Parallel Session

Mathematical Methods in Biology VIII

SPACE-TIME FRACTIONAL DIFFUSION EQUATIONS IN CHEMOTAXIS AND IMMUNOLOGY

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Keywords: Chemotaxis, Patlak-Keller-Segel equation, Nonlocal diffusion, Lévy walk.

In the presence of sparse attractants, the movement of both cells and large organisms has been shown to be governed by long distance runs, according to an approximate Lévy distribution. In this talk we clarify the form of biologically relevant PDE descriptions for such movements. Motivated by experiments including [3] and [4], we consider a microscopic velocity-jump model in which an individual performs occasional long jumps according to an approximate Lévy distribution. We derive the appropriate kinetic-transport equation, where the collision term describes the nonlocal motion. Under a perturbation argument and an appropriate hyperbolic scaling in space and time, we derive fractional Patlak-Keller-Segel equations [2] for the density ($\bar{u}$) of some chemotactic population in the presence of a chemoattractant (of concentration ρ):

$$\begin{aligned} \partial_t \bar{u} &= c_0 \nabla \cdot (D_\alpha \nabla^{\alpha-1} \bar{u} - \chi \bar{u} \nabla \rho), \\ \partial_t \rho &= D_\rho \Delta \rho + f(\bar{u}, \rho). \end{aligned} \tag{1}$$

We consider the implications of such biological diffusion in the context of T cell movement in the brain [5]. In response to *Toxoplasma gondii* infections, these cells have been shown to exhibit a mixed Lévy walk [1] in which an additional resting time occurs between directional changes. The resulting equation generates a time-fractional term in (1) and allows us to formally interpret the results of [1]. Consequently, we shed light on the extent to which Lévy flight behaviour impacts on the average time taken for T cells to locate the sparsely distributed infected targets. We use the PDE description to present numerical results.

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A MODELING AND SIMULATION STUDY OF THE INVASION PHENOMENON IN BIOFILM REACTORS

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Keywords: Biofilm, Invasion Model, Hyperbolic free boundary value problem, Numerical simulations, Anammox process.

Biofilm reactors represent the primary means to harness the biofilm usefulness for wastewater treatment by means of the synergistic interactions and biochemical transformations characterizing these microbial communities. The microbial invasion and colonization of preexisting biofilms has been found to play a significant role in the establishment of mixed species communities, as it can determine biofilm landscape and contribute to rapid alterations in biofilm populations. In this work, we introduce the free boundary value problem for the invasion phenomenon in biofilm reactors which takes into account the dynamics of the biofilm compartment as well as the bulk liquid phase in terms of both substrates and planktonic cells. The model is derived by coupling a reactor mass balance for planktonic cells and substrates with a full one-dimensional invasion model. The resulting mathematical problem consists of a system of nonlinear hyperbolic partial differential equations governing the microbial species growth and a system of semilinear elliptic partial differential equations describing the substrate diffusive trends. The model is completed with a system of elliptic partial differential equations governing the diffusion and reaction of planktonic cells, which are able to switch their mode of growth from planktonic to sessile when specific environmental conditions are found. Two systems of nonlinear differential equations for the substrate and planktonic cells mass balance within the bulk liquid are also considered. The free boundary evolution is governed by a differential equation which accounts for the displacement velocity due to the microbial biomass and the detachment flux as well. The model has been studied both by analytical methods and numerical studies. In particular, the existence and uniqueness of the solutions has been proved in the class of continuous functions. Numerical simulations have been developed for a real engineering/biological case which examines the invasion of specific microbial species, the Anammox bacteria, in a constituted wastewater biofilm. The invasion model has been adopted to illustrate the trends related to the establishment of such a multispecies community and to assess the effect of specific operational conditions on the biofilm colonization by Anammox bacteria. For all the cases analyzed, real data from existing literature are used to feed numerical simulations, which produce results in nice agreement with experimental findings.

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THE AUXILIARY REGION METHOD FOR COUPLING PDE AND BROWNIAN-BASED DYNAMICS FOR REACTION-DIFFUSION SYSTEMS

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Keywords: Hybrid modelling, Stochastic reaction-diffusion, Multiscale modelling, Auxiliary region.

Reaction-diffusion systems are important tools for the study of many biological and physical phenomena, many of which span many spatial scales. Within these, there are many examples which require very detailed descriptions in some regions of space, while in the rest of the domain, large particle numbers mean that continuum methods are appropriate. For example, we could be interested in the release of calcium ions through calcium-gated channels on the endoplasmic reticulum, or want to model the formation of defects in a liquid crystal. We present the auxiliary region method - a novel spatially-coupled hybrid method which interfaces Brownian-based microscopic dynamics to the corresponding mean-field PDE through the use of "auxiliary regions" which bridge the gap between the micro and macro scales. We describe the algorithm and demonstrate its effectiveness on a large array of problems; pure diffusion, morphogen gradient formation and a travelling wave problem, spanning over one and three dimensions. We also demonstrate that the method results in small errors with no bias for particles to gravitate towards either side of the interface.

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GAINING INFORMATION FROM SUBMODELS: MODELING LIVER INFECTIONS WITH REACTION-DIFFUSION EQUATIONS

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Keywords: Infection modeling, Reaction-diffusion equations, Model hierarchy.

Liver infections like hepatitis B and C are world wide spread and they tend to chronify. This leads to secondary diseases like liver cirrhosis. The underlying mechanisms of the chronification are not fully understood and therefore mathematical models are used for finding and testing new hypothesis about the development of the disease and possible interactions. The reaction-diffusion system in [1] is based on a predator-prey system and describes the interaction of virus and immune system, concluded as T cells. The model shows both infection courses healing and chronification, depending on the extension of the domain, the reaction change rate and the diffusion strength. Since the underlying mechanisms are not well known, the reaction terms are uncertain.

In this talk, we open the view on the used reaction terms by deducing indispensable properties of the reaction functions to get a model covering both infection courses. In the limit case of a very fast immune reaction, the two-component reaction-diffusion system reduces to a one component quasilinear parabolic partial differential equation with homogeneous Neumann boundary conditions for the virus. We analyse under which conditions stationary spatial inhomogeneous solutions, which are interpreted as chronic infections courses, occur. We study the stability by minimising an energy functional and an entropy function for the system to concretise the assumptions on the reaction function for the virus.

Finally, we test the assumptions on the reaction function by going back to the two component reaction-diffusion system which inherits properties of the parabolic sub-system. We regard the two models as part of a model family, establish a hierarchy and conclude differences, similarities and connections.

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