

# Guillaume LOUVEL

## Professional experiences

2021/01–2023/04

**Postdoctoral researcher**, *Diversity, Ecology and Evolution of Microbes*, Université Paris-Saclay, France.  
Deep phylogenetics: causes of incongruence in gene trees of Asgard archaea and Eukaryotes. Direction: Dr. Laura EME.

## Education

2016/09–2020/09

**PhD**, *Dyogen team, Institut de Biologie de l'École Normale Supérieure*, Paris, France.  
Dating within gene trees: speciations, duplications, losses. Direction: Prof. Hugues ROEST CROLLIUS.

2018/05

**EMBO Course: Computational Molecular Evolution (CoME)**, *Hellenic Center for Marine Research*, Heraklion, Greece, 61h.

2017/12

**Population genetics course: Genomes, Populations, Species**, *École Normale Supérieure*, Paris, 30h.  
Coordination: Prof. Guillaume Achaz

2015–2016

**Master's degree 2<sup>d</sup> year: Molecular and Cellular Biology (BMC), specialisation Bioinformatics and Modelling (BIM)**, *Pierre and Marie Curie University (UPMC)*, Paris, with high honours (Mention Bien).

2014–2015

**Internships for the ENS Diploma (cf. internships)**, *École normale supérieure (ENS) of Paris*.

2013–2014

**Master's degree 1<sup>st</sup> year: Ecology, Biodiversity, Evolution (EBE)**, *École normale supérieure (ENS), Pierre and Marie Curie University (UPMC)*, Paris.

2012–2013

**Bachelor's degree in Life Science**, *ENS, UPMC*, Paris, with honours.

2010–2012

**Classes Préparatoires aux Grandes Écoles BCPST (Biology, Chemistry, Physics and Earth Sciences)**, *Sainte-Geneviève high school*, Versailles, France.

2010

**Baccalauréat, scientific serie**, *Nantes local education authority–Lycée Nicolas Appert*, Orvault, France, with highest honours.

## Teaching

2018–2019

**32h, ENS.**  
Biostatistics lectures, Evolutionary genomics, Bioinformatics assistant in practicals (Bachelor, Master)

2017–2018

**32h, ENS.**  
Assistant in bioinformatics and phylogenetics practicals (Bachelor, Master)

2017, 2018, 2019

**3×3h, volunteer via the student association of IBENS.**  
Introduction to the phylogenetic comparative methods

2013

**Biology oral examiner in CPGE**, *Sainte-Geneviève high school*, Versailles, France.

## Undergraduate internships

- February–June 2016 **Master 2 internship**, *Dyogen team, Institut de biologie de l'École normale supérieure (IBENS), Paris, France.*  
Retained functions of gene duplicates in vertebrates. Supervision: Prof. Hugues ROEST CROLLIUS
- March–July 2015 **Own-initiative internship**, *Paleomix group, Centre for GeoGenetics, Natural History Museum of Denmark.*  
A pipeline for ancient metagenomics. Supervision: Assoc. Prof. Ludovic ORLANDO
- Sept. 2014–Jan. 2015 **Own-initiative internship**, *South African Iziko's Museum, Cape Town, South Africa.*  
Palaeontology of the South-African Karoo: Juvenile aggregations of Permian reptiles.  
Supervision: Prof. Roger SMITH
- February–June 2014 **Master 1 internship**, *Paleomix group, Centre for GeoGenetics, Natural History Museum of Denmark.*  
Deciphering ancient epigenomes. Supervision: Assoc. Prof. Ludovic ORLANDO
- June–July 2013 **Bachelor internship**, *Biology of Genomes, UMR 7238 CNRS, UPMC, Paris.*  
Establishment of the substitution patterns and rates on several chromosomal loci of the yeast *Lachancea kluyveri*. Supervision: Prof. Gilles FISCHER

## Other professional experience

- 2009 **BAFA diploma**, France & Germany, Youth leadership certificate in holiday camp.

