

Wet/Drylab MSc Project: Integrative Epigenomics in mouse ESC system

We make use of cutting edge epigenome mapping strategies including quantitative MINUTE-ChIP, CUT&Tag, ATAC-seq, single cell omics. We are developing additional technologies to map epigenome dynamics. We are interested in the underpinnings of pluripotency and lineage commitment.

We are looking for a highly motivated student that could either work on the experimental or analysis side (or both). For a bioinformatics project, excellent programming skills and knowledge in next-gen sequencing analysis are a requirement. For an experimental project, experience in mammalian tissue culture and molecular biology are expected.

The scope of the thesis will be a subset of the following:

- to perform cell culture based experiments with pluripotent stem cells
- to perform MINUTE-ChIP, CUT&Tag, ATAC-seq
- to use standard NGS suites to process primary data and extract relevant information (bowtie2, samtools, picard, deep tools) based on bash scripting
- Perform custom analyses, e.g. genome-wide correlation, peak overlap analysis to correlate datasets (R and other packages)
- Develop custom data aggregation, transformation and visualizations with R

Please contact me for more detail.

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