# POROUS MEDIA MODELLING OF DIFFUSION IN PATIENT-SPECIFIC BRAIN MESHES.

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**Key words:** Biomechanical, MRI, Glymphatic, Patient-specific, Diffusion.

**Summary.** We have demonstrated a computational methodology of MRI-contrast diffusion in the brain based on MRI measurements. The computational methodology is a pipeline from MRI via Freesurfer to FEniCS to construct patient-specific meshes, which makes it feasible to test the theory of the glymphatic system.

## 1 INTRODUCTION

The role of water flow in the ageing brain has recently received significant attention, as the water seems to play an important role in the development of dementia which is a growing problem in the western world. In particular, there has been a paradigmatic change in the understanding of the fluid flow in the human brain,that is; the development of dementia has been linked to a malfunctioning waste clearance system in the extracellular fluid of the brain. While still a controversial topic, it has been proposed that the waste clearance of the extracellular system is driven by a hydrostatic pressure gradient between the arterial and venous part of the capillary bed. The fluid pathway is called the glymphatic[1] system and needs to be verified by modelling as well as experimental means.

In our project we consider the brain as a porous media and investigate if it is feasible to use a computational model to test the theory of the glymphatic system given established values of permeability and pressure. In particular, we consider the diffusion of contrast agents in patient-specific computational models of the human brain. The modelling is compared with novel magnetic resonance imaging (MRI) measurements conducted at Rikshospitalet[2]. The modelling is performed using the finite element software package FEniCS[3] and the MRI segmentation package FreeSurfer[4].

## 2 THEORY

MRI works by detecting the magnetization of hydrogen atoms, due to an external magnetic field. The MRI measurements from Rikshospitalet show the distribution of MRI-contrast in the brain at different times, as seen in Fig.1. The MRI-contrast molecule will bind with water and will cause the relaxation time to be shortened, resulting in a local increase in intensity as displayed in Fig.1. The MRI are taken with the sequence known as gradient echo recall, where the signal intensity is given as

$$SI = N(H)\sin\alpha \frac{\exp^{-TE/T2^*}(1 - \exp^{-TR/T1})}{1 - \cos\alpha \exp^{-TR/T1}}, \tag{1}$$

with $N(H)$ is the number of mobile protons. Here $TR$, $TE$ and $\alpha$ are sequence specific variables known as repetition time, echo time and flip angle. While $T1$ is longitudinal(spin-lattice) relaxation time for the given medium. The $T2^*$ is transverse magnetization caused by a combination of spin-spin relaxation and magnetic field inhomogeneity[5]. Given a linear dependence on the contrast concentration $c$ and the relaxation times, we can write Eq.2 as

$$SI(c) = N(H)\sin\alpha \frac{\exp^{-TE(1/T2^*+r_2c)}(1 - \exp^{-TR(1/T1+r_1c)})}{1 - \cos\alpha \exp^{-TR(1/T1+r_1c)}}. \tag{2}$$

with $r_1$ and $r_2$ as the relaxivity constants.

The concentration of MRI-contrast is modelled as an isotropic diffusion process

$$\frac{\partial c}{\partial t} = \nabla \cdot (k\nabla c), \tag{3}$$

where $c$ is the concentration in mM and $k$ is the apparent diffusion coefficient. We will use the measurements conducted at Rikshospitalet to estimate the initial condition and boundary conditions. This is done by registering the different time steps to an initial MRI without MRI-contrast. Then we construct a residual, and solve the concentration as a non-linear problem.

The human brain is a complex organ with significant geometric differences between individuals. Thus we need a patient-specific mesh to accurately compute changes in the brain. The construction of these meshes are done by using MRI of the patient's brain. MRI data is loaded into the MRI segmentation package FreeSurfer, which will produce surfaces of the right and left hemisphere of the brain. These surface are then convert to readable format for the FEniCS module mshr, which is used to create the mesh seen in Fig.2.

## 3 RESULTS

In the left panel of Fig.3 we see the result of a 5 hour simulation with initial condition based on the concentration after 1 hour. The distribution of the concentration do not correspond with concentration after 6 hours, which can be seen in right panel of Fig.3.

We can see the difference near the inlets on the left and right side of the surface. These inlets are created by Freesurfer, since only the brain is included in the segmentation.

The amount of MRI-contrast present after 6 hours is also significantly higher than after 1 hour, which can also be seen in Fig.1. Thus the simulation would also require an influx of MRI-contrast.

