1027-92-66   **Tomas Gedeon*** (`gedeon@math.montana.edu`), Department of Mathematical Sciences, Bozeman, MT 59715, and **Kate Rardin** (`rardin@montana.edu`), Department of Mathematical Sciences, Bozeman, MT 59715. *Modelling the stability and robustness of lysogen in the bacteriophage* λ. Preliminary report.

Bacteriophage λ is the best studied example of a gene regulation switch. The phage-infected cell can follow lytic pathway which leads to production of new phages and lysis of the cell. Alternatively, the infected cell can follow lysogenic pathway, in which the virus establishes stable association with the host. In the last 20 years a number of experiments elucidated gene regulation mechanisms that are behind the choice of alternative states and their maintence.

In this work we study bifurcation structure of model due to Mackey and Santillian, which is based on Ackers chemical equilibrium description of the promoter binding by the regulatory factors. We describe how the model captures results of perturbation experiments which removed some feature of the switch mechanism. After establishing correspondence between the model and the experiments, we use the model to predict outcome of some experiments, which biologists were (so far, and for technical reasons) unable to not perform. (Received February 14, 2007)

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