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# Thomas BRAZIER

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38 years old

16, rue de la ville en pierre  
35 500 Vitré, FRANCE

One child  
Civil partnership

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<https://thomasbrazier.github.io>

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## INTERESTS

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Population Genomics  
Evolutionary Biology  
Deep Learning

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## SKILLS

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Statistics & Data Science  
R, Python, Bash/Unix  
Neural Networks  
Torch & Tensorflow  
Bioinformatics, Snakemake  
HPC

French (native speaker)  
English (written, spoken)

Driving license

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## ACADEMIC BACKGROUND

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**2022 – now. Post-doc CNRS. ECOBIO UMR 6553**  
Rennes. Qualified for MCU position (2024)

**2019 – 2022. PhD Recombination Landscapes and Genome Evolution in Angiosperms**  
CNRS/Rennes I University  
ECOBIO UMR 6553, EvoAdapt Team  
(Genome Evolution and Adaptation)  
Supervisor: Sylvain Glémin

**2017 – 2019. MSc Biodiversity Ecology & Evolution**  
Rennes I University – with honors  
(first of the class)

**2017. BSc Biology of Organisms**  
Aix-Marseille University – with honors  
(first of the class)

**2015 – 2016. BSc Life Science**  
Paris 6 University Pierre et Marie Curie / FOAD

**2007 – 2010. ENS Louis Lumière**  
Cinema, Photography & Sound School  
École Nationale Supérieure Louis Lumière –  
with honors

**2004 – 2007. Bachelor of Arts**  
Paris X Nanterre University – with honors

**2004. High School Diploma**  
Science – with honors

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## PROFESSIONAL BACKGROUND

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**2010-17. Grip/Key grip. Cinema and television**

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## POST-DOCTORAL EXPERIENCE

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**2024-2026** (24 months). Project: ERC EvoSV  
Claire Mérot.

Structural Variation & genetic diversity (macro-scale): How variable and how similar are structural diversity and evolutionary patterns driven by SVs across the tree of life, and why?

**2023-2024** (18 months). Project: ANR CisTransEvol  
Sylvain Glémin, Thomas Lenormand et al.  
Evolution of gene expression and the runaway process.

**2023 - Free collaboration with Claire Mérot (ECOBIO),  
Claire Lemaitre (INRIA) and the Wellcome Sanger Institute (Cambridge)**  
Development of a Structural Variant Calling pipeline.  
This collaboration is associated with an SV calling pipeline I developed (see below).

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## PUBLICATIONS

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- Brazier T. & Glémin S. (in revision).** Mating system and the evolution of recombination rates in seed plants. *Minor Revision in JEB*.
- Brazier T.,** Zarzoso-Lacoste D., Lehnen L., Jan P.-L., Puechmaille S.J., Petit E.J. **(2024).** The geometry of gametic dispersal in a flying mammal, *Rhinolophus hipposideros*. bioRxiv 2024.10.24.620000; doi: <https://doi.org/10.1101/2024.10.24.620000>
- Brazier, T., & Glémin, S. (2024).** Diversity in Recombination Hotspot Characteristics and Gene Structure Shape Fine-Scale Recombination Patterns in Plant Genomes. *Molecular Biology and Evolution*. <https://doi.org/10.1093/molbev/msae183>
- Brazier T. & Glémin S. (2022).** Diversity and determinants of recombination landscapes in flowering plants. *PLoS Genetics*. <https://doi.org/10.1371/journal.pgen.1010141>
- Brazier T.,** Cherif E., Martin J.F., Gilles A., Blanchet S., Zhao Y., et al. **(2022).** The influence of native populations' genetic history on the reconstruction of invasion routes: the case of a highly invasive aquatic species. *Biol Invasions*. <https://link.springer.com/10.1007/s10530-022-02787-6>
- Foley N.M., Petit E.J., **Brazier T.,** Finarelli J.A., Hughes G.M. Touzalin F., Puechmaille S.J., Teeling E.C. **(2020).** Drivers of longitudinal telomere dynamics in the long-lived bat species, *Myotis myotis*. *Mol Ecol*. <https://doi.org/10.1111/mec.15395>

## IN PREPARATION

Siri Birkeland S., Gustafsson A.L.S., Gizaw A., Chala D., Fraccasetti M., **Brazier T.,** Schrøder-Nielsen A., Slotte T., Rieseberg L.H., Brysting A.K., Glémin S., Nowak M.D., Brochmann C. What drives the rapid buildup of sterility barriers in the Arctic crucifer *Draba nivalis*?

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## SOFTWARE

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EasyMareyMap, R package to estimate recombination maps

<https://github.com/ThomasBrazier/EasyMareyMap>

Marey map data associated available at <https://lbbe-shiny.univ-lyon1.fr/MareyMapOnline/>

LD-based recombination maps, Snakemake pipeline

<https://github.com/ThomasBrazier/ldhat-snakemake-pipeline>

Structural Variant calling from long reads, Snakemake pipeline

<https://github.com/ThomasBrazier/evolsv>

Collaboration with Claire Merot (ECOBIO), Claire Lemaitre (INRIA) and the Wellcome Sanger Institute (Cambridge)

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## COMMUNICATIONS (PRESENTING)

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Recombination gradients within plant genic regions shaped by recombination hotspots.

2024. PopGroup 57. Oral

2023. Jacques Monod Conference. Sex unfolded. Poster

Diversity and determinants of recombination landscapes in flowering plants.

