

MASTER STUDENT PROJECT: EXPLORING THE TRANSCRIPTIONAL SIGNATURES OF AML ACROSS DIFFERENT NICHEs USING PUBLIC TRANSCRIPTOMICS DATA (BIOINFORMATICS)

Project Background

Acute myeloid leukemia (AML) is a severe type of blood cancer, characterized by the abnormal proliferation of immature myeloid cells (blasts) in the bone marrow (BM). Despite significant advances in our understanding of the disease, outcomes remain poor with a median overall survival of 8.5 months and a 5-year survival rate of only 24%, the lowest of all leukemia types (Shallis et al., 2019).

In the course of the disease, leukemic cells may occasionally disseminate from the BM niche and infiltrate other tissues – a phenomenon known as extramedullary disease. This occurs in approximately 2% of patients at diagnosis, but its incidence increases substantially in relapsed cases, affecting around 20% of patients who relapse following hematopoietic stem cell transplantation (DiNardo et al., 2023). We now plan to analyze publicly available single-cell transcriptomic data to identify transcriptional signatures characteristic of bone marrow or extramedullary AML.

Your Tasks

You will analyze public single-cell RNA-seq data of already sequenced AML cells in different niches. You will develop hands-on experience in common bioinformatics methods, such as: unsupervised clustering, label transfer, differential analysis or gene set enrichment analysis. Depending on your progress, you will also have the chance to explore other omics data generated in the lab to integrate with transcriptional profiles and build a multi-omic analysis.

Your Profile

We are seeking a master student with a strong background in bioinformatics, computational biology or biostatistics with the following skills:

- R programming
- Basic bash/shell scripting
- Basic knowledge of sequencing technologies

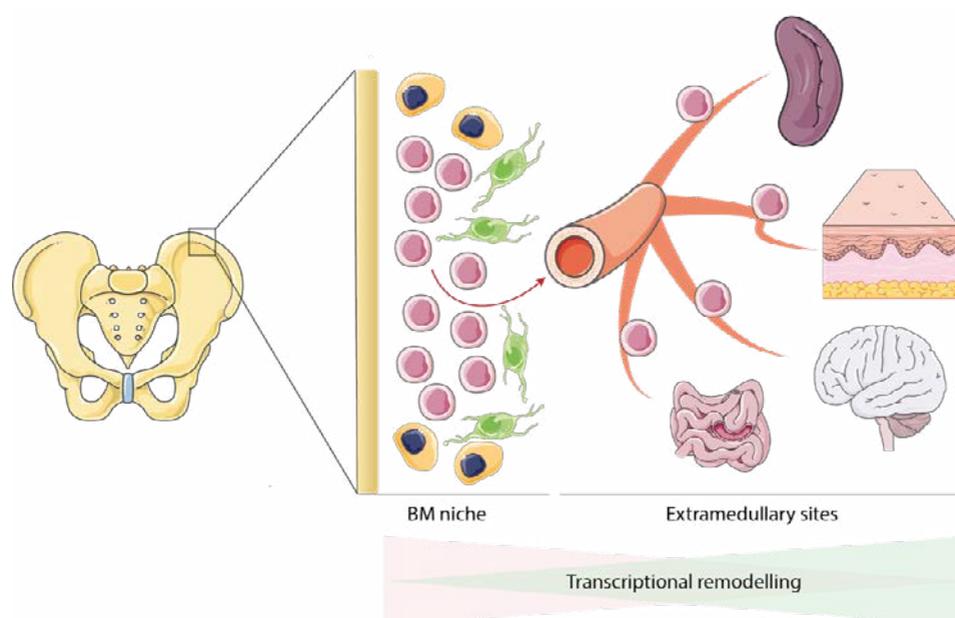
What we offer

You will join the Blood Cancer Biology and Immunotherapy (BCIM) lab (<https://www.apostolovalab.com/>) and be supervised by a skilled team of biologists, clinicians and a bioinformatician. Through our connections in oncology, hematology and bioinformatics, you will also have the possibility to develop a strong professional network in the University of Basel and in the University Hospital Basel for your future career. Depending on the results of the project, you will have the chance to become a co-author of the resulting research article.

How to apply

Please send an updated CV, a motivation letter and - if available - the contact information of one or more referees to petya.apostolova@unibas.ch and Anthony.sonrel@unibas.ch.

We will be happy to welcome you in our team as soon as possible, ideally before Summer 2026.



Visual abstract: We hypothesize that AML cells undergo a transcriptional switch impacting multiple cellular functions upon exiting the bone marrow niche. Our study plans to analyze the transcriptomic profiles of AML blasts across different niches. Yellow and green cells represent different types of BM niche cells. Pink cells represent AML blasts. Illustration created in part with images from Servier Medical Art, licensed under CC BY 4.0.

Literature:

- DiNardo, C. D., Erba, H. P., Freeman, S. D., & Wei, A. H. (2023). Acute myeloid leukaemia. *Lancet*, 401(10393), 2073-2086. [https://doi.org/10.1016/S0140-6736\(23\)00108-3](https://doi.org/10.1016/S0140-6736(23)00108-3)
- Shallis, R. M., Wang, R., Davidoff, A., Ma, X., & Zeidan, A. M. (2019). Epidemiology of acute myeloid leukemia: Recent progress and enduring challenges. *Blood Rev*, 36, 70-87. <https://doi.org/10.1016/j.blre.2019.04.005>