Lorenzo Bini

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Education

University of Geneva, Ph.D. Candidate - Department of Computer Science & CUI — Nov 2022 – Ongoing

- Major: Artificial Intelligence and Machine Learning.
- Research interests: Graph neural networks, adversarial learning, representation learning, active and self-supervised learning. Generative AI for medicine and healthcare, including 3D genomics and scRNA data generation. Implementation of robust adversarial models within weak/self-supervised training strategies to reduce label acquisition costs.

Polytechnic of Turin, Master of Science in Physics of Complex Systems — Sep 2020 – Sep 2022

- GPA: 4.0/4.0

Alma Mater Studiorum - University of Bologna, Bachelor degree in Physics & Astronomy Systems — Sep 2017 – Sep 2020

- GPA: 4.0/4.0

Experience

Research Assistant, Hôpitaux Universitaires de Genève (HUG) – Geneva, Switzerland — Nov 2022 - Ongoing

- Detection of minimal residual disease (MRD) of acute lymphoblastic and myeloid leukemia (AML/ALL) from flow cytometry data.
- Development of fast training/inference deep learning models (e.g, Graph Transformers) for single-cell classification in weak/self-supervised contexts.
- Development of generative models (e.g., DDPMs, Flow Matching) for 3D genomics, flow cytometry, scRNA-seq, spatial transcriptomic, and multiomics data.
- LLMs to streamline routine hospital processes.

Teaching Assistant, University of Geneva – Department of Computer Science & CUI — Nov 2022 – Ongoing

- Introduction to Computational Finance - 14X030;
- TALN: Traitement de la langue approches linguistiques et approches empiriques (NLP) - 34C2161;
- Information Retrieval - 14X060;
- Data Science - Analyse et Traitement de l'Information -14X026;
- Selected Chapters - Game Theory -14X060;

Research Assistant - Intern, Quantum Technology Group - University of Norway — Feb 2022 - July 2022

- Worked on quantum theory for entanglement and non-locality in optomechanics continuous variable systems. Developed quantum frameworks to analyze two-cavity optomechanics systems.

Research Intern, Jian Ma's Lab - Comp. Science Dept., Carnegie Mellon University — Sep 2025 - Mar 2026

- Developed and implemented symmetry-aware flow-matching models for 3D genome ensembles operating directly in 3D coordinate space.
- Built multi-modal conditioning pipelines combining genomic data sources to generate realistic chromosome conformational ensembles.
- Designed and integrated LLM-based multi-modal encoders to fuse epigenomic signals and imaging data.
- Implemented scalable training & inference (subchain batching, sparse graphs, RMSD alignment) and evaluation tooling (contact-map, SCC, insulation score, radius-of-gyration).
- Optimized memory and runtime (sparse attention) to enable large-region generation.

Publications

LapDDPM: A Conditional Graph Diffusion Model for scRNA-seq Generation with Spectral Adversarial Perturbations Jun 2025

Lorenzo Bini, Stéphane Marchand-Maillet

ICML'2025 + GenBio Workshop: The Second Workshop on Generative AI and Biology, Vancouver.

Self-Supervised Graph Learning via Spectral Bootstrapping and Laplacian-Based Augmentations May 2025

Lorenzo Bini, Stéphane Marchand-Maillet

Preprint. To appear in 2025, under double-blind review as a conference paper.

Massive Activations in Graph Neural Networks: Decoding Attention for Domain-Dependent Interpretability Oct 2024

Lorenzo Bini, Marco Sorbi, Stéphane Marchand-Maillet

ECAI'2025, Bologna (oral presentation) + ICLR'2025 Workshop XAI4Science: From Understanding Model Behavior to Discovering New Scientific Knowledge, Singapore.

Injecting Hierarchical Biological Priors into Graph Neural Networks for Flow Cytometry Prediction Jul 2024

Lorenzo Bini, Stéphane Marchand-Maillet

ICML'2024 + Workshop on Accessible and Efficient Foundation Models for Biological Discovery, Wien, Austria.