2022. Petit Pois Déridé. Poster

2022. Scientific Days of the Doctoral School. Poster

2021. Evolution. Talk

2021. Post-Docs and Student Meiosis Conference. Talk

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## ACADEMIC INTERNSHIPS

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**2019.** bachelor's degree (6 months), INRAE UMR DECOD. Supervisor: Scott McCairns  
Inferring invasion pathways and source population of the topmouth gudgeon (*Pseudorasbora parva*) in Europe with Machine Learning and ABC  
**(Published in Biol. Invasions)**

**2018.** bachelor's degree (4 months), INRAE UMR DECOD. Supervisor: Eric Petit  
Limited male dispersal and mating system in lesser horseshoe bats (*Rhinolophus hipposideros*):  
estimates from parentage assignment **(submitted to PCI Ecology)**

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## REVIEW ACTIVITY

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Reviewer for eLife, Evolution Letters, GBE and Journal of Evolutionary Biology

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## TEACHING & SUPERVISION

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### **2024. Supervisor of Remy Delage, M.Sc. internship (M2)**

Recombination gradients and GC gradients within plant genomes.

### **2023. Project Tutoring (2 M2 students, 3 hours)**

During one semester, I have been tutoring two Master students (M2) for a practical programming project which I designed and led (one hour per week effectively). They had to code quality controls and visualisation tools which will be integrated in our own SV calling pipeline.

### **2023. Co-supervisor of Lune Angevin, M.Sc. internship (M1)**

Lune implemented a bioinformatic pipeline to detect and call genomic structural variants based on the Darwin Tree of Life data.

### **2019 – 2022. Teaching assistant (3 years, 192 hours)**

Practicals in bio-informatics & statistics (B.Sc. & M.Sc., 160 hours).

Practicals in Ecology (B.Sc., 20 hours).

Jury Member of Oral Defenses (M.Sc., 12 hours).

### **2021. Co-supervisor of Elise Rolland, M.Sc. internship (M2)**

Elise implemented a bioinformatic pipeline to estimate recombination landscapes at fine scale from population data.

### **2020. Co-supervisor of Léo Salema-Gabrelle, M.Sc. internship (M1)**

Léo studied the evolution of recombination patterns and their genomic consequences in angiosperms.

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## GRANTS

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2023. ECOBIO Grant. Funding for a 6-month M2 internship (2024).

Recombination and GC gradients in plant genomes.

2022. ECOBIO Grant for a metagenomic study of micro-organisms communities in forest soil between ancient and recent forest lands (€ 5000). In this project I developed skills for sampling forest soil, DNA extraction and sequencing micro-organisms.

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## WORKSHOPS & COURSES

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- 2024. Workshop Programming with Julia (HPC/Applied mathematics department Rennes)
- 2023-2024. Deep Learning Specialization (MOOC Coursera, 3 months, 10 hours/week)
- 2023. Phylogenomic. CNRS Formation led by Stephan Guindon (Montpellier)
- 2022. Docker (MOOC OpenClassrooms)
- 2021. Ethic & Integrity (MOOC FUN)
- 2021. CNRS Summer school. Detection and Annotation of Transposable Elements
- 2021. Biogenouest Platform. Introduction to Genome Assembly/Annotation with Galaxy
- 2021. Python programming: from fundamentals to advanced concepts (MOOC FUN)
- 2020. GDR Ecolstat. Statistics for Ecology workshop (Rennes)
- 2019. Introduction to Wolfram Mathematica
- 2019. C++ programming. M.Sc. class (Rennes, Engineer School)
- 2017. Wood Anatomy (MOOC FUN)
- 2016. Des rivières et des hommes : hydrologie, hydraulique et géomorphologie
- 2015. Stem Cells (MOOC FUN)
- 2015. Python programming. (MOOC FUN)

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## ADDITIONAL INFORMATION

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### *Laboratory life*

- 2021 – now. Volunteer for the Labo I.5 initiative in the ECOBIO laboratory
- 2020 – 2023. Elected member of the Doctoral School advisory board (Rennes)
- 2020 – 2022. Book club led by **Martin Lascoux** (Uppsala University)
- 2019 – now. Recurrent animator of the ECOBIO laboratory journal club

### *Collaborations outside the laboratory*

**Claire Lemaitre (INRIA, Rennes).** Claire L. is a partner for methodological developments to address the diversity of Structural Variation within Eukaryotes genomes of the Darwin Tree of Life.

**Anne-Marie Chèvre and Mathieu Rousseau-Gueutin (INRAE IGEPP, Rennes).**

I helped them to estimate recombination maps in a polyploid Brassicaceae species.

**Adam Eyre-Walker (University of Sussex, UK).** Adam Eyre-Walker is focused on the rate, pattern and effects of mutations. As the effect of recombination can mimic mutagenic effects and selection in favours of certain nucleotides, I began to discuss with him for paper based on my thesis. Besides, I am also involved with him in a project aiming to estimate effective population sizes based on patterns of linkage disequilibrium. As such, I am invited to give a seminar at his lab (April 2024).

**Laurent Duret and Nicolas Lartillot (LBBE, Lyon University).** I am involved in the HotRec French ANR project, which is studying meiotic recombination in metazoans, while I'm studying in parallel recombination patterns in plants. I did recurrent meetings and travels at the LBBE.

**Christian Brochmann (Oslo University).** I was involved in the Speciation Clock project in Norway, for which I applied population genetics methods to study population structure and demography between populations of the Arctic crucifer *Draba nivalis*.