Nucleosome

A nucleosome is a basic unit of DNA packaging in eukaryotes, consisting of a segment of DNA wound in sequence around eight histone protein cores.

This structure is often compared to thread wrapped around a spool.

Nucleosome occupancy changes across cell types and environmental conditions and such changes often have profound influence in transcription. It's of importance to identify the differential nucleosome regions (DNRs) where the nucleosome occupancy level differs across cell types. Here we developed DNMHMM, a Hidden Markov Model (HMM) based algorithm, to detect the DNRs with nucleosomal DNA sequenced dataset. The performance evaluation indicates that DNMHMM is advisable for multi-cell type comparison. Upon testing this model in yeast mutants, where the modifiable histone residues were mutated into alanine, we found that DNA sequences of the dynamic nucleosomes lack 10-11 bp periodicities and harbor binding motifs of the nucleosome remodelling complex. Moreover, the highly expressed genes have more dynamic nucleosomes at promoters. We further compared nucleosome occupancy between resting and activated human CD4+ T cells with this model. It was revealed that during the activation of CD4+ T cells, dynamic nucleosomes are enriched at regulatory sites, hence, up to some extent can affect the gene expression level. Taken together, DNMHMM offers the possibility to access precise nucleosome dynamics among multiple cell types and also can describe the closer association between nucleosome and transcription [1).

[1)

Xie J, Cai Y, Li H, Wu J, Zhao X, Luo K, Sharma A, Xie J, Sun X, Liu H. DNMHMM: an approach to identify the differential nucleosome regions in multiple cell types based on a Hidden Markov Model. Biosystems. 2019 Sep 18:104033. doi: 10.1016/j.biosystems.2019.104033. [Epub ahead of print] PubMed PMID: 31541672.