

# Gierer-Meinhardt nonlinear system for pattern formation: An analytical and computational approach

Zakir Hossine<sup>1</sup>, Afia Farzana<sup>2</sup>, Md. Abdur Rafe<sup>3</sup>, and Md. Kamrujjaman<sup>4\*</sup>

<sup>1,2,3</sup>Department of Applied Mathematics, University of Dhaka, Dhaka 1000, Bangladesh

<sup>4</sup>Department of Mathematics, University of Dhaka, Dhaka 1000, Bangladesh

\*Corresponding author Email : [kamrujjaman@du.ac.bd](mailto:kamrujjaman@du.ac.bd)

**Abstract:** In the universe, an infinite number of patterns are visible, which is the premier beauty of nature. Mathematical modeling is a powerful tool to decorate the patterns in scientific computation. This paper studied the Gierer-Meinhardt reaction-diffusion model of pattern formation to visualize a class of patterns for different animals and plants. It is also noted that many biological and chemical phenomena can be explained using the Gierer-Meinhardt model. We have analyzed the linear stability to get the stability and instability conditions of a system of reaction-diffusion equations with diffusion and in the absence of diffusion. Finally, as an application, a series of different types of patterns are presented using numerical simulation of the model.

**Keywords:** Gierer-Meinhardt Model; stability analysis; Turing pattern; reaction-diffusion; numerical analysis.  
*AMS Subject Classification 2010:* 92D25, 35K57, 35K50, 37N25, 53C35.

## Introduction

The pattern is a common phenomenon in nature. We have found patterns almost everywhere in the surroundings. For example, the formation of clouds, rivers, water waves, and crystals all are followed a specific pattern. People are always curious about these patterns in nature. They always want to know these different patterns in nature, how they formed, and the evolution of patterns. To answer all these questions, the scientist uses mathematical modeling. Alan Turing was the first scientist who used mathematical modeling to describe the pattern in nature (Teuscher and Hofstadter, 2004). He suggested that shapes and patterns found in nature might be explained by two biological substances moving and interacting with one another in a mathematically predictable way. Turing mathematical modeling came up with a system of coupled differential equation (Kondo, 2017). However, solving that system with the computational technique available at that time was undoubtedly hard. However, Turing did complete the painstaking task once, which produced a pattern that resembled a cow's skin (Green and Sharpe, 2015). Although pattern formation is a broad topic, it is mainly used in biological science. Pattern creation in biology refers to the process by which genes create intricate arrangements of cells' fates in time and space (Meinhardt and Klingler, 1987). The traditional reaction-diffusion model by Alan Turing is included in the numerical simulations of

pattern formation in bio-molecules. The behavior of two species (substances) interacting with each other can be easily simulated using the reaction-diffusion equation (Harrison, 2005). The species (substances) are transformed into each other, the reaction that yields a higher concentration of the given substances at a spot. At the same time, they also dissolve, which is the diffusion, outspreading themselves over the area. The interaction between two or more species (or objects) is a reaction. One dimensional reaction is the interaction in which the species reacts with zero, either increasing the density of itself or decreasing (Nakamasu et al., 2009). For instance, a decaying reaction can be described by the system

$$\frac{du}{dt} = -u = f(u)$$

In other words, we can also say that the reactive term  $f(u)$ , describes the changes in concentration of  $u$  depending on its local value. On the other hand, the word diffusion describes the concept of spreading out. In Physics, diffusion is used to explain how liquids spread in the surrounding area when the gas particles (Glover et al., 2017). The model solution and visible natural patterns are shown in Figure 1.

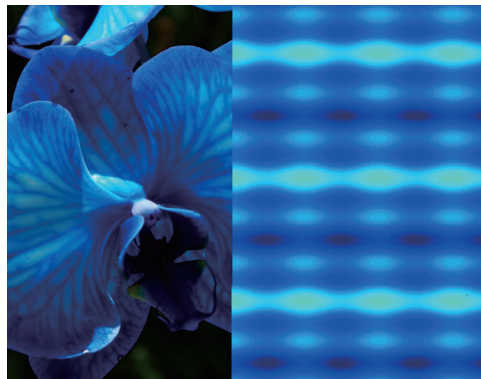


Figure 1: A comparative diagram between computer simulated results and natural patterns.

Let  $u(x, t)$  be the chemical's (species) concentration which is at the real line on  $x$  at time  $t$ . Then the reaction-diffusion equation is,

$$\frac{\partial u}{\partial t} = \mu \frac{\partial^2 u}{\partial x^2} + f(u), \tag{1}$$

where  $\mu$  is the diffusion coefficient and  $f(u)$  describes how  $u$  grows or decays based on the concentration (Hentschel et al., 2004). A lot of physical phenomena can be described by using this reaction-diffusion equation. In the present work, we mainly focused on a particular reaction-diffusion model by which we can describe the pattern formation on an animal's skin. The considered model is a Gierer-Meinhardt model, consisting of two partial differential equations. The findings significantly present the novel results which are matching with the existing multiple animal's pattern.

The main objective of this paper is to show the effects of parameters on pattern formation and compare the theoretical results with the existing pattern available in nature to compare the findings visually. The paper is organized as follows: the mathematical model (2) is take place and described in Section . We discuss the stability analysis and develop the analytic results in Section . The computational results are presented in Section , where we consider different values of the parameter and varying boundary conditions while the others are fixed. It is remarked that the significant change of the domain and changing time satisfy the stability criteria for certain large values of time,  $t$ . In Section , we have compared the simulations and exiting pattern to ensure the results and validity of the model. Finally, we conclude a summary and future direction of the study as presented in Section .

