University of Basel

DBM Basel
Department of Biomedicine

PROJECT PROPOSAL

Computational Analysis of Gene Regulatory Networks and Cell Fate Plasticity

Project Background

Cell fate plasticity plays a crucial role in development and disease, with transcription factors (TFs) acting as key regulators by stabilizing lineage commitment. Recent work, including studies on PROX1 as a safeguard repressor in cancer, has highlighted the importance of TFs in restricting unwanted cell state transitions. However, many such repressors remain unidentified, particularly in the hematopoietic system.

This project focuses on the computational identification of **safeguard repressors** that regulate cell fate plasticity using **gene regulatory networks (GRNs)**. We will integrate **single-cell RNA and chromatin accessibility data** to reconstruct lineage-specific GRNs, applying methods such as **SCENIC+ and scGRaNIE**. Additionally, **GRaNPA**, a tool for GRN benchmarking, will be used to assess network quality and identify important TFs involved in plasticity regulation.

Your Tasks

The master's student will work on the **computational aspects** of the project, performing **GRN inference, entropy-based plasticity analysis, and TF candidate selection.** The role will involve data analysis, visualization, and interpretation, with potential opportunities to refine computational methods. This project offers experience in **single-cell bioinformatics, gene regulatory networks, and transcriptional regulation,** with applications in both fundamental biology and disease research.

How to Apply

Please send us an updated CV, including previous lab experience and a motivation letter to judith.zaugg@unibas.ch.