

# Sébastien Gradit

## Computational Biologist Data Scientist

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## About Me

Highly accomplished PhD Computational Biologist with over five years of experience, specializing in bridging AI/ML solutions and Bioinformatics to transform complex multi-omics data into actionable insights for R&D. My expertise includes advanced computational methods and data-driven approaches to accelerate tool deployment and integration, with a strong focus on reproducibility and multi-disciplinary collaboration.

## Languages

- English: Fluent (TOEIC 955/990)

## Skills

- **Core Programming:** Python [advanced], C++ [Intermediate], R [Intermediate], High Performance Computing [Slurm], Cloud [AWS], Versioning [Git, GitHub]
- **Data Science / ML:** Machine Learning [Keras, TensorFlow, PyTorch, SciKit-Learn], SQL [Intermediate], Interactive Dashboards [Streamlit, Shiny]
- **Data Management / Workflow:** Continuous Integration/Continuous Development [GitHub Actions, Snakemake, Makefile], Containerization [Docker, Singularity]
- **Bioinformatics:** Package Development [PyPI, Conda], Multi-Omics Integration, Automation of Mapping and Downstream Analyses (NGS), High-Throughput Omics Data Analysis [RNA-Seq, ChIP-Seq, Hi-C, Single-cell Omics]

## Soft Skills

- Analytical Thinking, Complex Problem-Solving
- Adaptability, Agility, Continuous Learning
- Creative Thinking, Innovation
- Effective Communication, Interdisciplinary Collaboration

## Extracurricular Activities

- **JeBiF PRESIDENT (2022–24):** Led bioinformatics talent structure/energy; Fostered N/I collaborations; Promoted/popularized bioinformatics; Organized community events.

## Working Experience

### Bioinformatician

*Pasteur Institute, Paris*

2021-2024

- Led comprehensive PhD research focused on deciphering hidden chromatin contacts from repeated genomic elements via advanced statistical profiling.
- Developed Hicberg, a novel computational tool for reconstructing missing chromatin contacts in repeated regions, extensible to pair-ended omics data, leading to new insights into the spatial organization of genomes.
- Applied Hicberg to investigate *Saccharomyces cerevisiae* rDNA behavior and chromatin dynamics under various stress conditions (e.g., heat, oxidative) and kinetics.
- Leveraged Deep Learning to predict 2-micron plasmid interactions with the yeast genome based on nucleosome occupancy data.

### Biomedical Engineer

*Siemens Healthcare - LIPADE, Paris*

02/2020 – 08/2020

- Spearheaded the development of Machine Learning-driven automatic segmentation tools for bone lesion identification in (x)SPECT volumes, significantly enhancing diagnostic workflow efficiency and providing radiologists with data-driven insights for more confident decision-making in oncology.
- Engineered an end-to-end pipeline for automated extraction of radiomic features from xSPECT volumes, accelerating objective region of interest classification and segmentation to deliver critical, actionable data for diagnostic support.

### Biomedical Engineer

*Danone Research, Saclay*

02/2019 – 09/2019

- Pioneered the implementation and benchmarking of Area Under the Curve(AUC) computation techniques for bioequivalence assays, optimizing data reliability.
- Engineered an interactive user interface for bioequivalence assay analysis, enabling real-time computation, visualization, and comparative insights.
- Integrated Machine Learning models to refine clinical trial plans, directly supporting data-driven decision-making

### Biomedical Engineer

*CABOMA - UdeM, Montreal*

05/2018 – 08/2018

- Optimized biomechanical models for patient morphology tailored orthotic design.

## Education

### PhD in Bioinformatics

*Pasteur Institute, Sorbonne University*

2021-2024

### M.Sc. in Image Processing and A.I | Honors

*Télécom Paris - Sorbonne University*

2019-2020

### Master's Degree in Engineering (Dipl. Ing.) | Highest Honors

*ISBS - ESIEE Paris*

2016 – 2019

## Publications

### Hicberg: Reconstruction of genomic signals from repeated elements - BiorXiv 2025

*Gradit S., Ortion S., Larrous P., Koszul R., Cournac A.*

## Selected Scientific Communication

### JOBIM 2024, Toulouse, France

Poster | Prediction of omics signals from repeated elements.

2024

### JeBiF@JOBIM 2024, Toulouse, France

Workshop | Good practices in bioinformatics.

2024

### ICTE, St-Malo, France

Poster | Prediction of omics signals from repeated elements.

2024

### 31<sup>th</sup> Intelligent Systems For Molecular Biology, Lyon, France

Poster and Talk | Statistical inference of repeated sequence contacts in Hi-C maps.

2023

## Certifications

### DeepLearning.AI,

TensorFlow Advanced Techniques Specialization and Deep Learning Specialization

2023

### DeepLearning.AI - Stanford,

Machine Learning Specialization

2023

## Honors - Awards

### 1<sup>st</sup> Prize of Read Write Grow European SynBio Hackathon, SynBee

Classification of protein sequence safety through LLM and AI for Synthetic Biology designs

2025

### INCEPTION Program Grant, France

Awarded a highly competitive grant covering the final 3 months of the PhD program demonstrating recognition of research merit and strategic value in the field

2024

### 1<sup>st</sup> Prize of D4GEN Hackathon, Genopole - Evry

Predicting contacts between nuclear parasites and host genome

2022