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

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`https://github.com/jingrebeccali/SpinDoctor/`

Introduction

Understanding the relationship between the cellular structure and the diffusion MRI signal is essential to probe tissue micro-structure non-invasively and in-vivo [Bihan1968]. Numerous biophysical models subdivide the tissue into compartments described by spheres, cylinders (or sticks), and the extra-cellular space [novikov2019]. Due to the complexity of realistic neuron structure, these simplfied models could not be optimal [palombo2019]. Numerical simulations and realistic neuron models can help refine the models. Our work provides both a fast and accurate diffusion MRI simulator (SpinDoctor) and a set of high quality realistic neuron meshes. We present our work through the following steps:

- Show the pipeline for constructing the realistic neuron meshes;
- Validate the accuracy of SpinDoctor and the quality of the neuron meshes;
- Demonstrate three experiments to show the potential of our framework.

Construction of finite element meshes of neurons

We started with the morphological descriptions (SWC files) published in *NeuroMorpho.Org*. These surface descriptions of the neurons cannot be used directly by SpinDoctor to generate finite elements meshes due to self-intersections and proximities. We designed a pipeline (see Figure 1) that takes the SWC format files to the tetrahedral meshes in the MSH format. We also broke the neuron meshes into the soma and dendrite branches (see Figure 2).
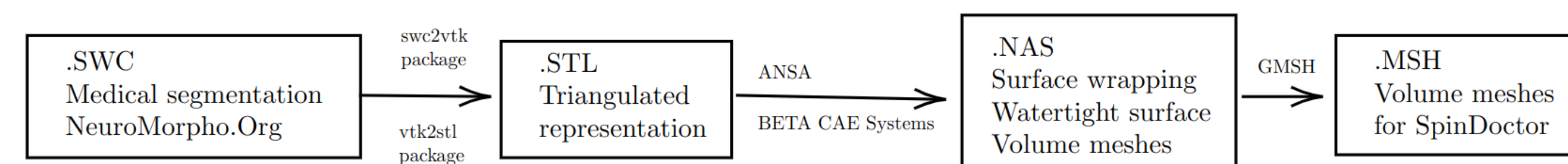

