Modelling and Analysis of MiRNA Regulation

Svetoslav G. Nikolov[1,2,3]
[1] Institute of Mechanics, Bulgarian Academy of Sciences, Acad. G. Bonchev Str., bl. 4, 1113 Sofia, Bulgaria
[2] Department of Systems Biology and Bioinformatics, University of Rostock, 18051 Rostock
[3] University of Transport, Geo Milev Str., 158, 1574 Sofia, Bulgaria
S.Nikolov@imbm.bas.bg

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MicroRNAs (miRNAs) are endogenous small non-coding RNA molecules (typically $\approx$ 22nt size in human) that regulate gene expression by binding to target messenger RNAs (mRNA) and including translational repression, cleavage or destabilization of the target. MiRNA regulation has direct implications for fundamental biology - disease etiology and treatment. It is well-known that the processes related to gene expression (transcription and translation) induce time delays in the response of biochemical systems. In this context, the interplay between gene transcription and translation time delay and the miRNA synthesis delay (miRNA biogenesis) can have important consequences on the timing and dynamics of expression patterns for miRNA-repressed genes.

In this article, a nonlinear mathematical model with three discrete time delays is used to investigate the complex dynamics of the gene expression regulated by the miRNA. Using a specific theoretical approach (obtained in (Nikolov, 2013)) and Hopf bifurcation theorem it is predicted the occurrence of a limit cycle bifurcation for the time delay parameters. From the accomplished analytical results and numerical simulations, it is becomes clear that time delays have destabilization dynamical role, as for some specific numerical values of the model parameters a complex (non-regular) behavior of the model is demonstrated.

References

[1] S. Nikolov, *Stability and Andronov-Hopf bifurcation of a system with three time delays*, Journal of Mathematics **2013** art. ID 347071 (11 pages), 2013.