## Mathematical Model

The Gierer-Meinhardt model depicts the concentration of an activator, a short-range autocatalytic substance that controls the synthesis of its inhibitor, a long-range antagonist substance. Although it is a very simple model, it is a theoretical link connecting observations and the inference of the fundamental molecular-genetic pathways (Alonso García, 2016; Schneider, 2012). In this study, we have studied the following mathematical model (Meinhardt, 2006),

$$\begin{cases} u_t = \frac{u^2(t, x)}{v(t, x)} - bu(t, x) + \mu\Delta u(t, x), & t > 0, x \in \Omega, \\ v_t = u^2(t, x) - v(t, x) + \nu\Delta v(t, x), & t > 0, x \in \Omega, \\ u(t, x) = \beta_1(t, x), v(t, x) = \beta_2(t, x), & t > 0, x \in \partial\Omega, \\ u(0, x) = u_0(x), v(0, x) = v_0(x), & x \in \Omega. \end{cases} \quad (2)$$

Here,  $u(t, x)$  represents the activator and  $v(t, x)$  represents the inhibitor. The rate of the change of activator concentration is represented by  $u_t$  and the rate of the change of inhibitor concentration is represented by  $v_t$ . The term  $\mu\Delta u(t, x)$  describes the diffusion term of the activator and similarly,  $\nu\Delta v(t, x)$  is for the inhibitor dispersal. The reaction term for the activator is represented by  $\frac{u^2(t, x)}{v(t, x)} - bu(t, x)$  while the reaction term for the inhibitor is  $u^2(t, x) - v(t, x)$  (Doelman et al., 2007; Lengyel and Epstein, 1992). In order to study this model, first of all, we need to perform a stability analysis of this model, from which we will get some stability conditions for which our considered model may have a stable solution. Then, we will use numerical analysis and MATLAB code to visualize the results.

## Steady states and mathematical analysis

The defined model is a system of non-linear partial differential equations, and finding the stability conditions for the exact system is challenging. In order to find the behavior of the solution, it will be convenient if we approximate the system. We may use the linearized approximation method for approximation as it will be easier for analysis. First, we will attempt to determine the stability conditions of the system without considering the diffusion effect on the system. Finally, we will also try to find out the stability condition of the system with diffusion effect (Hossine et al., 2021; Hossine and Kamrujjaman, 2019; Salazar-ciudad and Jernvall, 2004). Let us now consider the system (2) without diffusion such that

$$\begin{aligned} \frac{du}{dt} &= \frac{u^2}{v} - bu \\ \frac{dv}{dt} &= u^2 - v \end{aligned}$$

In case of steady state solution, it is obtained that  $u_0 = 0, \frac{1}{b}$  and  $v_0 = 0, \frac{1}{b^2}$ . Hence, linearizing about the steady state  $[u_0, v_0] = [\frac{1}{b}, \frac{1}{b^2}]$ , we find the Jacobian matrix is:

$$J = \begin{bmatrix} f_u & f_v \\ g_u & g_v \end{bmatrix}$$

$$\Rightarrow J|_{(\frac{1}{b}, \frac{1}{b^2})} = \begin{bmatrix} -b + \frac{2u}{v} & -\frac{u^2}{v^2} \\ 2u & -1 \end{bmatrix}_{(\frac{1}{b}, \frac{1}{b^2})} = \begin{bmatrix} b & -b^2 \\ \frac{2}{b} & -1 \end{bmatrix}$$

In order to find the stability, we have to satisfy the following two conditions,

$$\det(J) > 0, \quad \text{and} \quad \text{tr}(J) < 0,$$

which yields  $b > 0$ ,  $b < 1$  such that the limit of  $b$  is  $0 < b < 1$

Therefore, Gierer-Meinhardt model without diffusion is stable as long as  $0 < b < 1$  (Hossine et al., 2021).

Now, it's time to recall the governing problem (2) with diffusion. We have introduced a minor perturbation apart from the stable equilibrium to analyze this system, and then we will determine the parameter values.

Consider  $u(x, t) = u_o + \tilde{u}$  and  $v(x, t) = v_o + \tilde{v}$ , with  $\tilde{u}$  and  $\tilde{v}$  are very small. Then, the linearized system has the form,

$$\begin{aligned} \frac{\partial \tilde{u}}{\partial t} &= b\tilde{u} - b^2\tilde{v} + \mu \frac{\partial^2 \tilde{u}}{\partial x^2} \\ \frac{\partial \tilde{v}}{\partial t} &= \frac{2\tilde{u}}{b} - \tilde{v} + \nu \frac{\partial^2 \tilde{v}}{\partial x^2} \end{aligned}$$

So,  $f_u = b$ ,  $f_v = -b^2$  and  $g_u = \frac{2}{b}$ ,  $g_v = -1$ . Now, the solution of this system is,

$$\tilde{u}(x, t) = \dot{u}e^{\sigma t} \sin \alpha x \quad \text{and} \quad \tilde{v}(x, t) = \dot{v}e^{\sigma t} \sin \alpha x,$$

where above equations are the Fourier models. Therefore, the modified first equation of (2) is,

$$\begin{aligned} \sigma e^{\sigma t} \dot{u} \sin \alpha x &= -\alpha^2 \mu \dot{u} e^{\sigma t} \sin \alpha x + f_u \dot{u} e^{\sigma t} \sin \alpha x + f_v \dot{v} e^{\sigma t} \sin \alpha x \\ \Rightarrow \sigma e^{\sigma t} \dot{u} \sin \alpha x &= -\alpha^2 \mu \dot{u} e^{\sigma t} \sin \alpha x + b \dot{u} e^{\sigma t} \sin \alpha x - b^2 \dot{v} e^{\sigma t} \sin \alpha x \end{aligned} \quad (3)$$

Dividing both sides of the equation (3) by  $e^{\sigma t} \sin \alpha x$ , we get

$$\sigma \dot{u} = -\alpha^2 \mu \dot{u} + b \dot{u} - b^2 \dot{v}.$$

Similarly, the second equation of (2) becomes

$$\sigma \dot{v} = -\alpha^2 \nu \dot{v} + \frac{2}{b} \dot{u} - \dot{v}.$$

Combining the immediate last two equations, we have modified Jacobian matrix,

$$J = \begin{bmatrix} f_u - \alpha^2 \mu & f_v \\ g_u & g_v - \alpha^2 \nu \end{bmatrix} = \begin{bmatrix} b - \alpha^2 \mu & -b^2 \\ \frac{2}{b} & -1 - \alpha^2 \nu \end{bmatrix}$$

