

## **Master Thesis Project in Computational Single Cell Biology –**

### **Computational analysis of tRNA expression at a single-cell level**

The labs of Florian Büttner and Michael Rieger are looking for a motivated Master student to develop a computational workflow for the analysis of tRNA expression single cell data. The Büttner and Rieger labs are internationally renowned in the fields of computational cancer research and stem cell research. Moreover, the collaborative environment of the University Hospital Frankfurt fosters interdisciplinary excellence and provides an ideal research infrastructure. Furthermore, the topic has been defined as an emerging field of the Excellence Cluster Cardio-Pulmonary Institute, with excellent support for early career researchers.

Our labs are currently developing a method to quantify transfer RNAs (tRNAs) at a single cell level. We have established experimental protocols, generated preliminary datasets and we need to develop a specific computational approach. This will allow to elucidate how tRNA abundance and codon usage orchestrate cellular systems, focusing on hematopoietic stem cells and primary leukemia cells. The applicant will analyze single-cell sequencing data (tRNAs and mRNA transcriptomes) from patient derived material, visualize the results and discuss their findings with the other scientists involved in the project of both research groups.

The computational analysis of tRNAs at a single cell level pose multiple exciting challenges:

- The accurate genome mapping is made difficult by the high sequence similarity between tRNAs and by their post-transcriptional modifications;
- The functional analysis can be performed at multiple levels: single tRNAs, isodecoder (all tRNAs sharing a specific anticodon), and isoaccepter (all tRNAs carrying the same amino-acid).
- Some tRNA genes are located in introns of coding genes; therefore tRNA expression could be regulated independently or conditioned to mRNA expression, the genomic position of the tRNAs should therefore be considered in the analysis

We will consider applicants studying Bioinformatics, Biology, Molecular Medicine, Pharmaceutical Sciences or any related field. The optimal candidate has strong programming skills (Python, R, linux command) and a good understanding of sequence alignment algorithms and analysis of transcriptomic data. Beyond the focus on bioinformatic analyses of the data, the applicant has the possibility to contribute to the wet lab research.

If you are interested, please send your CV, a short cover letter and a copy of your Bachelor's degree to: Adrien Jolly ([a.jolly@dkfz-heidelberg.de](mailto:a.jolly@dkfz-heidelberg.de)) and/or Marius Külp ([marius.kuelp@em.uni-frankfurt.de](mailto:marius.kuelp@em.uni-frankfurt.de))