

Tiffany M. Delhomme

4TH YEAR PHD CANDIDATE

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Looking for a postdoctoral position in computational cancer genomics

Education

International Agency for Research on Cancer (IARC)

PH.D. IN COMPUTATIONAL CANCER GENOMICS

[Lyon, France](#)

Nov. 2015 - currently

- Thesis: Dealing with NGS errors to produce an efficient variant calling. Application to early cancer detection.

ENS Lyon, IXXI (Rhône-Alpes Complex Systems Institute)

M.D. IN THEORETICAL COMPUTER SCIENCE

[Lyon, France](#)

Sept. 2014 - July. 2015

- Major in complex system modelisation, minor in algorithms

Université Claude Bernard

M.D. IN BIOINFORMATICS AND EVOLUTIONARY BIOLOGY

[Lyon, France](#)

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 platform)
Statistical Programming Languages	R
Scientific Reproducibility	Docker, DockerHub, Singularity, SingularityHub, Git, GitHub
Workflow writing and data format	Nextflow, CWL, JSON, YAML

Publications

Identification of Circulating Tumor DNA for the Early Detection of Small-cell Lung Cancer

[EBioMedicine](#)

Lynnette Fernandez-Cuesta*, Sandra Perdomo*, Patrice H. Avogbe*, Noemie Leblay, **Tiffany M. Delhomme et al.**

Aug. 2016

[link](#)

KRAS mutations in blood circulating cell-free DNA: a pancreatic cancer case-control study

[Oncotarget](#)

Florence Le Calvez-Kelm, Matthieu Foll, Magdalena B. Wozniak, **Tiffany M. Delhomme et al.**

Oct. 2016

[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](#)

SUBMITTED

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

[Clinical Chemistry](#)

Maria Zvereva, Gabriel Roberti, Geoffroy Durand, Catherine Voegelé, MinhDao Nguyen, Matthieu Foll, **Tiffany M. Delhomme et al.**

sub. Nov 2018

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 Gkantous, **Tiffany M.Delhomme** *et al.*

Nature Communications

sub. Nov 2018

IN PREPARATION

needlestack: an ultra-sensitive variant caller for multi-sample deep next generation sequencing data

Tiffany M.Delhomme *et al.*

expected sub. Dec. 2018

[link](#)

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. 2018

Communications

POSTERS

needlestack: an ultrasensitive variant caller for multisample deep next generation sequencing data

Journées Ouvertes Biologie, Informatique et Mathématiques (JOBIM), Clermont Ferrand, France

June 2015

needlestack: an ultrasensitive variant caller for multisample deep next generation sequencing data

RECOMB-Computational Cancer Biology, Paris, France

Apr. 2018

TALKS

needlestack: an ultrasensitive variant caller for multisample deep next generation sequencing data

Journées Ouvertes Biologie, Informatique et Mathématiques (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

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James McKay

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