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Research Experience and Education

	November	GenPhySE, INRAE, Researcher (CR), Toulouse.
— 2	017-Present	Genetics and epigenetics of farm animals, notably multi-omics approach of heat tolerance and adaptation $\&$ epigenome editing.
_	2015–2017	Roslin Institute, University of Edinburgh , <i>Post-doctoral fellow</i> , Edinburgh. Bioinformatics and transcriptionnal regulation in the team of Anagha Joshi.
_	2011–2014	Cancer Research Centre of Lyon, <i>PhD student</i> , Lyon. PhD in epigenetics and cancer. Supervisor: Robert Dante, in the team of Patrick Mehlen.
_	2007–2011	ENS de Lyon , <i>Licence and Master</i> , Lyon. Biosciences. <i>Normalien. Agrégé.</i>

Professional training

- Docker and Kubernetes, April 2023
- 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, and conitnuous training (2019, 2020, 2022).
- Git & GitLab, Nathalie Vialaneix, 2018-03-29
- Proteomics Bioinformatics, EBI, December 2016

Supervision & teaching experiences

Students supervision

- Post-doctoral Researcher, 2024–, epigenetic editing in pig intestinal cells.
- PhD student, 2023–, molecular QTL in pigs (co-supervision).
- PhD student, 2020-2023, transgenerational epigenetic inheritance in quails (co-supervision).
- Master student, 6 months (2023), eQTL detection for pig adaptation to heat stress.
- Master student, 6 months (2022), DNA and mRNA transfection of intestinal cell lines and organoids.
- 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

- 11 hours of teaching (epigenomics bioinformatics), join Master 2 ENSAT INSA Toulouse (2023).
- 192 hours of teaching (embryology and genetics) 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

- epistack, visualisation of epigenetic profiles in stacks.
- 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

- Co-head of the local organisation committee of JOBIM 2024
- Member of the R user group EdinbR (2015–2017) and founding member of R-Toulouse (2018–present).
- Writer for the blog bioinfo-fr.net.
- Reviewing for F1000Research, Scientific Reports, Genomics, Bioinformatics, PLOS ONE, Genes, GSE, PLOS Pathogens.
- Treasurer of the local section of an union. (2021–present).
- Treasurer of the post-doctoral society of the *Roslin Institute*. (2015–2017).

Selected conferences & seminars

- JOBIM 2024
- EAAP 2023
- Digestive Pig Physiology, 2022
- 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, 2022
- 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

- → **Devailly, Guillaume**, Katia Fève, Safia Saci, Julien Sarry, Sophie Valière, Jérôme Lluch, Olivier Bouchez, Laure Ravon, Yvon Billon, Hélène Gilbert, Juliette Riquet, Martin Beaumont, and Julie Demars. Divergent selection for feed efficiency in pigs altered the duodenum transcriptomic response to feed intake and its dna methylation profiles. *Physiological Genomics*, 56(5):397–408, May 2024.
- \rightarrow Guillaume Devailly and Anagha Joshi. Comprehensive analysis of epigenetic signatures of human transcription control. *Molecular Omics*, 17(5):692–705, 2021.
- \rightarrow 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.
- \rightarrow 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.
- \rightarrow 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.
- \rightarrow 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.
- \rightarrow 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.

Martin Beaumont, Corinne Lencina, Katia Fève, Céline Barilly, Laurence Le-Normand, Sylvie Combes, **Devailly, Guillaume**, and Gaëlle Boudry. Disruption of the primocolonizing microbiota alters epithelial homeostasis and imprints stem cells in the colon of neonatal piglets. *The FASEB Journal*, 37(10), September 2023.

Eloïse Mussard, Corinne Lencina, Lise Gallo, Céline Barilly, Maryse Poli, Katia Feve, Mikael Albin, Laurent Cauquil, Christelle Knudsen, Caroline Achard, **Guillaume Devailly**, Laura Soler, Sylvie Combes, and Martin Beaumont. The phenotype of the gut region is more stably retained than developmental stage in piglet intestinal organoids. *Frontiers in Cell and Developmental Biology*, 10, August 2022.

C. Cerutti, S. Leroux, D. Gourichon, Y. Labrune, I. David, T. Zerjal, V. Coustham, **G. Devailly**, and F. Pitel. Short communication: Effects of in-ovo injection of endocrine disruptors and methyltransferase inhibitor on quail growth and egg-laying performances. *Animal*, 16(3):100464, March 2022.

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.

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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.

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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 $ERR\alpha$ 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.

Last update : 2024/07/18