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[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 tumours 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.

13'273 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: [mfoll/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](https://doi.org/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), Istanbul (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](https://doi.org/10.1093/gigascience/giae008); PMID: [38451475](https://pubmed.ncbi.nlm.nih.gov/38451475/)
Alcala N, Voegelé C, Mangiante L, Sexton-Oates A, Clevers H, Fernandez-Cuesta L, Dayton TL, Foll M.
GitHub: [IARCbioinfo/MS_panNEN_organoids](https://github.com/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](https://doi.org/10.1016/j.ccell.2023.11.007); PMID: [38086335](https://pubmed.ncbi.nlm.nih.gov/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](https://doi.org/10.1200/EDBK_390794); PMID: [37229617](https://pubmed.ncbi.nlm.nih.gov/37229617/)
Fernandez-Cuesta L, Sexton-Oates A, Bayat L, Foll M, Lau SCM, Leal T.
- 2023[#] **Multitomic analysis of malignant pleural mesothelioma identifies molecular axes and specialized tumor profiles driving intertumor heterogeneity.**
Nature Genetics. DOI: [10.1038/s41588-023-01321-1](https://doi.org/10.1038/s41588-023-01321-1); PMID: [36928603](https://pubmed.ncbi.nlm.nih.gov/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](https://doi.org/10.5220/0011865900003417)
Mathian E, Liu H, Fernandez-Cuesta L, Samaras D, Foll M, Chen L.
GitHub: [IARCbioinfo/HaloAE](https://github.com/IARCbioinfo/HaloAE).
- 2022[#] **A molecular phenotypic map of malignant pleural mesothelioma.**
Gigascience. DOI: [10.1093/gigascience/giac128](https://doi.org/10.1093/gigascience/giac128); PMID: [36705549](https://pubmed.ncbi.nlm.nih.gov/36705549/)
Di Genova A, Mangiante L, Sexton-Oates A, Voegelé C, Fernandez-Cuesta L, Alcala N, Foll M.
GitHub: [IARCbioinfo/MESOMICS_data](https://github.com/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](https://doi.org/10.1007/s00428-020-02980-9); PMID: [33411030](https://pubmed.ncbi.nlm.nih.gov/33411030/)
Fernandez-Cuesta L, Mangiante L, Alcala N, Foll M.
- 2020[#] **A molecular map of lung neuroendocrine neoplasms.**
Gigascience. DOI: [10.1093/gigascience/giaa112](https://doi.org/10.1093/gigascience/giaa112); PMID: [33124659](https://pubmed.ncbi.nlm.nih.gov/33124659/)
Gabriel AAG, Mathian E, Mangiante L, Voegelé C, Cahais V, ..., Foll M.
GitHub: [IARCbioinfo/DRMetrics](https://github.com/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](https://doi.org/10.1093/gigascience/giac128); PMID: [36705549](https://pubmed.ncbi.nlm.nih.gov/36705549/)
Delhomme TM, Avogbe PH, Gabriel AAG, Alcala N, Leblay N, ..., Foll M.
GitHub: [IARCbioinfo/needlestack](https://github.com/IARCbioinfo/needlestack).