For stability, there are two conditions such that,  $\det(J) > 0$  and  $\text{tr}(J) < 0$ . Trace of the Jacobian matrix is:

$$\begin{aligned} f_u + g_v - \alpha^2(\mu + \nu) &< 0 \\ \Rightarrow b - 1 - \alpha^2(\mu + \nu) &< 0, \end{aligned}$$

and determinant of the Jacobian matrix implies

$$\begin{aligned} (f_u - \alpha^2 \mu)(g_v - \alpha^2 \nu) - f_v g_u &> 0 \\ \Rightarrow (b - \alpha^2 \mu)(-1 - \alpha^2 \nu) + 2b &> 0. \end{aligned}$$

Now, consider the determinant,

$$\begin{aligned} \det(J) &= (f_u - \alpha^2 \mu)(g_v - \alpha^2 \nu) - f_v g_u \\ &= \alpha^4 \mu \nu - \alpha^2(-\mu + b\nu) - b + 2b, \end{aligned}$$

which employ the instability if  $\alpha^4 \mu \nu + \alpha^2(\mu - b\nu) - b + 2b < 0$ .

We have seen that the determinant of the Jacobian matrix is a quadratic function of  $\alpha^2$ . We know from algebra that a quadratic equation has an equal or distinct real root depending on the value of the discriminant of that equation which is dependent on the coefficient of that quadratic equation. Our derived quadratic equation will have zero, one, or two real roots, depending on  $b$ . We will get patterns from the numerical simulation of the model when the derived quadratic equation has real solutions (Liehr, 2013). In order to get two real roots for the quadratic, we must have

$$\begin{aligned} \mu\nu \left( \frac{-b\nu + \mu}{2\mu\nu} \right)^2 + (-b\nu + \mu) \left( \frac{-b\nu + \mu}{2\mu\nu} \right) - b + 2b < 0 \\ \Rightarrow (-b\nu + \mu)^2 > 4\mu\nu b \end{aligned}$$

Because of second condition required for instability ( $b > 0$ ), it follows that

$$-b\nu + \mu > 2\sqrt{\mu\nu b}.$$

This further implies

$$f_u\nu + g_v\mu > 0.$$

For better representation of our findings clarity, we will restate all four conditions here for which diffusion-driven stability will occur:

Condition i:  $tr(J) = f_u + g_v < 0 \Rightarrow tr(J) = b - 1 < 0$

Condition ii:  $det(J) = f_u g_v - f_v g_u > 0 \Rightarrow det(J) = b > 0$

Condition iii:  $f_u\nu + g_v\mu > 0 \Rightarrow b\nu - \mu > 0$

Condition iv:  $f_u\nu + g_v\mu > 2\sqrt{\mu\nu(f_u g_v - f_v g_u)} \Rightarrow b\nu - \mu > 2\sqrt{\mu\nu b}.$

## Computational approach and examples

To get the visualized results using numerical simulation, we have constructed a MATLAB program that can generate some dynamic simulations of the pattern. This program can represent a complete dynamic pattern simulation over time that shows how pattern formation executes after initial time and then changes unstably over time till it reaches its stable point. After getting stable, it remains unchanged no matter how much time we input. In this program, we have considered fixed  $b$ ,  $\mu$ ,  $\nu$  and time step-size  $\Delta t$ . In particular, we have chosen  $b = 0.2$ ,  $\mu = 0.5$ ,  $\nu = 35$ ,  $\Delta t = 0.00001$ . We have chosen these parameters' values so that stability conditions are satisfied.

### Gierer-Meinhardt model and numerical simulations

Regarding numerical calculations, We have employed the finite difference method to discretize the partial differential equations by designing a MATLAB code to simulate the numerical result. MATLAB code will show us how to numerically simulate the 2D Gierer-Meinhardt system and create a simplified version in the Turing instabilities. The code executes and represents figures of the concentration of activator and inhibitor at every point in the given time range. We have generated all the simulations for same initial conditions  $u_0(x, y) = \pi \sin(x) \sin(y) + \cos(\pi y)$  and  $v_0(x, y) = 1.25 + 0.5 \sin(y) \cos(x)$  with different boundary conditions. For each simulation, we represent five sets of figures of a certain time that are titled in the figures.

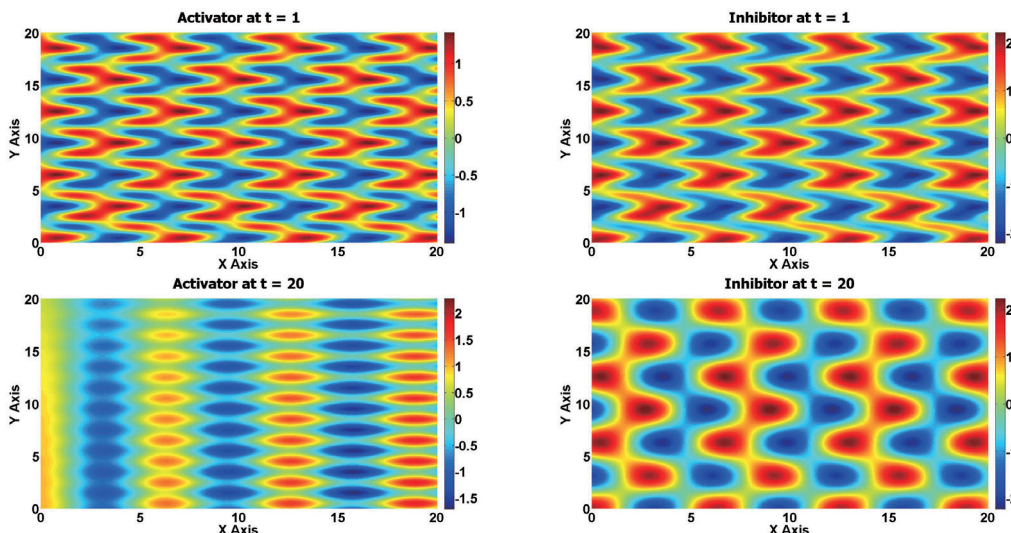


Figure 2: Patterns of the model with boundary conditions  $\beta_1(t, x, y) = \sin(x\pi) \sin(\frac{y}{t}) + \cos(\frac{y}{t}) \cos(y)$  and  $\beta_2(t, x, y) = \sin(\frac{x\pi}{t}) \sin(y) + 2 \cos(x) \cos(y)$  for  $t = 1$  and  $t = 20$ .

