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# Diffusion MRI simulation of realistic neurons with SpinDoctor and the Neuron Module

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**INTRODUCTION:** The simulation of diffusion MRI arising from realistic neuron models can help investigate the cellular microstructure<sup>1,2</sup>. However, ensuring correct connectivity between the distinct compartments comprising the system while minimizing the computational burden is one of the main challenges in our community<sup>3</sup>. The design of accurate and efficient simulation algorithm and the construction of high quality neurons meshes are two difficulties in addressing this problem. Our previous work includes a MATLAB Toolbox called SpinDoctor that is a diffusion MRI simulation pipeline based on solving the Bloch-Torrey partial differential equation using finite elements and an adaptive time stepping method<sup>4</sup>. The first version of SpinDoctor focus on the brain white matter whose biophysical models subdivide the tissue into compartments described by ellipsoids, cylinders, and the extra-cellular space. In this study, we present a new module of SpinDoctor called the Neuron Module that enables neuron simulations for a group of 36 pyramidal neurons and a group of 29 spindle neurons whose morphological descriptions were found in the publicly available neuron repository NeuroMorpho.Org<sup>5</sup>.

**METHODS:** The key to making accurate simulation possible is the use of high quality meshes for the neurons. For this, we started with the morphological reconstructions published in NeuroMorpho.Org<sup>5</sup>. These surface descriptions contain many self-intersections and proximities. We then used licensed software from ANSA-BETA CEA Systems<sup>6</sup> to correct and improve the quality of the neuron surface descriptions and produced new surface triangulations that are ready to be used for finite elements mesh generation. The new surface triangulations are passed into the software GMSH<sup>7</sup> to obtain volume tetrahedral meshes. To further study the diffusion MRI signal of neurons, we broke the neurons into disjoint geometrical components. As an illustration, we show in Figure 1 the spindle neuron 03a\_spindle2aFl volume tetrahedral mesh broken into sub-meshes of the soma and the two dendrite branches.

These finite elements meshes are used as input files in the Neuron Module, where they can be further refined if required using the built-in option in SpinDoctor. Currently, the spin exchange across the cell membrane is assumed to be negligible in the Neuron Module. Through the Neuron Module, these neuron and components finite element meshes can be seamlessly coupled with the functionalities of SpinDoctor to provide the diffusion MRI signal attributable to spins inside neurons.

**RESULTS:** We first validate our simulations by refining in space (making the finite elements smaller) and refining in time (decreasing the error tolerance of the ODE solver). The reference signal has the finest finite element size and the smallest error tolerance among the simulated signals. The signal difference between the reference signal and the simulated signals for the neuron 25o\_pyramidal18aFl is plotted in Figure 2. In this case, we see that the signal difference is less than 2.5% for b = 4000s/mm² and less than 1% for b=1000 s/mm². In Figure 3 and Figure 4, we show 2D and 3D high angular resolution diffusion imaging simulations respectively. The average computational time per gradient direction is around 30 seconds which is much faster than the Monte-Carlo simulations using Camino⁴. By visual inspection, the signals in the whole neuron are close to the volume weighted sums of the signals from the three geometrical components.

In [8] it was shown experimentally that the diffusion MRI signal of tubular structures such as axons exhibit a certain high b-value behavior, namely, the diffusion direction averaged signal,  $S_{ave}(b)$ , is linear in  $1/\sqrt{b}$  at high b-values. Because the dendrites of neurons also have a tubular structure, we test whether the diffusion direction averaged signal,  $S_{ave}(b)$ , of dendrite branches also exhibit the above high b-value behavior.

We computed  $S_{ave}(b)$  for the neuron 03a\_spindle2aFl as well as their associated dendrite branches averaged over 31 diffusion directions uniformly distributed in three dimensions. The results are shown in Figure 5. We see

clearly the linear relationship between  $S_{ave}(b)$  and  $1/\sqrt{b}$  in the dendrite branches for b-values in the range

 $2500s/mm^2 \le b \le 20000s/mm^2$ . In contrast, in the whole neuron, due to the presence of the soma, such linear relationship is not exhibited.

