

# Sébastien Gradit

COMPUTATIONAL BIOLOGIST · DATA SCIENTIST

Issy-les-Moulineaux, France

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Highly accomplished PhD Computational Biologist with over five years of experience, specializing in leveraging **AI and Bioinformatics** to transform complex **multi-omics** data into **actionable insights** for precision medicine. My expertise includes **advanced computational methods** and data-driven approaches to accelerate therapeutic discovery, with a strong focus on **reproducibility** and **collaborative innovation**.

## Experience

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### Pasteur Institute

Paris, France

PHD CANDIDATE

Oct. 2021 – Dec. 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.

### Siemens HealthCare - LIPADE

Paris, France

BIOMEDICAL ENGINEER

Feb. 2020 - Sept. 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.

### Danone Nutricia Research

Saclay, France

BIOMEDICAL ENGINEER

Feb. 2019 - Sept. 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.

### CABOMA - Université de Montréal

Montréal, Canada

BIOMEDICAL ENGINEER

May. 2018 - Aug. 2018

- Design and optimization of biomechanical models for foot orthotics design tailoring based on patient morphology.

## Education

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### PhD in Bioinformatics

Paris, France

PASTEUR INSTITUTE - SORBONNE UNIVERSITY

Oct. 2021 - Dec. 2024

Spatial Regulation of Genomes lab | Genomes and Genetics department

### M.Sc. in Image Processing and Artificial Intelligence | With honors

Paris, France

TÉLÉCOM PARIS - SORBONNE UNIVERSITY

Sept. 2019 - Sept. 2020

Advanced Image Processing and Artificial Intelligence applied to biomedical imaging

### M.Sc. in Biomedical Engineering (Engineer Diploma.) | With highest honors

Créteil - Noisy le Grand, France

INSITUT SUPÉRIEUR DES BIOSCIENCES (ISBS) - ESIEE

Sept. 2016 - Sept. 2019

Bioinformatics, Drug Development, Medical Image Processing, Machine Learning, Signal Processing, Biostatistics, Biomechanics, Biomaterials, Regulatory Affairs, Quality Assurance, Project Management.

# Skills

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<b>Core Programming</b>	<b>Python</b> [advanced], <b>C++</b> [Intermediate], <b>R</b> [Intermediate], <b>High Performance Computing</b> [Slurm], <b>Cloud</b> [AWS], <b>Versioning</b> [Git, GitHub]
<b>Data Science</b>	<b>Machine Learning</b> [Keras, TensorFlow, PyTorch, SciKit-Learn], <b>SQL</b> [Intermediate], <b>Interactive Dashboards</b> [Streamlit, Shiny]
<b>Data Management</b>	<b>Continuous Integration/Continuous Development</b> [GitHub Actions, Snakemake, Makefile], <b>Containerization</b> [Docker, Singularity]
<b>Bioinformatics</b>	<b>Package Development</b> [PyPI, Conda], <b>Multi-Omics Integration, Automation of Mapping and Downstream Analyses (NGS)</b> , <b>High-Throughput Omics Data Analysis</b> [RNA-Seq, ChIP-Seq, Hi-C, Single-cell Omics]
<b>Languages</b>	<b>French</b> [Native], <b>English</b> [Fluent: TOEIC 955/990]

# Soft Skills

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<b>Soft Skills</b>	<ul style="list-style-type: none"><li>Analytical Thinking &amp; Complex Problem-Solving</li><li>Adaptability, Agility &amp; Continuous Learning</li><li>Creative Thinking &amp; Innovation</li><li>Effective Communication &amp; Interdisciplinary Collaboration</li></ul>
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# Honors & Awards

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2024	<b>INCEPTION Program Grant</b> , Fellowship	<i>Paris, France</i>
<i>Awarded a highly competitive grant covering the final three months of the PhD program, demonstrating recognition of research merit and strategic value to the field.</i>		
2022	<b>1st Place</b> , Digital 4 Genomics Hackathon	<i>Genopole, Evry</i>

# Extracurricular Activity

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<b>Jeunes BioInformaticiens de France (JeBiF)</b>	<i>France</i>
PRESIDENT	2022 - 2024
<ul style="list-style-type: none"><li>Led strategic initiatives to <b>structure and energize</b> France's emerging bioinformatics talent.</li><li>Fostered <b>national and international collaborations</b> within the bioinformatics community.</li><li><b>Promoted and popularized</b> bioinformatics to public, private, and international stakeholders.</li><li>Organized <b>community-building events</b> and disseminated information on bioinformatics training.</li></ul>	

# Certificates

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2023	<b>TensorFlow Advanced Specialization</b> , DeepLearning.AI
2023	<b>Deep Learning Specialization</b> , DeepLearning.AI
2023	<b>Machine Learning Specialization</b> , Stanford - DeepLearning.AI

# Selected scientific communications

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2024	<b>JOBIM 2024, Toulouse</b> , Poster   Prediction of Omics Signal from Repeated Elements
2024	<b>JeBiF@JOBIM 2024, Toulouse</b> , Workshop   Good Practices in Bioinformatics
2023	<b>International Congress for Transposable Elements, St-Malo</b> , Poster   Prediction of Omics Signal from Repeated Elements
2023	<b>31st Intelligence Systems for Molecular Biology (ISMB), Lyon</b> , Poster and Talk   Statistical Inference of Repeated Elements Contacts in Hi-C maps

# Publications

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Hicberg: Reconstruction of Contact Signals from Repeated Elements **biorXiv**, 2025  
Gradit S., Ortion S., Larrous P., Delouis M., Koszul R., Cournac A.