SEMESTER/MASTER STUDENT POSITION IN COMPUTATIONAL BIOLOGY (ZAMPIERI LAB)

– Starting date: February 2026 or upon agreement.

The Zampieri group offers a semester research opportunity (semester project or master thesis) in the context of systems pharmacology, computational biology and metabolic regulation. The position will be based in the Department of Biomedicine (University website, Lab webpage) at Mattenstrasse 28 in Basel. We are seeking a highly motivated student for a 100% computation-al project, investigating how bacterial susceptibility to antibiotics depends on the metabolic and physiological states of bacteria. The mission of the group is to understand fundamental mech-anisms regulating short- and long-term metabolic adaptation to genetic and chemical perturba-tions to find new and unconventional therapeutic strategies, ranging from antibacterial to anti-cancer drugs. To this end, we develop new ways to combine state-of-the-art technologies in metabolomics with computational analysis.

Project Background

In this project, we aim to investigate the antimicrobial potential of drugs from a phytochemical library against bacteria. The selected candidate will analyse a large metabolome dataset – data are already available – from bacteria exposed to each drug of the library, assessing metabolic changes and their impact on bacterial growth. Additionally, the candidate will: (1) Compare these findings with datasets from bacteria grown in media that mimic human infection conditions. (2) Investigate whether metabolomic changes differ between laboratory strains and clinical isolates, uncovering variations in bacterial response.

Your Position

The candidate will have the opportunity to familiarize with the analysis and interpretation of large-scale metabolomics data to investigate how to pharmacologically interfere with fundamental mechanisms in the regulation of bacterial metabolism and the dependencies of these changes on growth media and bacteria strain. The selected candidate will receive strong supervision from experienced senior lab members who generated the data and specialize in metabolomic data analysis.

Your main tasks will be:

- Develop and apply model-based and statistical approaches to analyse and interpret large compendia of metabolome profiling of small molecules effects on bacteria.
- Adapting existing and developing improved analysis strategies for the high-throughput metabolomics analysis of drug-perturbed bacteria across different growth conditions.
- Unravel the hidden potential of apparently inactive molecules in hampering bacterial infection.
- Determining the underlying mechanisms that link antibacterial efficacy to the metabolic or physiological state of bacteria.

Your Profile

We are searching for a master student with strong bioinformatics background for a fully computational project.

Essential qualifications:

- Currently pursuing or completed studies in Computational Biology, Life Science or related fields.
- Strong statistic and programming skills.
- Excellent organizational and communication (in English) skills, with a proactive and dedicated attitude toward learning

Highly desirable:

- Experience in bioinformatic modelling of ‘omic’ technologies or regulatory/signalling network.
- Familiarity with datascience (R, python, MatLab) and large-scale dataset analysis

Application / Contact

Please send your application consisting of a motivation letter, CV and – if available – one (or more) reference letters by E-mail to: benjamin.demarco@unibas.ch.

Key References

1. Ortmayr, K., de la Cruz Moreno, R. & Zampieri, M. Expanding the search for small-molecule antibacterials by multidimensional profiling. Nat Chem Biol **18**, 584–595 (2022)
2. Anglada-Girotto, M., Handschin, G., Ortmayr, K. et al. Combining CRISPRi and metabolomics for functional annotation of compound libraries. Nat Chem Biol **18**, 482–491 (2022)
3. Zampieri, M., Hörl, M., Hotz, F. et al. Regulatory mechanisms underlying coordination of amino acid and glucose catabolism in Escherichia coli. Nat Commun 10, 3354 (2019)
4. Øyås O., Borrell S., Trauner A., et al. Model-based integration of genomics and metabolomics reveals SNP functionality in Mycobacterium tuberculosis. PNAS 117 (2020)
5. Campos A. and Zampieri M. Metabolomics-Driven Exploration of the Chemical Drug Space to Predict Combination Antimicrobial Therapies. Molecular Cell 74, 1291-1303 (2020)