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DK Seminar

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Time-dependent propagators for stochastic models of gene expression: an analytical method

The inherent stochasticity of gene expression in the context of regulatory networks profoundly influences the dynamics of the involved species. Mathematically speaking, the propagators which describe the evolution of such networks in time are typically defined as solutions of the corresponding Chemical Master Equation (CME). However, it is not possible in general to obtain exact solutions to the CME in closed form, which is due largely to its high dimensionality. In the present talk, we propose an analytical method for the efficient approximation of these propagators. We illustrate our method on the basis of two categories of stochastic models for gene expression that have been discussed in the literature. The requisite procedure consists of three steps: a probability-generating function is introduced which transforms the CME into (a system of) partial differential equations (PDEs); application of the method of characteristics then yields (a system of) ordinary differential equations (ODEs) which can be solved using dynamical systems techniques, giving closed-form expressions for the generating function; finally, propagator probabilities can be reconstructed numerically from these expressions via the Cauchy integral formula. The resulting ‘library’ of propagators lends itself naturally to implementation in a Bayesian parameter inference scheme, and can be generalised systematically to related categories of stochastic models beyond the ones considered here.