Binding of Transcription Factors to Non-Regulatory DNA:

The Gaussian Genome

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Recent studies in biophysics suggest transcription factor interactions with non-regulatory DNA are sequence-dependent and vary along the DNA strand [1]. This makes numerical calculation of the grand canonical partition function [2] cumbersome and renders predictions of genetic activity a seemingly insurmountable task. Using the cumulant-generating function of the normal distribution, we derive the partition function and define an effective energy, a single quantity which accounts for the contributions from the whole spectrum of binding energies. Applying our approach to the *lac* repressor and RNAP, two prominent *lac* operon transcription proteins, we obtain theoretical results which are in good accord with the actual biophysical picture.

[1]M. Lässig, BMC Bioinformatics 8(Suppl 6), S7 (2007).[2]F. M. Weinert et al., PRL 113, 258101 (2014)