



Master project 2024-2025

Personal Information

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Project

Computational genomics

Project Title:

Risk stratification of AML patients using RNA sequencing data and machine learning

Keywords:

Machine-Learning, RNA-sequencing, Leukemia, Cancer, modelling

Summary:

Current Next-Generation Sequencing (NGS) tests for acute myeloid leukemia (AML) detect genomic alterations, which impact patient prognosis. However, AML patients typically have multiple mutations, complicating interpretation and treatment decisions. Despite this, treatment options remain limited to chemotherapy and, in some cases, bone marrow transplantation. This project aims to use RNA sequencing (RNA-seq) to analyze the patient's transcriptome, focusing on mRNA expression levels correlated with increased survival. By developing machine learning models using RNA-seq data, the project seeks to predict clinically relevant features such as survival, drug resistance, and immune response in AML patients. The goal is to build a diagnostic platform enabling better understanding, stratification, and follow-up of AML patients using RNA-seq data. Additionally, the approach could be extended to other cancer types with similar mutational complexities.

Expected skills:

-Knowledge of programming languages commonly used in bioinformatics, such as R -Fundamental knowledge of molecular biology concepts, including gene expression regulation, RNA transcription, and cancer genetics -Ability to adapt and learn new techniques and methodologies as needed throughout the project
Desirable skills -Experience with statistical analysis and machine learning libraries in R and Python -Knowledge of machine learning algorithms and techniques

Possibility of funding:

To be discussed

Possible continuity with PhD:

To be discussed