Figure 1: The pipeline for constructing the finite element meshes of neurons.
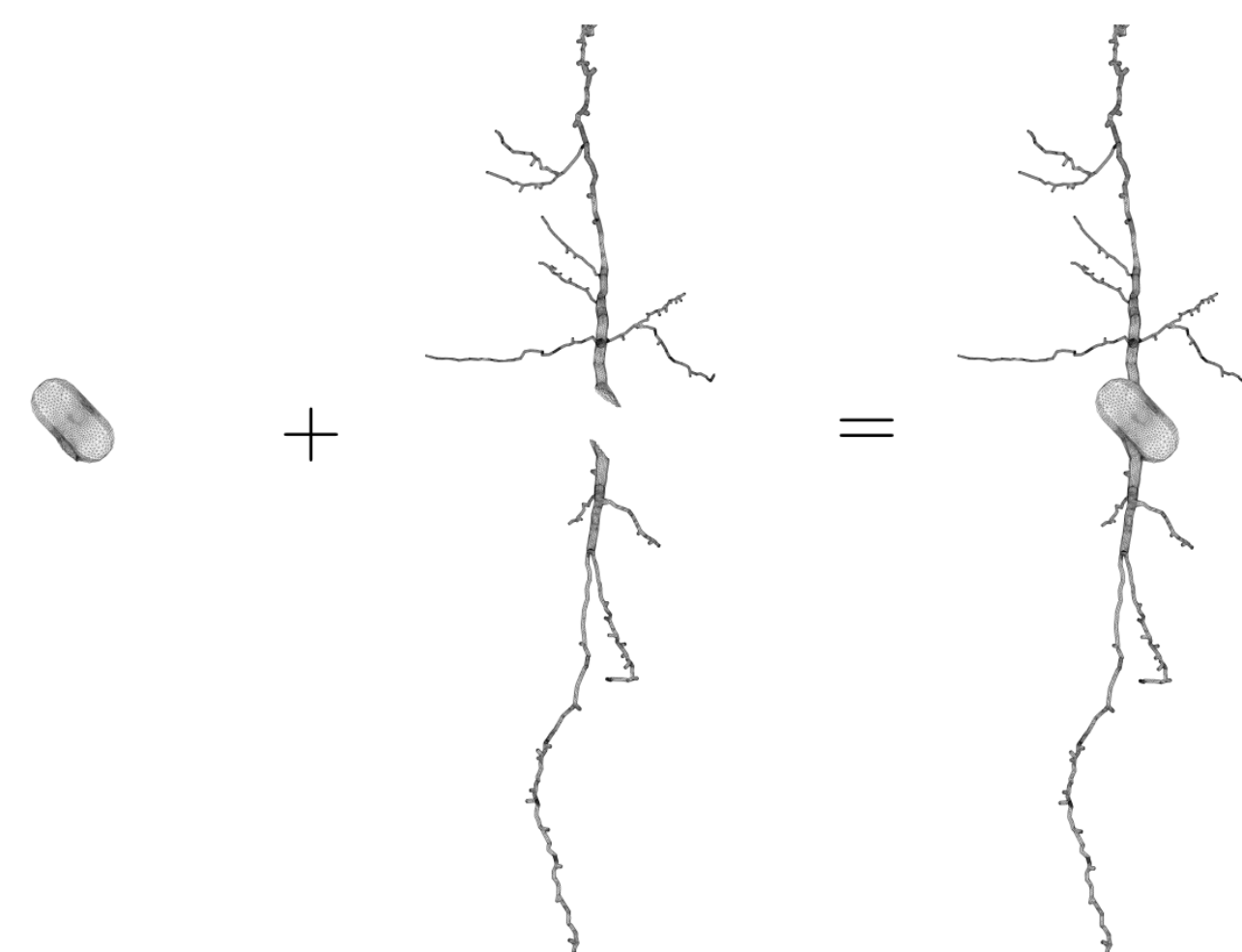

Figure 2: The mesh of the neuron *03a_spindle2aFI* is broken into three components.

