On Gierer - Meinhardt Model With Diffusion Constant Of Mean Reverting Process Type

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ABSTRACT: Many authors have considered varying the values of the diffusion constants, arbitrarily but within the context in order to get the turing instability which result in pattern formation in biology and medicine in form of spiky solutions within a defined domain. We study the dynamics of Gierer -Meinhardt(GM) model under the influence of stochastic diffusivity of the inhibitor of mean reverting stochastic differential equation, which varies in time and create Turing patterns in form of spikes. In order to have the random coefficient of diffusion not to be derived far away from the usual constants, it is allowed to oscillate stochastically around the long-run value using the mean-reverting idea. We show numerically how the spikes vanishes to a stable number for long time enough using the finite difference methods and the Matlab programming language. It is assumed that for long time enough, the new stochastic Gierer-Meinhardt model is approximated to deterministic GM model with certain probability.

1 Introduction

Many researchers have studied and explained the concept of reaction diffusion(RD) systems/models. For example [2] describes RD systems as the one involving constituents locally transformed into each other by chemical reactions and transported in space by diffusion. While [3] stated that RD systems are mathematical models that describe how the concentration of one or more substance distributed in space changes under the influence of two processes: Local chemical reactions in which the substances are converted into each other, and diffusion which causes the substances to spread out in space. As the two descriptions implies, reaction-diffusion systems arise quite naturally in Chemistry and Chemical Engineering. However, the equations can also describe dynamical process for the study of non-chemical nature such as in environmental(Geology, Physics, etc) and life sciences(Biology, Medicine). Mathematically, reaction-diffusion systems take the form of semi-linear or nonlinear Parabolic Partial differential equations.

The solutions of reaction-diffusion equations display a wide range of behaviours, including the formation of traveling waves and wave-like phenomena as well as other self-
organized patterns like **stripes, spots, hexagonal structures** or more intricate structures like dissipative solitons or **spikes**. 

In general the RD systems are the forefront for understanding the origin of endogenous rhythmic and patterning(pattern formation) phenomena observed in nature, such as in animal skins, embryology, cell division, genetics and technological applications.

Alan Turing [1] was the first to realize that under certain conditions two interacting chemicals can generate a stable inhomogeneous pattern if one of the substances diffuses much faster than the other. This kind of instability (Turing instability) generate biological patterns by gene activation.

Alens Gierer and Heins Meinhardt [12], and subsequently in [14, 15], twenty years after the popular paper of Turing, proposed that the instabilities in reacting and diffusing systems as a result of interaction of two biochemical substances with different diffusion rates can only occur if one of the substances(activator) influence the production of itself and that of the other one, while the other substance(inhibitor) inhibits the production. They assumed that the activator is a slowly diffusing substance while the inhibitor is a rapidly diffusing substance. Generally all models that exhibit this property are called ``Activator - Inhibitor models". Hence the model is named as Gierer – Meinhardt and is described by the following system of dimensionless equations on a spatial bounded domain $\Omega$:

$$
\begin{align*}
A_t &= \varepsilon^2 \Delta A - A + \frac{n_0}{H_{0}}, & x \in \Omega, & t > 0 \\
\tau H_t &= D \Delta H - \mu H + \frac{n_0}{H_{0}}, & x \in \Omega, & t > 0
\end{align*}
$$

(1)

with neumann bounary conditions

$$
\partial A = \partial H = 0, & x \in \partial \Omega.
$$

(2)

where $A$ and $H$ represent the activator and the inhibitor concentrations, $\varepsilon$ and $D$ are their diffusivities respectively, and where $\tau$ and $\mu$ are the reaction time rate and decay rate of the inhibitor; $D$ is assumed to be large and $\varepsilon$ and $\tau$ small (positive) and represent the diffusion coefficients of the activator and inhibitor respectively. The exponents $(p, q, r, s)$ are assumed to satisfy

$$
\begin{align*}
p > 1, & \quad q > 0, & \quad r > 0, & \quad s \geq 0, & \quad 0 < \frac{r-1}{s} < \frac{r}{s+1},
\end{align*}
$$

(3)

The mean-reverting process is a model employed in economics(in prices of commodities such as oil, electricity, stock market, interest rate, exchange rates etc ) to reconcile some of the more disturbing properties of Wiener paths with physical reality. In the Geometric Brownian Motion(GBM),given by the equation

$$
dx_t = \eta x_t dt + \sigma dW_t
$$

(4)

the price of a commodity can reach unrealistic levels for long period of time. The mean reverting process, ensures that the stochastic element gravitate over time towards the mean reversion stochastic element level. The mean-reverting process can be defined mathematically as a stochastic process $x_t$ given by the stochastic differential equation :
\[ dx_t = \eta(\bar{x} - x_t)dt + \sigma dW_t, \quad x(0) = x_0 \]  

(5)

where \( \eta \) is the speed of reversion (drift),

\( \bar{x} \) is the long-run equilibrium level (or the long-run value around which \( x_t \) tends to oscillate or revert),

\( \sigma \) is a volatility (or standard deviation) and

\( W_t \) is a standard Wiener process, \( W_t \equiv N(0, \sqrt{t}) \).

