Comparing Stochastic Models of Gene Expression

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Abstract
The nature of gene expression is intrinsically stochastic due to the small copy number of chemical species involved in this process. At transcriptional level, gene expression is mainly controlled by transcription factors that bind specifically at upstream promoter sites and modulate the transcriptional machine binding. Therefore, the regulation of transcriptional fluctuations depends on the binding mechanisms of transcription factors. It is known that transcriptional responses are generally sigmoid due to the presence of cooperative phenomena. Thus, many authors use Hill function to introduce cooperativity into models for transcriptional regulation. This approximation assumes simultaneous binding of transcription factors and infinite energies of interaction between them. However, in previous studies we found dependency of gene expression fluctuations with the cooperative interaction energy. In our approximation, the model includes several transcription factors binding sites and the sequential binding of them. Furthermore, the model assumes cooperative binding of transcription factors.
We explore these two approximations of transcription factors binding and the consequences in gene expression fluctuations using master equation formalism and computer simulation.
In their general form, both approximations differ when slow kinetics of transitions between promoter states and low interaction energies between transcription factors are considered. However, differences disappear when kinetics of transitions between promoter states and interaction energies between transcription factors are increased.

References:

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