Numerical validation

We 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 accuracy of the simulations was tuned using three simulation parameters, $Htetgen$ controls the finite element mesh size, $rtol$ is the relative residual tolerance, and $atol$ is the absolute residual tolerance. We took the simulation with the finest space discretization ($Htetgen = 0.05\mu m$) and the finest time discretization ($rtol = 10^{-6}$, $atol = 10^{-8}$) as the reference solution. In Figure 3, we show the relative signal errors (in percent) between several simulations and the reference solution. The relative errors are less than 1%.
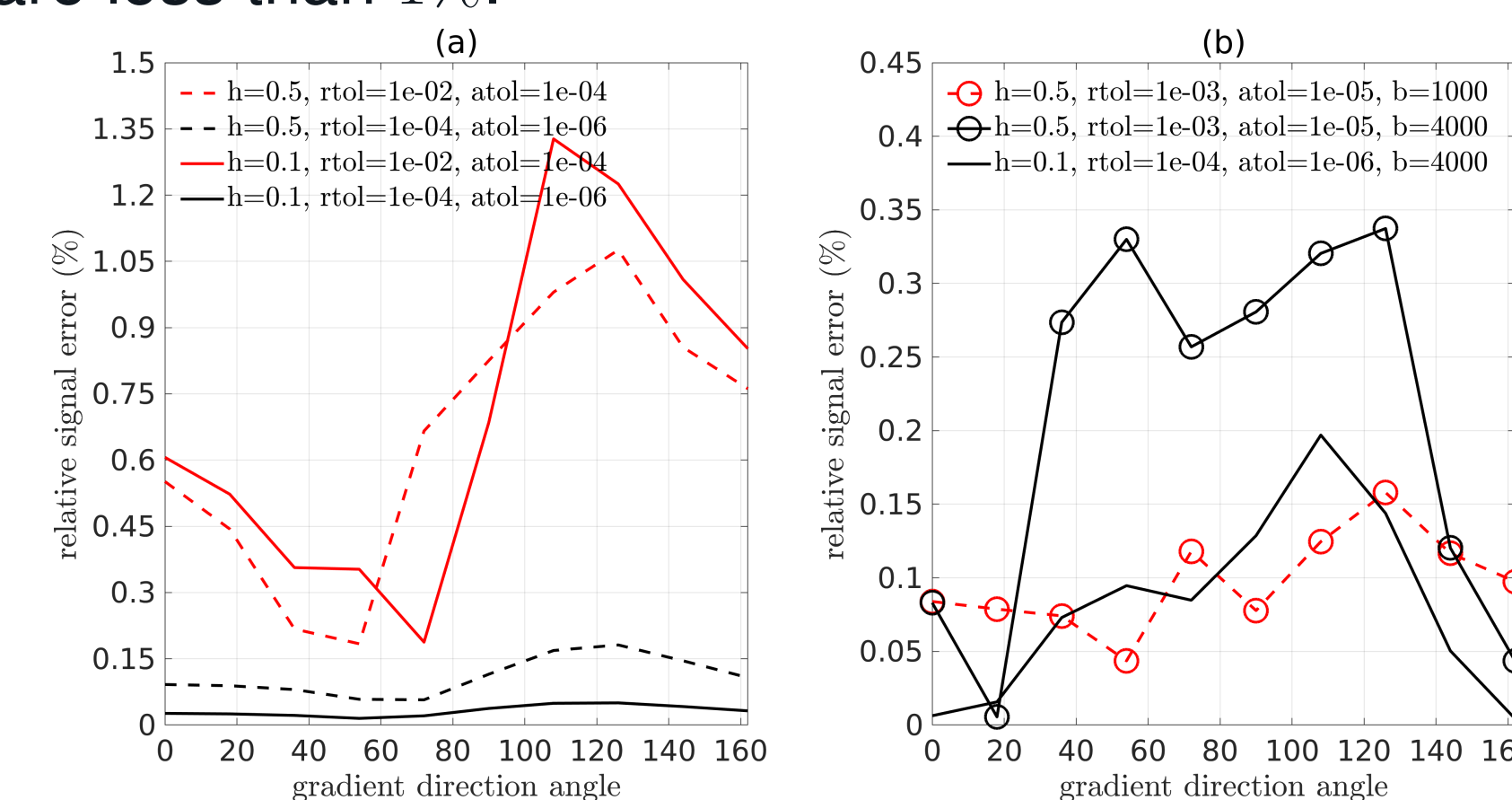

Figure 3: The relative errors for the neuron *03b_spindle4aACC* in 10 gradient directions.

