Marco Uderzo

PhD Student at Institut de Génomique Fonctionnelle de Lyon (IGFL)

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Profile

Computational Biologist with a background in Computer Science and Data Science, specializing in neuroscience and applied ML/DL for single-cell spatial omics. PhD Student in Computational Neurobiology at IGFL (ENS de Lyon), in the *Spatio-Temporal Logic of Adult Neurogenesis* team.

Areas of Expertise

Machine & Deep Learning - Computational Biology - Bioinformatics - Neurobiology - Computer Vision for Bioimaging

Professional Experience

PhD Student *(Institute of Functional Genomics, IGFL - ENS de Lyon)* **Lyon, France** *09/2025 - Present*

- Research focused on investigating the spatial molecular landscapes of neurogenic niches in the adult mouse brain, combining machine learning and spatial transcriptomics to identify shared and niche-specific molecular mechanisms of adult neurogenesis.
- Development of machine learning-based methods for spatial omics and analysis pipelines for 3D MERFISH data.

Bioinformatics Engineer *(Institute of Functional Genomics, IGFL)* **Lyon, France** *01/2025 - 08/2025*

Ingénieur d'études (CNRS) in the *Spatio-Temporal Logic of Adult Neurogenesis* team and Equipex+ *Spatial-Cell-ID* facility.

- Established and maintained Python-based analysis pipelines for high-resolution spatial transcriptomics data (Visium HD), used across multiple projects within the team and the *Spatial-Cell-ID* facility.
- Implemented and optimized workflows for spatial cell-type deconvolution, cell segmentation, custom binning, and feature extraction using Scanpy, Squidpy, SpatialData, Cell2Location, Bin2Cell, and Stardist.
- Developed BaCHClue, a novel tool for principled selection of clustering resolution in Scanpy-based analyses.

Research Intern *(Institute of Functional Genomics, IGFL)* **Lyon, France** *10/2024 - 12/2024*

Explored the application of spatial transcriptomics and machine learning methods to study adult neurogenesis in the mouse brain.

Student Trainee *(Dept. of Biomedical Sciences, University of Padua)* **Padua, Italy** *07/2024 - 08/2024*

Carried out a brief extracurricular wet-lab traineeship to gain hands-on experience in molecular biology and biochemistry techniques. Acquired familiarity with wet-lab protocols, experimental design, and hypothesis testing, complementing my computational background.

Software Engineering Intern *(Airlapp S.R.L.S.)* **Piove di Sacco, Padua, Italy** *07/2022 - 09/2022*

Analysis, Design and C# Implementation of Meta Avatars SDK in a R&D context, Metaverse-Oriented Virtual Reality prototyping on Oculus Quest platform. Gained experience with networked systems, real-time synchronization, and Unity-based development.

Education

Master's Degree, Data Science *University of Padua* **Padua (PD), Italy**

- Thesis: "Leveraging Spatial Transcriptomics and Machine Learning to Study Adult Neurogenesis Dynamics in the Mouse Brain"
- Relevant Courses: Machine Learning, Deep Learning, Introduction to Molecular Biology, Introduction to Human Diseases, Biological Data, Structural Bioinformatics, Fundamental and Applied Genomics, Computational Genomics, Statistical Learning, Mathematical Optimization, Stochastic Methods.

Erasmus, Biologie Moléculaire et Cellulaire *Université Claude Bernard Lyon 1* **Lyon, France**

MSc Erasmus semester focused on the study of Fundamental, Applied and Computational Genomics.

Bachelor's Degree, Computer Science *University of Padua* **Padua (PD), Italy**

- Thesis: "Meta Avatars SDK: study, analysis and development for Virtual Reality"
- Relevant Courses: Software Engineering, Algorithms and Data Structures, Calculus, Linear Algebra, Discrete Math, Numerical Methods, Object-oriented Programming, Computer Architecture, Databases, Automata and Formal Languages.

