Turing Stability and Natural Pattern Formation in the Gray-Scott Reaction-Diffusion System

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ABSTRACT

This paper examines the Gray-Scott model, a coupled system of nonlinear reaction-diffusion equations recognized for its capacity to produce intricate patterns. Our focus is on performing a Turing stability analysis to understand the conditions under which spatially heterogeneous structures emerge. By exploring the dynamics of the model under various parameter regimes, we demonstrate how the resulting patterns closely resemble those found in nature, such as animal coat markings, seashell textures, and chemical oscillations. The sensitivity of the model to its parameters reveals a rich spectrum of behavior, highlighting the profound connection between mathematical models and natural pattern formation.

Key words:
Reaction-Diffusion Systems, Turing Stability, Gray-Scott Model, Pattern Formation, Nonlinear Dynamics, Mathematical Biology

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INTRODUCTION

The contemporary theory of pattern generation originates from Turing's groundbreaking 1952 study, it employed linear analysis to define boundary criteria for the instability of spatially homogeneous equilibrium in typical two-component reaction-diffusion systems. Nonetheless, Turing's technique is confined to forms that are almost uniform in spatial distribution. Because spike-type solutions are common in many reaction-diffusion systems, it is difficult to predict their stability and behavior. Because the tuning method is not applicable in spike solutions, the stability and dynamics of these solutions are the main emphasis of this work (Diez et al., 2024).

A more recent requirement for formation of patterns was proposed by Gierer and Meinhardt (Gierer & Meinhardt, 1972) along with independently by Segel and Jackson (Segel & Jackson, 1972) they postulate that the following two conditions are necessary for pattern formation: local self-enhancement and long-range repression. Let us demonstrate how these two requirements are built into Gray-Scott models. In contrast, the Gray-Scott approach is classified in the category of activator-substrate system (Meinhardt & Gierer, 2000).

A comparable logic applies to the Gray-Scott model, where spike-type patterns arise given that D_u/D, is minimal. Note that these assumptions are in keeping with the primary work of Turing, where the unsteadiness was produced given that the ratio of the diffusion rate coefficients is either big or appropriately small (McGough & Riley, 2004).

A Brief Outline of the Gray-Scott Model

Two chemical species U and V are present in the reaction-diffusion system discussed here and variables u and v denote the concentration of these species at a specific location in space. As a result of their reaction, the two chemicals spread throughout the medium. Thus, the U and V degrees at any one place change with time and may not be the same as those at other locations (Madzvamuse et al., 2017).

The Gray-Scott model is a non-linear reaction-diffusion model of two chemical species U and V with the reactions are given by:

$U + 2V \rightarrow 3V$

$V \rightarrow P$

In this context P is considered an internal product. To keep things straightforward, reverse reactions are ignored, this makes sense in scenarios where a steady input of reactants stops the system from reaching equilibrium. Notably, V acts like a catalyst because it appears in both the reactants and the products of the primary reaction. The system's dynamics are governed by two key equations that describe how both U and V are generated and consumed through three main mechanisms:

$$\frac{\partial u}{\partial t} = D_u \nabla^2 u - uv^2 + F(1-u) \qquad (1)$$

$$\frac{\partial v}{\partial t} = D_v \nabla^2 v + uv^2 - (F+K)v \qquad (2)$$

Where $u = [U]$ represents U's concentration and $v = [V]$ represents V's concentration.. For the purpose of convenience, we think of D_u, D_v, F and K to be constants. Time and spatial quantization constants (Δt and Δx)are also employed in computer simulations to divide ∂t and ∇^2 and V into discrete intervals.

The pace at which the quantity u climbs is represented by the first equation. The equation consists of three components. The first term, $D_u \nabla^2 u$ represents diffusion. It indicates that the concentration of u changes in proportion to its Laplacian (a second-order spatial derivative capturing how much the local variation in the gradient) of u. When neighboring areas contain more U, the value of u increases. Conversely, if nearby concentrations are lower, the diffusion term($\nabla^2 u$) becomes negative, causing u to decrease. If we made an equation for u with only the first term, we would have $\frac{\partial u}{\partial t} = D_u \nabla^2 u$, which is a diffusion only system equivalent to the heat equation.

The second term $-uv^2$ represents the rate of reaction. This process requires one U molecule and two V molecules and it proceeds at a rate proportional to the square of the V concentration times the U concentration. Additionally, it changes U into V, thus a rise in v equals a fall in u (as shown by the positive $-uv^2$ in the second equation). There is no constant on the reaction terms, but the relative strength of the other terms can be adjusted through the constants D_u, D_v, F and K, and the choice of the arbitrary time unit implicit in ∂t. The third term, $F(1-u)$ is replenishment term. Since the reaction uses up U in order to create V, its concentration would totally drop in the absence of a source to replenish u. With F denoting the feed or supply rate of replenishment, this term raises u proportionately to its distance from the maximum value of 1.

The region where the reaction takes place in the systems this equation is modeling is physically close to a large supply of U and is isolated from it by a barrier that restricts its flow, resembling a semi-permeable membrane. Resupply occurs through diffusion across the membrane, driven by the concentration difference of $\Delta[U]$ on either side. The value 1 represents the concentration of U at the source, and F denotes the membrane's permeability.

