



## Master project 2021-2022

### Personal Information

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<b>Group</b>	pre-mRNA splicing

### Project

## Computational systems biology

#### Project Title:

Splicing Systems Biology

#### Keywords:

spliceosome, genome, intron, exon, splicing

#### Summary:

The information content of genomes can be greatly expanded by pre-mRNA splicing. Virtually all human pre-mRNAs need to be spliced to become mRNAs. Furthermore, most pre-mRNAs can be spliced into different mRNAs by alternative splicing, which thus constitutes an additional layer of regulation in gene expression. Pre-mRNA splicing is the task of the spliceosome, a ribonucleoprotein complex larger than the ribosome, and itself the target of a large number of regulatory factors that will shape its splicing output. In addition, as splicing takes place co-transcriptionally, the rate of pre-mRNA synthesis impacts its processing as well. We propose a combination of Bioinformatics and “wet lab” approaches to reveal novel splicing strategies that may contribute to the function of genomes. Using RNASeq data from multiple sources and evolution data we will address a number of questions, including (but not restricted to) (1) why some introns have specific properties like secondary structures in specific locations; (2) what may be the consequences for the splicing of a transcript from a sequence that includes a downstream start of transcription, or a transcription terminator in either strand; and (3) can we find common features in sets of related pre-mRNAs?

#### Expected skills::

In addition to a good Bioinformatics background, an ability to work independently and to integrate diverse data (mutational analyses, epigenetics, transcriptomics, and others) is desirable. Knowledge of python, bash, and R will be helpful.

#### Possibility of funding::

No

#### Possible continuity with PhD: :

To be discussed

