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Stochastic models of gene expression and post-transcriptional regulation HODJAT PENDAR, Department of Engineering Science and Mechanics, Virginia Tech, RAHUL KULKARNI, TAO JIA, Department of Physics, Virginia Tech — The intrinsic stochasticity of gene expression can give rise to phenotypic heterogeneity in a population of genetically identical cells. Correspondingly, there is considerable interest in understanding how different molecular mechanisms impact the 'noise' in gene expression. Of particular interest are post-transcriptional regulatory mechanisms involving genes called small RNAs, which control important processes such as development and cancer. We propose and analyze general stochastic models of gene expression and derive exact analytical expressions quantifying the noise in protein distributions [1]. Focusing on specific regulatory mechanisms, we analyze a general model for post-transcriptional regulation of stochastic gene expression [2]. The results obtained provide new insights into the role of post-transcriptional regulation in controlling the noise in gene expression.

[1] T. Jia and R. V. Kulkarni, *Phys. Rev. Lett.*,**106**, 058102 (2011)
[2] T. Jia and R. V. Kulkarni, *Phys. Rev. Lett.*, **105**, 018101 (2010)

Rahul Kulkarni
Department of Physics, Virginia Tech

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