

MARCELLO BARYLLI



- 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 Project 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
	Authoring scientific journal articles and applying 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).	