Modeling the Bacterial Clearance in Capillary Network Using Coupled Stochastic-Differential and Navier-Stokes Equations

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Abstract

The capillary network is a complex-interconnected structure. A single blood cell traveling from the arteriole to a venule via a capillary bed passes through, on average, $40 - 100$ capillary segments. The cardiovascular systems responsible of delivering blood to the tissue under sufficient pressure to exchange materials. This is a two way process, at which nutrients, Oxygen, and other materials, including bacteria, are carried to the tissue and cells during the outflow. On the other hand, blood is returned along with the wastes of cellular metabolism during the return flow. It is necessary to have an accurate model for the capillary-tissue exchange mechanism. This can be useful in many applications such as understanding the dispersion of drug particles, through vascular system, in human tissue [1, 2] as well as understanding the behavior of bacterial dispersion [3] and and the factors influencing its clearance [4–7].

Modeling the exchange process can be carried by means of coupling the classical diffusion (Fick's law) with Navier-Stokes equations. However, for a small number of particles, classical diffusion fails to introduce a satisfactory representation of the particle dispersion. It has been observed that the patterns of drug dispersion in human body organs exhibit certain irregularities (discontinuities) which can not be modeled with Fick's law of diffusion even using anisotropic and nonhomogeneous diffusivity. In order to accurately model the exchange process, we propose a stochastic based model of the diffusion process based on the well known Fokker Planck equation [8]. In order to account for the different mechanisms whereby capillary exchange can occur (diffusion and bulk flow), we model the capillary walls with means of pressure-dependent anisotropic diffusivity with slip conditions for the plasma flow inside the capillary. The main advantage of this technique lies in the fact that it accounts for both drift and random effects such as Brownian motion which are not accounted for in commonly used

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classical techniques based on Fick's law of diffusion. The extension to realistic geometry is straight forward since it can be dealt with using Finite Element Method.

This paper is organized as following order, first, we introduce the flow model using Navier-Stokes equations. Next, we utilize Fokker Planck equation with convection field to represent the probability function of the position of a particle (i.e, single bacteria) in the capillary-tissue region. Then, we compute the probabilities of absorption and transmission (clearance) of a single particle, using COMSOL multiphysics, and utilize them to compute the probability mass function (PMF) of the total number of bacterial particles. Finally, we expand our model to represent the different capillary segments and the blood-pressure dependency of the PMF.

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