Computational dissection of transcriptional regulation in metabolic disease

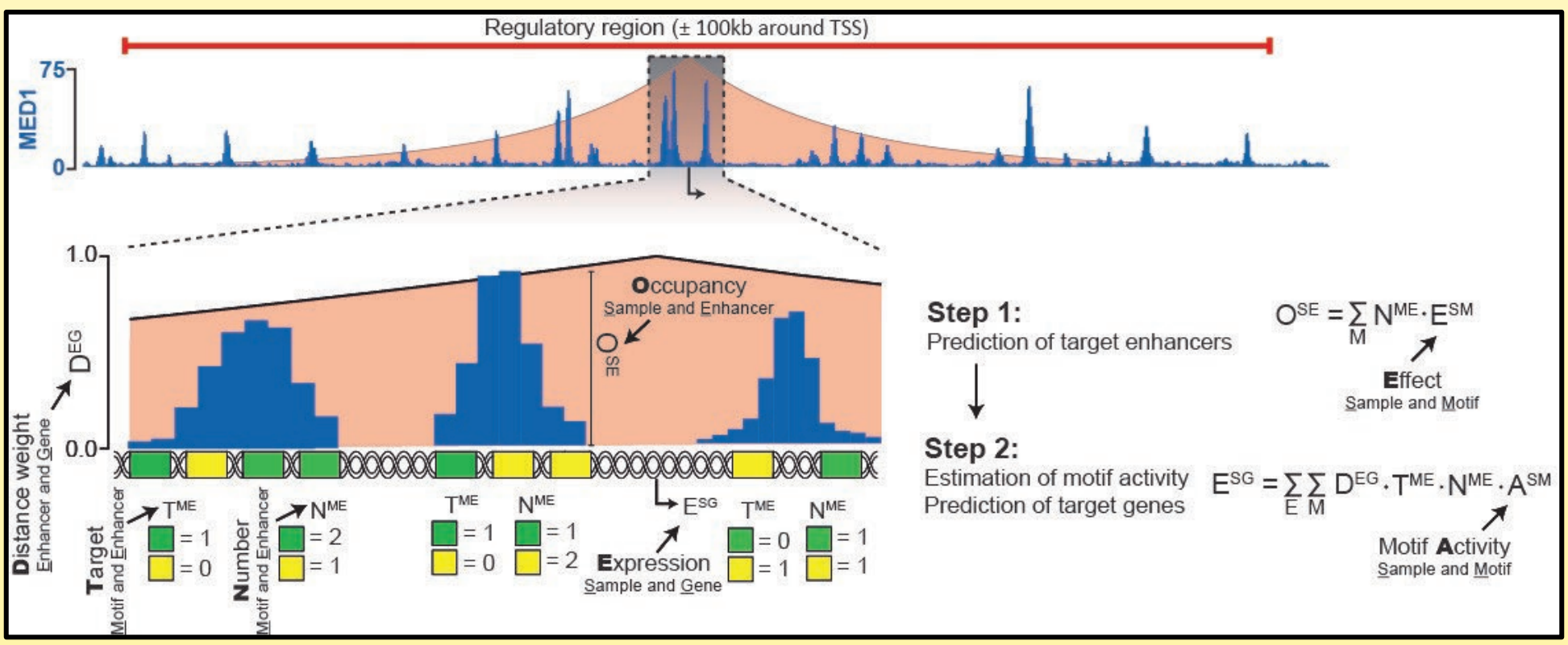
Forskningsleder Jesper Grud Skat Madsen

Gruppens kerneforskningsområder

Metabolic diseases, such as type 2 diabetes and obesity, are acquired over time. One of the key mechanisms underlying 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 the Madsen group, we only do computational biology (no laboratory) and 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 modelling, machine learning and exploratory data analysis on public data and data generated by collaborators.

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



Projekter	Beskrivelse
Disentangling transcriptional control in adipose tissue one cell at a time	Collaborative project, where my group identified optimal workflows and statistical methods for the analysis of single-cell RNA-seq and single-cell ATAC-seq from human adipose tissue.
Motif scoring methods for prediction of gene expression from sequence	In this project, we aim to identify the optimal method for scoring transcription factor motifs in order to predict gene expression from sequence of DNA.