## 4   CONCLUSION

We have in this paper demonstrated a computational methodology of MRI-contrast diffusion in the brain based on MRI measurements. The computational methodology is a pipeline from MRI via Freesurfer to FEniCS to construct patient-specific meshes, which makes it feasible to test the theory of the glymphatic system.
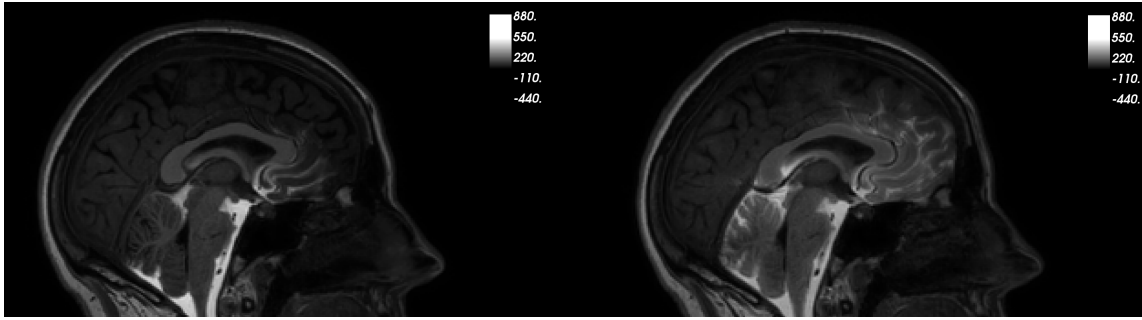


Figure 1: The left panel shows a MRI the patient's head with MRI-contrast after 1 hour. The right panel shows a MRI the patient's head with MRI-contrast after 6 hours.
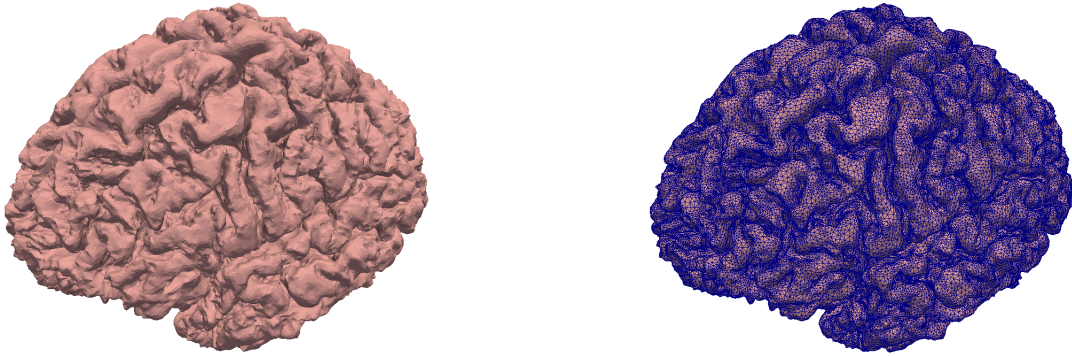


Figure 2: The left panel displays the mesh surface of the patient's brain without edges. The right panel displays the mesh surface of the patient's brain with edges.
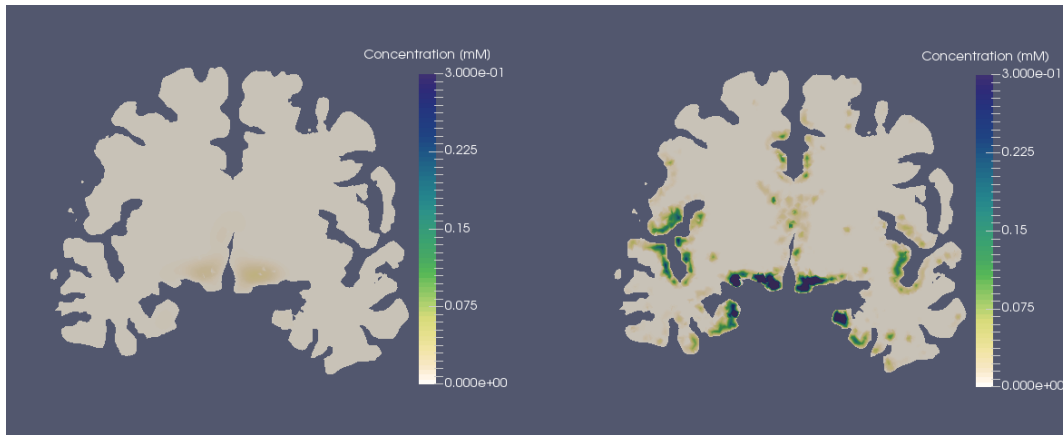
Figure 3: The left panel shows the concentration after 5 hours simulation based on the initial conditions after 1 hour. The right panel shows the estimated concentration after 6 hours.

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