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*Stochastic effects in gene transcription*

Gene transcription is typically the major source of noise in gene expression. We have developed models of gene transcription for both prokaryotes and eukaryotes. These models allow us to examine the effects of the kinetics of various elementary reaction steps on the overall statistical behavior of transcription, and in particular on the distribution of transcription times. Here we review a few results obtained from our models, emphasizing how these results impact large-scale gene network modeling.