Dr. Matthieu Foll

Curriculum Vitæ

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

Rare Cancers Genomics Team
Genomic Epidemiology Branch
International Agency for Research on Cancer (IARC-WHO)
25 avenue Tony Garnier, 69007 Lyon, France
Email: follm@iarc.who.int
Research Group: https://www.iarc.who.int/teams-rcg/

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), https://tumourclassification.iarc.who.int/

2023 **Young investigator award**, International Mesothelioma Interest Group (iMig), https://imig.org

2022–on **Chair of the of the Rare Cancers Working Group**, European Prospective Investigation into Cancer and Nutrition (EPIC), http://epic.iarc.who.int

2021–on **lung NET task force member**, European NEuroendocrine Tumors Society (ENETS), https://www.enets.org

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

Education

2004–2007 **PhD in Population Genetics and Evolution**, University of Grenoble, France. https://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

After studying applied mathematics and computer science, I completed a Ph.D. in population genetics and bioinformatics in 2007. During this time I gained a strong expertise in statistical genetics and bioinformatics methods, and I wrote several software now widely used in the field. After my PhD., I moved to the University of Berne as a postdoctoral researcher where I started to work more specifically on large human genomic data. I developed in particular several Bayesian models to identify genetic variants associated with phenotypes observed in different human populations or ethnic groups, being the consequence of local adaptation. In 2012, I was recruited as a Staff Research Scientist in the Swiss Federal Institute of Technology of Lausanne where I worked on new statistical and bioinformatics methods for the analysis Next Generation Sequencing data. In 2014 I been recruited as a staff scientist to develop computation cancer genomics projects and to coordinate the bioinformatics efforts in the International Agency for Research on Cancer (IARC-WHO). I am particularly involved in the molecular characterisation of rare thoracic tumors like lung neuroendocrine tumors and malignant mesothelioma, and since 2021 I am co-leading the IARC Rare Cancers Genomics team together with Dr. Lynnette Fernandez-Cuesta.

Publications

77 publications in international peer-reviewed scientific journals, including 9 publications as first/co-first author, and 14 publications as last/co-last/corresponding author.
13'415 total citations, h-index: 42 (source: Google Scholar).
Full list available at Google Scholar and My NCBI Bibliography.

Current 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

2023–2024 **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: https://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 the INSA Lyon engineering school (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

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: https://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, Annual 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

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 **Spotlight on Small-Cell Lung Cancer and Other Lung Neuroendocrine Neoplasms**.
American Society of Clinical Oncology Educational Book. DOI: 10.1200/EDBK_390794; PMID: 37229617
Fernandez-Cuesta L, Sexton-Oates A, Bayat L, Foll M, Lau SCM, Leal T.

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.

2016 **The past, present and future of genomic scans for selection**.
Molecular Ecology. DOI: 10.1111/mec.13493; PMID: 26745554
Jensen JD, Foll M, Bernatchez L.

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.

2012 **Genomic data reveal a complex making of humans**.
PLOS Genetics. DOI: 10.1371/journal.pgen.1002837; PMID: 22829785
Alves I, Srámková Hanulová A, Foll M, Excoffier L.

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
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.