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Asymptotic analysis of a chemotactic model of bacteria colonies

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Abstract

An estimate of the distance between spots generated by a bacterial colony model is obtained. The model describes the morphogenesis of a spot pattern in colonies of chemotactic strains of *Escherichia coli*. Asymptotic methods for other cell-chemotaxis models, which have been successfully used by previous researchers, can be applied also to this model. However the calculations and the result is more complicated for this model. The result is verified by comparing it with the results by numerical computations of solutions of the model. © 2005 Elsevier Inc. All rights reserved.

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1. Introduction

We consider an estimate of the distance between spots generated by the bacterial colony model developed by Kawasaki and Shigesada [6].

Much attention has been paid to pattern formation in the natural world. Especially, patterns of bacteria colonies have long been investigated, and mathematical models of pattern formation have recently developed extensively (for example, [1,6,5,7]).

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Colonies of chemotactic strains of the bacterium *Escherichia coli* show pattern with spots, when they are cultured under some environmental conditions [3]. Kawasaki and Shigesada [6] consider the mechanism of the morphogenesis of the spot pattern, using a reaction–diffusion model.

In this paper, we consider an estimate of the distance between spots for the model in one space dimension. Basically, we follow the methods mainly in [8,9]. However, due to slight differences in the linearized systems, our model needs more complicated calculations than that in [8].

In Section 2, we introduce the model developed in [6], and change it into a dimensionless form.

In Section 3, we linearize the system, and consider the exponential solutions. For the linear system, solutions can be constructed in the integral form by the superposition. By numerical simulations, we can see that the positions of the spots are almost determined while the disturbance is small (see Fig. 1). Hence we can use the linearized system instead of the original one.

In Section 4, we consider the leading edge, where the spots just begin to be generated. Here we use the numerical result that the propagation speed is almost constant (Fig. 1). Considering the leading edge, we can reduce the number of the independent variables. Thus, by the method of
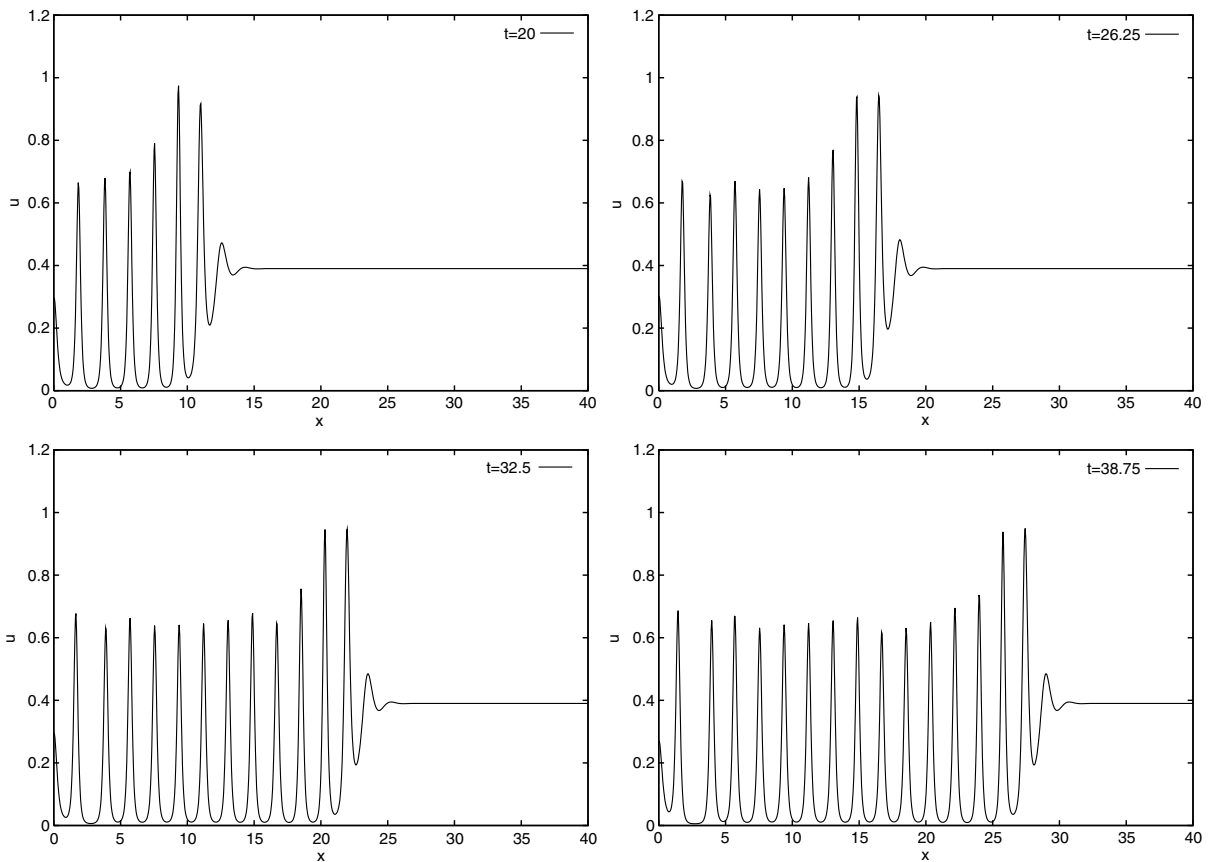

Fig. 1. A numerical solution shows spot generation. Each graph presents the density distribution of the bacteria for $t = 20$, $t = 26.25$, $t = 32.5$, $t = 38.75$, respectively.