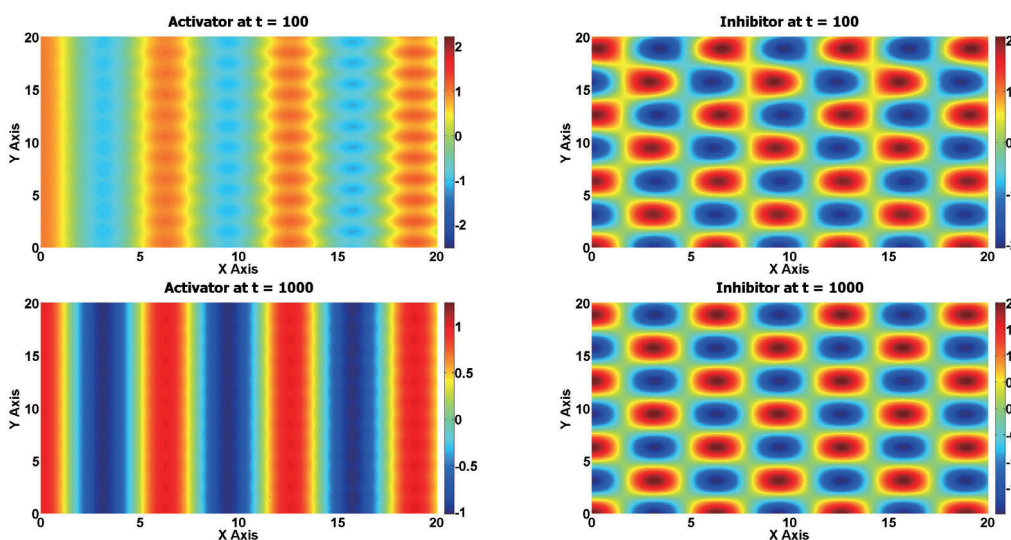


Figure 3: Patterns formation for  $\beta_1(t, x, y) = \sin(x\pi) \sin(\frac{y}{t}) + \cos(\frac{y}{t}) \cos(y)$  and  $\beta_2(t, x, y) = \sin(\frac{x\pi}{t}) \sin(y) + 2 \cos(x) \cos(y)$  at  $t = 100$  to  $t = 1000$ .

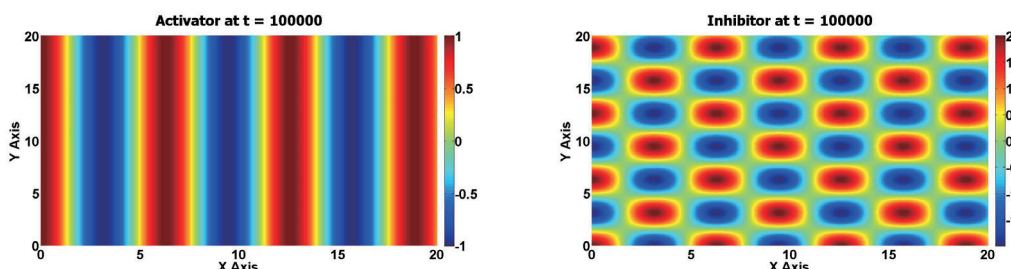


Figure 4: Stable patterns when  $\beta_1(t, x, y) = \sin(x\pi) \sin(\frac{y}{t}) + \cos(\frac{y}{t}) \cos(y)$  and  $\beta_2(t, x, y) = \sin(\frac{x\pi}{t}) \sin(y) + 2 \cos(x) \cos(y)$  for  $t = 100000$ .

We simulated the result of the Gierer-Meinhardt model with boundary conditions  $\beta_1(t, x, y) = \sin(x\pi) \sin(\frac{y}{t}) + \cos(\frac{y}{t}) \cos(y)$  and  $\beta_2(t, x, y) = \sin(\frac{x\pi}{t}) \sin(y) + 2 \cos(x) \cos(y)$  for different values of time  $t$ . It is seen from the outcome that the model's output oscillates at the beginning

of time and presented in Figure 2. Gradually the oscillation is being smaller (Figure 3), and after a certain time, the model's solution becomes stable, and we get a stable pattern as presented in Figure 4. At our current case the stable point is at  $t = 100000$ .

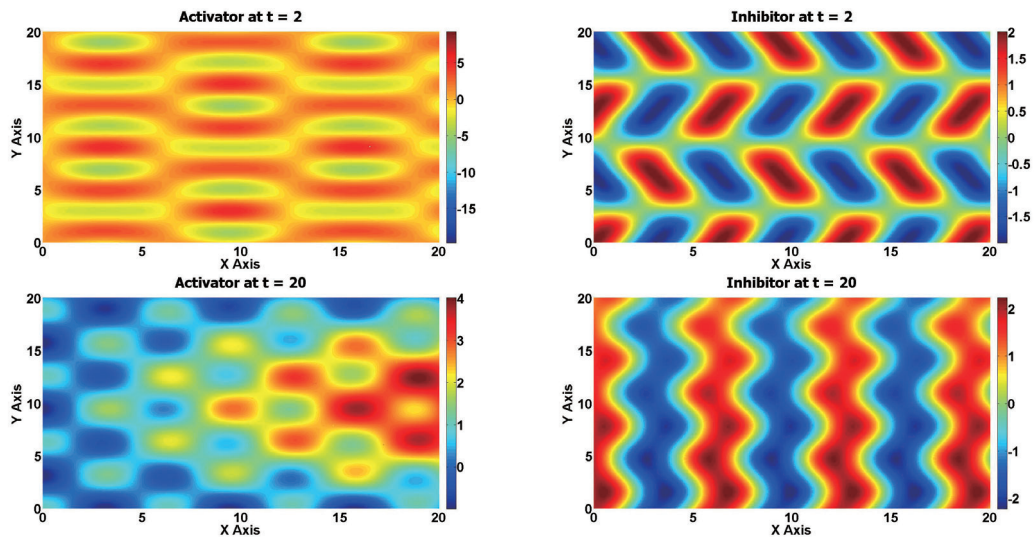


Figure 5: Result of the model with boundary conditions  $\beta_1(t, x, y) = 4 \sin(\frac{\pi x}{t}) \sin(\frac{y}{t}) + \cos(x) \cos(y)$  and  $\beta_2(t, x, y) = \sin(x) \sin(y) + 2 \cos(\frac{x}{t}) \cos(y)$  for  $t = 2$  and  $t = 20$ .

