

Abstract Submitted
for the MAR11 Meeting of
The American Physical Society

Regulation of gene expression by small RNAs via coupled stoichiometric degradation: a variational approach THIERRY PLATINI, Virginia Bioinformatics Institute, TAO JIA, RAHUL V. KULKARNI, Department of Physics, Virginia Tech — Regulatory genes called small RNAs (sRNAs) are known to play critical roles in cellular responses to changing environments. For several bacterial sRNAs, regulation is effected by coupled stoichiometric degradation with messenger RNAs (mRNAs). The nonlinearity inherent in this regulatory scheme implies that exact analytical solutions for the corresponding stochastic models are intractable. Based on the mapping of the master equation to a quantum evolution equation, we use the variational method (introduced by Eyink) to analyze a well-studied stochastic model for regulation by sRNAs. Results from the variational ansatz are in excellent agreement with stochastic simulations for a wide range of parameters, including regions of parameter space where mean-field approaches break down. The results derived provide new insights into sRNA-based regulation and will serve as useful inputs for future studies focusing on the interplay of stochastic gene expression and regulation by sRNAs.

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Date submitted: 16 Dec 2010

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