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STEADY-STATE PROPERTIES OF CYTOSINE METHYLATION AND DEMETHYLATION MODEL

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ABSTRACT

Epigenetic changes, apart from changes in the DNA sequence, are one of the most important factors determining the fate of cells in living organisms. The main epigenetic change is cytosine methylation in relevant regions of DNA. Recently, we published an article [1] in which we proposed a mathematical model of cytosine methylation and demethylation. In the presentation, we show an equilibrium analysis of this model. We present the conditions for its stability and aperiodic nature of the system's free response. In particular, we focus on the influence of the levels of enzymes involved in cytosine methylation and demethylation on the equilibrium coordinates. The conclusions from this analysis are important in understanding the biological basis of the behavior of cells in living organisms.

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REFERENCES

- [1] K. Kurasz, J. Rzeszowska-Wolny, R. Oliki, M. Foksiki, and K. Fajarewicz: *The Role of Different TET Proteins in Cytosine Demethylation Revealed by Mathematical Modeling*, *Epigenomes* **8(2):18** (2024), DOI 10.3390/epigenomes8020018.