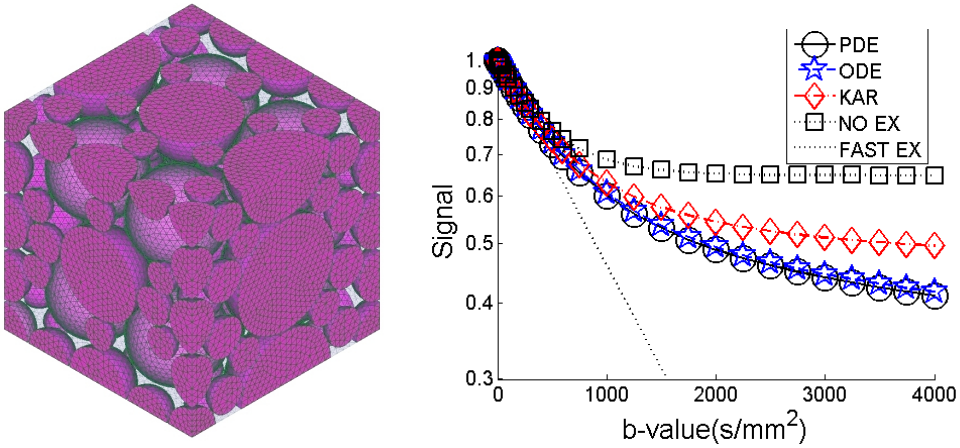
Direct and inverse models for Diffusion MRI

Houssem Haddar

INRIA Sacalay Ile de France and CMAP, Ecole Polytechnique, 91128, Palaiseau

Diffusion Magnetic Resonance Imaging is a promising tool to obtain useful information on the microscopic structure and has been extensively applied to biological tissues. We establish a new macroscopic model from homogenization theory for the complex transverse water proton magnetization in a voxel due to diffusion-encoding magnetic field gradient pulses in the case of intermediate water exchange across biological cellular membranes. Based on a particular scaling of the permeability condition modeling cellular membranes, this macroscopic model reproduces the memory effects often observed in experiments. Explicit formulae given by homogenization for the coefficients of this model emphasize their link to the relevant physiological quantities. In addition, we explicitly solve the macroscopic model to obtain an ODE model for the dMRI signal. The obtained model has a similar structure as so called Karger model, which was originally developed for micro-porous crystallites. However, the Karger model, that was obtained on the basis of phenomenological modeling, is only valid under a strong and often unrealistic assumption on the applied diffusion-encoding magnetic field gradient sequence. We shall validate our model for a variety of synthetic configurations as illustrated by the figure below.



(a) Finite elements mesh of periodicity cell C

(b) DMRI signals

Figure 1: (a) The computational domain $C = [-5\mu\text{m}, 5\mu\text{m}]^3$ contains 76 spheres with radii $0.6 - 2.55\mu m$. The volume fraction of the spheres is $v^s = 0.65$, and of the extra-cellular space is $v^e = 0.35$. The membrane permeability is set to $\kappa = 10^{-5}$m/s. (b) The dMRI signals: $S_{PDE}(b)$, $S_{ODE}(b)$, $S_{KAR}(b)$, $S_{NOEX}(b)$, $S_{FASTEX}(b)$. The gradient sequence is PGSE: $\delta = \Delta = 25$ms.

We shall also discuss numerical and theoretical issues related the inverse problem of retrieving the ODE model coefficients from (synthetic) dMRI signal data.

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