

# Monte Carlo simulations disambiguate the biophysical MECHANISMS OF DIFFUSION HINDRANCE ALONG TRACTS

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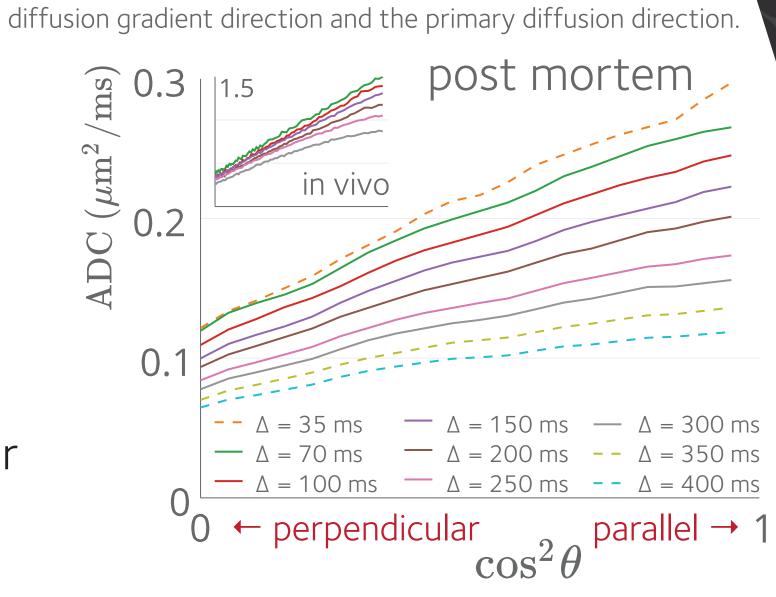
## BACKGROUND

- Diffusion imaging at long diffusion times ( $\Delta$ ) informs on microstructural tissue features up to the ~100 µm scale.
- Approximation of axons as straight cylinders might not hold, even for tissues that are generally assumed to be coherently organized, for example: the human corpus callosum (CC).
- Electron microscopy (Mikula 2012) and histology (Budde 2013) suggest that the CC is far from coherent: fibres bend, twist and undulate which might lead to specific signatures of hindrance along the tract.
- In this study, we investigated the diffusion time dependence of the <u>ap-</u> parent diffusion coefficient (ADC) along the fibres in the CC.
- Biophysical mechanisms of this dependence are explored by Monte Carlo simulations of various tissue models.

#### DIFFUSION TIME DEPENDENCE OF THE ADC IN THE CORPUS CALLOSUM

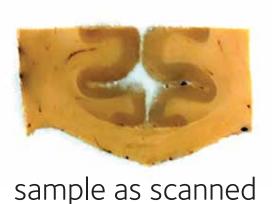
- The ADC in the corpus callosum decreases with diffusion time; to a comparable degree across and along the tract.
- This suggests considerable diffusion hinderance not only perpendicular to the fibres, but also in the tract direction.
- A model of infinitely long straight cylinders might thus be inappropriately simple, even for the (supposedly) most coherent WM tract.

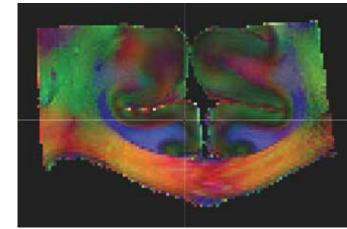
Figure 1. ADC plotted against cos<sup>2</sup> of the angle between the



#### MR MEASUREMENTS (POST MORTEM)

- 3x2 cm coronal block of a human corpus callosum
- soaked in PBS for 72h
- scanned in Fluorinert on a Varian 9.4T



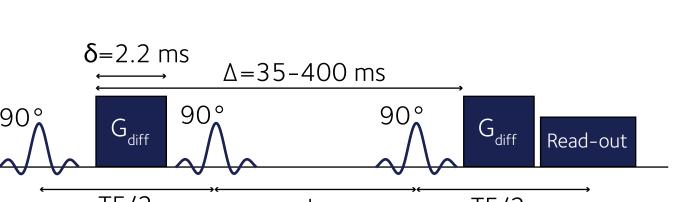


spin echo DTI fit

METHODS

acquiring DW-STEAM data with:

- 9 diffusion times: 35-400 ms
- 30 directions
- fixed q-value (0.14 rad/µm)
- TE=16 ms, TR=2.4-4.1 s
- 10 slices, 400 µm voxels

