Using Salomé to reproduce the structure and to observe the diffusion of water molecules in biological tissue

Dang Van Nguyen, Denis S Grebenkov, Jing-Rebecca Li

HAL Id: hal-00764328

https://inria.hal.science/hal-00764328

Preprint submitted on 12 Dec 2012

Using Salomé to reproduce the structure and to observe the diffusion of water molecules in biological tissue

*Dang Van Nguyen[1], Denis Grebenkov[2], and Jing-Rebecca Li[3]
[1]Neurospin, CEA Saclay, Gif-sur-Yvette, France, [2]LPMC, Ecole Polytechnique, Palaiseau, France,
[3]Equipe DEFI, INRIA Saclay, Palaiseau, France

Introduction

Diffusion magnetic resonance imaging (DMRI) can give useful information on cellular structure and its structural changes [1]. Salomé [2] is used to reproduce some complicated shapes in d-dimensions (d=2,3) that are used to represent the natural structures of various biological tissue. The meshes representing these shapes are used as inputs to a finite element code that we built upon FENICS C++ [3]. Results were obtained for a model of globlastoma (cerebral tumor) as a Voronoi diagram which was used to observe the convergence of the apparent diffusion tensor in long-time limit to the effective diffusion tensor computed by homogenization theory [4].

Problem formulation

(1) The black points in the globlastoma image are extracted to create a 2D Voronoi diagram by Matlab.
(2) The common segments of two adjacent Voronoi cells are thickened to create extra-cellular space (Fig.1) in which the interior compartment contains cells, and the exterior compartment is between the cells.
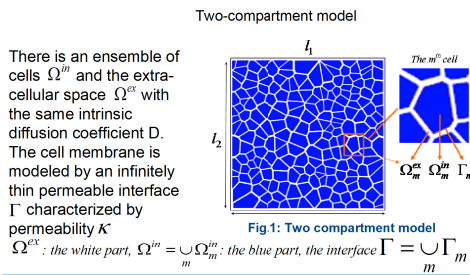(3) Simulation
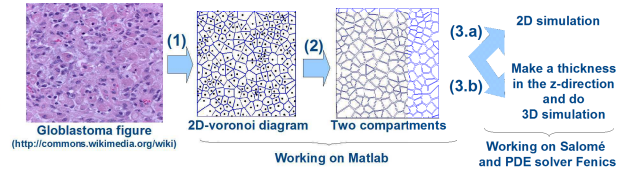
   (3.a) Generate the triangular mesh from step 2 using Salomé and perform simulation for 2D using our finite element code.

   (3.b) Make a thickness in the z-direction, create one layer, repeat this layer and put a thickness between two layers to create multi-layer structure, generate the tetrahedral mesh and do simulation for 3D.
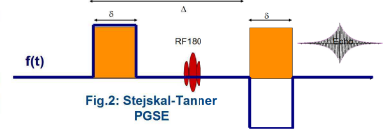
The DMRI signals from which we define the apparent diffusion tensors are obtained by solving Bloch-Torrey equation for a Stejskal - Tanner PGSE sequence (Fig.2) and the effective infinite time diffusion tensors are obtained by solving Laplace equation on the same domain Ω which contains a representative sample of the cellular structure $\Omega = \prod_{k=1}^{d} [a_k, b_k], (a_k < b_k)$.

Globlastoma figure (http://commons.wikimedia.org/wiki)
2D-voronoi diagram
Two compartments
Working on Matlab
2D simulation
Make a thickness in the z-direction and do 3D simulation
Working on Salomé and PDE solver Fenics

Fig.2: Stejskal-Tanner PGSE

Two-compartment model

There is an ensemble of cells Ω^{in} and the extra-cellular space Ω^{ex} with the same intrinsic diffusion coefficient D. The cell membrane is modeled by an infinitely thin permeable interface Γ characterized by permeability κ
Ω^{ex}: the white part, $\Omega^{in} = \cup_m \Omega_m^{in}$: the blue part, the interface $\Gamma = \cup_m \Gamma_m$

Fig1: Two compartment model

The mth cell

$\Omega_m^{ex} \ \Omega_m^{in} \ \Gamma_m$

Bloch-Torrey PDE and the apparent diffusion tensor D^A

$$\frac{\partial M(\vec{x},t)}{\partial t} = -i \gamma f(t) (\vec{g} \cdot \vec{x}) M(\vec{x},t) + \nabla\left(D \nabla M(\vec{x},t)\right)$$

with initial conditions are the uniform distribution

$$D \nabla M^{in}(\vec{x},t) \cdot \vec{n}^{in}(\vec{x}) = -D \nabla M^{ex}(\vec{x},t) \cdot \vec{n}^{ex}(\vec{x}) = \kappa(M^{ex}(\vec{x},t) - M^{in}(\vec{x},t)), \ \vec{x} \in \Gamma,$$