Circulation or cells in-to a nearby layer of tissue that constantly create the essential chemical or chemicals at rates regulated by enzymes might offer this "supply" in systems of life, like the skin of a growing embryo.

The main distinction between the two equations lies in the third term: one includes $F(1-u)$, while the other features $(F+K)v$. In the equation for v, the third term represents a decay or diminishment factor. Without this term, the concentration of V could grow indefinitely. Although V can accumulate over time without immediately hindering its own production, it eventually diffuses out of the system through a process similar to how fresh U is supplied. The decay term depends both on the current level of V and the combined values of the constants F and K. Here, F again represents the membrane's permeability to U, while K indicates the difference in permeability rates between U and V.

In the original stirred tank model, the symbol "F" stands for "feed" or "flow," indicating the rate at which pure U is added to the tank. The reaction $V \rightarrow P$ happens at a rate represented by K, which Karl Sims refers to as the "kill" rate. This reaction converts some of the V chemical into P, effectively removing V, which is why the term $K \times v$ is subtracted in the second equation.

The tank itself neither fills up nor empties; instead, liquid leaves through an outlet at the same rate it enters. The outflow of U is represented by the term $-F \times u$ in the first equation, while $-F \times v$ serves the same role in the second equation. Since the tank is well-stirred, the outflow is a mixture of u, v and P whose total volume equals one unit the amount of U pumped in during a given time period. The concentration of each chemical in the outflow reflects their current proportions inside the tank.

If the tank contains concentrations u, v and p of the chemicals U, V and P respectively, then their sum is always $u+v+p=1$(where 1 represents 100% concentration). Each concentration must be between 0 and 1 never negative or exceeding 1. Because the three values sum to one, there are effectively two degrees of freedom. The possible values of u and v lie within a triangle defined by the points where (u,v)=(0,0), (u,v)=(0,1) and (u,v)=(1,0).

FIGURATIVE REPRESENTATION OF GRAY-SCOTT MODEL

The Gray-Scott model is used to simulate the reaction and diffusion of two virtual compounds on a 2D grid (Amin & Mashat, 2021):

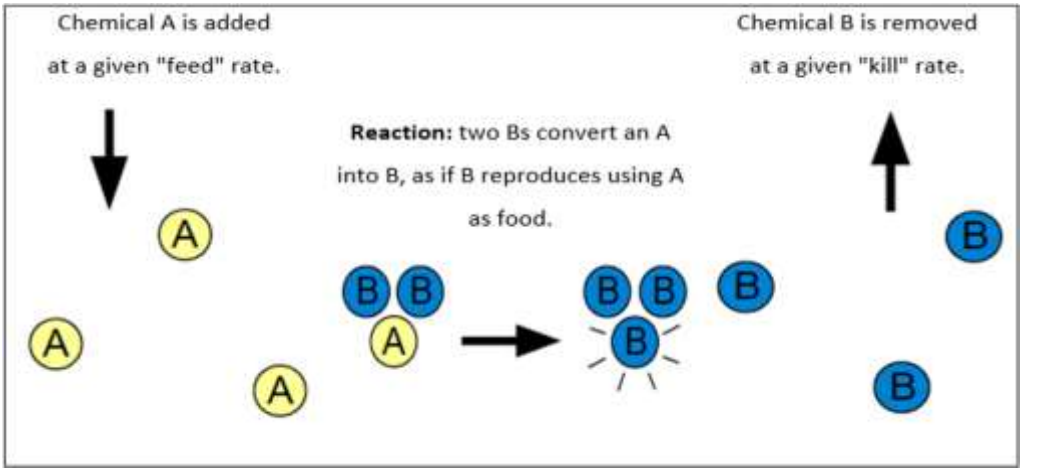


Figure 1: Explanation of Gray-Scott Model for the chemicals A and B.

Linear Stability Analysis:

Next, we will identify the steady states and perform a linear stability analysis of the Gray-Scott model. When diffusion is ignored (D_u=D_v=0), the system typically reaches a steady state where ($\frac{\partial u}{\partial t} = \frac{\partial v}{\partial t} = 0$) commonly at the point (u,v)=(0,0). Additionally, there are two other fixed points, which can be found by solving the following equations (Al-Bayati et al., 2008):

$$u_{1,2} = \frac{1}{2}\left[1 \pm \sqrt{1 - 4\frac{(F+K)^2}{F}}\right] \quad (3)$$

$$u_{1,2} = \frac{F}{2(F+K)}\left[1 \pm \sqrt{1 - 4\frac{(F+K)^2}{F}}\right] \quad (4)$$

This implies that these exist if $F \geq 4(F+K)^2$, meaning that the interior of the parabolic region is defined by $F = \frac{1}{2}\left[\left(\frac{1}{4} - 2K\right) \pm \sqrt{\frac{1}{16} - K}\right]$.

