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) — *Lyon, France*

PH.D. IN COMPUTATIONAL CANCER GENOMICS — *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) — *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

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

Circulating tumor-derived KRAS mutations in pancreatic cancer cases are predominantly carried by very short fragments of cell-free DNA — *Clinical Chemistry*

Maria Zvereva, Gabriel Roberti, Geoffroy Durand, Catherine Voegele, 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 — *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.* — *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 perfomance 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 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
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