

Master Thesis in Bioinformatics and the Microbiome

Our research group at the Institute of Medical Microbiology of University of Zurich (UZH) is searching for a Master student to perform a project aimed at developing a bioinformatic pipeline to automate the analysis of 16S sequencing data for microbiome characterization.

The research group led by Prof. Egli, focuses on understanding host-pathogen interactions to develop novel diagnostic tools. Utilizing cutting-edge next-generation sequencing and bioinformatics, we analyze whole genome and metagenomic data for our own research projects as well as with collaborators from the Swiss and international research communities.

Project background: The microbiome plays an important role in human health and disease. Next-generation 16S rRNA gene sequencing is a powerful technology used to characterize bacterial composition in samples like stool, aiding in the study of diseases such as infections, cancer, diabetes, neurodegenerative disease, and obesity. Microbiome analysis holds promise for disease diagnostics and integration into routine clinical microbiology. However, the complexity of bioinformatic analysis required for 16S sequencing data remains a major hurdle. Developing a streamlined pipeline to simplify this analysis is essential for its routine diagnostic use. **Goals:** The goal of the project is to build and validate a standardized bioinformatic pipeline and workflow for 16S rRNA gene sequencing analysis with general microbiome compositional outputs. **Methods:** QIIME2 will be used in conjunction with Nextflow to create a standardized 16S rRNA sequencing workflow for microbiome analysis. Microbiome sequencing and analytical data from routine diagnostics will be used to test and validate the workflow.

Professional and personal skills:

- Experience with bash, Linux, and R (preferable but not mandatory).
- Ability to work independently and in a team with a high level of self-motivation.
- Excellent organizational skills with a keen attention to detail.
- Interest in medical microbiology and applied research questions

What we offer:

- A collaborative, innovative workspace with opportunities to engage with bioinformaticians and researchers using cutting-edge technologies like next-generation sequencing and machine learning for microbiology.
- Microbiome data to develop and validate the 16S rRNA sequencing pipeline, with access to high-performance computing resources.

Are you interested? To apply, please send your updated CV and motivation letter to Dr. Ashley Rooney (Thesis mentor, email: arooney@imm.uzh.ch) and Prof. Adrian Egli (Institute director, email: aegli@imm.uzh.ch)