The research group of Dr. Florian Ingelfinger, Centre for Translational Cell Research (ZTZ), at the Medical Center – University of Freiburg, Department of Hematology, Oncology and Stem Cell Transplantation, invites applications from

Master Students/Internships (m/f/d)

Starting date: as soon as possible
Project: Deep Generative Modeling of Immune Phenotypes in Acute Myeloid Leukemia

Acute Myeloid Leukemia (AML) is an aggressive blood cancer with high heterogeneity, demanding rapid and precise diagnostics to guide therapy. Flow cytometry is one of the gold standards for AML diagnosis and risk stratification, but current clinical workflows rely on low dimensional measurements and subjective manual gating.

In this project, we will employ advanced generative AI modeling of antibody-based single cell technologies (flow cytometry, high throughput antibody screens, single cell genomics, etc.) to assemble one of the largest single cell atlases of AML patients to date. Our goal is to build an AML reference atlas across hundreds up to thousands of patients, refine it with targeted biomarker screens, and identify actionable biomarkers for clinical decision making.

As a Master or intern student, you will contribute to developing and applying computational and (optionally) experimental methods at the intersection of systems immunology, computational biology, and translational hematology. Your work will directly support the identification of robust biomarkers and the development of AI-driven diagnostic tools with translational impact for hematology.

Team:
The project is led by Dr. Florian Ingelfinger in collaboration with our clinical partners. You will join a highly interdisciplinary team spanning clinical hematology, systems immunology, and computational biology, with strong ties to both experimental and clinical research. Our group emphasizes creativity, collaboration, and innovation in addressing clinically relevant questions in immunology and hematology.

Tasks:
- Integration and imputation of massive flow cytometry datasets using deep generative modeling
- Development of computational methods for large scale analysis of sample-level heterogeneity in clinical cohorts
- Integration of clinical metadata and high-dimensional immune profiling data
- Development and benchmarking of machine-learning classifiers for biomarker candidate evaluation
- Optional: Experimental profiling of clinical samples using antibody-based single cell technology assays (fluorescent based or oligonucleotide based)
- Presentation and interpretation of results together with our clinical partners

Requirements:
- Master student in Bioinformatics, Computer Science, Molecular Medicine, Immunology, Biology, Biochemistry, or related field
- Solid skills in computational biology (Python and R, exploratory single-cell data analysis, machine learning)
- Experience with single-cell analysis frameworks (e.g. scanpy, scvi-tools) and at least basic knowledge of statistics
- Familiarity with Linux-based high-performance computing environments, including bash scripting and job

scheduling on HPC clusters

- Basic understanding of immunology and cancer biology is an advantage
- Prior exposure to deep learning frameworks and experience with computer vision is an advantage
- Experience in wet lab immunology (flow cytometry, single-cell genomics) is considered a plus
- Strong motivation to work at the interface of AI, immunology, and clinical translation
- Curiosity, attention to detail, and ability to work both independently and as part of a team

Applications should include:
1. Motivation letter
2. CV
3. Copy of Bachelor’s degree certificate
4. Relevant academic transcripts or certificates
5. Optional: Letter of recommendation

Please send applications to:

florian.ingelfinger@uniklinik-freiburg.de

For further inquiries, feel free to contact Dr. Florian Ingelfinger via email.