High School Diploma, Liceo Classico *Liceo Ginnasio G.B. Brocchi* **Bassano del Grappa (VI), Italy**

Main Projects

BaCHClue: BIC and Calinski-Harabasz Score Guided Transcriptome Clustering *PyPI, GitLab Repository*
BaCHClue is a Python-based tool for the identification of optimal clustering resolution in Scanpy-based single-cell and spatial transcriptomics analyses. It systematically evaluates multiple clusterings across a range of resolutions by computing statistical validation metrics such as the Bayesian Information Criterion (BIC) and the Calinski–Harabasz score in parallel, enabling principled, reproducible selection of biologically meaningful cluster structures in high-dimensional single-cell and spatial transcriptomics data.

Leveraging Spatial Transcriptomics & Machine Learning to Study Adult Neurogenesis in the Mouse Brain
MSc research internship and master's thesis conducted at IGFL (Lyon) in the "Spatio-Temporal Logic of Adult Neurogenesis" team (Supervisors: Dr. Zayna Chaker, Dr. Sergio Sarnataro). Performed integrative analysis of Visium and high-resolution Visium HD spatial transcriptomics datasets to investigate adult neurogenesis dynamics in the mouse brain. Built analysis workflows combining Scanpy, Squidpy, and SpatialData for preprocessing, visualization, and spatial gene expression analysis. Applied Cell2Location for spatial cell-type deconvolution of multiple Visium datasets from the mouse olfactory bulb. Performed cell segmentation and custom binning of high-resolution Visium HD datasets from the V-SVZ and DG using Bin2Cell and Stardist, followed by downstream analysis to identify shared molecular mechanisms across neurogenic niches.

Modelling and Functional Characterization of a Protein Domain Family *GitHub Repository*
Construction of Sequence Model, assessment of Taxonomic Lineage, Gene Ontology annotations assessment for Functional Enrichment, and identifications of conserved Short Linear Motifs within the Pyridoxamine Kinase/Phosphomethylpyrimidine Kinase Domain Family.

Classification of Contacts in Protein Structures with Deep Learning *GitHub Repository*
Classification of Residue-Residue Interactions in Protein Structures using Feed Forward Deep Neural Networks. Developed in Python using BioPython and Keras.

Zeroth-Order Frank-Wolfe Optimization for Black-Box Adversarial Attacks *GitHub Repository*
Thorough study of the respective papers and implementation of Faster Zeroth-Order Conditional Gradient Sliding (Gao et al.) and Stochastic Gradient-Free Frank-Wolfe (Sahu et al.) applied to Adversarial Attacks against MNIST Recognition Deep Neural Network.

Gradient Descent vs Block Coordinate Gradient Descent in Semi-Supervised Learning *GitHub Repository*
Implementation, evaluation and performance comparison between Gradient Descent (GD), Gauss-Southwell (GS-BCGD), and Randomized Block Coordinate Gradient Descent (R-BCGD) algorithms in semi-supervised learning problems.

Automated Retrieval and Custom Parsing of Protobuf-Encoded Telemetry Data *GitHub Repository*
Developed an end-to-end automated pipeline for large-scale data acquisition and custom parsing of Protobuf-encoded game telemetry. Reverse engineered and adapted an existing telemetry demo parser via code analysis and controlled testing, mapping low-level Protobuf network messages to semantically meaningful events and condensed raw telemetry into task-specific entity/action time series for LSTM-based player behavioral modeling and re-identification.

Courses and Workshops

- NEUBIAS Institut Pasteur Course on Bioimage Analysis – Paris, 2025
- AI/ML for the Analysis of single-cell Spatial Transcriptomics – Lyon, 2025

Technologies

- **Python Libraries and Frameworks:**: Scanpy, Squidpy, SpatialData, PyTorch, Tensorflow, Keras, Scikit-learn, OpenCV, BioPython, Pandas, NumPy, Matplotlib, Seaborn
- **Programming Languages:** Python, R, Bash, SQL, C, C++
- **Other:** LaTeX, Git

Languages

- **Italian** [Native]
- **English** [C1]
- **French** [A2/B1] - Learning