

# Élise Kerdoncuff

## Education and Professional Experience

- 2025-current **Postdoc**, Human Evolutionary Genetics team at Pasteur Institute, Paris, France. Tracing Ancestral Genomes from Genome-Wide Genealogies: Insights Into Human Genetic History in the Pacific.
- 2022-2025 **Postdoc**, Moorjani Lab at University of California, Berkeley, USA. Study of South Asian population evolutionary history and development of local ancestry inference methods.
- 2017-2021 **PhD**, *Detection of Recent Decline in Population by a Genomic Approach*, Stochastic Models for the Inference of Life Evolution group (CIRB, Collège de France) and Atelier de Bio-Informatique group (Muséum National d'Histoire Naturelle - MNHN). Supervised by Guillaume Achaz and Amaury Lambert, Sorbonne University.
- 2015-2017 **Master**, Ecology, Biodiversity, Evolution, speciality: Evolutionary Ecology, Sorbonne University.
- 2012-2015 **Bachelor**, Bi-disciplinary bachelor of biology and mathematics, Sorbonne University at the Roscoff Marine Station, France.
- Exchange**, 3<sup>rd</sup> year of bachelor (2014-2015) at the National University of Singapore, Singapore.

## Publications, Preprints

1. **Kerdoncuff, E.\***, Marohn M.\*, Cramer N., Dey S., Kardias S., Thangaraj K., Ségurel L., Lee J., Dey AB., Moorjani P. Revisiting the Evolution of Lactase Persistence: Insights from South Asian Genomes [bioRxiv preprint](#) (\*EK and MM contributed equally to this work)
2. **Kerdoncuff, E.\***, Skov L.\*, Patterson N., Zhao W., Lueng Y.K., Schellenberg G.D., Smith J., Ganna A., Dey AB., Kardias S., Lee J., Moorjani P. 50,000 years of Evolutionary History of India: Insights from 2,700 Whole Genome Sequences. [Cell](#) (\*EK and LS contributed equally to this work)
3. **Kerdoncuff, E.**, Ianni-Ravn, M., Roze, D., Novembre, J., Lambert, A., Achaz, G. How demography shapes linkage disequilibrium with or without recombination. [bioRxiv preprint](#)
4. Freund, F.\*, **Kerdoncuff, E.\***, Matuszewski, S., Lapierre, M., Hildebrandt, M., Jensen, J. D., Ferretti, L., Lambert, A., Sackton, T. B., Achaz, G. Interpreting the pervasive observation of U-shaped Site Frequency Spectra. (2023) [PLOS Genetics](#) (\*FF and EK contributed equally to this work)
5. Foutel-Rodier, F., Blanquart, F., Courau, P., Czappon, P., Duchamps, J., Gamblin, J., **Kerdoncuff, E.**, Kulathinal, R., Régner, L., Vuduc, L., Lambert, A., Schertzer, E. From individual-based epidemic model to McKendrick-von Foerster PDEs: a guide to modeling and inferring COVID-19 dynamics. (2022) [Journal of Mathematical Biology](#)
6. **Kerdoncuff, E.**, Lambert, A., Achaz, G. Testing for population decline using maximal linkage disequilibrium blocks. (2020) [Theoretical Population Biology](#).
7. Ribardièrre, A., Centanni, J., Dano, A., Coudret, J., Daguin-Thiébaud, C. Houbin, C., **Kerdoncuff, E.**, Jambut, S., Cordaux, R., Broquet, T. Female-biased sex ratios unrelated to *Wolbachia* infection in European species of the *Jaera albifrons* complex (marine isopods). (2018) [Journal of Experimental Marine Biology and Ecology](#).

## Presentations

### Invited

- *Gokcumen Lab Seminar*, October 2025, Online seminar, University of Buffalo, New-York, USA.
- *Anthropologie Génétique UMR seminar*, March 2025, Musée de l'Homme, Paris, France.

- *Human Evolutionary Genetics group weekly seminar*, May 2024, Pasteur Institute, Paris, France.
- *Workshop on Li-Stephens based methods and applications*, December 2022, Harvard, USA.
- *Center for Theoretical and Evolutionary Genetics weekly seminar*, April 2022, UC Berkeley, USA.
- *Workshop : Evolutionary Genomics and Life History Traits*, October 2019, Montpellier, France.
- *Séminaire du CESCO*, June 2019, MNHN, Paris, France.

### Contributed talks

- *Probabilistic Modeling in Genomics*, March 2025, Cold Spring Harbor, USA.
- *Bay Area Population Genomics*, November 2024, Berkeley, USA.
- *New Frontiers in Reconstructing Human Evolution History*, June 2023, Hannover, Germany.
- *Bay Area Population Genomics*, October 2022, Berkeley, USA.
- *Popgroup53*, January 2020, Leicester, Royaume-Uni.
- *GDR Approches Interdisciplinaires en Evolution Moléculaire (AIEM)*, November 2019, Toulouse, France.
- *Annual Meeting Society for Molecular Biology and Evolution (SMBE), Symposium: The Coalescent in the Era of Population-Scale Genomics*, July 2019, Manchester, Royaume-Uni.
- *Mathematical and Computational Evolutionary Biology (MCEB)*, May 2019, Porquerolles, France.
- *Séminaire de l'ISYEB*, May 2019, MNHN, Paris, France.
- *CIRB seminar*, February 2019, Collège de France, Paris, France.
- *Popgroup52*, January 2019, Oxford, Royaume-Uni.

