

# MARCELLO BARYLLI



- MSc graduate in computational science, with expertise in complex systems.
- Completed graduation project with excellence, securing funding for 2 subsequent publications.
- Currently researching the intersection of collective intelligence and AI, via multi-agent systems and graph neural networks.
- Drawing inspiration from biology to advance machine learning methods.

## Education

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, agent-based models and cellular automata, scientific computing.

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

**Thesis: VirACuDa - Virus Automated Curation of Datasets. Grade: 1.**

Advisor: Prof. Thomas Rattei

Development of software for genomic database filtering and automated grouping.

**Key Subjects:** Systems biology and bioinformatics, quantitative biology, mathematical biology, biophysics.

## Research Experience

2023 **Multi-Layer Network Models in Colorectal Cancer Subtype Analysis.** [University of Amsterdam](#)

- Investigated diffusion-based algorithms for graph neural networks.
- Reviewed nonlinear dimensionality reduction techniques for joint embedding.
- Developed a weighted Gaussian graphical model for network inference.
- Applied network diffusion PDEs for structural probing of inferred networks, determining key genes and modules in aggressive cancer subtypes.

Currently **Computational Biologist** [Amsterdam University Medical Center](#)

- Writing scientific journal articles: review and research papers.
- Applying an agent-based model to the tumour microenvironment.

## 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. Multi-Layer and Single Cell Network Models in Cancer.

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