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**Arcady Ponosov\*** (arkadi@umb.no), UMB/IMT, P.O.Box 5003, 1432 Aas, Norway, **Yuriy Nepomnyashchikh**, Maputo, Mozambique, **Andrei Shindiapin**, Maputo, Mozambique, and **Irina Shlykova**, Aas, Norway. *Gene regulatory networks with delay effects.*

A mathematical framework to study gene regulatory networks with time-delay effects, which is based on delay differential equations, is suggested and outlined. An essential feature of the gene regulatory networks is their “almost Boolean” structure, where the dynamics are governed by sigmoid-type nonlinearities which are close to the step functions. This is due to the fact that genes are only activated if certain concentrations are close to the respective threshold values. The delay effects arise from the time required to complete transcription, translation and diffusion to the place of action of a protein.

Any mathematical model describing such networks faces a problem of how to study the dynamics in the vicinity of the thresholds. A method of localizing stationary points and local stability analysis near the thresholds in the presence of delays is offered. The basic technical tools, which are systematically applied within the suggested framework, combine a special modification of the well-known “linear chain trick” with the perturbation analysis.

Some properties of gene regulatory networks with delay in comparison with the non-delay model are discussed as well.

The results are illustrated by a number of examples. (Received January 13, 2008)