Experiments

Diffusion MRI signals simulations in multiple diffusion directions
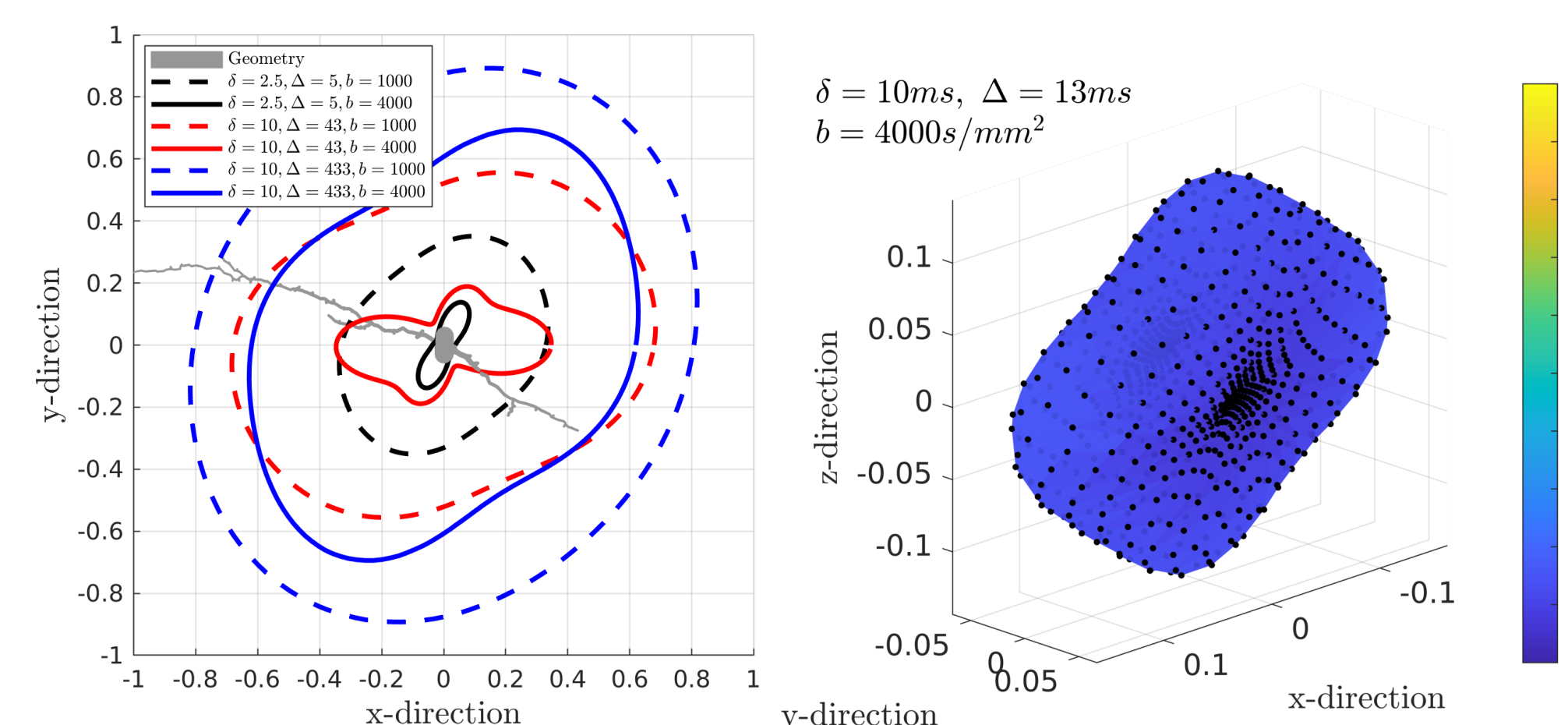

Figure 4: Left: The diffusion MRI signals for the neuron *03b_spindle4aACC* in 180 directions lying on the $x - y$ plane. The distance from each data point to the origin represents the magnitude of the normalized signal. Right: The normalized diffusion MRI signals for the neuron *03a_spindle2aFI* in 720 directions uniformly distributed on a unit sphere. The color and the distance to the origin of each data point represent the magnitude of the normalized signal.

Experiments

GPU Monte-Carlo vs. SpinDoctor

We compare the computational times used by SpinDoctor and a GPU Monte-Carlo program. For a fair comparison, we chose two set of simulation parameters with a comparable accuracy. Due to this difference between serial and parallel implementations, we show in Table 1 the computational times for one gradient direction. The time ratio (GPU Monte-Carlo/SpinDoctor) ranges from 24 to 72.

Computational time (s)		neuron		dendrite 1		dendrite 2		soma	
$\delta = 10ms, \Delta = 43ms$	b	E_{max}	$t\,(s)$	E_{max}	$t\,(s)$	E_{max}	$t\,(s)$	E_{max}	$t\,(s)$
SpinDoctor	1000	0.16	17.1	0.52	7.8	0.11	3.4	0.17	5.7
	4000	0.34	26.0	0.91	11.8	0.13	4.9	0.23	6.8
GPU Monte-Carlo	1000	0.14	537.8	0.65	337.3	0.51	116.1	0.29	311.2
	4000	0.60	1895.9	2.34	342.1	0.47	116.5	0.90	311.3

Table 1: The computational times of SpinDoctor and GPU Monte-Carlo simulations (in seconds). The maximum relative error E_{max} (in percent) is taken over 10 gradient directions in the $x - y$ plane.

