Thomas BRAZIER

38 years old

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

One child
Civil partnership

+33 (0)6 70 48 42 12

thomas.brazier@univ-rennes.fr

ORCID 0000-0001-5990-7545

https://thomasbrazier.github.io

INTERESTS

Population Genomics
Evolutionary Biology
Deep Learning

SKILLS

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

French (native speaker)
English (written, spoken)

Driving license

ACADEMIC BACKGROUND

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 1 University
ECOBIO UMR 6553, EvoAdapt Team
(Genome Evolution and Adaptation)
Supervisor: Sylvain Glémin

2017 – 2019. MSc Biodiversity Ecology & Evolution
Rennes 1 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

PROFESSIONAL BACKGROUND

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

POST-DOCTORAL EXPERIENCE

2024-2026 (24 months). Project: ERC EvolSV
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).

PUBLICATIONS

Brazier T., Stetsenko R., Roze D., & Glémin S. **(2025).** Mating system and the evolution of recombination rates in seed plants. *Accepted in JEB.*

Dallaire X., Normandeau E., **Brazier T.**, Harris L., Hansen M. M., Mérot C., Moore J-S. **(2024).** Leveraging whole genomes, mitochondrial DNA, and haploblocks to decipher complex demographic histories: an example from a broadly admixed arctic fish. bioRxiv 2024.12.11.628006; doi: https://doi.org/10.1101/2024.12.11.628006

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

SOFTWARE

ABCNN, R package for demographic inference with
Approximate Bayesian Computation and Bayesian Neural Networks.
Private github. Access upon request.

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)

COMMUNICATIONS (PRESENTING)

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

ACADEMIC INTERNSHIPS

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**)

REVIEW ACTIVITY

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

TEACHING & SUPERVISION

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.

GRANTS

2019. PhD grant of the Doctoral School. Three years.

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.

WORKSHOPS & COURSES

2025. Winter School Qlife. Polygenic selection. ENS Paris.
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 Ecostat. 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)

ADDITIONAL INFORMATION

Laboratory life

2025 - now. Scientific animator of the mailing list 'Big Data and AI for Ecology and Evolution'
2024 – now.   Elected member of the Laboratory Consultative Board
2021 – now.   Volunteer for the Labo 1.5 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.*