Can Mathematics Explain Fish Skin Patterns? A Turing Pattern Simulation Investigation

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Abstract

The diffusive aspect of morphological pattern formation, specifically on the Mbu puffer fish, was investigated by modelling the reaction-diffusion system of two skin pigmentation chemicals with the Brusselator. The evolution of the system in time was simulated using a combination of the finite differences and Euler methods with random initial chemical concentrations. By performing non-linear stability analysis on the system, a range over which to vary a bifurcation parameter was found, and the Mbu puffer fish skin pattern was successfully reproduced with a bifurcation parameter of $B = 7.5$, along with two other distinct patterns with bifurcation parameters of $B = 6.9$ and $B = 16.9$ respectively (with fixed parameters of $A = 4.5$, $D_U = 1$, and $D_V = 8$).

Introduction

Morphogenesis is the process during which tissues develop into patterns and shapes [1]. One of the first mathematical descriptions of how physical processes create these biological patterns was formulated in 1952 by English mathematician and computer scientist, Alan Turing [2]. He defined reaction-diffusion systems, the solutions of which resembled those created by morphogenesis in nature. These reaction-diffusion systems are mathematical models that correspond to various physical phenomena and have the form of semi-linear parabolic partial differential equations. They are especially applicable for the study of the spatial and time evolution of the concentration of chemicals because they describe reactions, during which substances are transformed into each other, and the effect of diffusion, which causes their movement on the spatial domain. Due to a small perturbation in an initially homogeneous spatial equilibrium state, these reaction-diffusion models can create stable spatial patterns, a phenomenon known as Turing instability [3]. The various self-organised shapes created as the solutions of these reaction-diffusion equations have been named Turing patterns, and are nowadays widely used in computer science to model the skin pigmentation pattern of animals [4].

The aim of this project was to find initial parameters that, after an arising Turing instability, create a pattern similar to the skin pigmentation of a Mbu pufferfish. Although there are several different reaction-diffusion models that describe Turing instabilities, in this project one of the simplest ones was used, called the Brusselator. This model was first proposed by Ilya Prigogine and his collaborators at the Université Libre de Bruxelles in 1968 [5]. A realistic system of equations would be very complicated, that is why they are replaced by a simplified set of equations, which are still effective in reproducing the observed patterns [6].

Theory

The Brusselator model for a reaction-diffusion system is a type of activator-inhibitor model based on the following reactions [5]:

$$\begin{aligned} A &\to U, \\ 2U + V &\to 3U, \\ B + U &\to V, \\ U &\to E, \end{aligned} \tag{1}$$

where the concentrations of A and B remain constant. It contains an activator U and an inhibitor V. In this case, U works to pigment the skin and promote the production of both itself and V. V works to inhibit the skin pigmentation caused by U. This means a small initial disturbance producing U quickly leads to a large increase in the concentrations of U and V. V then diffuses outwards, creating maxima of skin pigmentation contained within a characteristic length limited by the diffusion rate of V [7]. For this reason, the diffusion rate of V must be much larger than that of U. Based on these reactions, the kinetic equations with diffusion for the Brusselator model are given below:

$$\begin{aligned} \frac{\partial U}{\partial t} &= D_U \nabla^2 U + A - (B+1)U + U^2 V, \\ \frac{\partial V}{\partial t} &= D_V \nabla^2 V + BU - U^2 V, \end{aligned} \tag{2}$$

where U and V are the concentrations of the activator and inhibitor respectively, the concentrations A and B act as bifurcation parameters to be fixed and/or varied to produce different patterns, and the diffusion coefficients D_U and D_V define the relationship between the flux of U and V and their concentration gradient over a space according to Fick's law of diffusion.

The Brusselator system has a steady-state $U = A$, $V = B/A$. The evolution of small perturbations u, v of this state ($U = A + u$, $V = B/A + v$) is given by the linear equation $\partial_t \vec{x} = L\vec{x}$, where

$$L = \begin{pmatrix} D_U \nabla^2 + B - 1 & A^2 \\ -B & D_V \nabla^2 - A^2 \end{pmatrix} \quad \text{and} \quad \vec{x} = \begin{pmatrix} u \\ v \end{pmatrix}, \tag{3}$$

which has solutions of the form $\vec{x}_0 e^{\omega t + i\vec{k}\cdot\vec{r}}$. The amplitude $\vec{x}_0$ is not zero precisely when $|L - \omega I| = 0$. Turing bifurcation occurs when one of the roots of this quadratic equation vanishes [8], which happens if B is not smaller than the critical value B_c^T:

$$B \geqslant B_c^T = \left(1 + A\sqrt{\frac{D_U}{D_V}}\right)^2, \tag{4}$$

at which point stable patterns will form.