Potential biomarkers of the soma size

By leveraging the realistic neuron meshes, it is possible to find potential biomarkers that could reveal the tissue micro-structure. Figure 5 gives an example of using the inflection point of the direction-averaged signal to indicate the soma volume.
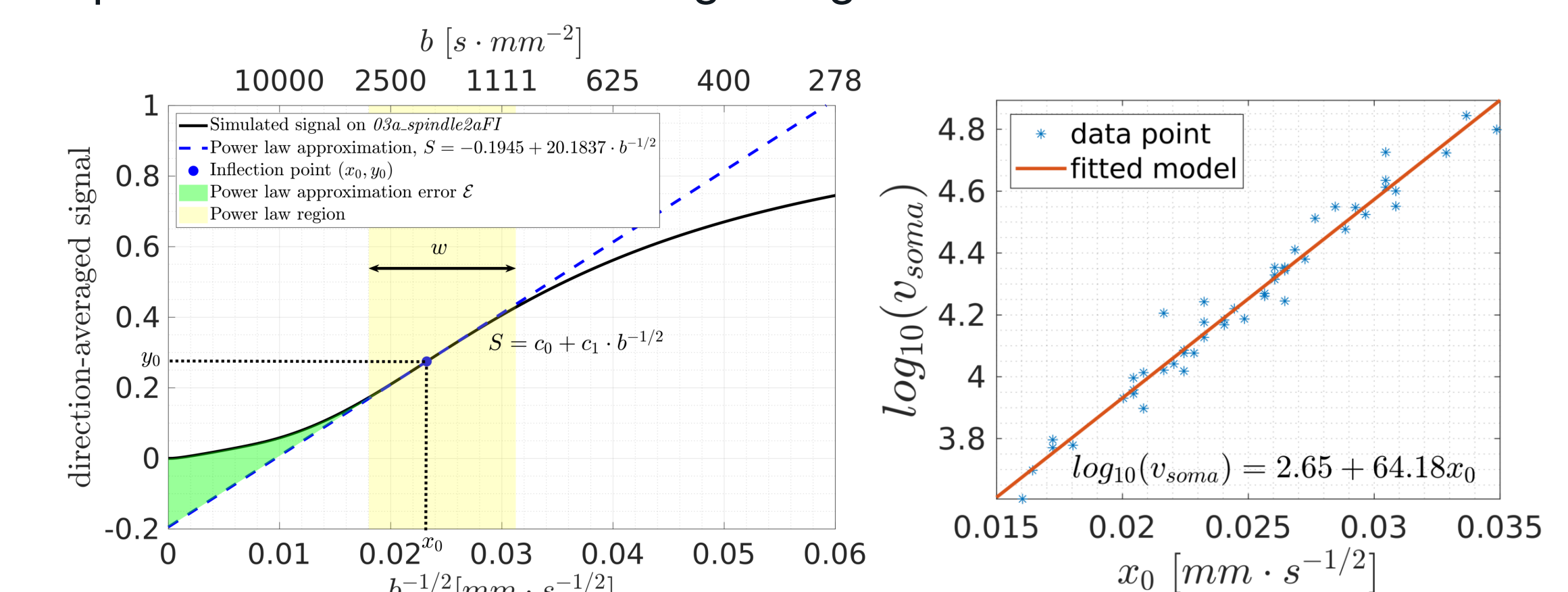

Figure 5: Left: The direction-averaged signal for the neuron *03a_spindle2aFI*. We show some candidate biomarkers in the figure. Right: A statistical study about the inflection point on the 65 neurons was performed. The inflection point serves as a potential biomarker for probing soma volume.

Takeaways

- SpinDoctor is a fast and accurate diffusion MRI simulator.
- Neuron Module provides 65 high quality realistic neuron meshes.
- Our framework enables fast hypothesis testing, model validation and new method design for diffusion MRI imaging.