



Offre de stage M2 2018/2019

Titre: Regulation of transcription factor binding by chromatin.

Description du projet :

Regulation of gene expression is driven by sequence-specific transcription factors (TFs) that bind to regulatory regions through the recognition of short specific DNA sequence motifs. However, while thousands of occurrences of specific TF motifs are found within genomes, only a small fraction is bound in a context-specific manner. Therefore, the specificity of TF binding must be controlled by other means. DNA methylation occurs on cytosines mostly within CpG dinucleotides and has the potential to block TF binding. However, it is still disputed which TFs are sensitive to DNA methylation and if DNA hypomethylation is a cause or consequence of TF binding.

The goal of this project is to integrate genomic data to explore which TFs are sensitive to DNA methylation in mammalian cells. First, you will predict TF binding sites using TF motifs information and DNA accessibility data (DNase I sequencing). Second, you will predict TF sensitive to DNA methylation by integrating TF binding sites to methylation data (whole genome bisulfite sequencing).

Potential candidate TFs predicted to be sensitive to DNA methylation will then be validated experimentally in our laboratory by chromatin immunoprecipitation followed by sequencing. Ultimately, the project will lead to a better understanding of how the chromatin context influences TF binding, which is critical to build predictive models of TF binding and gene regulation.

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 bioinformatics, genomics and DNA methylation for the success of the project.

This project can be extended into a PhD project.

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Masters concernés : Biologie Structurale Intégrative et Bioinformatique