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Modeling transcription factor occupancy profiles in Drosophila.

Transcriptional regulation is the result of transcription factors (TFs) binding the DNA and interacting with the basal transcriptional machinery, and with each other, to regulate gene expression. In recent years, chromatin immunoprecipitation (ChIP)-based genome-wide assays of TF occupancy have emerged as a powerful, high throughput method to understand transcriptional regulation, especially on a global scale. With the availability of ChIP-chip and ChIP-SEQ data sets, attempts have been made to correlate occupancy profiles to the TFÕs binding specificity as described by a motif. The ultimate goal is to be able to model a TFÕs occupancy profile in any given cellular condition. In this talk, I will present our on-going work towards this goal. We have analyzed TF-ChIP data sets in Drosophila using our statistical thermodynamics-based model of occupancy. While the baseline model uses only the TFÕs motif in predicting ChIP profiles, we incorporated additional features into the model, including TF concentration, competition and cooperation between TFs, and DNA accessibility, to test if these features make a significant contribution to measured occupancy. We find evidence for a variety of factors influencing TF-DNA interaction, some common across many ChIP data sets and some more specific to a few data sets.