



Offre de stage M2 2018/2019

Titre: Bioinformatic identification of DNA sequence and chromatin signatures of germline genes.

Description du projet :

DNA methylation plays pivotal roles in development and cancer. One of the main functions of DNA methylation is to repress promoters of germline genes in mammalian somatic cells. However the mechanisms responsible for specifically targeting DNA methylation to the promoters of germline genes are unknown. Transcription factors (TF) have the potential to regulate those specific DNA methylation and chromatin patterns through the recognition of specific DNA sequence motifs.

The goal of the project is to identify DNA sequence motifs and chromatin signatures that characterize the promoters of germline genes. To do so, you will collect epigenomics datasets from public databases (methylome, ChIP-seq, DNase-seq) and develop machine learning approaches to identify DNA sequence motifs and patterns of chromatin marks that differentiate the promoters of germline genes from the other gene promoters in mammalian cells. Ultimately, this will help to formulate hypotheses on the mechanisms that recruit DNA methylation to germline genes.

You will be part of a dynamic research team interested in the epigenetic regulation of mammalian genomes. You will benefit from our strong expertise in genomics and bioinformatics for the success of the project.

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Masters concernés : Biologie Structurale Intégrative et Bioinformatique