Abstract Submitted
for the MAR16 Meeting of
The American Physical Society

Deterministic and Stochastic Modeling of an Artificial Bistable Switch in E. coli DANIEL FINKELSTEIN, East Chapel Hill High School and Duke University, NICOLAS BUCHLER, SARGIS KARAPETYAN, Duke Universtity — Networks of mutually interacting genes are common in natural regulatory networks. To better understand these interactions, scientists have recently been constructing artificial genetic networks. Much of the effort is focused on creating genetic oscillators and bistable switches. In this project, we analyzed the possibility to create a bistable switch in E. coli. In this realization of the switch, the Repressor (basic leucine zipper CEBP/alpha) represses the transcription of the Inhibitor (artificial dominant negative 3HF). The Inhibitor, in turn, sequesters the Repressor by binding to it. Using deterministic modeling we identified a range of parameters suitable for bistability. We then analyzed the resulting solutions with the full model taking the reaction rates corresponding to E. coli and the including stochastic nature of gene expression. We have shown that the bistability in not destroyed by stochastic fluctuations if several copies of genes are present. Specifically, taking a realistic number of plasmids (10) we show that the number of proteins in the systems undergoes sizable fluctuations; however, the two states with low and high concentrations of inhibitor stay distinct in the relevant range of parameters.

gleb finkelstein
Duke Universtity

Date submitted: 06 Nov 2015 Electronic form version 1.4