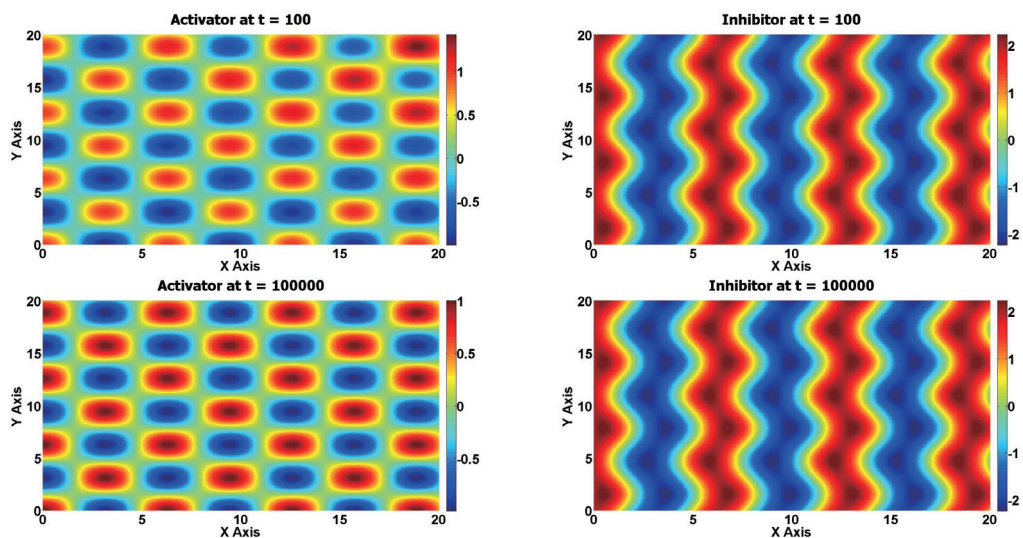


Figure 6: Result of the model with boundary conditions  $\beta_1(t, x, y) = 4 \sin(\frac{\pi x}{t}) \sin(\frac{y}{t}) + \cos(x) \cos(y)$  and  $\beta_2(t, x, y) = \sin(x) \sin(y) + 2 \cos(\frac{x}{t}) \cos(y)$  for  $t = 100$  to  $t = 100000$ .

The Figure 5 shows the result of the Gierer-Meinhardt model with boundary conditions  $\beta_1(t, x, y) = 4 \sin(\frac{\pi x}{t}) \sin(\frac{y}{t}) + \cos(x) \cos(y)$  and  $\beta_2(t, x, y) = \sin(x) \sin(y) + 2 \cos(\frac{x}{t}) \cos(y)$  with respect to time  $t$ . In activator and inhibitor, it shows that the patterns are stable after a certain time of oscillation (Figure 6), and in the present case, the stable point is  $t = 1000$ .

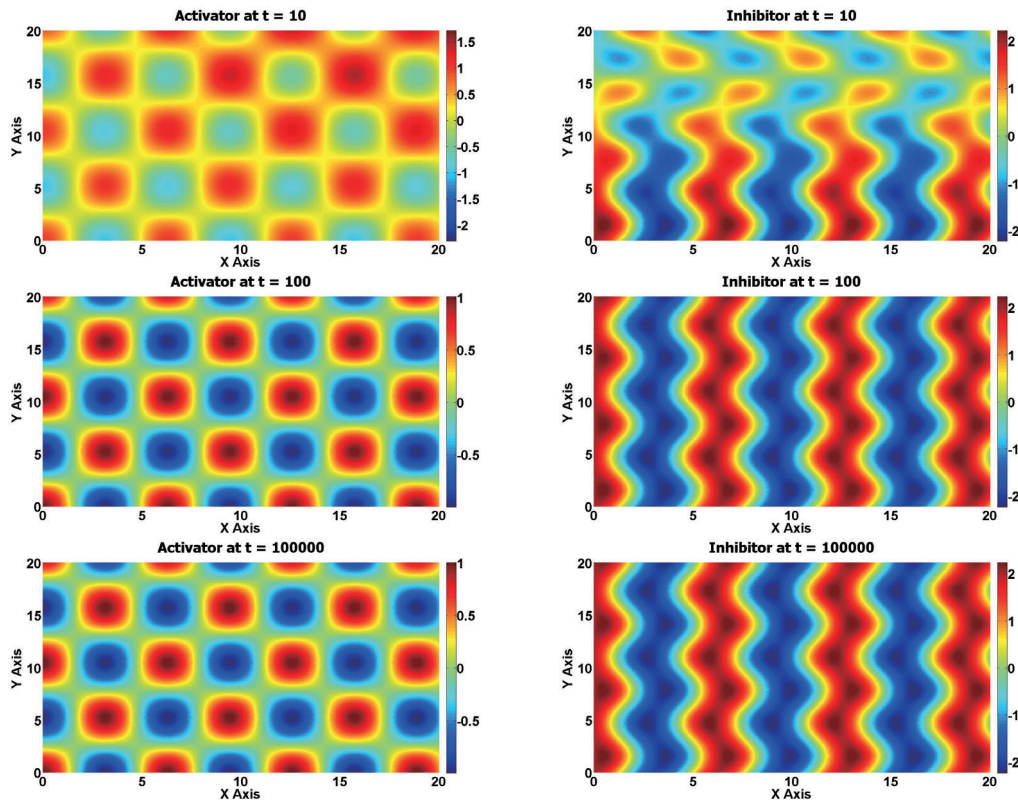


Figure 7: Patterns of the model with boundary conditions  $\beta_1(t, x, y) = \sin\left(\frac{x}{\pi t}\right) \sin\left(\frac{y}{t}\right) + \cos(0.6x) \cos(y)$  and  $\beta_2(t, x, y) = \sin(x) \sin(y) + 2 \cos\left(\frac{x}{t}\right) \cos(y)$ .

