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Exact protein distributions for stochastic models of gene expression RAHUL KULKARNI, Department of Physics, UMass Boston, HODJAT PENDAR, Department of Engineering Science and Mechanics, Virginia Tech, THIERRY PLATINI, Department of Applied Mathematics, Coventry University, UK — Stochasticity in gene expression gives rise to variations in protein levels across a population of genetically identical cells. Such fluctuations can drive phenotypic variation in clonal populations, hence there is considerable interest in quantifying noise in gene expression using stochastic models. However, obtaining exact analytical results for protein distributions has been an intractable task for all but the simplest models. We develop a novel mapping that significantly simplifies the analysis of stochastic models of gene expression. Using this mapping, we derive exact analytical results for steady-state and time-dependent protein distributions for the basic 2-stage model of gene expression. Considering extensions of the basic model, we obtain exact protein steady-state distributions for models that include the effects of post-transcriptional and post-translational regulation. The approach developed in this work is widely applicable and can contribute to a quantitative understanding of stochasticity in gene expression and its regulation.

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