Genomic Approaches in Malaria Diagnostics: A Tool for Targeted Treatment and Surveillance of Epidemiological Trends

Supervisor: **dr. Marcela Krůtová**

Malaria remains a life-threatening disease, with delayed diagnosis and drug resistance contributing to high mortality rates. Treatment failure of artemisinin-based therapies has been reported in Czech travellers, but the underlying mechanisms are unknown. This project aims to generate genomic data on Plasmodium spp. imported to the Czech Republic to detect molecular markers associated with treatment failure or disease severity.

Leveraging Multi-Omics for CSF-Based Insights into Brain Tumor Biology

Supervisor: **doc. Michal Zápotocký**

Brief synopsis: This project leverages a unique biobank of 200 cerebrospinal fluid (CSF) samples from pediatric brain tumor patients to advance innovative diagnostics and uncover tumor biology. We will employ DNA sequencing and methylation profiling for improved molecular classification and diagnostic precision. Additionally, proteomics will be utilized to explore the tumor microenvironment, identifying novel biomarkers and therapeutic targets.

Targeting metabolic adaptations in therapy-resistant leukemia

Supervisor: **dr. Júlia Starková**

Developing advanced tools to characterize the metabolic profiles of resistant leukemic cells that drive treatment failure. Our goal is to track resistant features in leukemic cell population and design alternative therapeutic strategies that can specifically eradicate these and improve patient survival.

Lineage Plasticity in Childhood Leukemia: Single-Cell and Computational Approaches

Supervisors: **dr. Jan Stuchlý, prof. Eva Froňková**

This project aims to unravel the mechanisms of lineage plasticity in childhood leukemia by integrating advanced single-cell multiomics and computational modeling approaches. The successful candidate will develop and apply analytical frameworks to identify and validate key regulatory dynamics driving leukemic cell fate transitions.

Unraveling Lineage Fate in ETP-ALL Leukemic Cells Through Mass Cytometry and Single-Cell RNA Sequencing

Supervisor: **dr. Daniela Kužílková, prof. Tomáš Kalina**

We aim to comprehensively characterise the biological basis of leukemic cells obtained from ETP-ALL patients at diagnosis using mass cytometry. To achieve this, we will (i) develop and (ii) validate a mass cytometry panel using cell line models. This panel will include immunophenotypic markers of hematopoietic progenitors, T-lymphoid and myeloid lineage markers, and intracellular proteins that regulate cell fate, such as transcription factors involved in lineage commitment, as well as markers of apoptosis and proliferation. We will define physiological developmental steps using healthy thymocytes and compare these with ETP-ALL samples. Finally, for selected patient samples, we will perform single-cell RNA sequencing to explore the relationship between RNA and protein expression trends.