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Topological-numerical analysis of the discrete-time two-gene Andrecut-Kauffman model

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We analyze the behavior of a gene expression model first introduced by Andrecut and Kauffman [1]. We identify chaotic and ordered dynamics using maximal Lyapunov exponent and perform numerical simulations for a wide range of parameters. We find parameter values resulting in the presence of multiple attractors, which have the potential for representing real-world phenomena [2]. Moreover, we obtain Morse decomposition of the system by utilizing a rigorous numerical algorithm. We compute isolating neighborhoods of attractors as well as unstable sets, providing a birds-eye view of the dynamics present in the system. We gain further insight into the model by computing Conley indices for the isolating neighborhoods, which are visualized using comprehensive Conley-Morse graphs. Our results showcase the utility of topological methods in analyzing complex biological systems and their advantages over simpler numerical simulations.

[1] M Andrecut and S A Kauffman. Chaos in a discrete model of a two-gene system. *Phys. Lett. A* **367(4-5)** (July 2007), 281–287. `https://doi.org/10.1016/j.physleta.2007.03.074`

[2] Mikołaj Rosman, Michał Palczewski, Paweł Pilarczyk, Agnieszka Bartłomiejczyk. Bistability and chaos in the discrete two-gene Andrecut-Kauffman model. *Discrete and Continuous Dynamical Systems - B* **30(11)** (2025), 4442–4461. `https://doi.org/10.3934/dcdsb.2025028`