Numerical studies by Gierer and Meinhardt [12] and more of recent by [10] Holloway have revealed that when \( \sigma \) is small and \( D \) is large and finite, GM model seems to have stable stationary solutions with the property that the activator concentration is localized around a finite number of points in \( \mathbb{R} \) in form of spikes. Further studies by [23, 21, 22], have shown that the spike solutions to GM model have been much explored through different approaches. In Matthias et al [24], the spiky patterns for GM system in which the diffusion constant of the inhibitor has jump discontinuities resulted in the existence of interior spikes located away from the jump discontinuity. In this research, we proposed to study the dynamics of GM model under the influence of stochastic diffusivity of the inhibitor, \( D_h \) of mean reverting stochastic differential equation, which varies in time and create Turing patterns in forms of spikes. Therefore in order to have the random coefficient of diffusion not to be derived far away from the usual constants, it will be allowed to oscillate stochastically around the long-run value using the mean-reverting idea. We expect that for long time enough, the new stochastic Gierer-Meinhardt model will converge to deterministic GM model with certain probability. This assertion is in line with the Large Deviations principles which gives the general asymptotic results for systems with large time and small noise problems resulting in the exponential decay of probability measures as is given in detail by J. Callen et al in [25]. Numerically, we have shown how the spikes vanishes to a stable number over time using the finite difference methods with the help of Matlab simulations by varying the noise, diffusion and time parameters in the model. The probability of convergence from stochastic model to deterministic has also been determined. The proposed model is given by the following system of equations obtained from the scaled Gierer-Meinhardt model:

\[ \begin{align*}
\alpha_t &= k\alpha_{xx} - \alpha + \frac{\alpha^2}{h}, \quad x \in \Omega, \quad t > 0 \\
h_t &= D\alpha_{xx} - h + \alpha^2, \quad x \in \Omega, \quad t > 0,
\end{align*} \]  

(6)

with the neumann boundary conditions

\[ n_\alpha = \alpha_x = 0, \quad x \in \partial \Omega. \]  

(7)

where the unknowns \( \alpha = \alpha(x, t) \) and \( h = h(x, t) \) represent the concentrations of activator and the inhibitor at a point \( x \in \Omega \) and time \( t > 0 \). \( \Omega \) is abounded smooth domain defined as \( \Omega = [0, 1] \). \( k \) and \( D \) are their diffusivities respectively. \( k = 1 \) (positive) \( D \) is assumed to be large and stochastic, given by the stochastic differential equation.
\[ d\mathcal{O} = c(\mathcal{O} - D)ds + \epsilon dW \]  

(8)

\( \mathcal{O} \) is the long-run equilibrium level (or the long-run value around which \( D \) tends to oscillate or revert),

\( c \) is the rate of reversion to the mean and

\( W \) is a standard Wiener process, with mean 0 and standard deviation \( \sqrt{\epsilon} \), \( \epsilon \) a volatility (or standard deviation) which determines the strength of the noise.

Our study is important in that it addresses the important questions about the effects of "classical" noise (disturbance) on the Gierer-Meinherdt Model. In particular it will answer the question that with the diffusion coefficient of mean reverting type (MRP), can we still get patterns. Biologically, this study will establish the effect of noise that will affects the development of patterns/organisms in Biology. In general, the results will provide interesting insights regarding the role of noise, convergence and the long term behaviour of models based on such stochastic processes.

2 Methodology/Theoretical Analysis

For the purpose of computer simulations of the model, we will use Matlab Programming languages by discretizing the model equations. This program is eloquent in its random number generation and computation as well as its capability of creating graphs. The discretization is a common tool for transforming a continuous problem into a discrete one from which approximations can be calculated that closely resemble the actual solutions.

The method of choice for this project is the Explicit Euler method or forward difference method derived from the Taylor’s polynomial theorem. Using a forward difference at time step \( t \) and spatial element at step \( j \), the derivative in time for the concentration of activator and inhibitor, respectively can be approximated by discretization, and for error terms \( R_a(x) \) sufficiently small, can be written as :

\[ a_z = \frac{a(t+1) - a(t)}{\Delta t} \]  

(9)

and

\[ h_z = \frac{h(t+1) - h(t)}{\Delta t} \]  

(10)

Similarly, the central-difference at time step \( t \) and spatial element at step \( j \), the second spatial derivative for the two substances, respectively, which represent their diffusions as:

\[ a_{xx} = \frac{a(t+1) - 2a(t) + a(t-1)}{\Delta x^2} \]  

(11)

and

\[ h_{xx} = \frac{h(t+1) - 2h(t) + h(t-1)}{\Delta x^2} \]  

(12)

However, for the second derivative in space, since indices of arrays in MATLAB must start at 1, not 0 or negative, we deviated slightly in the code. Similarly with \( D \) stochastic of mean
reverting process which is time dependent, the stochastic differential equation in (8) can be discretize as:

\[ D(i+1) - D(i) = c(Duv - D(i)) + \text{random} \]  

(13)

To calculate the approximations to \( u_{xnx}(i,j) \) and \( h_{xnx}(i,j) \) at \( x = 0 \) and \( x = 1 \), we need to use the boundary conditions (obc.), i.e., \( h(1,j) = 1 \), while the second derivatives of \( u \) and \( h \) we have \( \frac{2(a(i,j)-a(i+1))}{dx^2}, \frac{2(h(i,j)-h(i+1))}{dx^2} \) respectively.