In Figure 7, we have considered the boundary conditions  $\beta_1(t, x, y) = \sin\left(\frac{x}{\pi t}\right) \sin\left(\frac{y}{t}\right) + \cos(0.6x) \cos(y)$  and  $\beta_2(t, x, y) = \sin(x) \sin(y) + 2 \cos\left(\frac{x}{t}\right) \cos(y)$  and the patterns results are presented for different values of time  $t$ . Again the stable patterns are focused at  $t = 1000$  while the fluctuation was visible at the beginning of time.

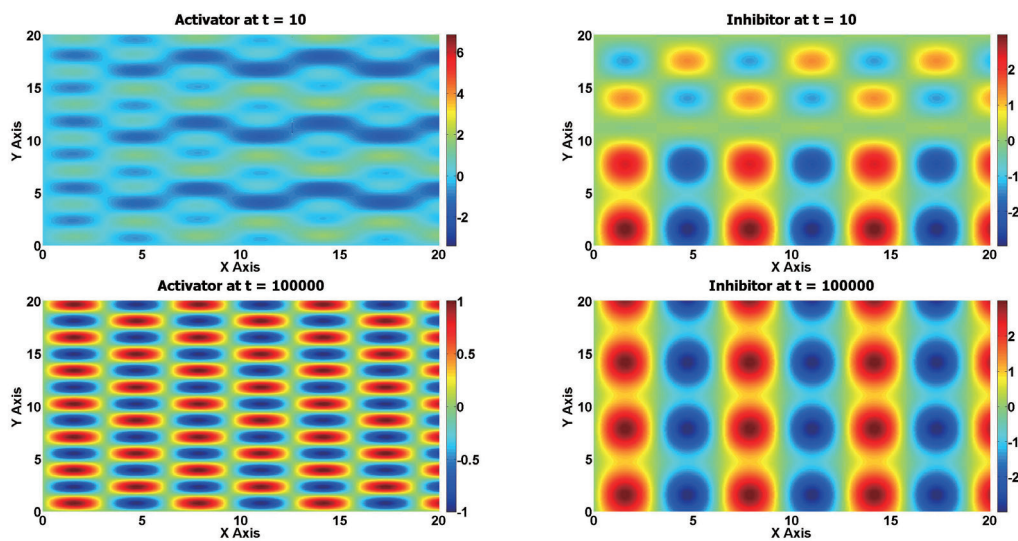


Figure 8: Result of the model with boundary conditions  $\beta_1(t, x, y) = \sin(2x) \sin(y) + \sin(x) \sin\left(\frac{y}{t}\right)$  and  $\beta_2(t, x, y) = \sin(x) \sin(y) + 2 \cos\left(\frac{x}{t}\right) \sin(y)$ .

The result of the Gierer-Meinhardt model is generated with boundary conditions,  $\beta_1(t, x, y) = \sin(2x) \sin(y) + \sin(x) \sin\left(\frac{y}{t}\right)$  and  $\beta_2(t, x, y) = \sin(x) \sin(y) + 2 \cos\left(\frac{x}{t}\right) \sin(y)$  and for different



values of time  $t$ . We have seen from the output that the model's output oscillates at the beginning of time, and after a certain time, the model's output becomes stable, and we get a stable pattern. At our current case the stable point is  $t = 1000$ .

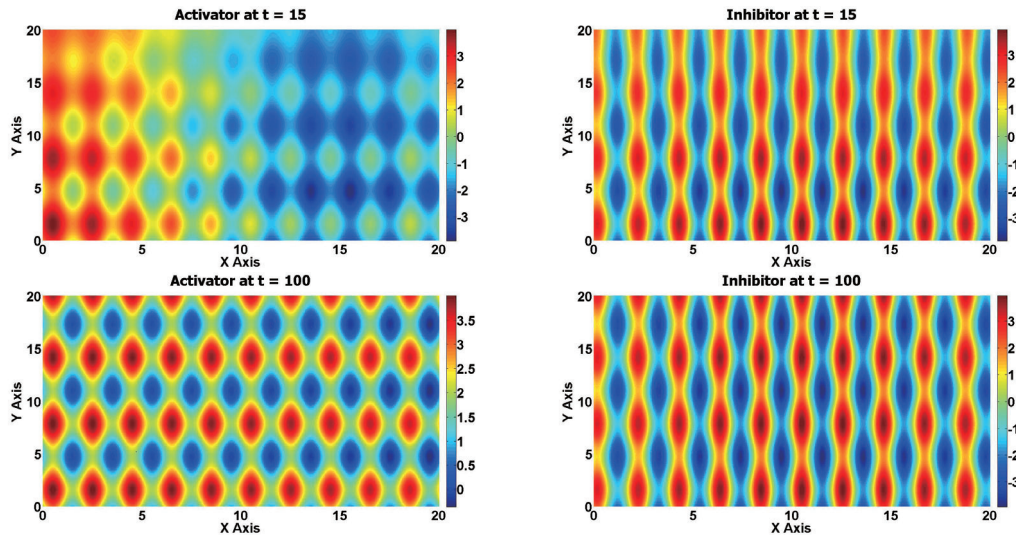


Figure 9: Result of the model with boundary conditions  $\beta_1(t, x, y) = \sin(x) \cos(\frac{x}{t}) + \sin(\pi y) \cos(\frac{x}{t}) + 2 \cos(\frac{y\pi}{t})$  and  $\beta_2(t, x, y) = \sin(x) \cos(\frac{x}{t}) + \sin(\pi y) \cos(\frac{x}{t}) + 2 \cos(3y)$ .

In Figure 9, we simulated the result of the problem with boundary conditions,  $\beta_1(t, x, y) = \sin(x) \cos(\frac{x}{t}) + \sin(\pi y) \cos(\frac{x}{t}) + 2 \cos(\frac{y\pi}{t})$ , and  $\beta_2(t, x, y) = \sin(x) \cos(\frac{x}{t}) + \sin(\pi y) \cos(\frac{x}{t}) + 2 \cos(3y)$  and for different values of time  $t$ . Similar results are visible compared with the previous results.

