MARCELLO BARYLLI

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- MSc graduate in computational science, with expertise in complex systems.
- Completed thesis with excellence, securing funding for 2 subsequent publications.
- Drawing inspiration from biology and self-organisation to advance machine learning methods.

Education

2025 - Present **PhD at GROW-AI** ITU Copenhagen

Self-Organising Artificial Intelligence
Advisor: Prof. Sebastian Risi

Key Subjects: Reinforcement Learning, Evolution, Neuroscience, Self-Organisation, Collective Intelligence.

2021 - 2024 **MSc, Computational Science, GPA: 8.3/10** University of Amsterdam

Thesis: Multi-Layer Network Models in Colorectal Cancer Subtype Analysis.
Grade: 9/10
Advisor: Dr. Vivek Sheraton Muniraj
Key Subjects: Theory of complex systems, complex systems simulation, machine learning, biosystems data analysis, agent-based models and cellular automata, scientific computing.

2017 - 2021 **BSc, Molecular Biology, GPA: 1.7 (A)** University of Vienna

Thesis: **VirACuDa - Virus Automated Curation of Datasets. Grade: 1 (A).**
Advisor: Prof. Thomas Rattei
Details: Development of software for genomic database filtering and automated grouping.
Key Subjects: Evolutionary theory, developmental biology, systems biology and bioinformatics, quantitative biology, neurobiology, cell culture, neuronal culture.

Research Experience

2024 **Computational Biologist** Amsterdam University Medical Center

Authored scientific journal articles and applied agent based models in cancer settings.

2023 **Multi-Layer Network Models in Colorectal Cancer Subtype Analysis.** University of Amsterdam

Investigated diffusion-based algorithms for graph neural networks, probabilistic graphical models for network inference, reviewed nonlinear dimensionality reduction techniques for joint embedding.

Work Experience

2020 - 2021 **Bioinformatician** CUBE: Computational Systems Biology

Installation and troubleshooting of software on the Life Science Compute Cluster (LiSC), metagenomic analysis, SQL database implementation and API testing.

Upcoming Publications

In Progress Barylli, M.; Saha, J.; Sheraton, V. M; and Hoekstra, A. G. Biological Multi-Layer and Single Cell Network-based Multiomics Models – a review.

In Progress Barylli, M.; Saha, J.; Sheraton, V. M; and Hoekstra, A. G. Multi-Omic Network Inference and Knockout Analysis (MONIKA).