Spectral Methods for Resolving Spike Dynamics in the Geirer-Meinhardt Model

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Received 23 December 2006; Accepted (in revised version) 5 July 2007

Available online 30 October 2007

Abstract. The Gierer-Meinhardt reaction-diffusion model is analyzed using a spectral collocation method. This reaction-diffusion system is governed by activator and inhibitor concentrations. Initially, the system is considered in one dimension and then in two dimensions; numerical results are presented for both cases. The algorithmic complexity and accuracy are compared to those of a moving finite element method. Finally, observations are made concerning when to use the proposed spectral method as opposed to the established moving mesh method.

AMS subject classifications: 65M70

Key words: Spike dynamics, Gierer-Meinhardt model, spectral collocation.

1 Introduction

In the 1970s, Gierer and Meinhardt [6] proposed a variety of models related to biological pattern formation [23]. These models are used to describe the reactions between two substances, an activator and an inhibitor; other models have also been suggested to study pattern formation including the Schnakenberg model [25]. In this paper, a spectral collocation method is proposed to solve one such model, now called the Gierer-Meinhardt model, that describes the concentrations of the activator and inhibitor as functions of space and time. In this model, the activator is an autocatalyst, that is, it has the ability to make more of itself. In contrast, the inhibitor lives off the activator and reduces the activator's concentration. By analyzing the concentrations at different times, we can see

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how these two substances interact. Also, by altering parameters that effect the reaction speed of the two concentrations, a variety of different states can be achieved [6,22].

The Gierer-Meinhardt (GM) model in dimensionless form is as follows:

$$A_t = \epsilon^2 \nabla^2 A - A + \frac{A^p}{H^q}, \tag{1.1a}$$

$$\tau H_t = \kappa \nabla^2 H - H + \epsilon^{-1} \frac{A^m}{H^s}, \quad x \in \Omega, \quad t > 0,$$
(1.1b)

$$\partial_n A = \partial_n H = 0, \qquad x \in \partial \Omega, \quad t > 0,$$
 (1.1c)

where *A* is the activator concentration, *H* is the inhibitor concentration, ϵ is the activator diffusivity satisfying $0 < \epsilon \ll 1$, κ is the inhibitor diffusivity satisfying $\kappa > 0$, τ is the reaction-time constant, and Ω is a bounded two-dimensional domain. ∂_n denotes the normal derivative with respect to the boundary $\partial\Omega$, and *x* is the spatial coordinate(s). The set of exponents (*p*,*q*,*m*,*s*) satisfies

$$p > 1$$
, $q > 0$, $m > 0$, $s \ge 0$, $\frac{p-1}{q} < \frac{m}{s+1}$

The GM model exhibits rich spike dynamics that vary depending on the parameters chosen; these spike solutions have been studied using finite element moving mesh methods described in [13, 18, 19]. Asymptotic analysis has also been applied to the spike dynamics problem to provide analytical insight into the reaction-diffusion model [8]. For the one-dimensional GM model, extensive asymptotic and numerical results have been presented for the case when $\tau = 0$, and also for $\tau > 0$ [13]. For the two-dimensional GM model there have been limited asymptotic and numerical results only for the case when $\tau=0$. Recently, numerical results have been presented for the case when $\tau > 0$ [18,19], but asymptotic results are as yet unavailable.

The main focus of this paper is to provide numerical results for the two-dimensional GM model for the case when $\tau > 0$ using spectral collocation. The purpose of this is to provide insight into the spike dynamics of the model, to introduce a computationally feasible way of solving spike dynamics problems, and to partially validate the results obtained in [19], since theoretical results are limited for this case. In Section 2, we outline the implementation of a Chebyshev spectral collocation method to the one-dimensional problem (2.1a), and present numerical results arising from the method. In Section 3, we show how to extend the Chebyshev spectral method to two spatial dimensions and present numerical results for the case $\tau > 0$. These results are compared to the ones in [18,19].

2 One-dimensional GM model

In one spatial dimension, the dimensionless GM model can be written as

$$A_t = \epsilon^2 A_{xx} - A + \frac{A^2}{H}, \qquad (2.1a)$$

$$\tau H_t = \kappa H_{xx} - H + \epsilon^{-1} A^2, \qquad (2.1b)$$

660