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Distribution of population averaged observables in stochastic gene expression BHASWATI BHATTACHARYYA, ZIYA KALAY, iCeMS, Kyoto University — Observation of phenotypic diversity in a population of genetically identical cells is often linked to the stochastic nature of chemical reactions involved in gene regulatory networks. We investigate the distribution of population averaged gene expression levels as a function of population, or sample size for several stochastic gene expression models to find out to what extent population averaged quantities reflect the underlying mechanism of gene expression. We consider three basic gene regulation networks corresponding to transcription with and without gene state switching and translation. Using analytical expressions for the probability generating function (pgf) of observables and Large Deviation Theory, we calculate the distribution of population averaged mRNA and protein levels as a function of model parameters and population size. We validate our results using stochastic simulations also report exact results on the asymptotic properties of population averages which show qualitative differences for different models. We calculate the skewness and coefficient of variance for pgfs to estimate the sample size required for population average that contains information about gene expression models. This is relevant to experiments where a large number of data points are unavailable.

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