

## Master project 2020-2021

### Personal Information

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<b>Group</b>	Cancer and Stem Cells

### Project

## Computational genomics

#### Project Title:

Comparative genomics and transcriptomics in stem cells and cancer

#### Keywords:

Transcriptomics, Genomics, leukemia, public repositories, cancer genetics

#### Summary:

Comparative genomics has become an essential tool for understanding genetic changes among different organisms, tissues and diseases. Alongside the latest development of powerful sequencing techniques and complex computational algorithms, researchers have been able to identify genetic drivers of cancer, as well as to provide insights into the biological pathways involved in carcinogenesis. Comparative genomics is thus considered a key element in cancer sciences, and bioinformatics is nowadays implemented in every multidisciplinary research team. The Stem Cells and Cancer group led by Anna Bigas is focused on the study of the molecular mechanisms involved in hematopoietic stem cells generation and hematologic malignancies, specially T-cell acute lymphoblastic leukemia (T-ALL). Moreover, it is implicated in the exploration of biological processes underlying colorectal cancer as it works in close cooperation with Colorectal Cancer group led by Lluís Espinosa. The expertise of Yolanda Guillén, a bioinformatics-trained biotechnologist, is crucial to perform the computational part of these projects and to understand the biological relevance of the results. We are glad to host an enthusiastic and motivated student willing to participate in:

- The implementation of different bioinformatics pipelines in ongoing projects. We do use multiple approaches to analyze transcriptional (RNA-Seq and microarrays), genomics (ChIP-Seq) and epigenomics (ATAC-Seq) data. The student will learn how to prepare, run and interpret the results, from the raw sequencing data to the final output. Importantly, we do have access to a supervised computational cluster, which will make the student possible to understand how to work in such computational environment.
- The exploration of transcriptional changes in T-ALL. Our main objective is to collect transcriptional data, mainly RNA-Seq, from public resources in order to screen for genetic expression changes in T-ALL. We are not only interested in identifying genes differentially expressed in T-ALL compared to normal cells, but to detect isoform switching patterns in cancer.

#### Expected skills::

Bash and R basic programming

#### Possibility of funding::

No

**Possible continuity with PhD: :**

To be discussed

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