The point (1, 0) is always a steady state. To determine the stability of the remaining two fixed points, one can examine the eigenvalues of the Jacobian matrix evaluated at those locations.

$$\begin{bmatrix} -(F + v^2) & -2uv \\ v^2 & -(F + K) + 2uv \end{bmatrix}$$

$$= \begin{bmatrix} -(F + v^2) & -2(F + K) \\ v^2 & -(F + K) \end{bmatrix}$$

Now the determinant is $\Delta = (v^2 - F)(F + K)$ and the trace $\boldsymbol{\tau} = -(v^2 - K)$. With these shorthand notations, the eigenvalues are

$$\lambda_{1,2} = \frac{1}{2}\left[\tau \pm \sqrt{\tau^2 - 4\Delta}\right] \quad (5)$$

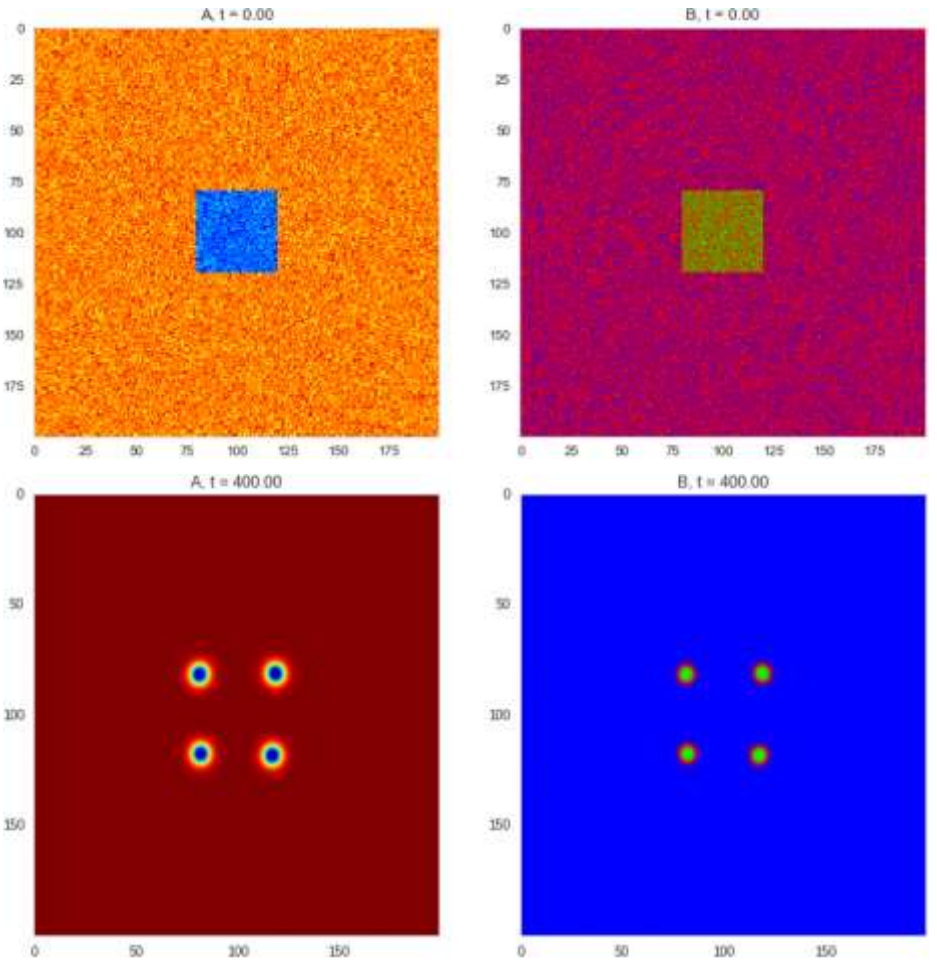
SPATIAL PATTERN IN THE GRAY-SCOTT MODEL

The response and dispersion of chemical entities may form a variety of patterns reminiscent of the ones observed in nature. The Gray-Scott equations represent this reaction (Lee et al., 1993).

Numerous numerical techniques are used to simulate the modeling of partial differential equations that represent this process. Even using a simple approach like forward finite-difference equations that arise from the spatial discretization of the Laplacian, we may anticipate respectable results. We have used the explicit finite difference method to numerically explore the problem. This method is clear and easy to implement in Python using all this information (Amin & Mashat, 2021).

In the following figure we see that some astonishing patterns arises in our nature by using Mathematical model. We use the irreversible Gray-Scott model and see that different values of the parameter setting creates some sports and stripes pattern which we showed in natural environment. Here we find the bacterial growth pattern, coral pattern, finger print pattern, and the worms' pattern can be imitated by using a Turing model.

Bacteria:



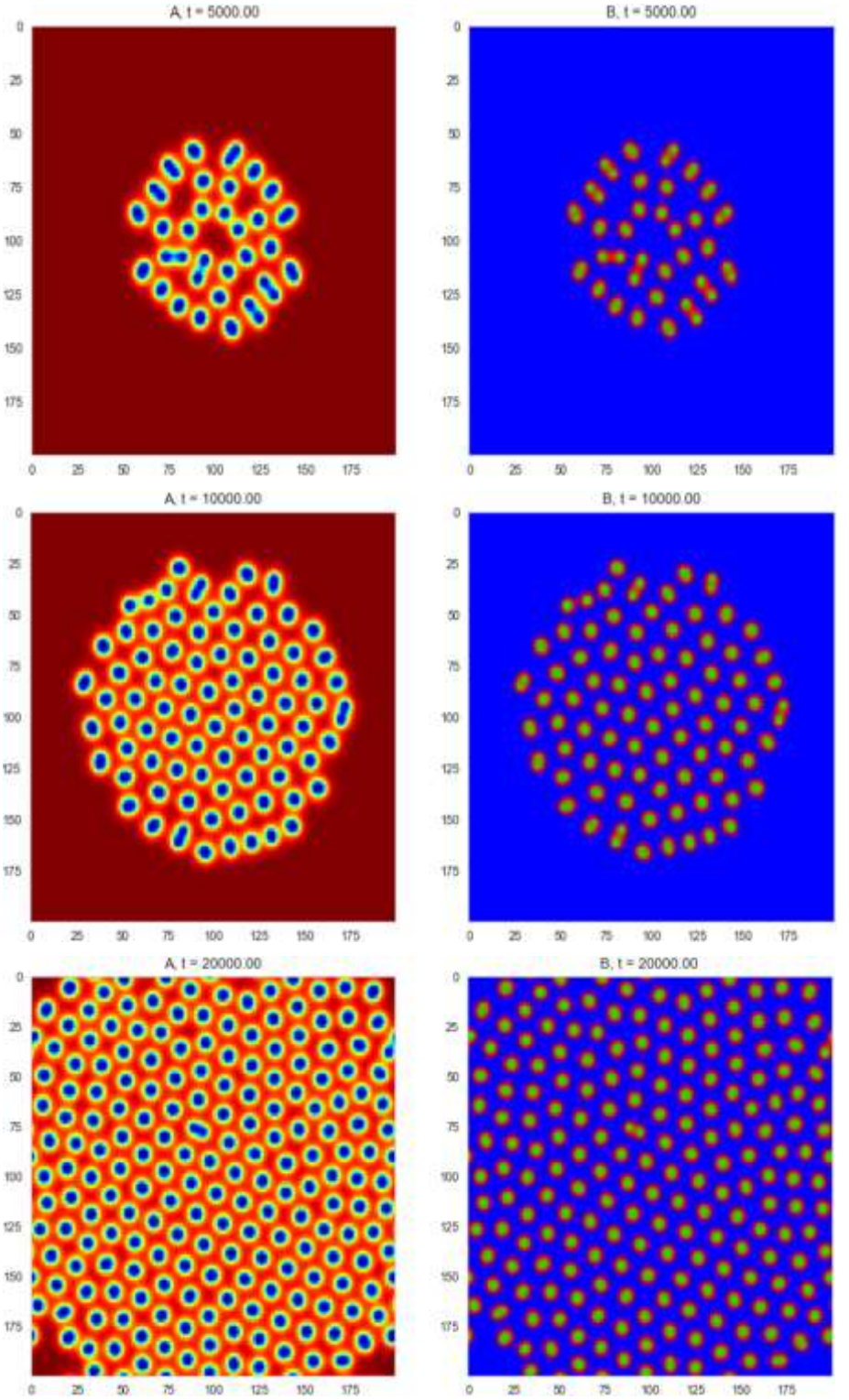
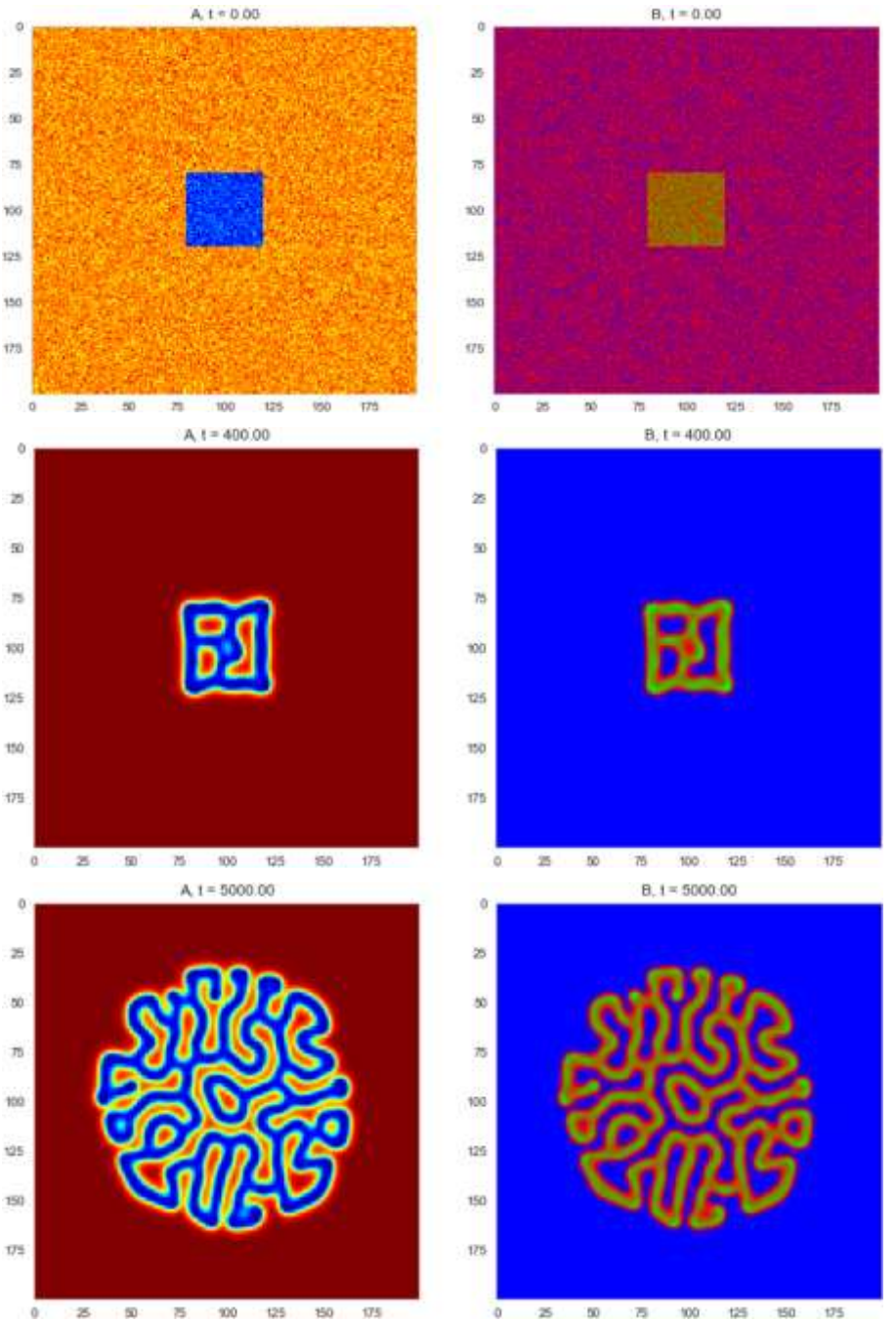

