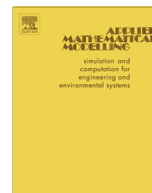




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Hyperbolic model for bacterial movement through an orthotropic two-dimensional porous medium

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ABSTRACT

In this paper an alternative hyperbolic model for bacterial movement is used to represent the migration of a bacterial population through an anisotropic porous medium filled with a nutrient. It is shown how this model can effectively reproduce bacterial wave fronts, which are observed in bacterial migration through porous media experiments. Time and length scales are defined where hyperbolic model preserves its physical validity and predicts very different bacterial concentration profiles in comparison with the classical Keller–Segel model for chemosensitive movement. Representative values of the hyperbolic model parameters are taken from experimental systems reported in literature and it is found that characteristic diffusion time is much smaller than characteristic growth time; in this way, the practical usefulness of the proposed model is limited to time scales when bacterial growth is negligible for the studied system. An analytical solution is presented and discussed for the two-dimensional diffusion of bacterial population within a square orthotropic porous medium, and it is shown that anisotropic properties of the medium lead to preferential bacterial flows.

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1. Introduction

The study of populations of bacterial microorganisms is important at different levels, because they are the most extended life form and can be involved in industrial processes like medicines production, bioremediation of polluted soils and food processing as well. Several kinds of bacterial microorganisms are provided with threadlike appendages or extensions which are used for motion in fluid media; in the case of flagellated bacteria, the movement of an individual is composed of straight-line runs which are interrupted by breaks when bacteria modifies its direction, the resulting path is a random walk and the macroscopic spread of the whole population is named random motility. The above-mentioned behavior could be altered by the presence of different stimuli in the surroundings; for example, bacteria like *Escherichia coli*, *Pseudomonas putida* and *Salmonella typhimurium*, can sense chemical gradients in their environment and be attracted to amino acids, carbohydrates and other beneficial nutrients; whereas they avoid extreme pH and metabolic waste that could reveal the existence of overpopulation. This biological phenomenon, called chemotaxis, performs an important role in degradation processes in natural environment, oil extraction and biological based waste treatment technologies as well. Several of such processes take place inside porous media with stagnant fluid phase(s); for instance, the microbial enhanced oil recovery which is used to improve

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the extraction of trapped oil in porous media and in situ bioremediation that applies microorganisms to degrade pollutants in the soils and surface or subsurface waters.

The most used model for chemotaxis is the classical Keller–Segel (KS) model for chemosensitive movement, which was established by Keller and Segel in 1970; they studied the aggregation behavior of the soil-living amoeba *Dictyostelium discoideum* [1]. KS model describes the movement process of bacterial population like a Brownian motion. Nevertheless, bacteria move in nearly straight-line, stop to change direction and continue the run in the new route. This characteristic movement is best described as a velocity jump process rather than a Brownian motion [2]. In addition, KS model presents the disadvantage of infinite speed of signal propagation. Therefore, it is justified to investigate alternative models for movement of bacterial populations; for example, Dolak and Hillen have derived models for chemosensitive movement based on Maxwell–Cattaneo’s law of heat propagation with finite speed to qualitatively describe pattern formation experiments with slime mold *D. discoideum* and bacteria *S. typhimurium* in petri dishes with semi-solid agar medium [3]. Filbet et al. derived hyperbolic models for chemosensitive movements through a Chapman–Enskog expansion and performed numerical simulations to model experiments with human endothelial cells on matrigel [4].

The Maxwell–Cattaneo (MC) equation has been extensively used to model a variety of energy and mass transfer processes as an alternative to classical diffusion laws of Fourier and Fick [5–7]. The main feature of MC equation is the prediction of finite speed of signal propagation through a medium, which avoids the inherent and nonphysical infinite speed of classical diffusion models. The coupling of MC equation with the corresponding balance equation leads to a hyperbolic differential equation that describes the time evolution of property concentration (energy or mass); for this reason, an energy transfer process is called hyperbolic heat conduction when MC equation is considered [8]. However, the MC equation’s validity is still under debate because many researchers have presented evidence in behalf of [9–11] and against it [12–15]. The arguments are both theoretical and experimental, while the principal issue is the lack of experimentally measured values of relaxation time parameters [16,17].

In this paper we apply the MC equation to model the diffusion and growth of a bacterial population through an anisotropic porous medium and verify its physical validity. The objective of this work is the qualitative analysis of the proposed model rather than a quantitative description of any experimental system. A characteristic relaxation time is introduced to represent the delay time between the bacterial mass flux and the bacterial and nutrient concentration gradients, and the medium anisotropy is characterized with a bacterial diffusion tensor (random motility tensor). First, to simplify the analysis, a one-dimensional system is considered and we use experimental data from studies reported in literature [18,19]; then an anisotropic two-dimensional case is investigated to evaluate the effect of the anisotropy of the medium. Specially, we focus on length and time scales where the MC equation predicts very different bacterial concentration profiles in comparison with the classical Keller–Segel model. The analyzed system has been studied both experimentally and theoretically [20], and consists of the bacteria *E. coli* strain RW262, which moves through a porous medium (sand column) filled with galactose (nutrient). The considered strain presents positive chemotaxis towards galactose and can metabolize it. Later, it is shown that diffusion time scale is much smaller than growth time scale; thus, we present an analytical solution for diffusion of bacteria with relaxation in a porous square orthotropic medium.

2. Mathematical model and solution

The analyzed system was selected because the availability of experimental data which are shown in Table 1. First, we consider a one-dimensional case and two experiments to evaluate time and length scales where hyperbolic chemotaxis model is physically valid. Experiment 1 represents a sand column filled with an initial uniform concentration of nutrient (galactose) and total absence of bacteria; suddenly, an end of the column is maintained with a constant concentration of bacteria. In Experiment 2 an amount of bacterial solution of known concentration is added to an extreme of the column and this is represented like an initial bacterial concentration profile.

The mass balance equations for bacterial population and nutrient are:

$$\frac{\partial B}{\partial t} + \nabla \cdot \mathbf{J}_B = R_B, \quad (1)$$

Table 1
Parameter values used to solve Eqs. (1)–(6) [3,20].

Parameter	Value
B_0	2.0×10^7 cells/mL
τ	10 s
μ_x	1.05×10^{-5} cm ² /s
D	1.61×10^{-6} cm ² /s
χ	8.40×10^{-5} cm ² /s
k_d	0.03 mM
k_s	0.03 mM
k_m	0.35 h^{-1}
ψ	0.2

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