# Master project 2021-2022

| Personal Information | |
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| **Website** | https://www.sebepedroslab.org/ |
| **Group** | Single-cell genomics and evolution |

| Project |
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## Computational genomics

**Project Title:**

Investigating animal cell type diversity, evolution and regulation using single cell genomics and epigenomics approaches

**Keywords:**

Evolutionary biology; Single-cell genomics; Genome regulation; Animal phylogenetics; Comparative genomics

**Summary:**

Projects and specific tasks We are looking for students to join our team to work on a computational project involving integrative analysis of high-throughput single-cell genomics and chromatin data in different animals and unicellular relatives of animals. You will analyse single-cell datasets from different species and perform comparative genomics analyses. The goal is to reconstruct the evolutionary origin and diversification of animal cell types. We also have a second position to work on the development of a phylogenetics pipeline to infer genome-wide gene orthologies. You will learn about phylogenetics methods, protein alignment tools, and gene family evolution. The goal is to set-up a robust orthology framework to integrate single-cell atlases from diverse organisms; as well as to focus on the evolution of particular multi-gene families that are important for animal multicellularity and cell type differentiation (e.g. transcription factors). About the group 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 (see Sebé-Pedrós 2018, Cell, Sebé-Pedrós 2018 NEE, Sebé-Pedrós 2016 Cell). 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.

**References:**

Check our website: https://www.sebepedroslab.org/

**Expected skills::**

We are seeking for creative and highly motivated students with an interest in evolutionary biology, genome regulation and/or comparative genomics. We are preferentially looking for dry/computational candidates, but there is also a possibility to work on dry+wetlab projects. Basic bioinformatics skills (command-line terminal, R/python scripting) are highly desirable, while ability to work in collaborative projects is a must. Possibility to continue with PhD after the master.

**Possibility of funding::**

To be discussed

**Possible continuity with PhD: :**

To be discussed