Tiffany M. **Delhomme**

PH.D.

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Looking for a postdoctoral position in computational cancer genomics

Education

International Agency for Research on Cancer (IARC) — *Lyon, France*

PH.D. IN COMPUTATIONAL CANCER GENOMICS — *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.

ENS Lyon, IXXI (Rhone-Alpes Complex Systems Institute) — *Lyon, France*

M.SC. IN THEORETICAL COMPUTER SCIENCE — *Sept. 2014 - July. 2015*

- Major in complex system modelisation, minor in algorithms

Universite Claude Bernard — *Lyon, France*

M.SC. IN BIOINFORMATICS AND EVOLUTIONARY BIOLOGY — *Sept. 2009 - 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

Integrative and comparative genomic analyses identify clinically relevant groups of pulmonary carcinoids and unveil the existence of supra-carcinoids — *Nature Communications*

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.* — *Aug. 2019*

Urinary TERT promoter mutations as non-invasive biomarkers for the comprehensive detection of urothelial cancer — *EBioMedicine*

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.* — *June 2019*

link

Integrative genomic profiling of large-cell neuroendocrine carcinomas reveals distinct subtypes of high-grade neuroendocrine lung tumors — *Nature Communications*

Julie George, Vonn Walter, Martin Peifer, Ludmil B. Alexandrov, Danila Seidel, Frauke Leenders, Lukas Maas, Christian Müller, Ilona Dahmen, **Tiffany M.Delhomme** *et al.* — *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

Under review

needlestack: an ultra-sensitive variant caller for multi-sample deep next generation sequencing data
Tiffany M.Delhomme *et al.*
Contribution: development of the algorithm and implementation (mostly in R, bash and nextflow). needlestack is based on a robust negative binomial regression and is implemented in nextflow to emphasize scientific reproducibility and efficient computations. Analyses on real and simulated tumor data to evaluate the perfomance of needlestack in case of germline, somatic and low allelic fraction somatic mutations.

Nucleic Acid Research - Genomics and Bioinformatics
link

Submitted

Urinary TERT promoter mutations as non-invasive biomarkers for the comprehensive detection of urothelial cancer
Ismail Hosen, Mahdi Sheikh, Maria Zvereva, Ghislaine Scelo, Nathalie Forey, Geoffroy Durand, Catherine Voegele, Hossein Poustchi, Masoud Khoshnia, Gholamreza Roshandel, Masoud Sotoudeh, Arash Nikmanesh, Arash Etemadi, Patrice H. Avogbe, Priscilia Chopard, **Tiffany M. Delhomme** *et al.*

Journal of the National Cancer Institute
Aug. 2019

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.*
Contribution: application of our needlestack algorithm on circulating tumor DNA data (two independent case/control cohorts) and development of variant filtering steps in order to increase the specificity obtained in Fernandez-Cuesta *et al.*

expected sub. Dec. 2019

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

Ph.D. Fellowship, La Ligue Nationale Contre le Cancer *2015-2018*

Referees

Matthieu Foll
GEN/GCS group
International Agency for Research on Cancer
Lyon, France
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James McKay
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