

Stochastic Dynamics in Transcription Models

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Abstract: The formalism of stochastic reaction networks (SRNs) provides building blocks for number of models in mathematical biology both at molecular and population levels (e.g., gene transcription or epidemic outbreak). In particular the SRNs allow to naturally incorporate both delay and multi-scale phenomena. In the first case the resulting models may be often expressed in the language of queuing theory, in the second case they lead to stochastic diffusions and ODE/PDE approximations. In this talk I will provide a brief overview of the applications of SRNs to modeling molecular biological systems emphasizing the recent work on multi-scaling for simple gene transcription model.

Related Articles: [Individual Molecules Dynamics in Reaction Network Models | SIAM Journal on Applied Dynamical Systems | Vol. 22, No. 2 | Society for Industrial and Applied Mathematics](#) and [Reduction for Stochastic Biochemical Reaction Networks with Multiscale Conservations | Multiscale Modeling & Simulation | Vol. 15, No. 4 | Society for Industrial and Applied Mathematics](#)