A, t = 5000.00
B, t = 5000.00
A, t = 10000.00
B, t = 10000.00
A, t = 20000.00
B, t = 20000.00
0
25
50
75
100
125
150
175

Figure 2: Time evolution of the concentration profile and formation of Bacterial growth pattern. Simulation of Gray-Scott Model using finite difference approximation for D_u=0.16, D_v = 0.08, F=0.035, K=0.065.

Coral:



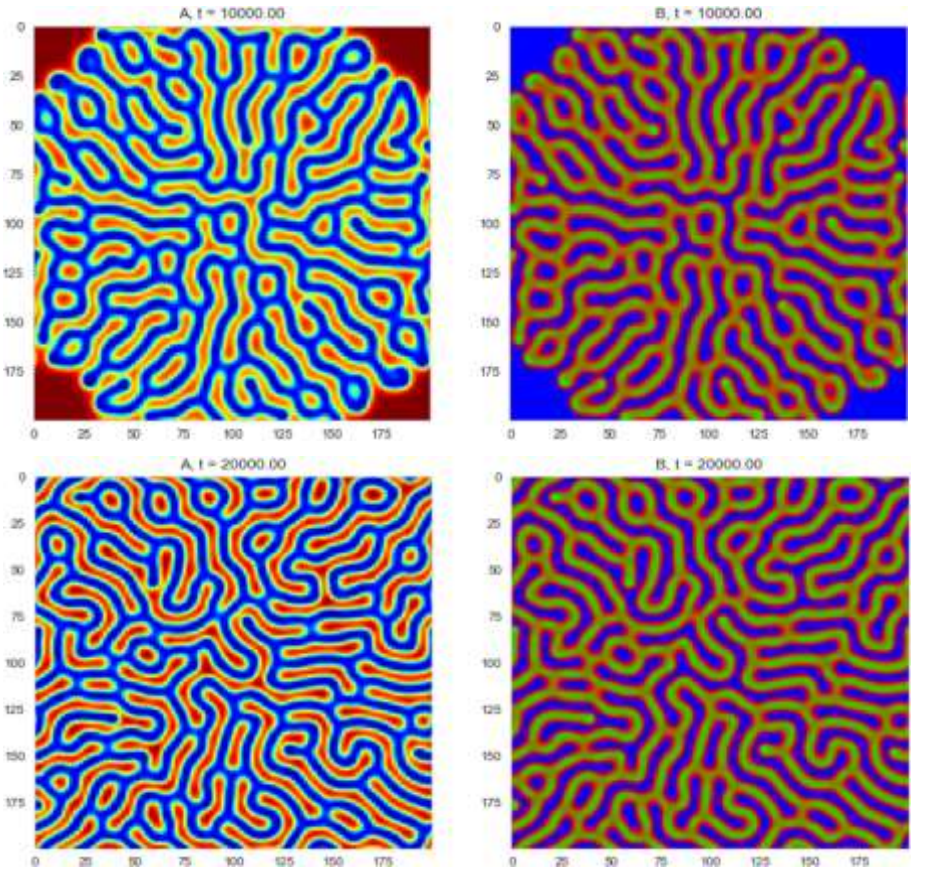
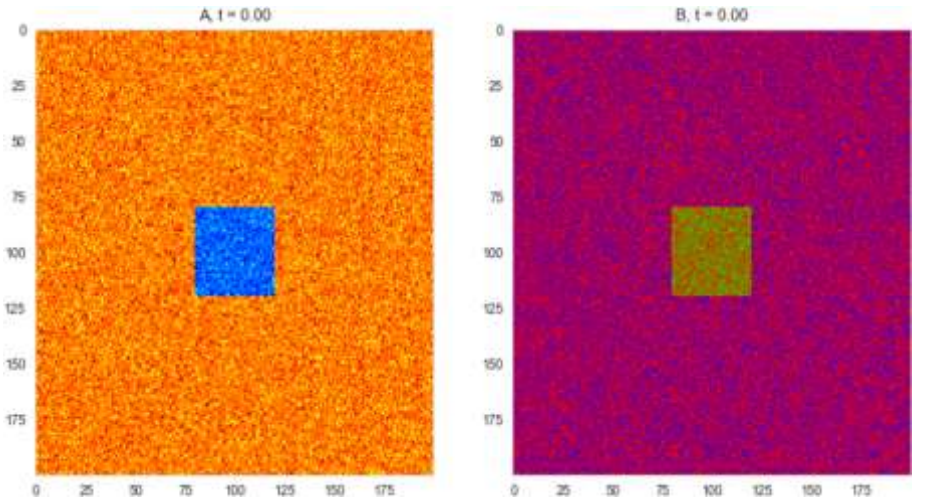


