and SNP data**. 🏆 1350 citations 🔓
PLOS Genetics. DOI: 10.1371/journal.pgen.1003905; PMID: 24204310
Excoffier L, Dupanloup I, Huerta-Sánchez E, Sousa VC, Foll M.

2013 **Approximate Bayesian computation**. 🏆 695 citations 🔓
PLOS Computational Biology. DOI: 10.1371/journal.pcbi.1002803; PMID: 23341757
Sunnåker M, Busetto AG, Numminen E, Corander J, Foll M, Dessimoz C.

2011[#] **fastsimcoal: a continuous-time coalescent simulator of genomic diversity under arbitrarily complex evolutionary scenarios**. 🏆 419 citations 🔓
Bioinformatics. DOI: 10.1093/bioinformatics/btr124; PMID: 21398675
Excoffier L, Foll M.
Code: cmpg.unibe.ch/software/fastsimcoal2.

2010[#] **Quantifying population structure using the F-model**.
Molecular Ecology Resources. DOI: 10.1111/j.1755-0998.2010.02873.x; PMID: 21565093
Gaggiotti OE, Foll M.

2009 **Genetic consequences of range expansions**. 🏆 1330 citations
Annual Review of Ecology, Evolution, and Systematics. DOI: 10.1146/annurev.ecolsys.39.110707.173414; Full text
L Excoffier, Foll M, RJ Petit

2009[#] **Detecting loci under selection in a hierarchically structured population**. 🏆 921 citations 🔓
Heredity (Edinb). DOI: 10.1038/hdy.2009.74; PMID: 19623208
Excoffier L, Hofer T, Foll M.
Code: cmpg.unibe.ch/software/arlequin35/.

2008[*] **A genome-scan method to identify selected loci appropriate for both dominant and codominant markers: a Bayesian perspective**. 🏆 2867 citations 🔓
Genetics. DOI: 10.1534/genetics.108.092221; PMID: 18780740
Foll M, Gaggiotti O.
GitHub: mfoll/BayeScan.

2006[*] **Identifying the environmental factors that determine the genetic structure of populations**. 🏆 418 citations 🔓
Genetics. DOI: 10.1534/genetics.106.059451; PMID: 16951078
Foll M, Gaggiotti O.
Code: leca.osug.fr/-Genomique-des-populations-.

*: first/co-first author.
#: last/co-last/corresponding author.
🏆: >20 citations/year.
🏆: >50 citations/year (on average since publication, source: Google Scholar).
🔓: Open Access publication.