



European
Research
Council

Position in Genomics and Bioinformatics

The **López-Bendito** Lab is interested in understanding the cellular and molecular mechanisms involved in the development and plasticity of sensory circuits (<http://lopezbenditolab.com>). In particular, our aim is to uncover the principles underlying the formation and specification of sensory systems and the plasticity and adaptations of these connections triggered by early sensory deprivation, through an integrated and innovative experimental programme.

This project seeks to understand the transcriptional control of the formation of sensory nuclei in the developing thalamus, a central sensory station. A detailed understanding of the pool of guidance receptors that is expressed by distinct populations of thalamic neurons is essential to determine the mechanistic program involved in the correct pathfinding and development of this connectivity. In the laboratory, we have been developing strategies to selectively label distinct populations of thalamic nuclei and their projections using specific transgenic mouse lines that includes *in vivo* imaging of brain activity, manipulation of gene expression, cell and molecular biology, genome-wide analysis, cell culture and electrophysiology (Martini et al. 2021 Neuron; Herrero-Navarro et al. 2021 Science Adv.; Anton-Bolaños et al., 2019 Science; Moreno-Juan et al., 2017 Nat Comm.; Gezelius et al., 2017 Cereb Cortex; Mire et al., 2012 Nat Neuro). One of the aims of this project is to isolate thalamic neurons from different nuclei to study their gene profile at distinct developmental time points.

The laboratory offers an excellent and multidisciplinary working atmosphere at the Institute of Neuroscience in Alicante, located in the south-east of Spain at the University of Miguel Hernández-CSIC campus. The host institute is composed by several research groups exploring the development, structure and function of the nervous system in normal and pathological conditions (<http://in.umh.es/>).

The candidate will analyze high-throughput genomic data available in our lab from transgenic mouse models: bulk population RNA-seq, bulk population ATAC-seq, single-cell RNA-seq, etc, to dissect the mechanisms orchestrating epigenome and transcriptome rewiring of thalamocortical neurons during early development.

We believe this is an exciting opportunity for an enthusiastic candidate to join a consolidated team with a strong commitment to basic and translational research. You will receive help and supervision on the project at multiple levels and will be offered possibilities to grow scientifically.

Requirements:

- Knowledge in bioinformatic analysis of scRNA-seq, RNA-Seq, ATAC-seq, and ChIP-Seq datasets. Knowledge of expression data analysis and/or sequencing-based, and experience in developing analysis strategies and workflows in transcriptomics.
- Experience in data-science techniques (regression, machine learning).

- Working knowledge of Linux and programming expertise (e.g., Perl or Python). Good knowledge of R (and the BioConductor libraries).
- Strong problem-solving ability, and the aptitude and zeal to acquire new skills necessary for the job.
- Rigorous and well organized; good verbal and written English communication skills.

Desirable skills

- Demonstrated experience in working out proof of concept workflows, analysis tools or visualizations.
- Broadly applicable general bioinformatics skills (pathway analysis, data and text mining, querying databases, and repositories in the public domain).

Possibility of funding

This position offers a superb opportunity for a highly motivated MSc who want to pursue a (funded) PhD thesis at the host lab.

Contact information:

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