

Master project 2020-2021

Personal Information

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Group	Single-cell genomics and evolution

Project

Computational genomics

Project Title:

Evolutionary modeling of cell type gene regulatory networks using single cell genomics data

Keywords:

evolution; gene regulation; cell types; transcription factors; chromatin accessibility

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 analyse 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 at single-cell resolution, we now aim at dissecting the evolution of cell types and their underlying gene regulatory networks. We are seeking highly motivated master students to join our team and work on inferring and comparing cell type gene regulatory networks (GRNs) across species. Methodologically, this project will involve the integrative computational analysis high-throughput single-cell genomics and chromatin data in different systems.

References:

<https://www.ncbi.nlm.nih.gov/pubmed/29856957>
<https://www.ncbi.nlm.nih.gov/pubmed/27114036>

<https://www.ncbi.nlm.nih.gov/pubmed/29942020>

Expected skills::

R and Python programming; experience working on a computing cluster; good understanding of functional genomics methods and experience analyzing genomic data.

Possibility of funding::

No

Possible continuity with PhD: :

To be discussed
