

Exploring Chaotic Dynamics in Gene Expression Model

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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:

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

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.

References

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

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