

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 (Rhone-Alpes Complex Systems Institute)

M.D. IN THEORETICAL COMPUTER SCIENCE

[Lyon, France](#)

Sept. 2014 - July. 2015

- Major in complex system modelisation, minor in algorithms

Universite 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
Language	French: native, English: good writing and communication, Spanish: notions

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

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.

[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

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

Clinical Chemistry

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 Ghantous, **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

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 performance of needlestack in case of germline, somatic and low allelic fraction somatic mutations.

[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

Contribution: application of needlestack on two new cohorts and development of variant filtering steps in order to increase the specificity obtained in Fernandez-Cuesta *et al.*

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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