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The effect of axon shape and myelination on diffusion MRI signals in a realistic Monte Carlo simulation environment

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Abstract:

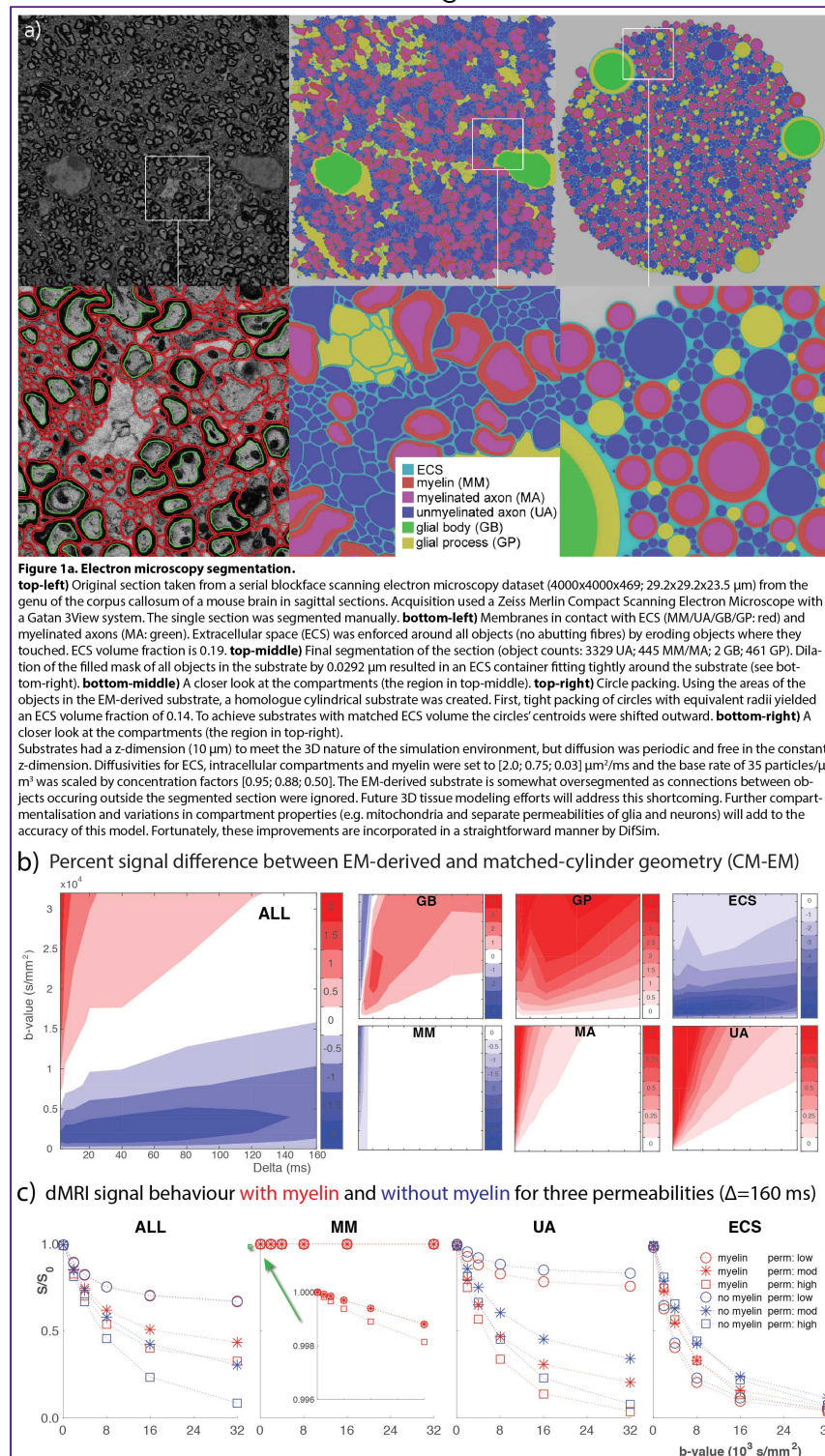
Diffusion MRI (dMRI) microstructure techniques, e.g. axon diameter and membrane permeability estimation, are often validated using Monte Carlo (MC) simulations. The geometric substrates are usually oversimplified cylindrical models. This work investigates more realistic geometry derived from electron microscopy (EM) data and aims to showcase how subtle microstructural features can be explored.

An EM section from mouse corpus callosum was segmented into 6 compartments: unmyelinated/myelinated axons; myelin; glial bodies/processes; extracellular space (Figure1a). MC simulations were performed using MCell (Stiles et al., 1996), with DifSim (Balls and Frank, 2009) calculating the dMRI signal from the phase of protons diffusing under a PGSE sequence with diffusion times $\Delta=2-160$ ms, b-values 100-32000 s/mm² in 30 perpendicular directions. The effects of two tissue features were assessed:

(A) Shape, by comparing EM-derived vs. cylindrical geometry with equivalent radii (Figure1b): The aggregate dMRI signal averaged over directions is similar for EM-derived vs. cylindrical geometry, lending validity to modeling axons in cross-section as circles. Two regimes where shape is relevant: i) short Δ , where lower signal in EM-derived geometry appears driven by irregularly-shaped cell processes; ii) lower b-values, where higher signal in EM-derived geometry might be due to more tortuous diffusion in ECS around realistic cell packings.

(B) Myelination, by comparing EM-derived vs. geometry with myelinated axons replaced by unmyelinated axons under various permeability conditions (Figure 1c): at low permeability, only a modest effect of myelination on the dMRI signal is seen, suggesting myelination does not contribute much to signal attenuation in healthy tissue.

The EM-based geometry and simulation environment presented here has been developed to provide researchers with a flexible tool for investigating the role of a range of tissue features. Here, we have presented two examples: shape and myelination. Ongoing work extends these realistic simulations in full 3D using SBFSEM.



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