Tiffany M. **Delhomme**

Ph.D.

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Experience

Postdoctoral researcher (Juan de la Cierva fellow) — *IRB Barcelona, Spain*

Genome Data Science Lab (PI: Pr. Supek) — *Jan. 2020 - present*

- Scientific projects: mining genomics data in order to explore how exogenous and endogenous factors can impact mutational processes in the soma

Ph.D. in Computational Cancer Genomics — *Lyon, France*

International Agency for Research on Cancer (IARC) — *Nov. 2015 - July 2019*

- Thesis: Using the systematic nature of errors in NGS data in order to efficiently detect mutations. Computational methods and application to early cancer detection.

Education

Ph.D. in Computational Cancer Genomics — *Lyon, France*

International Agency for Research on Cancer (IARC) — *Nov. 2015 - July 2019*

- Thesis: Using the systematic nature of errors in NGS data in order to efficiently detect mutations. Computational methods and application to early cancer detection.

M.Sc. in Theoretical Computer Science — *Lyon, France*

ENS Lyon, IXXI (Rhone-Alpes Complex Systems Institute) — *Sept. 2014 - July. 2015*

- Major in complex system modelisation, minor in algorithms

M.Sc. in Bioinformatics and Evolutionary Biology — *Lyon, France*

Universite Claude Bernard — *Sept. 2012 - June. 2014*

- Major in Bioinformatics and biostatistics, minor in evolution and biometry

Skills

Omics	NGS, somatic and germline variant calling and filtering, RNA-seq analysis, TCGA data
Cancer Evolution	Neutral tumor evolution, repeated tumor evolution
Cancer Biomarkers	Circulating tumor DNA for early cancer detection
Machine Learning	Supervised learning and semi-supervised learning (random forest) Unsupervised learning (cluster-then-label)
Statistics	Hypothesis testing and probability theory, bayesian inference, (generalized) linear models
Discrete Mathematics	Graph theory, clustering, biological networks
Programming	Bash, Python, cloud computing (SevenBridges Genomics plateform)
Statistical Programming Languages	R
Scientific Reproducibility	Docker, DockerHub, Singularity, SingularityHub, Git, GitHub
Workflow writing and data format	Nextflow, CWL, JSON, YAML
Language	French: native, English: good writing and communication, Spanish: notions

Publications

The PI3K/mTOR pathway is targeted by rare germline variants in patients with both melanoma and renal cell carcinoma — *Cancers*

Jean-Noël Hubert, Voreak Suybeng, Maxime Vallée, **Tiffany M Delhomme** *et al.* — *May 2021*

link

TP53 Targeted Deep Sequencing of Cell-Free DNA in Esophageal Squamous Cell Carcinoma Using Low-Quality Serum: Concordance with Tumor Mutation — *Int. J. Mol. Sci.*

Dariush Nasrollahzadeh, Gholamreza Roshandel, **Tiffany M Delhomme** *et al.* — *May 2021*

link

The PI3K/mTOR Pathway Is Targeted by Rare Germline Variants in Patients with Both Melanoma and Renal Cell Carcinoma
Jean-Noël Hubert, Voreak Suybeng, Maxime Vallée, **Tiffany M Delhomme** *et al.*
Cancers
2021
link

Development of sensitive droplet digital PCR assays for detecting urinary TERT promoter mutations as non-invasive biomarkers for detection of urothelial cancer
Ismail Hosen, Nathalie Forey, Geoffroy Durand, Catherine Voegele, Selin Bilici, Patrice H. Avogbe, **Tiffany M Delhomme** *et al.*
Cancers
2020
link

needlestack: an ultra-sensitive variant caller for multi-sample deep next generation sequencing data
Tiffany M.Delhomme, Patrice H. Avogbe, Aurelie AA. Gabriel *et al.*
Nucleic Acid Res. - Genomics and Bioinformatics
June 2020
link

Integrative and comparative genomic analyses identify clinically relevant groups of pulmonary carcinoids and unveil the existence of supra-carcinoids
Nicolas Alcala*, Noemie Leblay*, Aurelie Gabriel*, Lise Mangiante, David Hervas Marin, Theo Giffon, Anne-Sophie Sertier, Anthony Ferrari, Jules Derks, Akram Ghantous, **Tiffany M.Delhomme** *et al.*
Nat. Commun.
Aug. 2019

Urinary TERT promoter mutations as non-invasive biomarkers for the comprehensive detection of urothelial cancer
Patrice H. Avogbe, Arnaud Manel, Emmanuel Vian, Geoffroy Durand, Nathalie Forey, Catherine Voegele, Maria Zvereva, Ismail Hosen, Sonia Meziani, Berengere De Tilly, Gilles Polo, Olesia Lole, Pauline Francois, **Tiffany M. Delhomme** *et al.*
EBioMedicine
June 2019
link

Integrative genomic profiling of large-cell neuroendocrine carcinomas reveals distinct subtypes of high-grade neuroendocrine lung tumors
Julie George, Vonn Walter, Martin Peifer, Ludmil B. Alexandrov, Danila Seidel, Frauke Leenders, Lukas Maas, Christian Müller, Ilona Dahmen, **Tiffany M.Delhomme** *et al.*
Nature Communications
Mar. 2018
link

KRAS mutations in blood circulating cell-free DNA: a pancreatic cancer case-control study
Florence Le Calvez-Kelm, Matthieu Foll, Magdalena B. Wozniak, **Tiffany M.Delhomme** *et al.*
Oncotarget
Oct. 2016
link

Identification of Circulating Tumor DNA for the Early Detection of Small-cell Lung Cancer
Lynnette Fernandez-Cuesta*, Sandra Perdomo*, Patrice H.Avogbe*, Noemie Leblay, **Tiffany M.Delhomme** *et al.*
Contribution: development of needlestack, an highly sensitive variant caller that can detect low abundance mutations such as tumor-derived mutations from circulating tumor DNA data. In this study, we applied needlestack to Small-cell Lung Cancer cases and matched controls in order to use circulating tumor DNA as an early cancer biomarker.
EBioMedicine
Aug. 2016
link

Submitted

Disentangling heterogeneity of Malignant Pleural Mesothelioma through deep integrative omics analyses
Lise Mangiante*, Nicolas Alcala*, Alex Di Genova*, Alexandra Sexton-Oates*, [+14], **Tiffany M. Delhomme** *et al.*
Nat. Commun. 2022

In preparation

Assessment of the diagnostic value of circulating RB1 and TP53 mutations for early detection of small cell lung cancers
Patrice H. Avogbe*, **Tiffany M.Delhomme*** *et al.*
expected sub. Dec. 2021

Communications

Posters

needlestack: an ultra-sensitive variant caller for multisample deep next generation sequencing data
Journees Ouvertes Biologie, Informatique et Mathematiques (JOBIM), Clermont Ferrand, France *June 2015*

needlestack: an ultra-sensitive variant caller for multisample deep next generation sequencing data
RECOMB-Computational Cancer Biology, Paris, France *Apr. 2018*

Talks

needlestack: an ultra-sensitive variant caller for multisample deep next generation sequencing data
Journees Ouvertes Biologie, Informatique et Mathematiques (JOBIM), Lyon, France *Aug. 2016*

IARC nextflow pipelines: toward efficient cancer genomics analyses
Nextflow workshop, **invited speaker**, Barcelona, Spain *Nov. 2018*

Honors & Awards

Fellowships

Postdoctoral Fellowship, "Juan de la Cierva", Spanish Ministry of Science *2020-2022*
Ph.D. Fellowship, La Ligue Nationale Contre le Cancer *2015-2018*

Referees

Dr. Matthieu Foll
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