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Studying the effects of single mutations on nucleosome positioning with deep neural network.

The MNase protocol makes it possible to experimentally study the positioning of the nucleosomes along the genome. Studying the effects of point mutations on this positioning can help us to understand how the DNA sequence encodes nucleosomes positions.

We propose to use deep neural networks to provide a tool to study the effect of single mutations at a genome wide scale . We trained a deep neural network to predict the nucleosome landscape in S.cerevisiae from the underlying DNA sequence. Being able to faithfully reproduce experimental results the neural network acts like the S.cerevisiae nucleosome positioning machinery. With this tool in hand, we can test the effect of the mutation of every single nucleotide in the genome. This allows us to detect nucleotides and sequence motives that are the most important for nucleosomes positioning.

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