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Stochastic Modeling of Regulation of Gene Expression by Multiple Post-transcriptional Regulators CHARLES BAKER, TAO JIA, RAHUL KULKARNI, Virginia Polytechnic Institute and State University — New research indicates that post-transcriptional regulators, such as small RNAs (sRNAs), are key components of global regulatory networks. In particular, it has been discovered that these networks often comprise multiple sRNAs which control expression of a critical master regulator protein. However, the regulation of a single protein by multiple sRNAs is not currently well understood and the impact of multiple sRNA on stochastic gene expression remains unclear. To address these issues, we analyze a stochastic model of regulation of gene expression by multiple sRNAs. We derive exact closed form solutions for the regulated protein distribution, including compact expressions for its mean and variance. The derived results provide novel insights into the roles of multiple sRNAs in fine-tuning the noise in gene expression. In particular, we show that, in contrast to regulation by a single sRNA, multiple sRNAs provide a mechanism for independently controlling the mean and variance of the regulated protein distribution.

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