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Stochastic modeling of protein-based post-transcriptional regulation TAO JIA, RAHUL KULKARNI, Virginia Tech — Recent experiments have enabled monitoring gene expression in living cells at the level of single proteins. Data from such experiments for protein burst-size distribution and burst frequency can be used to obtain analytical expressions for the steady-state protein distribution across a population. We extend this analysis to the case of modulation of gene expression by binding/unbinding of a post-transcriptional regulatory protein. Closed-form analytical expressions and results from stochastic simulations will be presented. In the case that regulator binding results in complete repression of protein expression, the steady-state protein distribution has the same functional form as the unregulated case, once the mRNA degradation rate is appropriately renormalized. For the general case, wherein binding can result in partial repression or even activation of protein expression, we derive an analytical expression for the steady-state distribution which generalizes the result for the unregulated case.

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