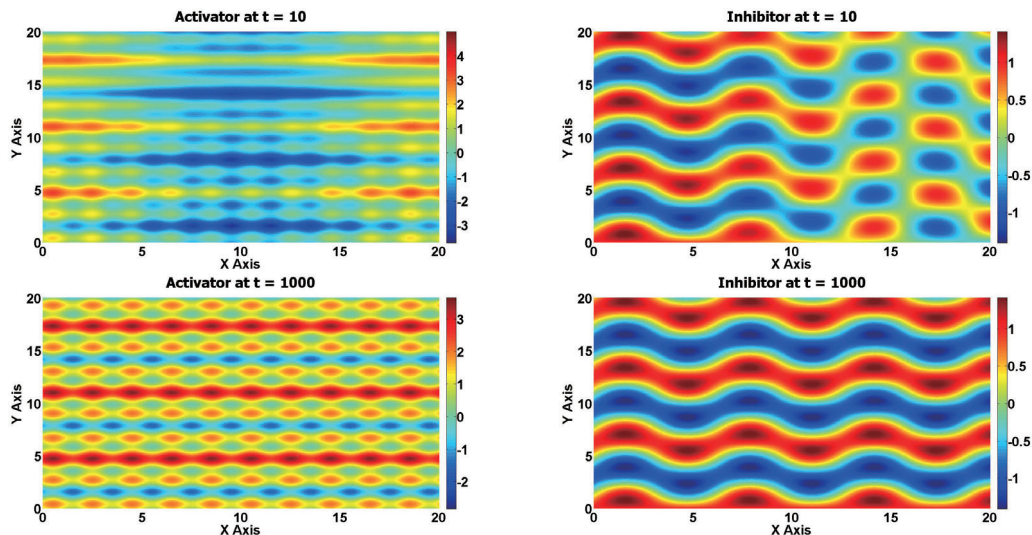


Figure 10: Result of the model with boundary conditions  $\beta_1(t, x, y) = 2 \sin(x) \cos(2x) + \frac{1}{2} \sin(\pi y) \cos(\frac{x}{t}) + 2 \cos(\frac{y\pi}{t})$  and  $\beta_2(t, x, y) = \sin(x) \sin(y) + \cos(x) \cos(\frac{y}{t}) + 2 \cos(3y)$ .

The above result of the Gierer-Meinhardt model as shown in Figure 10 with boundary conditions,  $\beta_1(t, x, y) = 2 \sin(x) \cos(2x) + \frac{1}{2} \sin(\pi y) \cos(\frac{x}{t}) + 2 \cos(\frac{y\pi}{t})$ , and  $\beta_2(t, x, y) = \sin(x) \sin(y) + \cos(x) \cos(\frac{y}{t}) + 2 \cos(3y)$  and for various time  $t$ . It is noted that the fluctuation patterns are seen for a lower time, and gradually the solution patterns become stable. At our current case the stable point is  $t = 3000$ .

## Actual pattern vs computer model

Creation and nature are full of various patterns. In the surroundings, we can see different patterns with different colors. Above we have done by computer programming and established the results and figures. Now we will compare those figures with the skin patterns of different animals.

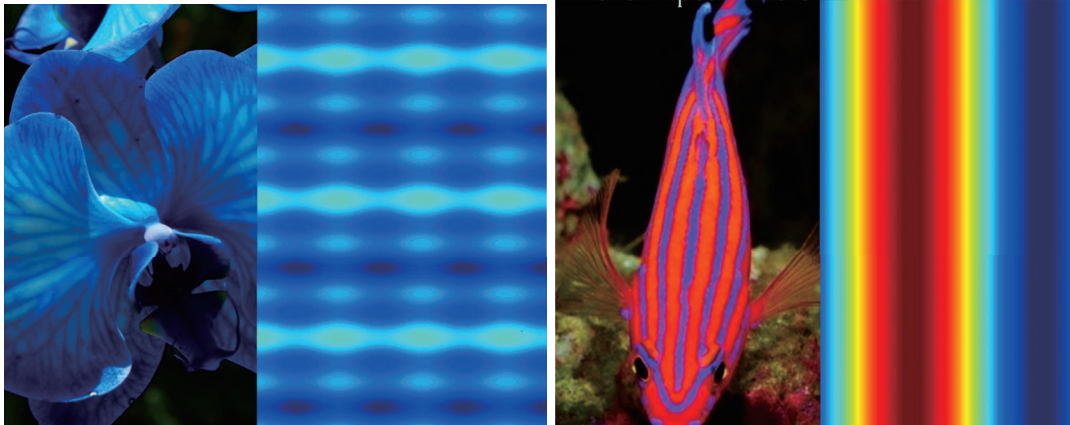


Figure 11: Different types of natural pattern compared with computer simulated pattern.

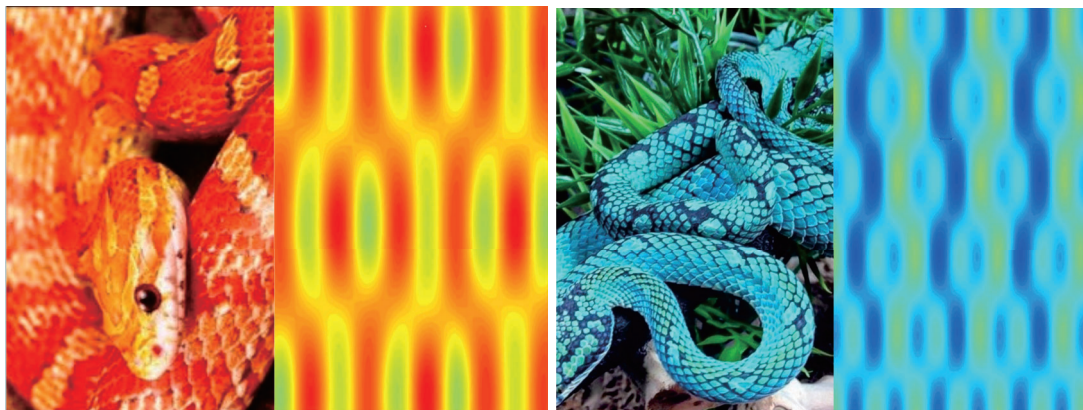


Figure 12: Different types of natural pattern compared with data simulated results.