**CONCLUSION:** We presented the Neuron Module which we implemented in the Matlab-based diffusion MRI simulation toolbox SpinDoctor. We have created high quality volume tetrahedral meshes for a group of 36 pyramidal neurons and a group of 29 spindle neurons. In the current study, we illustrated the usefulness of the Neuron Module in providing simulated HARDI signals at various b-values and diffusion times. In addition to calculating the HARDI signals from whole neurons, we also simulated the HARDI signals of neuron components such as the soma and the dendrite branches. In particular, we compared the high b-value behavior of the diffusion MRI signals from dendrite branches and from whole neurons, confirming the linear relationship

between the diffusion direction averaged signal and  $1/\sqrt{b}$  for tubular structures. These meshes and the source code of the Neuron Module are made available to the public as an open-source package<sup>9</sup>.

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**Synopsis:** The simulation of diffusion MRI arising from realistic neuron models can help investigate the cellular microstructure. However, ensuring correct connectivity between the distinct compartments comprising the system while minimizing the computational burden is one of the main challenges in our community. The design of accurate and efficient simulation algorithm and the construction of high quality neurons meshes are two difficulties in addressing this problem. The Neuron Module can perform HARDI simulation of realistic neurons at various b-values and diffusion sequences with high accuracy. The computational time per gradient direction is around 30 seconds which is much faster than some Monte-Carlo simulators. The linear relationship between the diffusion direction averaged signal and one over square root of b for tubular structures is validated by our simulations. We believe our work can add substantially to the understanding of the imaging of neuronal microstructure.

**Summary of Main Findings:** The diffusion MRI signal arising from realistic neurons can be numerically simulated by the Neuron Module which are implemented in the Matlab-based diffusion MRI simulation toolbox SpinDoctor.

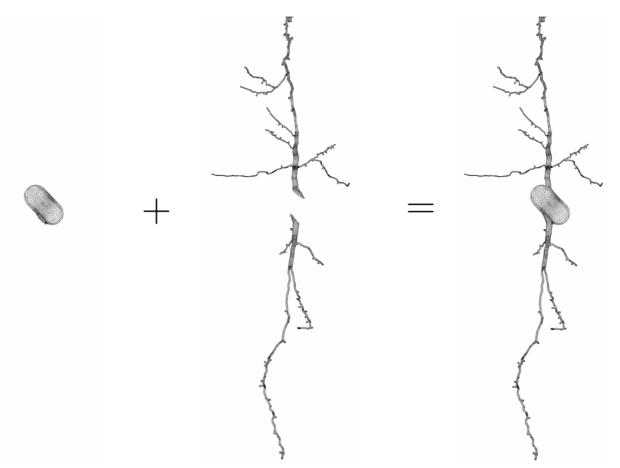


Figure 1: The volume tetrahedral mesh of the spindle neuron 03a\_spindle2aFl is broken into three geometrical components: the soma and two dendrite branches.

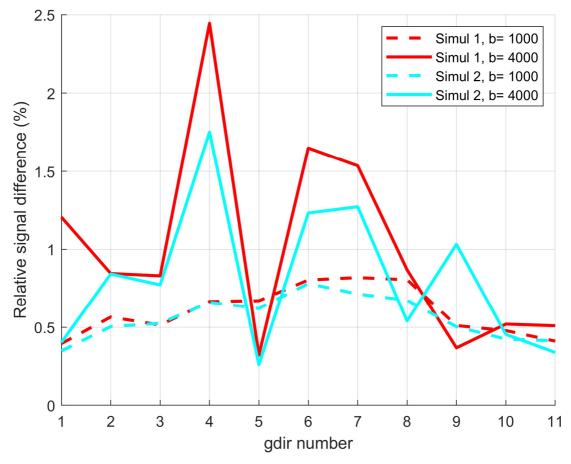


Figure 2: The signal differences between the reference signal and the simulated signals for the neuron 25o\_pyramidal18aFl.

