Krajowa Konferencja Zastosowań Matematyki w Biologii i Medycynie

Zdynia, 17th–21st September 2024

EXPLORING CHAOTIC DYNAMICS IN GENE EXPRESSION MODEL

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ABSTRACT

In the context of genetic regulatory networks, the interplay between genes and proteins orchestrates the activation or inhibition of gene expression. Transcription factors, proteins that bind to specific regulatory sites known as promoters on DNA, play a pivotal role in this process. They can modulate the transcription of other transcription factors as well as their own.

Andrecut and Kauffman [1] proposed a simplified model where transcription and translation are merged into a single reaction: RNA polymerase binding to the promoter site, resulting in the production of both mRNA and protein monomers. Within this framework, the dynamic relationships between the expression levels of two genes, denoted as x and y, is illustrated in terms of their interactions and feedback mechanisms:

$$
\begin{aligned}
x_{t+1} &= \frac{\alpha}{1+(1-\varepsilon)x_t^n+\varepsilon y_t^n}+\beta x_t \\
y_{t+1} &= \frac{\alpha}{1+\varepsilon x_t^n+(1-\varepsilon)y_t^n}+\beta y_t.
\end{aligned}
$$

To further explore the dynamics of the model and unveil novel behaviours, we introduce a slight modification by relaxing the assumption of a uniform α parameter across genes. By allowing distinct values of α for each gene, we observe different behaviours and chaotic dynamics within the model.

By employing an array of numerical methods we perform a qualitative analysis of the behaviour of the system under various parameter values. We consider Lyapunov spectra to partition the extended parameter space into regions corresponding to chaotic, hyperchaotic and stable states of the model. Complex relationships governing the system are visualised using bifurcation diagrams and parameter planes.

Furthermore, we present limitations of global metrics, such as the maximal Lyapunov exponent, when applied to this model. We reveal how the system's dynamics can be strongly influenced by initial conditions for a fixed choice of parameters, including strange attractors coexisting with stable orbits in the state space. Successful detection and classification of such nuanced behaviours requires a significantly more cautious approach than for systems with uniform dynamics.

Lastly, we assess the feasibility of using genetic regulatory network simulations as predictive tools for physical systems and outline potential applications of these simulations in real-world scenarios.

REFERENCES

[1] M. Andrecut and S. Kauffman: *Chaos in a discrete model of a two-gene system*, Phys. Lett. **A 367** (2007), 281-287.