By plugging these discretization into the activator equation in (6), after some rearrangements and letting \( \frac{kdt}{dx^2} = s \), we obtain the following equation

\[ a(i+1,j) = s(a(i,j+1) + a(i,j-1)) + (-2s)a(i,j) + (1 - dt)a(i,j) \]

\[ + dt((a(i,j))^2)/h(i,j) \]

Similarly for the inhibitor, the equation is given by:

\[ h(i+1,j) = u(h(i,j+1) + h(i,j-1)) + (-2u)h(i,j) + (1 - dt)h(i,j) \]

\[ + dt((a(i,j))^2)/h(i,j) \]

where \( \frac{kdt}{dx^2} = s \).

For the system to be stable, according to Euler forward method, the values of \( \frac{dx}{dt} \) and \( \frac{dt}{dx} \) should be chosen appropriately so that \( 0 < s \leq 0.5 \), similarly with \( u \). Let \( n = 100 \) be the number of times the interval \([0,1]\) is divided, then \( \frac{dx}{dt} = 1/(n+1) \) and let also timesteps = 100 and \( \frac{dt}{dx} = 0.0001 \). Therefore the Matlab code will have, for each time step, algebraic equations with 202 unknowns \([a(i,j), h(i,j)]\). Variations of these approximations, together with the initial and boundary conditions are used to simulate the solution for the system.

3 Results and Discussions

Here we present the results of various simulations showing how the spikes vanishes using different values of \( u \) and time-steps. The blue solid line and dash red line represents the concentrations of activator and inhibitor respectively.
Figure 1: Initial condition with t-steps=1,e=0.01,mav=0.01

Figure 2: 4 spikes,t-steps=10^5,e=0.01,mav=0.01
Figure 3: 2 spikes, t-steps=3\times10^5, e=0.01, mav=0.01
Moreover, increasing the strength of the noise to \( \sigma = 0.1 \), we notice formation of spikes but with low amplitude as can be seen below:
Figure 5: 15 regular spikes with t-steps=$10^5$, e=0.1, mav=0.01
Figure 6: 4 spikes, t-steps=$1.5 \times 10^5$, $e=0.1$, $mav=0.01$
Figure 7: 2 spikes, t-steps = 5 x 10^4, e = 0.1, mav = 0.01

Figure 8: 1 spike, t-steps = 5 x 10^4, e = 0.1, mav = 0.01
However, with strength of noise, $\sigma = 2$ no regular patterns are formed at lower time steps (1-80000) as can be seen below:

Figure 9: 15 irregular spikes with t-steps=$10^4$, $\sigma=2$, mav=0.01
Figure 10: 13 irregular spikes, t-steps=3 \times 10^4, e=0.1, mav=0.01

Figure 11: 2 spikes, t-steps=9 \times 10^4, e=2, mav=0.01
3.1 Determination of Probability of convergence from Stochastic to Deterministic model.

According to the large deviation principle and as shown by [25], as the level of noise, $\sigma$ falls over time, with a constant mean reverting pull, $c$; constant $\overline{D}$, representing the fundamental or stable(long-run) equilibrium point, and constant variance $\sigma$ while $W(t)$ is the Wiener process, the following diffusion process, $dD_t$, converges (in probability) to the fundamental value exponentially quickly:

$$
\begin{align*}
\frac{dD_t}{D(0)} &= c(\overline{D} - D)dt + \sigma dW(t) \\
\text{This equation is similar to (8), with additional initial condition. Given that } &D_0(t) = \exp(-ct) \text{ is the solution to the corresponding deterministic equation, then for any } \delta > 0, T > 0, \\
\lim_{\delta \to 0} \log P_{0 \leq t \leq T} |D_x(t) - D_0(t)| > \delta & = -\kappa \delta^2 \frac{\exp(\frac{\epsilon^2}{\sigma^2})}{\exp(1)} \\
\text{taking the exponential of both sides} &P_{0 \leq t \leq T} |D_x(t) - D_0(t)| > \delta = \exp(-\frac{\kappa \delta^2}{\epsilon^2}) \exp(\frac{\epsilon^2}{\sigma^2}) \\
\text{and as } T \to \infty, &P_{0 \leq t \leq T} |D_x(t) - D_0(t)| > \delta = \exp(-\frac{\kappa \delta^2}{\epsilon^2})
\end{align*}
$$

4 Conclusion

We established the turing instability inform of spiky solutions and the stochastic gierer - meinhardt model can be approximated to deterministic model with certain probability. The
biological implication of this findings is that the presence of small noise inform of shortage of food, influence of weather, small shocks etc cannot affect pattern formation.

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