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Randomness in the Expression of Genes

The process by which the genetic code comes to life is a fundamentally stochastic process. In order to begin to quantify this randomness, this work models transcription using a population density approach. In the model, a single gene of interest fluctuates stochastically between an inactive state, in which transcription cannot occur, and an active state, in which discrete transcription events occur; and the individual mRNA molecules are degraded stochastically in an independent manner. The random dwell times in the inactive and active states are independent random variables drawn from any specified distributions. Previously, this sort of model with exponential dwell times has been successful in explaining experimental estimates of the distribution of random mRNA copy number within a population of isogenic cells.

I will present efficient numerical methods for computing steady-state mRNA distributions, an analytic formula for the mRNA autocovariance function, and a procedure for model identification based on laboratory data. It will be shown that the autocovariance function can, in some situations, be used to disambiguate gene switching models. Temporal data beyond the autocovariance function is required in general to characterize gene switching. It is hoped that these theoretical advancements will lead to a better understanding of stochastic gene expression, in theory and experimentally.