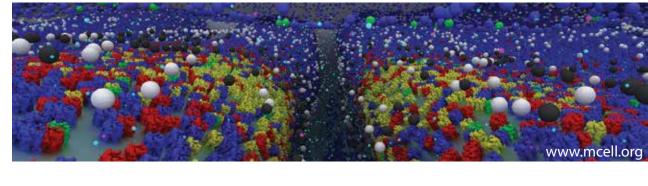


#### Monte Carlo diffusion simulations

• Geometries created with CellBlender: blender

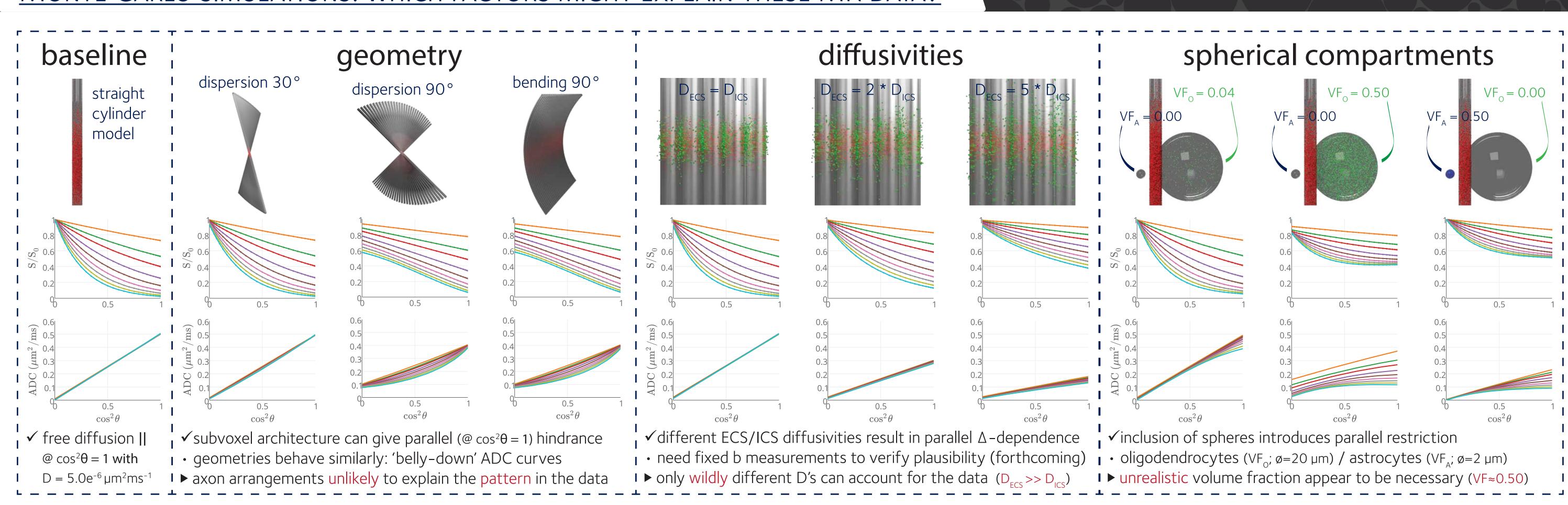
$$-L_{axon} = 160 \mu m$$
$$-d_{axon} = 3 \mu m$$

- Particle trajectories from MCell (Stiles 1996): MCell
  - $D = 0.5 \mu m^2/ms$
  - $dt = 100 \mu s$
  - 400000 particles
  - impermeable walls

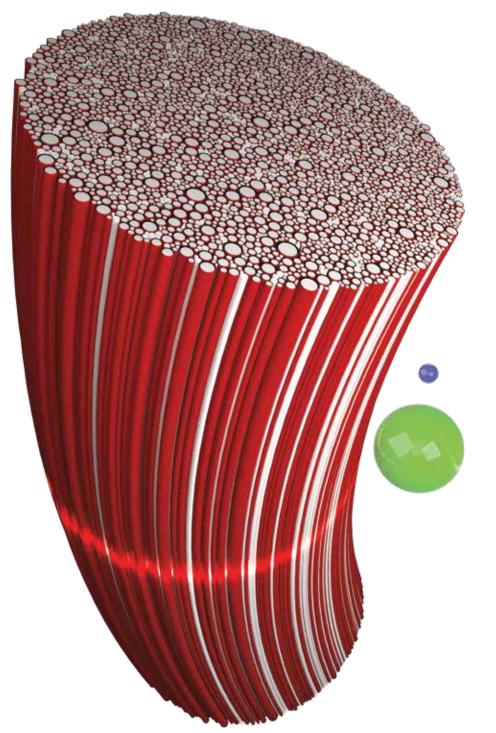


- dMRI signals calculated with DifSim (Balls 2009):
  - STEAM MR protocol (as above)
  - T2 decay not simulated

## Monte Carlo simulations: which factors might explain these MR data?



#### COMBINING FACTORS FOR A BIOPHYSICALLY PLAUSIBLE MODEL



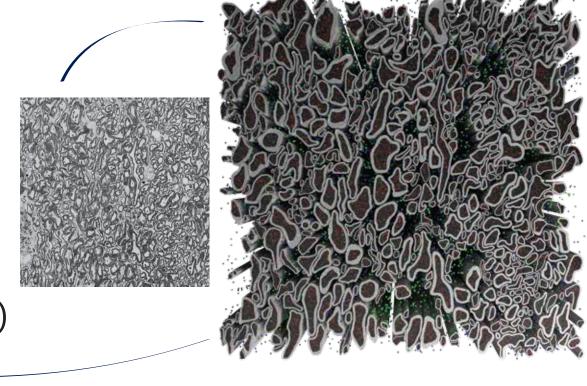
- sensible combination of all of the above approximates the data
- MODEL: gamma-distributed cylinders N=3573;  $<\emptyset>=0.5 \mu m$ ; g-ratio=0.8bending of 30° compartments: 25% ECS (D= $5.0e^{-6}\mu m^2/ms$ ) 10% myelin (D= $1.0e^{-6}\mu m^2/ms$ ) 40% axons (D= $4.0e^{-6}\mu m^2/ms$ ) 10% oligodendrocytes (D=D<sub>FCS</sub>) 10% astrocytes (D=D<sub>FCS</sub>) 5% mitochondria (D=1.0e<sup>-6</sup>µm<sup>2</sup>/ms)
- glial volume fractions might still be too high
- 0.2 0.5  $\cos^2 \theta$

#### CONCLUSIONS

- The ADC parallel to the bundle is diffusion time dependent
- Monte Carlo simulations suggest the explanation has to involve a combination of microstructural factors
- This work demonstrates a framework for assessing micro structure MRI: from simple cylinders to complex geometry

### OUTLOOK: USING EM DATA

- electron microscopy as ground truth for  $\mu$ -dMRI
  - realistic geometries for MC simulations (2½D&3D)



CONCLUSION