Figure 3: Time evolution of the concentration profile and formation of Coral pattern. Simulation of Gray-Scott Model using finite difference approximation for D_u=0.14, D_v=0.060, F=0.035, K=0.062

Finger Print:



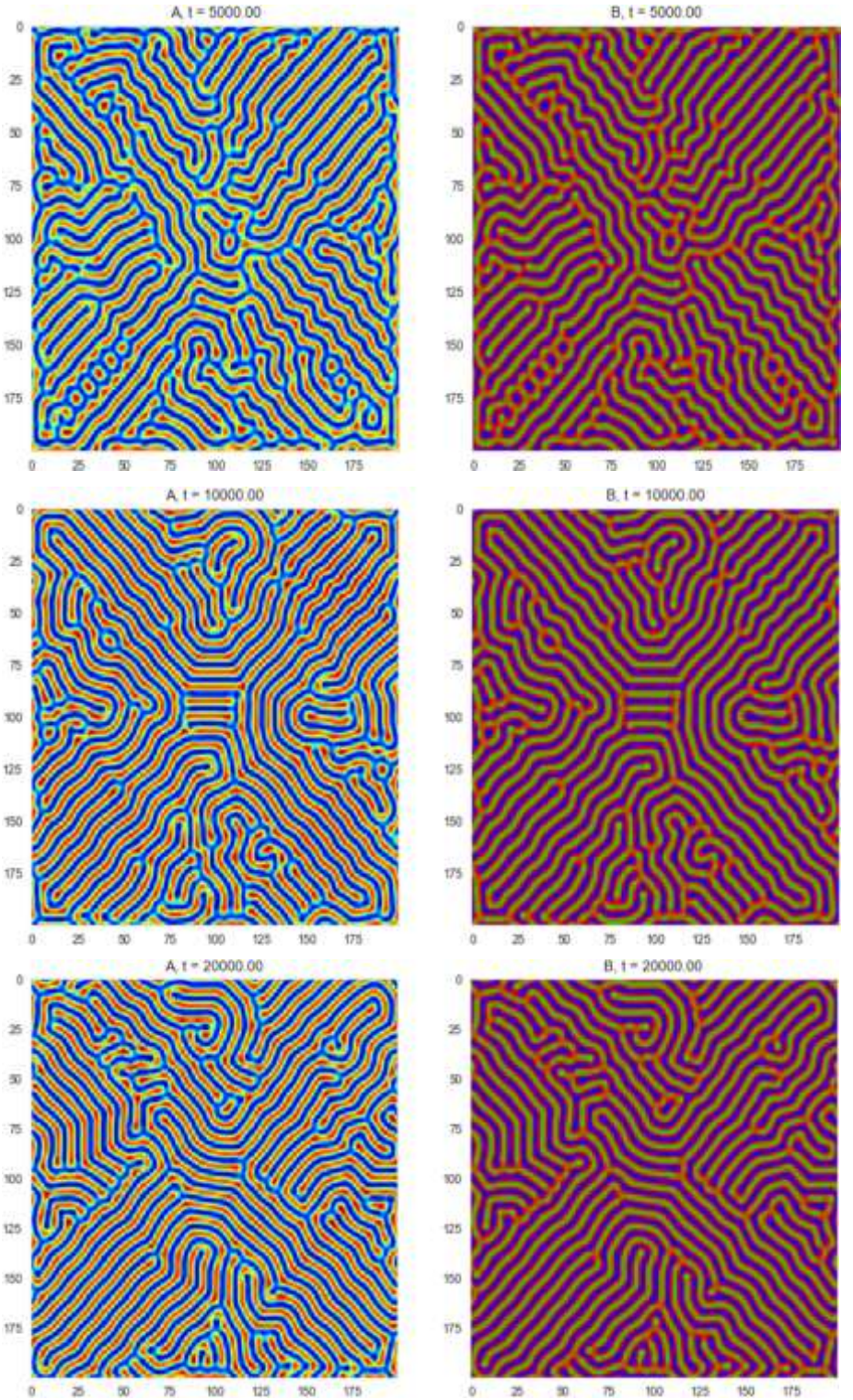

A, t = 5000.00
B, t = 5000.00
A, t = 10000.00
B, t = 10000.00
A, t = 20000.00