## Languages

English	fluent
French	native
German	good

## Computer skills

### Work environnements

- o GNU Linux, Mac OS X
- o UNIX command line
- o code versioning: Git
- o High Performance Computing: Slurm, HTCondor

### Programming languages

- o Python, expert
- o Bash, expert
- o R, proficient
- o Perl, familiar
- o Vimscript, familiar
- o C++, learning

### Bioinformatics

- o workflow managers (snakemake, GNU make)
- o NGS, alignments, phylogenetics

### Data analysis

- o Python packages: Numpy, Scipy, Pandas, Statsmodels, Scikit-learn
- o Statistical modelling: PCA, multiple linear regression, Lasso regression, mixed models, bayesian statistics

## Software projects

Multipurpose tools for phylogenetics:  
Metagenomics pipeline for ancient DNA:  
Reconciliation algorithm (gene tree - species tree):  
Contributions:

[github.com/DyogenIBENS/Phylorgs](https://github.com/DyogenIBENS/Phylorgs)  
[bitbucket.org/Glouvel/metabit](https://bitbucket.org/Glouvel/metabit)  
[github.com/Gullumluv1/Genarium](https://github.com/Gullumluv1/Genarium)  
APE (R), simclock (R), Ete3 (Python)

## Publications

### PhD publications

- Louvel, G.** and Roest Crolius, H. Aug. 14, 2023. “Factors influencing the accuracy and precision in dating single gene trees”. In: *bioRxiv*: 10.1101/2020.08.24.264671v2. DOI: 10.1101/2020.08.24.264671. *submitted*.
- Szenker-Ravi, E., Ott, T., Khatoor, M., Moreau de Bellaing, A., Goh, W. S., Chong, Y. L., Beckers, A., Kannesan, D., and **Louvel, G.**, et al. 2022. “Discovery of a genetic module essential for assigning left–right asymmetry in humans and ancestral vertebrates”. In: *Nature Genetics* 54.1, pp. 62–72. DOI: 10.1038/s41588-021-00970-4.

### Previous publications

- Louvel, G.**, Der Sarkissian, C., Hanghøj, K., and Orlando, L. May 2016. “metaBIT, an integrative and automated metagenomic pipeline for analyzing microbial profiles from high-throughput sequencing shotgun data”. In: *Mol. Ecol. Resour.* DOI: 10.1111/1755-0998.12546.
- Gillet-Markowska, A., **Louvel, G.**, and Fischer, G. Nov. 2015. “bz-rates: A Web Tool to Estimate Mutation Rates from Fluctuation Analysis.” In: *G3 (Bethesda)*. 5.11, pp. 2323–7. DOI: 10.1534/g3.115.019836.
- Seguin-Orlando, A., Gamba, C., Der Sarkissian, C., Ermini, L., **Louvel, G.**, Boulygina, E., Sokolov, A., Nedorozhko, A., and Lorenzen, E. D., et al. Jan. 2015. “Pros and cons of methylation-based enrichment methods for ancient DNA.” In: *Sci. Rep.* 5, p. 11826. DOI: 10.1038/srep11826.

## Scientific communications

- 2023/01 **ALPHY (Alignments and Phylogeny)**, *Grenoble*.  
Causes for discord in eukaryotic protein domains inherited from Archaea
- 2023/01 **ISEP Virtual Meeting (International Society for Evolutionary Protistology)**, *Online*.
- 2017/02 **ALPHY (Alignments and Phylogeny)**, *Paris*, MNHN.  
Genomic markers of species diversification in Vertebrates

## Personal interests

### Community involvement

- Member of the organising comity of the YRLS conference, 2017 (Young Researchers in Life Sciences), Paris.
- Vice-treasurer of the association Phoenix de Montrouge, 2017–2019 (ultimate frisbee)

### Sciences

- Evolution;
- fauna and flora ;
- paleontology, history of Earth and life;
- ...

### Other

- running, ultimate frisbee, hiking, climbing;
- Bicycle repair;
- Science-fiction, fantasy;
- Psychedelic rock.