### Poster

- *Annual Meeting Society for Molecular Biology and Evolution (SMBE)*, July 2024, Puerto Vallarta, Mexico.
- *Population, Evolutionary, and Quantitative Genetics Conference*, June 2022, Asilomar, USA.
- *Probabilistic Modeling in Genomics*, October 2019, Aussois, France.
- *GDR AIEM*, November 2018, Lille, France.
- *MCEB*, June 2018, Saint-Martin-de-Londres, France.
- *GDR AIEM*, November 2017, Lyon, France.

### Media

2024-2025 Interviews on the Indian Evolutionary History:

- General audience newspapers: *Times of India*, *San Francisco Chronicle*
  - Scientific newspapers: *New scientist*, *Live Science*
  - Radio/Podcast : *Sher-E-Punjab AM 600 Vancouver*, *The Coffee House Experience Podcast*
- 2021 Podcast episode of *Chercheuses* on my PhD journey: [In French](#)

### Teaching Experience

- 2022 *University of California, Berkeley*, Quantitative Biology Bootcamp, Teaching Assistant (15h).
- 2022 *University of California, Berkeley*, Computational Biology Skill Seminar, lecture (1h, [Video](#)).
- 2018-2019 *Sorbonne Université, Paris*, Python, Teaching Assistant (40h).
- 2017-2018 *IUT de Vélizy*, C Language, class and tutorials (45h).

### Mentoring/Supervision

- 2023-current **Meaghan Marohn**, PhD Candidate UC Berkeley.  
Revisiting the evolution of lactase persistence : insights from South Asian genomes.
- 2024 **Mara Baylis**, Rotation student UC Berkeley, 3 months.  
Description, origin and functional impact of the haplotype carrying the BTNL2 gene inherited from Denisovan and present in human populations.
- 2021 **Pierre Imbert**, M2 Bio-Informatique Paris Diderot, 6 months.  
Benchmark of inference methods: a focus on population decline.
- 2019 **Ludovic Fourteau**, M1 Bio-Informatique Paris Diderot, 3 months.  
Effect of a single recombination event on the diversity in a population.

2019 **Rebecca Clodion**, M1 Bio-Informatique Paris Diderot, 3 months.  
The mysterious U spectrum: a population analysis of the genetic diversity.

## Grants/Scholarship

2024 Symposium SMBE 2024 (Organisation grant 4,250\$).  
2023 Keystone Symposia Future of Science Fund scholarship (Travel grant 1,200\$).  
2020-2021 ATER Collège de France grant for a fourth year of PhD (Salary >20,000€).  
2017-2020 Interfaces pour le vivant (IPV) doctoral school grant for a three year PhD (Salary >50,000€).

## Service

**Reviewer:** *Nature communications* (2025), *Human Genetics and Genomics Advances* (2025), *BMC Biology* (2025), *American Journal of Human Genetics* (2024), *Molecular Biology and Evolution* (2024), *Human Population Genetics and Genomics* (2024-2025), *European Journal of Human Genetics* (2022-2023)

**Symposium organiser:** *Haplotype-based methods and frameworks for inference of evolutionary history*. SMBE 2024, Puerto Vallarta, Mexico.

**Student/postdoc representative of the ISYEB (elected member):** Institute meetings participation. Organisation of monthly seminars and yearly Young Research day; from 2018 to 2021.

**Jury:** Best poster and best presentation of the symposium 'Evolutionary Ecology' of the 6th Young Natural History Scientists' Meeting, 12-16 mars 2019, MNHN, Paris, France.

**Volunteer at conferences:** Evolution 2018, Montpellier, France.

**Student representative of the SDUEE Master (elected member):** Council meetings participation; from 2016 to 2018.

## Computer skills

Languages C, PYTHON

Familiar with the usage of a computer cluster

Github

- Scripts of paper *50,000 years of Evolutionary History of India* ([github.com/MoorjaniLab/LASI-DAD](https://github.com/MoorjaniLab/LASI-DAD))
- Scripts and data of paper *Interpreting the pervasive observation of U-shaped Site Frequency Spectra* ([github.com/fabfreund/usfs\\_mmc](https://github.com/fabfreund/usfs_mmc))
- Code of the four gamete test chopping algorithm into Maximum Linkage Disequilibrium blocs ([github.com/Ekerdoncuff/algo\\_4GT\\_genome](https://github.com/Ekerdoncuff/algo_4GT_genome))

## References/Collaborators

- Priya Moorjani, Postdoc advisor, Assistant Professor at *UC Berkeley*: [moorjani@berkeley.edu](mailto:moorjani@berkeley.edu)
- Guillaume Achaz, PhD advisor, Professor at *Université Paris-Cité*: [guillaume.achaz@mnhn.fr](mailto:guillaume.achaz@mnhn.fr)
- Amaury Lambert, PhD advisor, Professor at *École Normale Supérieure*: [amaury.lambert@ens.fr](mailto:amaury.lambert@ens.fr)