Computer simulation allows us to investigate (with suitable precision) the evolution of the system over time using the Euler method. With randomised initial concentrations, the equations for U and V are iterated over a large number of time steps of size δt which must be sufficiently small to preserve the stability of the simulation:

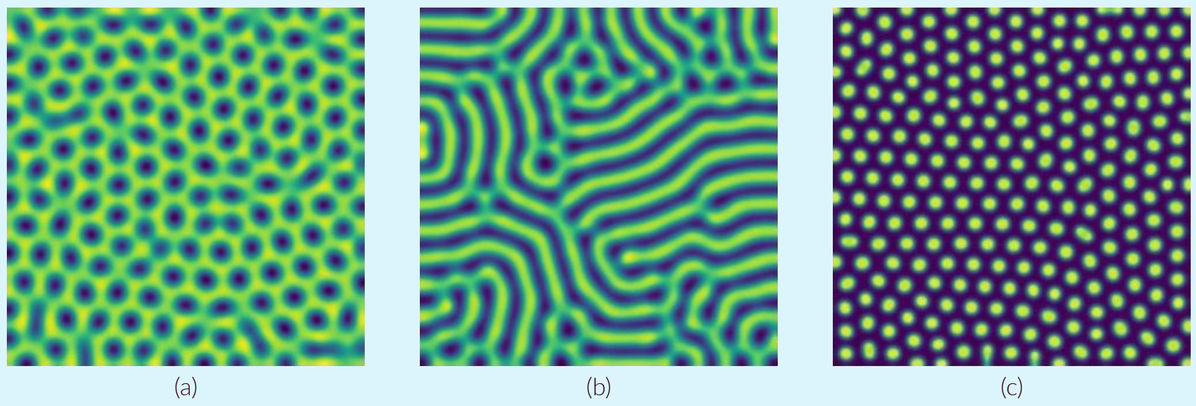
$$\begin{aligned} U(t + \delta t) &\approx U(t) + (D_U \nabla^2 U + A - (B+1)U + U^2 V)\delta t, \\ V(t + \delta t) &\approx V(t) + (D_V \nabla^2 V + BU - U^2 V)\delta t, \end{aligned} \tag{5}$$

wherein we have discretised the Laplace operator ∇^2 using the finite differences method with spatial step size h, applying Neumann boundary conditions which require that U and V have zero flux at the boundaries:

$$\nabla^2 f(x,y) \approx \frac{f(x-h,y) + f(x+h,y) + f(x,y-h) + f(x,y+h) - 4f(x,y)}{h^2}. \tag{6}$$

Results

A value of $B_c^T = 6.7$ was calculated with $A = 4.5$, $D_U = 1$ and $D_V = 8$. The simulation was then run for 200 randomised initial U and V concentrations over a period of 100 seconds (with $\delta t = 0.001$), varying B over the range $6.8 < B < 20.8$. The QR code in the top right corner shows the evolution of the patterns as B is varied. Over this range, three distinct patterns were found, seen below in Figure 1.



(a) (b) (c)

Figure 1. Chemical concentration patterns produced from simulations of Brusselator model with varied values of B (fixed $A = 4.5$, $D_U = 1$, $D_V = 8$). For (a) $B = 6.9$, for (b) $B = 7.5$ and for (c) $B = 16.9$.

A pattern of hexagonal cells was observed for B values near critical instability, as shown in Figure 1a, and a dotted pattern when $B \gg B_c^T$, shown in Figure 1c. At a value of $B = 6.9$ a labyrinth-like pattern was observed, shown in Figure 1b, which was the most recognisably puffer fish-like, see Figure 2.

Discussion

The simulation successfully reproduced a pattern similar to the skin pigmentation of a Mbu pufferfish. The similarity between the simulated pattern and the real fish images indicates that the model captures important features of the biological system. The reproduction of other distinct patterns suggests the Brusselator model could be a useful tool for studying morphogenesis in other species as well.

Figure 2. Skin pigmentation on the Mbu pufferfish, side [9] and front [10].

While the Brusselator is a simple and effective reaction-diffusion model for reproducing observed patterns, there are other models that can be used for similar simulations. For example, the Gray-Scott model is another well-known reaction-diffusion model that has been used to simulate various patterns, including those found in zebrafish skin. Results obtained using the Brusselator and Gray-Scott models could be compared to see how they differ in terms of pattern formation and accuracy in reproducing observed biological patterns.

It should be noted that the simulation only captures the skin pigmentation pattern and does not take into account other factors that might affect morphogenesis, such as gene expression. Another model that has been used for simulating fish skin patterns is the reaction-diffusion model with directional feedback, which incorporates both chemical diffusion and mechanical interactions between cells. This model has been shown to produce more realistic and intricate patterns than the Brusselator, but it is also more difficult to analyze and interpret.

Additionally, the use of higher-order numerical methods for discretising the Laplacian and iterating the equations, such as finite element methods or spectral methods, would improve the accuracy and efficiency of the simulation.

Conclusion

Despite the relative success in pattern reproduction through simulation, further analysis could include exploring the evolution of the system with non-uniform initial conditions and comparing results to other biological systems using different models such as the Gray-Scott model. The accuracy and efficiency could be improved by using higher-order numerical methods for discretising the Laplacian, and the role of different chemical species and their interactions in the pattern formation process could also be investigated.

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