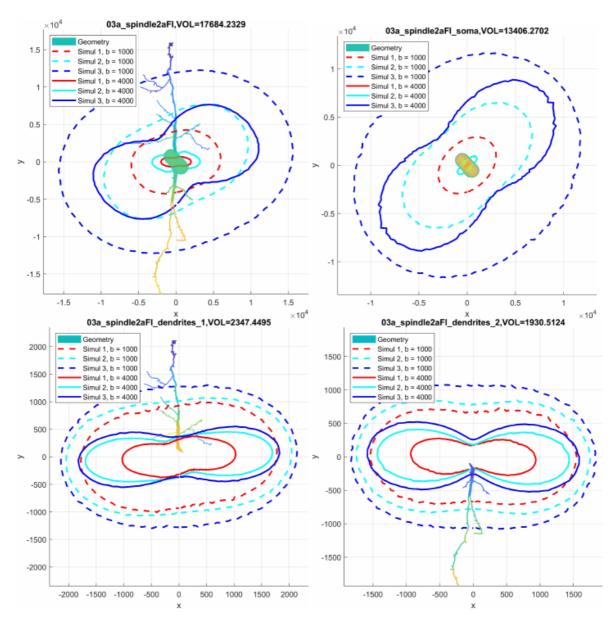


Figure 3: The diffusion MRI signals in 90 directions lying on the x-y plane, uniformly distributed on the unit circle. Top left: the whole neuron 03a\_spindle2aFI. Top right: the soma. Bottom left: the upper dendrite branch. Bottom right: the lower dendrite branch.

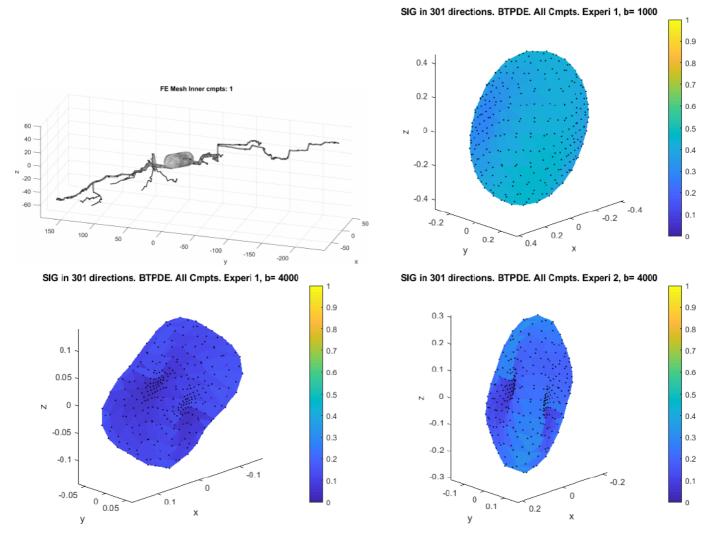


Figure 4: Top left: the finite elements mesh of the spindle neuron 03a\_spindle2aFl, the unit is  $\mu m$ . The other three plots: HARDI simulations in 301 diffusion directions. The color gives the magnitude of the signal attenuation.

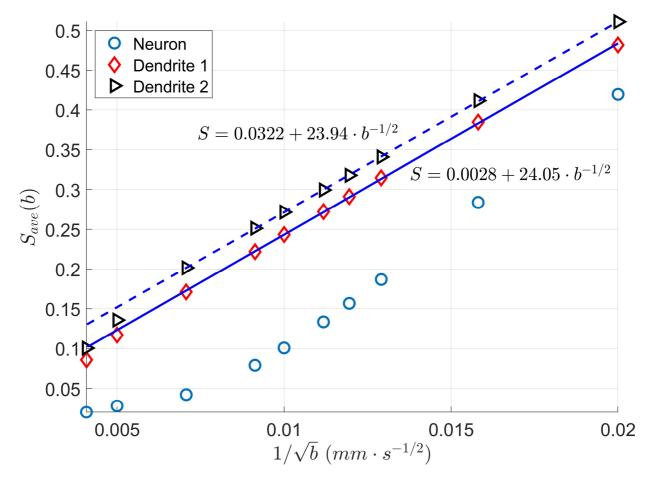


Figure 5: The diffusion direction averaged signal,  $S_{ave}(b)$ , as a function of  $1/\sqrt{b}$ .  $S_{ave}(b)$  is normalized so that  $S_{ave}(b=0)=1$ .

The b-values are  $b = \{60000, 40000, 20000, 12000, 10000, 8000, 7000, 6000, 4000, 2500\}$   $s/mm^2$ .