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*Molecular distributions in gene regulatory networks*

Extending the work of Friedman et al. (2006), we study the stationary density of the distribution of molecular constituents in the presence of noise arising from either bursting transcription or translation, or noise in degradation rates. We examine both the global stability of the stationary density as well as its bifurcation structure. We have compared our results with an analysis of the same model systems (either inducible or repressible operons) in the absence of any stochastic effects, and shown the correspondence between behaviour in the deterministic system and the stochastic analogs. We have identified key dimensionless parameters that control the appearance of one or two stable steady states in the deterministic case, or unimodal and bimodal densities in the stochastic systems, and detailed the analytic requirements for the occurrence of different behaviours. This approach provides, in some situations, an alternative to computationally intensive stochastic simulations. Our results indicate that, within the context of the simple models we have examined, bursting and degradation noise cannot be distinguished analytically when present alone.