B, t = 20000.00
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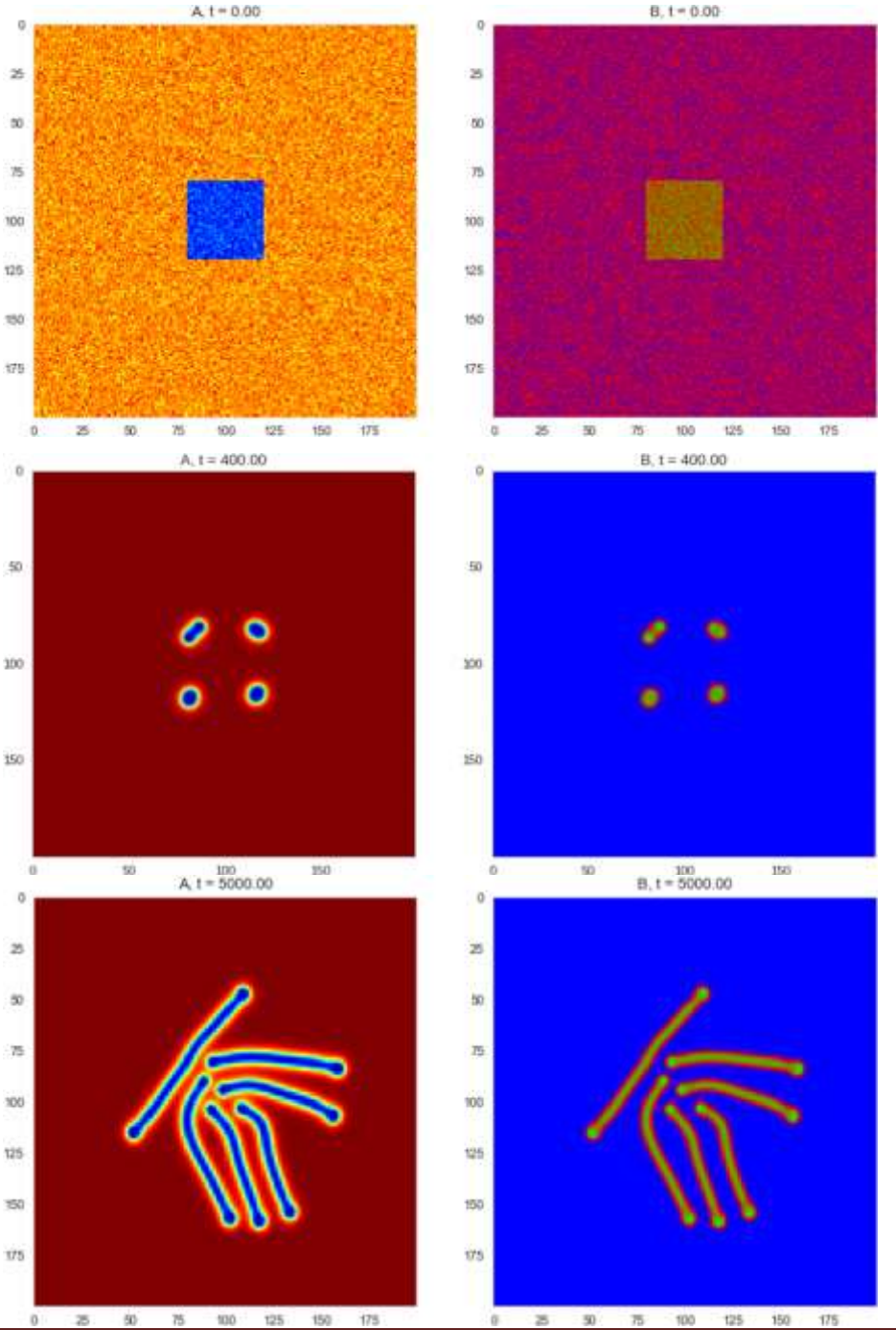
Figure 4: Time evolution of the concentration profile and formation of Finger Print pattern. Simulation of Gray-Scott Model using finite difference approximation for D_u=0.19, D_v=0.05, F=0.06, K=0.062.

Worms:



