

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

31th 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

1st Prize of Read Write Grow European SynBio Hackathon, SynBee

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

2025

INCEPTION Progran 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

1st Prize of D4GEN Hackathon, Genopole - Evry

Predicting contacts between nuclear parasites and host genome

2022

