MSLS: Applied Computational Life Sciences **Master's**

Thesis

Title of project / Thesis	Antimicrobial resistance prediction from MALDI-TOF mass spectra.
Topic / Key words	Antimicrobial resistance, machine learning, programming
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External partners	Universitätsspital Zürich
Place(s) of work	Wädenswil
Abstract	Early use of effective antimicrobial treatments is critical for the outcome of infections and the prevention of treatment resistance. Antimicrobial resistance testing enables the selection of optimal antibiotic treatments, but current culture-based techniques can take up to 72 hours to generate results. In this project a machine learning approach to predict antimicrobial resistance directly from matrix-assisted laser desorption/ionization - time of flight (MALDI-TOF) mass spectra profiles of clinical isolates shall be implemented to: 1. Reproduce research results published in [1]. 2. Enhance the state of the art in antimicrobial resistance prediction on the DRIAMS clinical routine database [2]. A dataset of MALDI-TOF mass spectra from more than 300,000 clinical isolates from four different diagnostic laboratories in Switzerland. The work will help to establish a foundation for a mass spectra-based machine learning solution as important tool for treatment optimization and antibiotic stewardship.
Requirements	- Basic knowledge and/or willingness to learn some scripting language such as R, Python Matlab, Julia etc. - Fundamental machine learning knowledge
Comments	[1] Weis, C. et al. (2022). Direct antimicrobial resistance prediction from clinical MALDI-TOF mass spectra using machine learning. *Nature Medicine*, *28*(1), 164–174. https://doi.org/10.1038/s41591-021-01619-9 [2] https://doi.org/10.5061/dryad.bzkh1899q
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