

# Sébastien Gradit

Data Scientist  
Bioinformatician

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## Social Network

S. Gradit    sebgra

## About Me

PhD-trained bioinformatician from the Pasteur Institute seeking to apply expertise in data science and biological interpretation to advance research. Proven ability to leverage machine learning and statistical modeling to solve complex biological problems.

## Languages

- English: Fluent (TOEIC 955/990)
- French: Mother tongue

## Hard Skills

- Basic programming: Bash, Python, R, C++, HPC (Slurm, AWS)
- Bioinformatics: Multiomics integrative analysis, Automation of mapping and genomics analysis
- Data analysis: Data mining, interactive dashboards (Shiny, Streamlit), SQL databases
- Machine learning: TensorFlow, Keras, Scikit-learn
- Workflow: CI/CD automation (git, Snake-make, Nextflow)
- Containerization and deployment (Docker, Singularity)
- Web: Static (HTML, CSS)

## Soft Skills

- Adaptability
- Communication
- Problem solving
- Scientific inquiry

## Working Experience

- |                   |   |                                    |
|-------------------|---|------------------------------------|
| 2021-2024         | <b>PhD candidate</b><br>Development of statistical modeling to address missing data in genomics, with focus on genome contacts.   | Pasteur Institute, Paris           |
| 02/2020 – 08/2020 | <b>Biomedical Engineer</b><br>Applied machine learning techniques to xSPECT imaging for automated segmentation of bone lesions, enhancing the objectivity and precision of cancer treatment monitoring compared to traditional SPECT imaging.                               | Siemens Healthcare - LIPADE, Paris |
| 02/2019 – 09/2019 | <b>Biomedical Engineer</b><br>Benchmark of bioequivalence assays, development of interactive interface for clinical trial statistical plans visualization, and machine learning methods implementation for clinical trial plan refactoring for data-driven decision-making. | Danone Research, Saclay            |
| 05/2018 – 08/2018 | <b>Biomedical Engineer</b><br>Design and optimization of biomechanics models within proprietary software, tailoring foot orthotics designs to individual patient morphology for improved treatment outcomes.  | Caboma, Montréal                   |

## Education

- |             |  |   |
|-------------|--|---|
| 2021 – 2024 | <b>PhD in bioinformatics</b><br>Regulation Spatiale des Genomes lab.   | Pasteur Institute - Sorbonne University |
| 2019 – 2020 | <b>M.Sc. in Image Processing</b><br>Advanced medical images processing and A.I.   <i>Honors</i>                      | Télécom Paris - Sorbonne University     |
| 2016 – 2019 | <b>Master's Degree in Engineering (Dipl. Ing.)</b><br>Bioinformatics, Medical Image and A.I.   <i>Highest Honors</i> | ISBS - ESIEE Paris                      |

## Publications

- |         |  |
|---------|--|
| Pending | <b>Hicberg: Reconstruction of genomic signals from repeated elements - BiorXiv</b><br><i>Gradit S., Ortion S., Larrous P., Koszul R., Cournac A.</i> |
|---------|--|

## Selected Scientific Communication

- |      |   |                  |
|------|---|------------------|
| 2024 | <b>JOBIM 2024</b><br>Poster   Prediction of omics signals from repeated elements.   | Toulouse, France |
| 2024 | <b>JeBIF@JOBIM 2024</b><br>Workshop   Good practices in bioinformatics.   | Toulouse, France |
| 2024 | <b>ICTE</b><br>Poster   Prediction of omics signals from repeated elements.   | St-Malo, France  |
| 2023 | <b>31<sup>th</sup> Intelligent Systems For Molecular Biology</b><br>Poster and Talk   Statistical inference of repeated sequence contacts in Hi-C maps. | Lyon, France     |

## Certifications

- |      |  |
|------|--|
| 2023 | <b>DeepLearning.AI</b><br>TensorFlow Advanced Techniques Specialization and Deep Learning Specialization |
| 2023 | <b>DeepLearning.AI - Stanford</b><br>Machine Learning Specialization                                     |

## Awards

- |      |   |                 |
|------|---|-----------------|
| 2022 | <b>1<sup>st</sup> Prize of D4GEN Hackathon</b><br>Predicting contacts between nuclear parasites and host genome | Genopole - Evry |
|------|---|-----------------|