FlowCyt: A Comparative Study of Deep Learning Approaches for Multi-Class Classification in Flow Cytometry Benchmarking Jun 2024

Lorenzo Bini, Margarita Liarou, Thomas Matthes, Stéphane Marchand-Maillet

Conference on Health, Inference, and Learning (CHIL'24), New-York, NY.

Why Attention Graphs Are All We Need: Pioneering Hierarchical Classification of Hematologic Cell Populations with LeukoGraph Feb 2024

Lorenzo Bini, Thomas Matthes, Stéphane Marchand-Maillet

Preprint arXiv:2402.18610, under double-blind review as a conference paper.

HemaGraph: Breaking Barriers in Hematologic Single Cell Classification with Graph Attention Dec 2023

Lorenzo Bini, Thomas Matthes, Stéphane Marchand-Maillet

Preprint arXiv:2402.18611, under double-blind review as a conference paper.

Awards & Oral Presentations

Oral Presentation at the Second Workshop on Explainable Artificial Intelligence for the Medical Domain - ECAI'25, Bologna Oct. 2025

- Invited oral presentation of the accepted paper "Massive Activations in Graph Neural Networks: Decoding Attention for Domain-Dependent Interpretability" at European Conference on Artificial Intelligence (ECAI'25), Bologna.

PhD Symposium - CHIL'24 at Cornell Tech University, NY Jun. 2024

- Winner of the PhD Symposium money-prize to attend and present PhD work "Adversarial Robust GNNs: Enhancing Learning with Knowledge Injection in Single-Cell Data" at CHIL'24, conference held by Cornell Tech University, New York.

CHAIR Structured Learning Workshop - Chalmers University of Technology Oct. 2023

- Oral presentation of the "Knowledge Distillation in Acute Myeloid Leukemia Classification: Tabular Data Meets Graph Neural Networks" poster at the AI Structured Learning 2023 Workshop in Götebor, Sweden.

Winner of Thesis on Proposal 2021/2022 Feb. 2022

- Winner of the "Thesis on Proposal 2021/2022" call for bids for Master's Thesis on "Entanglement and nonlocality in optomechanics continuous variable systems" under the supervision of Prof. Francesco Pietro Massel & Prof.

Vittorio Penna.

- Received grants for research period at USN-Kongsberg.

Projects

Flow Cytometry Deep Learning Benchmark FlowCyt-Benchmark

- Developed the first publicly available deep learning benchmark for single cell classification and clustering on flow cytometry data. Tested on a cohort of 30 patients selected by expert hematologists, from bone marrow and peripheral blood samples. Benchmarked SOTA classification/generative models including GNNs, GraphTransformers, Diffusion Models (DDPMs) and VAEs.
- Tools Used: Python, CSS, HTML.

Hackathons & Competitions 2019 - Ongoing

- Regular participation at Kaggle/LeetCode competitions and Hackathons; runner-up BR41N.IO 2021 Hackathon@PoliTO, runner-up UNIBO-IBM-Unipol Hackathon 2019, 3rd classified QuHack4IA 2023.
- Tools Used: Python - Compatitive Programming.

Math/Physics Olympiad Sep 2014 - Sep 2019

- 2x winner of the Italian Regional Math Olympiad.
- 1x winner of the Italian Regional Physics Olympiad.

Visiting Student, City Montessory School, Lucknow - Uttar Pradesh, India USN Aug 2016 - Sep 2016

- Visited the City Montessory School together with the italian cultural association "CinemíCinemá" to provide help and needs to elementary/mid school students.

Oxfam Volunteering 2016 - Ongoing

- I do regularly serve as volunteer for charity organization, such as Oxfam Italy.

Technologies

- **Programming Languages**: Python, Julia, R, , Matlab, Mathematica, C/C++, CUDA.
- **Frameworks**: Pytorch, Pytorch-Lightning, Tensorflow, Keras, Jupyter.
- **AI/ML**: SciPy, scikit-learn, Github, GitLab, Numpy, Pandas, Matplotlib, Seaborn, wandb, PyG.
- **Tools**: Git, Linux, ssh, SLURM, pip, Anaconda, Docker, VSCode, Bash (Shell).

Software Licenses: Kaluza Analysis Software, Zemax OpticStudio | Comprehensive Optical Design Software, TeXstudio, BioVinci Software.