- 2020 **EURACAN/IASLC Proposals for Updating the Histologic Classification of Pleural Mesothelioma: Towards a More Multidisciplinary Approach.**
Journal of Thoracic Oncology. DOI: [10.1016/j.jtho.2019.08.2506](https://doi.org/10.1016/j.jtho.2019.08.2506); PMID: [31546041](https://pubmed.ncbi.nlm.nih.gov/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](https://doi.org/10.21037/tlcr.2019.11.08); PMID: [32038931](https://pubmed.ncbi.nlm.nih.gov/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](https://doi.org/10.1016/j.ebiom.2019.09.003); PMID: [31648983](https://pubmed.ncbi.nlm.nih.gov/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.**
Nature communications. DOI: [10.1038/s41467-019-11276-9](https://doi.org/10.1038/s41467-019-11276-9); PMID: [31431620](https://pubmed.ncbi.nlm.nih.gov/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.**
Science. DOI: [10.1126/science.aav3824](https://doi.org/10.1126/science.aav3824); PMID: [30705186](https://pubmed.ncbi.nlm.nih.gov/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.**
Nature. DOI: [10.1038/s41586-018-0317-6](https://doi.org/10.1038/s41586-018-0317-6); PMID: [29988082](https://pubmed.ncbi.nlm.nih.gov/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](https://doi.org/10.1016/j.jtho.2016.12.019); PMID: [28034829](https://pubmed.ncbi.nlm.nih.gov/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](https://doi.org/10.1111/mec.13493); PMID: [26745554](https://pubmed.ncbi.nlm.nih.gov/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](https://doi.org/10.1111/1755-0998.12280); PMID: [24834845](https://pubmed.ncbi.nlm.nih.gov/24834845/)
[Foll M](#), Shim H, Jensen JD.
 GitHub: [mfoll/WFABC](https://github.com/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](https://doi.org/10.1016/j.ajhg.2014.09.002); PMID: [25262650](https://pubmed.ncbi.nlm.nih.gov/25262650/)
[Foll M](#), Gaggiotti OE, Daub JT, Vatsiou A, Excoffier L.
 GitHub: [mfoll/BayeScanHierarchical](https://github.com/mfoll/BayeScanHierarchical).
- 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](https://doi.org/10.1073/pnas.1402875111); PMID: [25136101](https://pubmed.ncbi.nlm.nih.gov/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](https://doi.org/10.1371/journal.pgen.1004185); PMID: [24586206](https://pubmed.ncbi.nlm.nih.gov/24586206/)
[Foll M](#), Poh YP, Renzette N, Ferrer-Admetlla A, Bank C, ..., Jensen JD.
- 2013# **Robust demographic inference from genomic and SNP data.**
PLOS Genetics. DOI: [10.1371/journal.pgen.1003905](https://doi.org/10.1371/journal.pgen.1003905); PMID: [24204310](https://pubmed.ncbi.nlm.nih.gov/24204310/)
 Excoffier L, Dupanloup I, Huerta-Sánchez E, Sousa VC, [Foll M](#).
- 2013 **Approximate Bayesian computation.**
PLOS Computational Biology. DOI: [10.1371/journal.pcbi.1002803](https://doi.org/10.1371/journal.pcbi.1002803); PMID: [23341757](https://pubmed.ncbi.nlm.nih.gov/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](https://doi.org/10.1371/journal.pgen.1002837); PMID: [22829785](https://pubmed.ncbi.nlm.nih.gov/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.**
Bioinformatics. DOI: [10.1093/bioinformatics/btr124](https://doi.org/10.1093/bioinformatics/btr124); PMID: [21398675](https://pubmed.ncbi.nlm.nih.gov/21398675/)
Excoffier L, Foll M.
Code: cmpg.unibe.ch/software/fastsimcoal2.
- 2010[#] **Quantifying population structure using the F-model.**
Molecular Ecology Resources. DOI: [10.1093/bioinformatics/btr124](https://doi.org/10.1093/bioinformatics/btr124); PMID: [21398675](https://pubmed.ncbi.nlm.nih.gov/21398675/)
Gaggiotti OE, Foll M.
- 2009 **Genetic consequences of range expansions.**
Annual Review of Ecology, Evolution, and Systematics. DOI: [10.1146/annurev.ecolsys.39.110707.173414](https://doi.org/10.1146/annurev.ecolsys.39.110707.173414)
L Excoffier, Foll M, RJ Petit
- 2009[#] **Detecting loci under selection in a hierarchically structured population.**
Heredity (Edinb). DOI: [10.1038/hdy.2009.74](https://doi.org/10.1038/hdy.2009.74); PMID: [19623208](https://pubmed.ncbi.nlm.nih.gov/19623208/)
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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.**
Genetics. DOI: [10.1534/genetics.108.092221](https://doi.org/10.1534/genetics.108.092221); PMID: [18780740](https://pubmed.ncbi.nlm.nih.gov/18780740/)
Foll M, Gaggiotti O.
GitHub: [mfoll/BayeScan](https://github.com/mfoll/BayeScan).
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Genetics. DOI: [10.1534/genetics.106.059451](https://doi.org/10.1534/genetics.106.059451); PMID: [16951078](https://pubmed.ncbi.nlm.nih.gov/16951078/)
Foll M, Gaggiotti O.
Code: leca.osug.fr/~Genomique-des-populations-.

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#: last/co-last/corresponding author