

Bioinformatics MSc Project: Integrative Epigenomics in mouse ESC system

We make use of cutting edge epigenome mapping strategies including quantitative ChIP-Seq, transient transcriptomics (TT-Seq), DNA feature mapping (BLISS and S1-Seq) to understand the unique properties of stem cell chromatin. We are developing additional technologies to map epigenome dynamics. Integrating the different datasets with the wealth of published epigenome data provides a powerful strategy to identify mechanistic connections and regulatory patterns.

We are looking for a highly motivated bioinformatics student with excellent programming skills and knowledge in next-gen sequencing analysis. The scope of the thesis will be:

- 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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