On the Well-Posedness of a Class of Mathematical Models Describing Processes in Spatially Heterogeneous Biofilm Communities

Hermann J. Eberl¹, Messoud A. Efendiev², <u>Stefanie Sonner³</u> ¹ University of Guelph, Canada heberl@uoguelph.ca ² Institute of Biomathematics and Biometry, Helmholtz Center Munich, Germany messoud.efendiyev@helmholtz-muenchen.de ³ BCAM Basque Center for Applied Mathematics, Spain ssonner@bcamath.org

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Biofilms are dense aggregations of microbial cells encased in a slimy extracellular matrix forming on biotic or abiotic surfaces in aqueous surroundings. Such multicellular communities are a very successful life form and able to tolerate harmful environmental impacts that would eradicate free floating individual cells. Biofilms play an important role in various fields and mathematical models of biofilms have been studied for several decades. They range from traditional one-dimensional models describing biofilms as homogeneous flat layers, to more recent two- and three-dimensional biofilm models that account for the spatial heterogeneity of biofilm communities.

The prototype of the models we address is a deterministic multidimensional biofilm growth model, which was first proposed in [2]. The model describes the growth of a bacterial biofilm community consisting of only one species, and is formulated as a highly non-linear reaction-diffusion system for the biomass density and the concentration of the growth-controlling substrate. The main difficulty is to model the spatial spreading mechanism of biomass: Expansion occurs locally only where and when the biomass density approaches values close to the maximal possible cell density, and biofilm and liquid surroundings are separated by a sharp interface. While the substrate concentration satisfies a standard semi-linear parabolic equation, the spatial spreading of biomass exhibits two non-linear diffusion effects. The biomass diffusion coefficient possesses a polynomial degeneracy which is well-known from the porous medium equation and shows super diffusion. Both non-linear diffusion effects are necessary to reflect the experimentally observed characteristic growth behavior of biofilms, and the highly irregular structure causes difficulties in the mathematical analysis. The single-species single-substrate model is in good agreement with experimental findings and was analytically studied in [3], where its well-posedness was established.

Various applications require to take further biofilm processes into account and to distinguish between multiple biomass components. The prototype biofilm model was therefore extended to model biofilms which consist of several types of biomass and account for multiple dissolved substrates. The model introduced in [1] describes the diffusive resistance of biofilms against the penetration by antibiotics. In [4] an amensalistic biofilm control system was modelled, where a beneficial biofilm controls the growth of a pathogenic biofilm. The structure of the governing equations of the multi-species models differs essentially from the mono-species model, and the analytical results for the prototype model could not all be carried over to the more involved multi-species case. In both articles, the model behavior was studied numerically and the existence of solutions was established. The question of uniqueness of solutions, however, remained unanswered in both cases.

Recently, one further multi-component biofilm model was proposed, that describes quorum-sensing in growing biofilm communities. Quorumsensing is a cell-cell communication mechanism used by bacteria to coordinate behavior in groups. It comprises a similar structure as the previous multi-component models [1] and [4], but has the particularity that adding the governing equations for the involved biomass components we recover exactly the mono-species biofilm model. Taking advantage of the known results for the prototype model we were able to prove the existence and uniqueness of solutions and its continuous dependence on initial data in [5]. It was the first time that a uniqueness result was obtained for multi-species reaction-diffusion models of biofilms that extend the single-species model [2]. The solution theory developed in [5] can be extended to more general multicomponent models and provides a positive answer to the question of uniqueness of solutions for the models [1] and [4].

We give an overview of the analytical results obtained for the multicomponent biofilm models in [1], [4] and [5] and present numerical simulations that illustrate the model behavior.

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