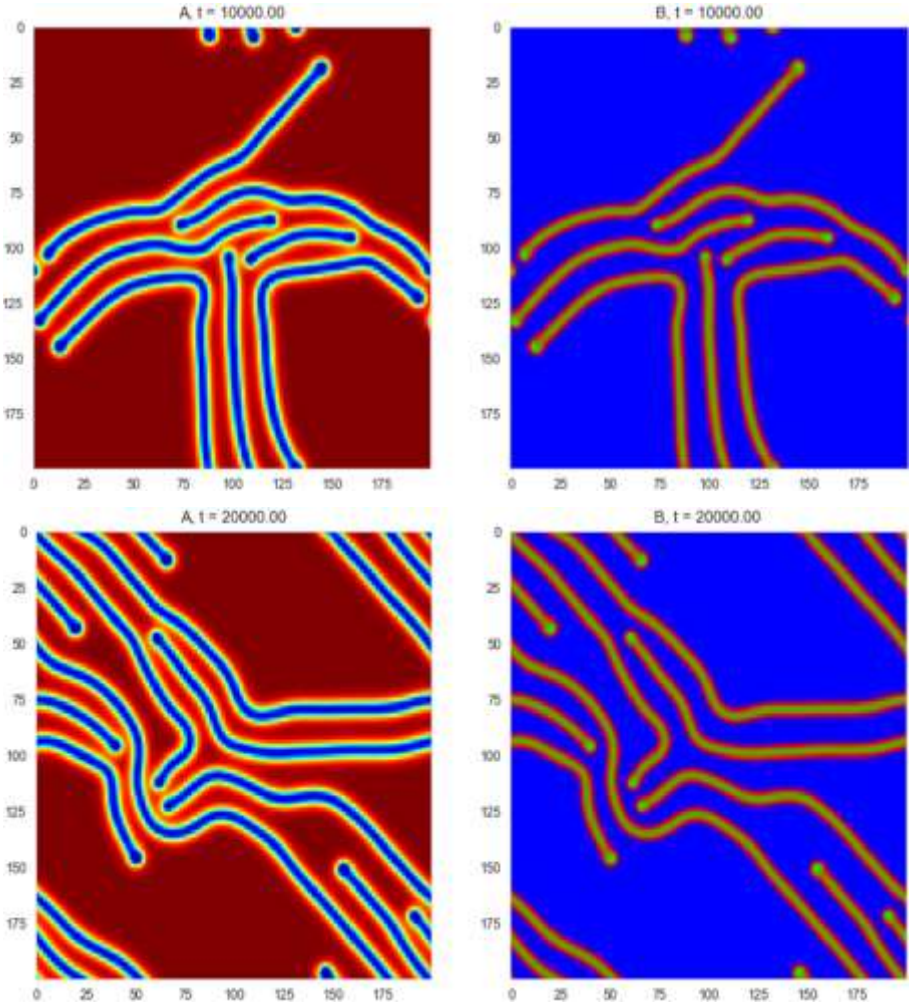


Figure 5: Time evolution of the concentration profile and formation of Worms pattern. Simulation of Gray-Scott Model using finite difference approximation for D_u=0.16, D_v=0.08, F=0.05, K=0.065.

DISCUSSION

A numerical simulation of the system is performed in a two-dimensional lattice. All of our numerical simulations use the boundary conditions that are periodic. We choose a time step of 0.01 and a space step of 1. Here we use Python programming language for numerical simulations. From the above figure 2, 3, 4, 5 it was show that the time evolution of the concentration profile and formation of the Bacterial growth pattern, Coral pattern, Finger print pattern and Worms pattern.

In figure 2, the pattern has been generated by a computer simulation starting from a random state. We choose the parameters D_u=0.16, D_v=0.08, F=0.035, K=0.065. Here we find the bacterial growth pattern. In this pattern we see that when t=0 then there is no bacteria exists in the medium. But when t=400, then we can see small amount of bacteria in the medium.

When t=5000 then we can see some bacteria whose amount are larger than previous. When t=10000, then we can see many bacteria. When t=20000, then we can see the whole medium filled with bacteria.

In figure 3, the pattern has been generated by a computer simulation starting from a random state. We choose the parameters D_u=0.14, D_v=0.06, F=0.035, K=0.062. Here we find the coral pattern. In this pattern we see that when t=0 then there is no coral exists in the medium. But when t=400, then we can see the size of the coral is small in the medium. When t=5000 then we can see some coral whose amount are larger than previous. When t=10000, then we can see many corals. When t=20000, then we can see the whole medium filled with the coral pattern.

In figure 4, the pattern has been generated by a computer simulation starting from a random state. We choose the parameters for D_u=0.19, D_v = 0.05, F=0.06, K=0.062. Here we find the finger print pattern. In this pattern we see that when t=0 then there is no pattern exists in the medium. But when t=400, then we can see the size of the pattern is small in the medium. When t=5000 then we can see some pattern whose amount are larger than previous. When t=10000, then we can see many pattern. When t=20000, then we can see the whole medium filled with the finger print pattern.

In figure 5, the pattern has been generated by a computer simulation starting from a random state. We choose the parameters D_u=0.16, D_v = 0.08, F=0.05, K=0.065. Here we find the worms pattern. In this pattern we see that when t=0 then there is no worms exists in the medium. But when t=400, then we can see the size of the pattern is small in the medium. When t=5000 then we can see some worms whose amount are larger than previous. When t=10000, then we can see many worms than previous. When t=20000, then we can see the many large worms pattern.

CONCLUSION

In this work, we looked at the formation of natural patterns using the Gray-Scott reaction-diffusion model. We started by talking about the model's basic process and doing the linear consistency (Turing) analysis to find out when patterns appear.

We then implemented a Python-based simulation to observe the formation and evolution of diverse structures resembling bacteria, coral, fingerprints, and worms from random initial conditions. Our results demonstrate the model's capability to replicate a wide range of biologically inspired patterns through simple nonlinear interactions.

Future research could extend this analysis by incorporating stochastic effects, domain growth, or more realistic boundary conditions to better mimic biological environments. Additionally, coupling the Gray-Scott model with other biochemical or mechanical models could provide deeper insight into multi-scale pattern formation processes in developmental biology and ecological systems.

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