Guillaume Devailly

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Research Experience and Education

November 2017–Present — **GenPhySE, INRAE**, *Researcher (CR)*, Toulouse.
Genetics and epigenetics of farm animals, notably multi-omics approach of heat tolerance and adaptation & epigenome editing.

2015–2017 — **Roslin Institute, University of Edinburgh**, *Post-doctoral fellow*, Edinburgh.
Bioinformatics and transcriptionnal regulation in the team of Anagha Joshi.

2011–2014 — **Cancer Research Centre of Lyon**, *PhD student*, Lyon.
PhD in epigenetics and cancer. Supervisor : Robert Dante, in the team of Patrick Mehlen.

2007–2011 — **ENS de Lyon**, *Licence and Master*, Lyon.
Biosciences. *Normalien. Agrégé.*

Professional training

— Nextflow at Genotoul, October 2020
— Systems biology and gene networks inference, Tony Reverter (CSIRO), November 2018
— Advanced SLURM scheduler, 2018-11-08
— FAIR, FAIRDOM & SEEK training 2018-10-27
— Animal experimentation, FELASA, Veterinary school of Toulouse, September 2018
— Git & GitLab, Nathalie Vialaneix, 2018-03-29
— Proteomics Bioinformatics, EBI, December 2016

Supervision & teaching experiences

Students supervision

— PhD student, 2020–, transgenerational epigenetic inheritance in quails (co-supervision).
— Master student, 6 months (2021), the duodedom transcriptomic response to feed intake in pigs.
— Master student, 6 months (2020), impact of a maternal heat stress on chick embryo DNA methylation.
— Visiting PhD student, 5 months (2017), analysis of mouse and rat transcriptomic data.
— Master student, 2 months (2017), single cell RNA-seq.
— High school student, 1 month (2016), data visualisation of the GEISHA database .

Teaching experiences

— 192 hours of teaching at the Claude Bernard University of Lyon 1 (2011-2014).
— Cell signalling tutorials for vet school students, University of Edinburgh (2016).
— Tutoring in french and mathematics, secondary school students (Lyon, 2007-2008).

Fundings

— 2020 : ANR Flash Open Science : 76k€ for developing interactive visualisations of FAANG data.
— 2019 : Animal Genetics Department, INRAE : 35k€ for developing epigenetic editing tools & studying satiety regulation in pigs intestine.
— 2015 : Cascade Fellows, 40k£ to support post-doctoral research.
— 2014 : *Ligue contre le cancer* (cancer charity), 6 months funding extension for last year of PhD.

Software & web application

— Heat*seq, a web application to compare publicly available NGS experiments (web application).
— PEREpigenomics, visualisations of the Roadmap Epigenomics data (web application).
— scFeatureFilter, informed feature-filtering of single cell RNA-seq data (Bioconductor package).

Other responsibilities

— Member of the R user group EdinbR (2015–2017) and founding member of R-Toulouse (2018–2020).
— Writer for the blog bioinfo-fr.net.
— Reviewing for *F1000Research*, *Scientific Reports*, *Genomics*, *Bioinformatics*, *PLOS ONE*, *Genes*.
— Treasurer of the post-doctoral society of the *Roslin Institute*. (2015–2017).

Selected conferences & seminars

— Epigenetic Inheritance Symposium (ETHZ), 2021
— VizBi 2021
— QMUL epigenetics : New Horizon in Genomics, 2020
— Adebiotech Epigen 2018 (invited speaker)
— ICSB 2018
— JOBIM 2106, 2017, 2021
— Game Of Epigenomics (Dubrovnik), 2016
— Coming of Age : The Legacy of Dolly at 20, scientific symposium (Edinburg), 2016
— Epigenetics : in dialog with the genome (Edinburg), 2015
— GRC Cancer genetics & Eppigenetics, 2013

Prizes

— Toulouse Dataviz competition Hackaviz 2018, Special prize of the Jury.
— Edinburgh Genomics conference (2016), second best poster prize.

Publications

→ **Guillaume Devailly** and Anagha Joshi. Comprehensive analysis of epigenetic signatures of human transcription control. 17(5) :692–705, 2021.

→ **Guillaume Devailly** and Anagha Joshi. Insights into mammalian transcription control by systematic analysis of ChIP sequencing data. *BMC bioinformatics*, 19(Suppl 14) :409, nov 2018.

→ Pía Francesca Loren Reyes, Tom Michoel, Anagha Joshi, and **Guillaume Devailly**. Meta-analysis of liver and heart transcriptomic data for functional annotation transfer in mammalian orthologs. *Computational and Structural Biotechnology Journal*, 15 :425–432, 2017.

→ **Guillaume Devailly** and Anagha Joshi. Transcription control in human cell types by systematic analysis of ChIP sequencing data from the ENCODE. In *Bioinformatics and Biomedical Engineering*, pages 315–324. Springer International Publishing, 2017.

→ **Guillaume Devailly**, Anna Mantsoki, and Anagha Joshi. Heat*seq : an interactive web tool for high-throughput sequencing experiment comparison with public data. *Bioinformatics (Oxford, England)*, 32(21) :3354–3356, nov 2016.

→ **Guillaume Devailly**, Anna Mantsoki, Tom Michoel, and Anagha Joshi. Variable reproducibility in genome-scale public data : A case study using ENCODE ChIP sequencing resource. *FEBS letters*, nov 2015.

