Computational dissection of transcriptional regulation in metabolic disease

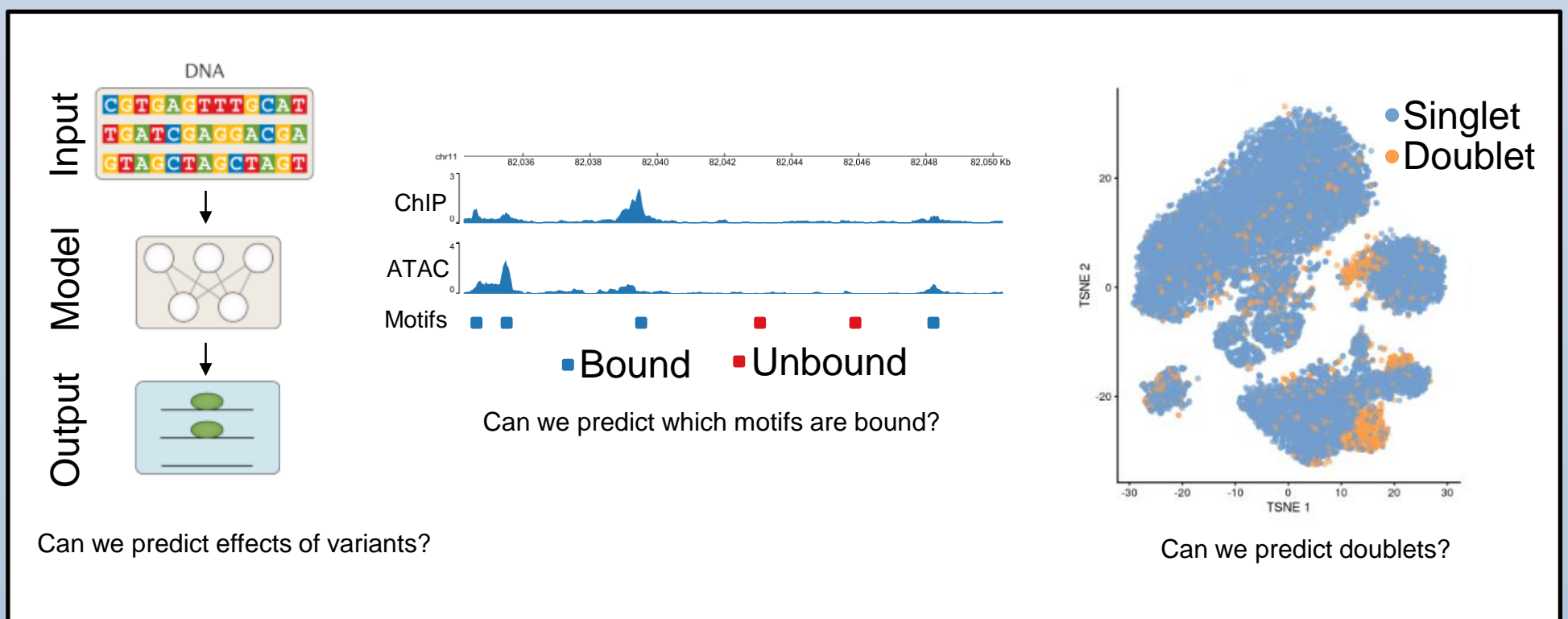## Forskningsleder Jesper Grud Skat Madsen

Gruppens kerneforskningsområder

Metabolic diseases, such as **type 2 diabetes and obesity**, are acquired over time. One of the key mechanisms underlying the progression of non-acute, slow-progressing diseases is **transcriptional regulation**. Through transcriptional regulation, cells in various metabolic tissues slowly, but persistently, change from a healthy towards an unhealthy state.

In MadLab, we are experts in **computational biology**, and therefore, we do not have access to laboratories. We are focused on developing new and applying existing computational methods to dissect transcriptional regulation in metabolic disease. To that end, we use **statistical programming** (e.g., R and Python) to perform statistical modeling, machine learning, and exploratory data analysis on public data and data generated by collaborators.

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Can we predict effects of variants?

Can we predict which motifs are bound?

Can we predict doublets?

Projects	Description
Mapping genetic variation using deep learning	In this project, we develop new deep learning architectures that can predict the effect of genetic variants on the epigenome. This has exciting applications in understanding genetic mechanisms of disease.
Transcription factors, variants and chromatin accessibility.	In this project, we aim to explore the determinants of transcription factor binding by analyzing transcription factor affinity and chromatin accessibility in a genome-wide manner. This will generate important insights into mechanisms of gene regulation.
Identifying doublets in single-nucleus ATAC-seq datasets	In this project, we want to test existing and develop a new ensemble method for detecting doublets in single-nucleus ATAC-seq and paired RNA-seq and ATAC-seq datasets. This will yield important insights into best practices for data analysis.

Er du interesseret i at skrive projekt i gruppen, så kontakt jgsm@bmb.sdu.dk

MADLAB

Functional Genomics & Metabolism

ATLAS CENTER FOR FUNCTIONAL GENOMICS AND TISSUE PLASTICITY

NOVO NORDISK FOUNDATION CENTER FOR GENOMIC MECHANISMS OF DISEASE AT BROAD INSTITUTE