

David van Dijk, Marten Postma, Jaap Kaandorp & Peter Slood  
Computational Science, University of Amsterdam

Transcriptional regulation is the result of regulatory proteins binding to DNA where they have an activating and repressing role in RNA polymerase activity. Protein-DNA binding is a thermodynamic process where temperature, concentration and sequence specific binding affinity influence the configuration space of the molecules bound to the DNA. The distribution of these configurations of regulatory proteins, like nucleosomes and transcription factors, is what influences gene expression. In order to predict binding probabilities and study the configurations of regulatory proteins we introduce a framework for stochastic simulation of DNA binding molecules. In this framework Monte Carlo simulation is used to sample from the configuration space to determine the occupancy of the DNA at thermodynamic equilibrium. Using different sampling techniques we are able to study DNA binding along spatial as well as temporal dimensions. MC simulation of diffusion in a potential is used to study configuration change over time. To validate our method we perform MC simulation of nucleosome binding and compare the results to existing prediction techniques and experimental data.