



Global existence and asymptotic stability of smooth solutions to a fluid dynamics model of biofilms in one space dimension



Roberta Bianchini^a, Roberto Natalini^{b,*}

^a *Dipartimento di Matematica, Università degli Studi di Roma “Tor Vergata”, via della Ricerca Scientifica 1, I-00133 Rome, Italy*

^b *Istituto per le Applicazioni del Calcolo “M. Picone”, Consiglio Nazionale delle Ricerche, via dei Taurini 19, I-00181 Rome, Italy*

ARTICLE INFO

Article history:

Received 5 June 2015

Available online 21 October 2015

Submitted by P.G. Lemarie-Rieusset

Keywords:

Fluid dynamics models

Dissipative hyperbolic equations

Biofilms

Global existence

Asymptotic stability

ABSTRACT

In this paper, we present an analytical study, in the one space dimensional case, of the fluid dynamics system proposed in [3] to model the formation of biofilms. After showing the hyperbolicity of the system, we show that, in an open neighborhood of the physical parameters, the system is totally dissipative near its unique non-vanishing equilibrium point. Using this property, we are able to prove existence and uniqueness of global smooth solutions to the Cauchy problem on the whole line for small perturbations of this equilibrium point and the solutions are shown to converge exponentially in time at the equilibrium state.

© 2015 Elsevier Inc. All rights reserved.

1. Introduction

A biofilm is a complex gel-like aggregation of micro-organisms like bacteria, algae, protozoa and fungi. They stick together, attach to a surface and embed themselves in a self-produced extracellular matrix of polymeric substances, called EPS.

In this paper, we study a fluid dynamics model, introduced in [3], to describe the space–time growth of biofilms. This model was built in the framework of mixture theory, see [10] or [1], and conserves the finite speed of propagation of the fronts. For simplicity reasons, the model describes a biofilm in which there is just one species of micro-organisms, or better, all species are lumped together, but it can be extended to other situations. It has been derived starting from the equations for mass and momentum conservation, and some physical constraints and assumptions about the behavior of the biological aggregates and their interaction with the surrounding liquid. Here we assume that the complex structure of biofilms is described by four different phases: bacteria $B(x, t)$, extracellular matrix EPS $E(x, t)$, dead cells $D(x, t)$ and a liquid phase $L(x, t)$. The quantities B, E, D, L are the volume fraction of each component, then $B, E, D, L \in [0, 1]$.

* Corresponding author.

E-mail addresses: bianchin@uniroma2.it (R. Bianchini), roberto.natalini@cnr.it (R. Natalini).

Since we are dealing with a one dimensional model, then we have $x \in \mathbb{R}$, $t > 0$. Therefore, in this paper we consider the whole x -axis. Clearly, the problem with a finite x -domain, i.e. the interval $[a, b]$, with $a, b \in \mathbb{R}$, $a < b$, is another interesting problem, but, in this case, our proof of global existence does not work and so this problem will be considered in a future work.

For simplicity reasons, we assume that B, E, D have the same transport velocity v_S . The reaction terms are indicated by Γ_Φ , with $\Phi = B, E, D, L$. Imposing the total balance of mass and momentum for each phase Φ , we can write the model, see [3] for all details. This model was originally proposed in all space dimensions, and in the present case of one space dimension, is given by a system of six partial differential equations, which read:

$$\begin{cases} \partial_t B + \partial_x(Bv_S) = \Gamma_B, \\ \partial_t E + \partial_x(Ev_S) = \Gamma_E, \\ \partial_t D + \partial_x(Dv_S) = \Gamma_D, \\ \partial_t L + \partial_x(Lv_L) = \Gamma_L, \\ \partial_t((1-L)v_S) + \partial_x((1-L)v_S^2) = -(1-L)\partial_x P - \gamma\partial_x(1-L) \\ \qquad\qquad\qquad + (M - \Gamma_L)v_L - Mv_S; \\ \partial_t(Lv_L) + \partial_x(Lv_L^2) = -L\partial_x P - (M - \Gamma_L)v_L - Mv_S. \end{cases} \quad (1.1)$$

To reformulate our model in a more suitable form, we assume the following volume constraint:

$$L = 1 - (B + E + D), \quad (1.2)$$

that is the assumption that the mixture is saturated and no empty space is left. In addition to the balance mass of each component, we also have the total conservation of the mass of the mixture by the following assumption:

$$\Gamma_B + \Gamma_E + \Gamma_D + \Gamma_L = 0. \quad (1.3)$$

The mass constraint in (1.3) states that the mixture is closed, i.e. there is no net production of mass for the mixture. According to [3], the reaction terms are given by:

$$\Gamma_B = K_B BL - K_D B; \quad (1.4)$$

$$\Gamma_D = \alpha K_D B - K_N D; \quad (1.5)$$

$$\Gamma_E = K_E BL - \epsilon E. \quad (1.6)$$

The birth of new cells at a point depends on the quantity of liquid available in the neighborhood of the point, that is why the birth term in Γ_B is a product between the volume fraction B of active cells and the volume fraction L of liquid. In this way, the mass production term Γ_B is the difference between a birth term and a death term, where the second is proportional to the fraction B of bacteria, with rate k_D . The death term in the expression of Γ_B gives rise to a creation term of the mass exchange rate for dead cells Γ_D , with a proportional coefficient α , since a part of the active cells goes into liquid when the cell dies. In Γ_D , we also find a natural decay of dead cells with a constant decay rate k_N . The EPS is produced by active cells in presence of liquid and therefore the production term will be proportional to BL , where k_E is the growth rate of EPS. There is also a natural decay of EPS with rate ϵ . To conclude this explanation about the mass exchange terms, we choose Γ_L in order to enforce condition (1.3). See again [3] for more details.

Download English Version:

<https://daneshyari.com/en/article/6417577>

Download Persian Version:

<https://daneshyari.com/article/6417577>

[Daneshyari.com](https://daneshyari.com)