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Modeling Epigenetic Silencing

Anirvan Sengupta

*Department of Physics and Astronomy
Rutgers, The State University of New Jersey
136 Frelinghuysen Road
Piscataway, NJ 08854-8019
USA
anirvans@physics.rutgers.edu*

Abstract

We formulate a mathematical version of the conventional model of maintenance of silencing in *S. cerevisiae* and analyze the conditions for bistability as well as for formation of stationary boundaries. Although the model is perhaps too simple, the structure of the bifurcation diagram, describing parameter regions with different kinds of qualitative behavior, is likely to be more robust. We can place some of the known mutants in different regions of this diagram. One interesting finding of this study is that, under some conditions, the lowering of acetylation rates might have non-obvious consequences for silencing. Possible improvements of the model as well as experimental tests are discussed at the end.