Master project 2024-2025

Personal Information

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Group	Comparative regulatory genomics

Project

Computational genomics

Project Title:

Investigating the origin and evolution of eukaryotic chromatin, from heterochromatin to regualtory loops

Keywords:

Chromatin; Transcription factors; Gene regulation; Evolution; Phylogeny

Summary:

Our group studies genome regulation from an evolutionary systems perspective. In particular, we are interested in deciphering the evolutionary dynamics of animal cell type programs and in reconstructing the emergence of genome regulatory mechanisms linked to cell type differentiation (from transcription factor binding through chromatin states to the physical architecture of the genome). To this end, we apply advanced single-cell genomics and chromatin experimental methods to molecularly dissect cell types and epigenomic landscapes in phylogenetically diverse organisms. We also develop computational tools to integrate these diverse data sources into models of cell type gene regulatory networks and we use phylogenetic methods to comparatively analyze these models. Our recent work has provided the first whole-organism cell type atlases in different species and mapped key regulatory genome features underlying these cellular programs. By sampling additional species and chromatin features, we now aim at dissecting the evolutionary history of eukaryotic chromatin and gene regulation.

Expected skills:

We are seeking a highly motivated candidate to join our team to work on an interdisciplinary project (experimental and computational) involving comparative genomics and chromatin profiling in different systems. The research program for this position focuses on studying the evolution of animal transcription factor and their sequence binding specificities, as the key players orchestrating cell type identity gene regulatory networks. To this end, you will apply phylogenetic methods to infer the evolutionary history transcription factors and chromatin proteins, in vitro experiments (SELEX-seq), as well as in silico modelling, to interrogate transcription factor binding motifs, and chromatin profiling methods (ChIP-seq, ATAC-seq, microC) to interrogate the architecture of the regulatory genome. Our laboratory has advanced molecular biology infrastructure regularly applies all the methodologies involved in this project (e.g. Micro-C, ChIP-seq, SELEX-seq). Previous experience in basic molecular biology and/or functional genomics data analysis is an advantage. Creativity and intellectual independence are essential, as is the ability to work collaboratively.

Possibility of funding:

To be discussed

Possible continuity with PhD:

Yes