



Chloé Aujoulat

Bioinformatician

Profile

I am currently looking for a fixed-term or a permanent contract to work in genomic/transcriptomic data analysis.

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Skills

Genomic data analysis (genome assembly, QC, trimming, sequence alignment)	Data visualisation
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Programming (Python, R, Bash, Nextflow)	Oral presentation
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HPC

Conferences / Papers

[Jobim](#) - Toulouse (2024) and Bordeaux (2025)

[Review 2023](#) - Guide of mathematical modelling of metabolism: from the bench to the console and the way back.

[Poster ISGSB Innsbruck 2022](#) - Graph theory as a driver for multi-omic mechanistic model construction applied to Tomato Glandular Trichomes.

[Poster NWK Brandenburg 2022](#) - Diagnostics meets Genealogy: Evaluation of Sequence Variations in the Sheep Poodle Genome.

Languages

French: Native ; English: Professional
German: A1

Hobbies

Swimming ; Reading ; Theatre ; Painting

Experiences

ERA-Bio-IT (Company) | June 2024 - Nov 2025 - Bioinformatician

Construction and analysis of a maize pangenome (Python, Bash, Nextflow, R). Use of Minigraph, PGGB and Minigraph-Cactus to build pangenomes.

Pangenome analysis: partitioning the pangenome using Panacus, variant calling using VG tools (VG deconstruct). Statistical analysis (VG stats). Filtering variants (VCFtools).

Participation in the creation of a R&D project to submit a technical proposal: project suggestions related to pangenomic and modelisation. HPC SLURM.

RWTH Aachen (University) | Aug 2022 – Oct 2023 – Research Assistant (PhD)

Study from the genotype to the phenotype on tomato glandular trichomes, using metabolic modelling (Python, pandas, plotly, scikit-learn, PyMC). Git.

Part of HDS-LEE graduate school (RWTH Aachen and Research Center in Jülich).

Teaching assistant for data visualization. Establishment of a notation system enhancing all skills and in favor of students who try to do something, instead of punishment. Participation in the Night of Science.

Hochschule Mittweida (University) | Jan 2022 - July 2022 – Research Assistant (Master thesis)

Detection and evaluation of sequence variations in the sheep poodle genome (dog) (Python, Bash, pandas and plotly). Designing pipeline using FastQC, SAMtools, BCFtools, Clustal Omega, MUSCLE, Iq-tree, and VSEARCH. Performing in silico SNP-array. Phylogenetic reconstruction. Manipulation of GEO database, Nanopore sequencing data, and Illumina SNP-probe data. Visualization of Nanopore manipulation. Git. Statistical analysis.

IPK Gatersleben (Research center) | Apr 2021 - July 2021 - Research Assistant (Master)

Metabolic modelling using Flux Balance Analysis (Python, pandas and use of Conda and plotly). Mapping of metabolites, reactions and genes using different databases (NCBI, ENSEMBL, BiGG and ModelSEED). API. Git.

I.N.R.A. | 2019 – Research Assistant (Master thesis)

Transformation of tomato protoplasts, qRT-PCR, statistical analysis using R.

I.J.P.B. | 2018 – Research Technician (Master)

Analysis of genetic sequences, DNA extractions & PCR on *Arabidopsis thaliana*.

I.E.E.S. | 2017 – Laboratory Technician (Bachelor thesis)

In vitro culture, NeuronJ manipulation, *Arabidopsis thaliana*, GWAS .

Projects in bioinformatics and genetics

C.R.C.L. (Lyon - Cancer Research Center) | Sept 2020 - Dec 2020

Creation of an automated pipeline for the analysis of genetic variations in rRNAs: use of GitLab, Conda, Nextflow, MultiQC, FastQC, Trimmomatic, Bowtie2, IGV. Programming in Bash, Python, Nextflow. Statistical analysis in R.

L.B.B.E. (Lyon - public laboratory) | Jan 2021 - Apr 2021

Bioinformatic pipeline to detect horizontal gene transfers between parasitoids and their hosts: use of Conda, Nextflow, BUSCO, Augustus, Mmseq and Bash.

L.B.B.E. (Lyon - public laboratory) | Sept 2021 - Dec 2021

Genomic and transcriptomic evolution of the genome of *D. suzukii* after a selection experiment: use of GitHub, Conda, SAMtools, BCFtools, GATK, repeatmasker, repeatmodeler, TEcount.

Education

Master Bioinformatics (Lyon1) | 2020 - 2022

Methods of analysis of genomic, transcriptomic and proteomic data – Programming in Python, Bash and R – Data visualization – Structural bioinformatics – Machine learning – Data science – Design of bioinformatic pipelines - Statistical analysis in R - Git - NGS

Master Plant Biology (Bordeaux1) | 2017 – 2019

Plant biology and biotechnology – NGS - Statistical analysis in R - Genetics, genomics and epigenetics in plants

Bachelor in Biology (Paris - Sorbonne) | 2013-2017

General biology: molecular biology – Genetics – Biochemistry - Statistical analysis