We have the following conclusion as presented in Figures 11 and 12:

- In the first figure, we have compared **Blue Phalaenopsis orchid** (orchidrepublic) with the computer output generated in Figure 7 (Activator at  $t=100000$ ).
- In the second figure, we have compared **Red Candy Basslet's skin (Liopropoma carmabi)** (Wikipedia) with the computer output generated in Figure 2 (Activator at  $t=100000$ ).
- In the third figure, we have shown the comparison between **Corn snake's skin** (Wikipedia) and the computer output generated in Figure 5 (Activator at  $t=2$ ).
- In the fourth figure, a comparative findings between **Sri Lanka Pit Viper's skin (Trimeresurus trigonocephalus)** (Agefotostock) and the computer output generated in Figure 8 (Activator at  $t=10$ ).

## Summary and concluding remarks

In this study, we studied the Gierer-Meinhardt model to develop the patterns of various animals and plants and compared the existing scenario and the modeling outcome. The results concluded that different natural patterns could be simulated through mathematical modeling and many models exhibiting a pattern. In forming a pattern, a model must be satisfied all the conditions for Turing instability. By changing parameters, first, we checked Turing instability. If the model is stable, we took different initial conditions to get different patterns. From this general Gierer-Meinhardt model, we got some spot and stripe patterns by using random initial conditions and applying Dirichlet boundary conditions. These patterns are different in colors and also different types. Finally, we compared these figures with some animals' skin patterns.

## Acknowledgments

The author, M. Kamrujjaman research, was partially supported by the University Grants Commission (UGC) and Bose Center for Advanced Study and Research in Natural Sciences, University of Dhaka, Bangladesh.

## Conflict of interest

The authors declare no conflict of interest.

## References

- Agefotostock. Sri lanka pit viper (*trimeresurus trigonocephalus*). URL <https://www.agefotostock.com/age/en/details-photo/sri-lanka-pit-viper-trimeresurus-trigonocephalus-sri-lanka/IBR-6954783>. [Online].
- L. A. Alonso García. Reaction-diffusion systems and pattern formation. 2016.
- A. Doelman, T. J. Kaper, and K. Promislow. Nonlinear asymptotic stability of the semistrong pulse dynamics in a regularized gierer–meinhardt model. *SIAM Journal on Mathematical Analysis*, 38(6):1760–1787, 2007.
- J. D. Glover, K. L. Wells, F. Matthäus, K. J. Painter, W. Ho, J. Riddell, J. A. Johansson, M. J. Ford, C. A. Jahoda, V. Klika, et al. Hierarchical patterning modes orchestrate hair follicle morphogenesis. *PLoS biology*, 15(7):e2002117, 2017.
- J. B. Green and J. Sharpe. Positional information and reaction-diffusion: two big ideas in developmental biology combine. *Development*, 142(7):1203–1211, 2015.
- L. G. Harrison. *Kinetic theory of living pattern*. Number 28. Cambridge University Press, 2005.
- H. Hentschel, T. Glimm, J. A. Glazier, and S. A. Newman. Dynamical mechanisms for skeletal pattern formation in the vertebrate limb. *Proceedings of the Royal Society of London. Series B: Biological Sciences*, 271(1549):1713–1722, 2004.
- Z. Hossine and M. Kamrujjaman. On the interplay of geometrical shapes and the analysis of a dispersal model for pattern formations. *Journal of Advances in Mathematics and Computer Science*, pages 1–10, 2019.

- Z. Hossine, O. Khanam, M. M. I. Y. Adan, and M. Kamrujjaman. Spatio-temporal brusselator model and biological pattern formation. *Annual Research & Review in Biology*, pages 88–99, 2021.
- S. Kondo. An updated kernel-based turing model for studying the mechanisms of biological pattern formation. *Journal of Theoretical Biology*, 414:120–127, 2017.
- I. Lengyel and I. R. Epstein. A chemical approach to designing turing patterns in reaction-diffusion systems. *Proceedings of the National Academy of Sciences*, 89(9):3977–3979, 1992.
- A. Liehr. *Dissipative solitons in reaction diffusion systems*, volume 70. Springer, 2013.
- H. Meinhardt. Gierer-meinhardt model. *Scholarpedia*, 1(12):1418, 2006.
- H. Meinhardt and M. Klingler. A model for pattern formation on the shells of molluscs. *Journal of Theoretical Biology*, 126(1):63–89, 1987.
- A. Nakamasu, G. Takahashi, A. Kanbe, and S. Kondo. Interactions between zebrafish pigment cells responsible for the generation of turing patterns. *Proceedings of the National Academy of Sciences*, 106(21):8429–8434, 2009.
- orchidrepublic. Blue phalaenopsis orchid[online]. URL <https://orchidrepublic.com/blogs/news/blue-orchids>. [Online].
- I. Salazar-ciudad and J. Jernvall. How different types of pattern formation mechanisms affect the evolution of form and development. *Evolution & development*, 6(1):6–16, 2004.
- J. T. Schneider. Perfect stripes from a general turing model in different geometries. 2012.
- C. Teuscher and D. R. Hofstadter. *Alan Turing: Life and legacy of a great thinker*, volume 54. Springer, 2004.
- Wikipedia. The candy basslet (*Liopropoma carmabi*). URL [https://en.wikipedia.org/wiki/Liopropoma\\_carmabi](https://en.wikipedia.org/wiki/Liopropoma_carmabi). [Online].
- Wikipedia. Corn snake. URL [https://en.wikipedia.org/w/index.php?title=Corn\\_snake&oldid=1089960712](https://en.wikipedia.org/w/index.php?title=Corn_snake&oldid=1089960712). [Online].



This paper DOI: [10.5281/zenodo.7619195](https://doi.org/10.5281/zenodo.7619195)

Journal Old Website: <http://ijgsw.comze.com/> is no longer used

Journal New Website: <https://ijgsw.net/>  
You can submit your paper to email: [Jichao@email.com](mailto:Jichao@email.com)  
Or [IJGSW@mail.com](mailto:IJGSW@mail.com)