

# MARCELLO BARYLLI



## Upcoming Publications

- |         |  |
|---------|--|
| 2024    | Multi-Layer and Single Cell Network Models in Cancer. <i>Barylli, Marcello; Saha, J.; Sheraton, V. M; and Hoekstra, A. G.</i>        |
| 2024-25 | Multi-Omic Network Inference and Knockout Analysis (MONIKA). <i>Barylli, Marcello; Saha, J.; Sheraton, V. M; and Hoekstra, A. G.</i> |

## Education

- |             |   |                         |
|-------------|---|-------------------------|
| 2021 - 2024 | <b>MSc, Computational Science, GPA: 8.3/10</b><br><b>Thesis: Multi-Layer Network Models in Colorectal Cancer Subtype Analysis. Grade: 9/10</b><br><b>Key Subjects:</b> <ul style="list-style-type: none"><li>Theory of Complex Systems</li><li>Complex Systems Simulation</li><li>Machine Learning</li><li>Agent-Based Modeling</li></ul>                                 | University of Amsterdam |
| 2017 - 2021 | <b>BSc, Molecular Biology, GPA: A</b><br><b>Thesis: VirACuDa - Virus Automated Curation of Datasets. Grade: A.</b><br>Development of a Python script for genomic database filtering.<br><b>Key Subjects:</b> <ul style="list-style-type: none"><li>Systems Biology, Bioinformatics</li><li>Statistics and Mathematics</li><li>Structural Biology and Biophysics</li></ul> | University of Vienna    |

## Experience

- |                 |   |                                     |
|-----------------|---|-------------------------------------|
| 03/2024-Present | <b>Computational Biologist</b><br>Developing an integrated pipeline for network-based cancer analysis   | Amsterdam University Medical Center |
| 10/2020-10/2021 | <b>Bioinformatician</b> <ul style="list-style-type: none"><li>Installation and troubleshooting of bioinformatics software on the Life Science Compute Cluster (LiSC), a Tier-2 HPC system with &gt;2000 CPU cores and &gt;1PB network storage.</li><li>Metagenomic analysis of environmental (fresh water) samples for the MetaBac research platform, utliising LiSC.</li><li>Implementation of a SQL database for the storage and access of bacterial genomes and their associated phages.</li><li>Testing of an API for accessing viral genomic information. Prototyping new features, such as annotation from raw sequences.</li></ul> | CUBE: Computational Systems Biology |
| 09/2019         | <b>Microbiology Intern</b> <ul style="list-style-type: none"><li>Bacterial cultivation.</li><li>Growth inhibition experiments.</li><li>Isolation of organic compounds.</li></ul>  | Esse, South Africa                  |

- » Staffing ambulances.
- » Response to emergency calls.
- » Care for patients during transport to and from hospitals.