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Stochastic Gene Expression in Networks of Post-transcriptional Regulators CHARLES BAKER, TAO JIA, HODJAT PNDAR, RAHUL KULKARNI, Virginia Polytechnic Institute and State University — Post-transcriptional regulators, such as small RNAs and microRNAs, are critical elements of diverse cellular pathways. It has been postulated that, in several important cases, the role of these regulators is to modulate the noise in gene expression for the regulated target. Correspondingly, general stochastic models have been developed, and results obtained, for the case in which a single sRNA regulates a single mRNA target. We generalize these results to networks containing a single mRNA regulated by multiple sRNAs and to networks containing multiple mRNAs regulated by a single sRNA. For these systems, we obtain exact expressions relating the mean levels of the sRNAs to the mean levels of the mRNAs. Additionally, we consider the convergence of the original model to an approximate model which considers sRNA concentrations to be high; for the latter model we derive an analytic form for the generating function of the protein distribution. Finally, we discuss potential experimental protocols which, in combination with the derived results, can be used to infer the underlying gene expression parameters.

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