Noise propagation in biochemical networks

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Stochasticity is an unavoidable aspect of biochemical transformations. Given the complex interdependency of cellular processes, a full description of the noisy dynamics of the molecular copy numbers requires modeling and analysis at the network level. The chemical master equation as a modeling framework is not always well-suited for this task. Here we present an alternative approach that focuses on the fate of individual molecules. In its simplest version, molecules in question are treated as independent random walkers on the network. We show that population level statistics can be readily recovered from the autocorrelation function of arrival and departure events at individual nodes of the network.
For non-interacting walkers, exact relations are obtained for the arrival statistics at consecutive nodes along a linear pathway. We introduce the Poissonian and non-Poissonian components of the autocorrelation function which are shown to propagate differently, with the latter decreasing in magnitude along a transport channel. Consequently, an initially bursty signal broadens as it propagates on the network. Our analysis for the linear pathway can be extended to the more general case of converging and diverging pathways, as well as cascade reactions as in gene transcription and signaling.