$$[M(\vec{x},t)]_{y_i=a_i} = [M(\vec{x},t)]_{y_i=b_i} \exp\left(i(\vec{g} \cdot \vec{e}_i)\gamma l_i \int_0^t f(s)ds\right) \quad \left[\frac{\partial M(\vec{x},t)}{\partial x_k}\right]_{x_i=a_i} = \left[\frac{\partial M(\vec{x},t)}{\partial x_k}\right]_{x_i=b_i} \exp\left(i\gamma(\vec{g}\cdot\vec{e}_i) l_i \int_0^t f(s)ds\right)$$

$$\vec{g} := \vec{q}/\gamma \qquad \Psi(\vec{q},t) = \int_\Omega M(\vec{x},t)d\vec{x} \qquad \ln\Psi(\vec{q},t) = \vec{q}^T D^A \vec{q} \int_0^u du \left(\int_0^u f(s)ds\right)^2 + O(\|\vec{q}\|^4)$$

Laplace's equation and the effective diffusion tensor D^{eff}

$$\nabla\left(D \nabla v_j(\vec{x})\right) = 0$$

$$D\nabla v_j^{in}(\vec{x}) \cdot \vec{n}^{in}(\vec{x}) = -D\nabla v_j^{ex}(\vec{x}) \cdot \vec{n}^{ex}(\vec{x}) = \kappa(v_j^{ex}(\vec{x}) - v_j^{in}(\vec{x})), \ \vec{x} \in \Gamma$$

$$[v_j(\vec{x})]_{x_k=a_k} = [v_j(\vec{x})]_{x_k=b_k} - (\vec{g}\cdot\vec{e}_k)l_k$$

$$\left[\frac{\partial v_j(\vec{x})}{\partial x_k}\right]_{x_k=a_k} = \left[\frac{\partial v_j(\vec{x})}{\partial x_k}\right]_{x_k=b_k} \qquad D^{eff} = [D_{jk}^{eff}]_{j=1..d,k=1..d}$$

$$D_{jk}^{eff} = D \int_\Omega \nabla v_j \cdot \vec{e}_k \, d\vec{x}$$

$\vec{e}_k$ is the unit vector in the kth direction

Results

We simulated on 2D and 3D voronoi cells in the box $[-25 \mu m ; 25 \mu m]^d$ (Fig.2 and Fig.3) by taking the same intrinsic diffusion coefficient D=$3.10^{-3} \ \mu m^2/\mu s$ for interior and exterior compartments. The permeablity of the inter-compartment interface was $\kappa = 10^{-5} \mu m/\mu s$. Seven b-values were taken from 0 to 4000 to get a curve of signal attenuation from which we obtain the tensor D^A.

Fig.2: 2D sample with 202 cells

Fig.3: 3D sample with 202x5 cells

Fig.4: The signal attenuation
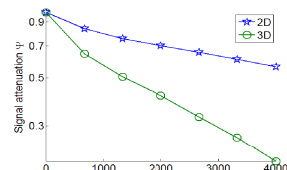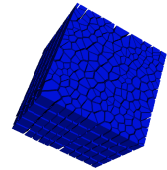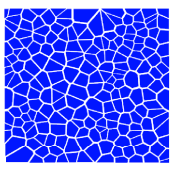
The signals in both 2D and 3D were obtained at $\delta = \Delta = 10$ms in Fig.4. The computation for 7 b-values costs about 11 minutes for 2D with the mesh-size of 8565 vertices and 1.5 hours for 3D with the mesh-size of 49035 vertices.

$$b-value = \gamma^2 \vec{g}^2 \delta^2 (\Delta - \delta/3)$$

Fig.5 shows the convergence of the apparent diffusion coefficient D^A to the effective diffusion coefficient D^{eff} in 2D for $\delta = 20$ms and $\Delta = 20..180$ms.
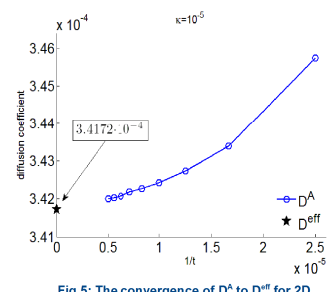
The computation for each D^A computed from 7 b-values costs between 20 minutes to 50 minutes.

Fig.5: The convergence of D^A to D^{eff} for 2D

Conclusion and future works

A Voronoi diagram was created to observe the diffusion in globlasma in both 2D and 3D. Preliminary results showed that Salomé gives good meshes for this application.
More realistic shapes are currently under development such as random cylinders to approach the structure of the human cerebral grey matter.
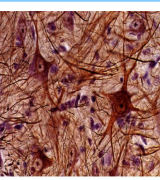

Fig.6: Human visual cortex (Le Bihan et al. PNAS 2006).

References

[1] LeBihan (2007) Phys Med Bio 52.
[2] http://www.salome-platform.org/
[3] A. Logg, K.-A. Mardal, G. N. Wells et al. (2012). Automated Solution of Differential Equations by the Finite Element Method, Springer.
[4] Bensoussan et al. (1978) Asymptotic analysis for periodic structures, North-Holland, Amsterdam.

* For futher information--correspondant's email: dang.1032170@gmail.com