→ **Guillaume Devailly**, Mélodie Grandin, Laury Perriaud, Pauline Mathot, Jean-Guy Delcros, Yannick Bidet, Anne-Pierre Morel, Jean-Yves Bignon, Alain Puisieux, Patrick Mehlen, and Robert Dante. Dynamics of MBD2 deposition across methylated DNA regions during malignant transformation of human mammary epithelial cells. *Nucleic acids research*, 43(12) :5838–54, 2015.

Mahmood F. Bhutta, Jane Lambie, Lindsey Hobson, Debbie Williams, Hayley E. Tyrer, George Nicholson, Steve D.M. Brown, Helen Brown, Chiara Piccinelli, **Devailly, Guillaume**, James Ramsden, and Michael T. Cheeseman. Transcript analysis reveals a hypoxic inflammatory environment in human chronic otitis media with effusion. *Frontiers in Genetics*, 10 :1327, 2020.

Deepti Vipin, Lingfei Wang, **Guillaume Devailly**, Tom Michoel, and Anagha Joshi. Causal Transcription Regulatory Network Inference Using Enhancer Activity as a Causal Anchor. *International Journal of Molecular Sciences*, 19(11), nov 2018.

Angeles Arzalluz-Luque, **Guillaume Devailly**, and Anagha Joshi. scFeatureFilter : Correlation-based feature filtering for single-cell RNAseq. In *Bioinformatics and Biomedical Engineering*, pages 364–370. Springer International Publishing, 2018.

Anna Mantsoki, **Guillaume Devailly**, and Anagha Joshi. Dynamics of promoter bivalency and RNAP II pausing in mouse stem and differentiated cells. *BMC Developmental Biology*, 18(1), feb 2018.

P Mathot, M Grandin, **G Devailly**, F Souaze, V Cahais, S Moran, M Campone, Z Herceg, M Esteller, P Juin, P Mehlen, and R Dante. DNA methylation signal has a major role in the response of human breast cancer cells to the microenvironment. *Oncogenesis*, 6(10) :e390, oct 2017.

Ángeles Arzalluz-Luque, **Guillaume Devailly**, Anna Mantsoki, and Anagha Joshi. Delineating biological and technical variance in single cell expression data. *The International Journal of Biochemistry & Cell Biology*, 90 :161–166, sep 2017.

Mélodie Grandin, Pauline Mathot, **Guillaume Devailly**, Yannick Bidet, Akram Ghantous, Clementine Favrot, Benjamin Gibert, Nicolas Gadot, Isabelle Puisieux, Zdenko Herceg, Jean-Guy Delcros, Agnès Bernet, Patrick Mehlen, and Robert Dante. Inhibition of DNA methylation promotes breast tumor sensitivity to netrin-1 interference. *EMBO molecular medicine*, 8(8) :863–77, aug 2016.

A Griveau, **G Devailly**, L Eberst, N Navaratnam, B Le Calvé, M Ferrand, P Faull, A Augert, R Dante, J M Vanacker, D Vindrieux, and D Bernard. The PLA2R1-JAK2 pathway upregulates ERRα and its mitochondrial program to exert tumor-suppressive action. *Oncogene*, 35(38) :5033–42, sep 2016.

Anna Mantsoki, **Guillaume Devailly**, and Anagha Joshi. Gene expression variability in mammalian embryonic stem cells using single cell RNA-seq data. *Computational biology and chemistry*, 63 :52–61, aug 2016.

Anna Mantsoki, **Guillaume Devailly**, and Anagha Joshi. CpG island erosion, polycomb occupancy and sequence motif enrichment at bivalent promoters in mammalian embryonic stem cells. *Scientific reports*, 5 :16791, 2015.

Roxane M Pommier, Johann Gout, David F Vincent, Lindsay B Alcaraz, Nicolas Chuvin, Vanessa Arfi, Sylvie Martel, Bastien Kaniewski, **Guillaume Devailly**, Geneviève Fourel, Pascal Bernard, Caroline Moyret-Lalle, Stéphane Ansieau, Alain Puisieux, Ulrich Valcourt, Stéphanie Sentis, and Laurent Bartholin. TIF1-γ Suppresses Tumor Progression by Regulating Mitotic Checkpoints and Chromosomal Stability. *Cancer research*, 2015.

David Vindrieux, **Guillaume Devailly**, Arnaud Augert, Benjamin Le Calvé, Mylène Ferrand, P Pigny, L Payen, Gérard Lambeau, Michael Perrais, Sebastien Aubert, Hélène Simonnet, R Dante, and David Bernard. Repression of PLA2R1 by c-MYC and HIF-2alpha promotes cancer growth. *Oncotarget*, 5(4) :1004–1013, 2014.

Andrea Paradisi, Marion Creveaux, Benjamin Gibert, **Guillaume Devailly**, Emeline Redoulez, David Neves, Elsa Cleyssac, Isabelle Treilleux, Christian Klein, Gerhard Niederfellner, Philippe A. Cassier, Agnés Bernet, and Patrick Mehlen. Combining chemotherapeutic agents and netrin-1 interference potentiates cancer cell death. *EMBO Molecular Medicine*, 5(12) :1821–1834, 2013.