Are DW-MRI signals from crossing fibers well represented by sums of signals from single fibers?

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Introduction:

Diffusion-weighted MRI (DW-MRI) is a widely used tool in brain microstructure mapping. A particularly challenging task is to retrieve microstructural properties such as the axonal radius or density in regions where multiple fascicles of axons intersect. Most models (e.g. [Ass04,Scher12,Scher15,Schu10,Tuch02]) assume that the DW-MRI signals arising from crossing fascicles is equal to the sum of the signals arising from each fascicle independently, although the diffusion of water molecules in the interstitium is hindered by all fascicles simultaneously. Whether this approximation is valid in standard microstructure with common acquisition sequences remains an open question that we investigate here numerically.

Methods:

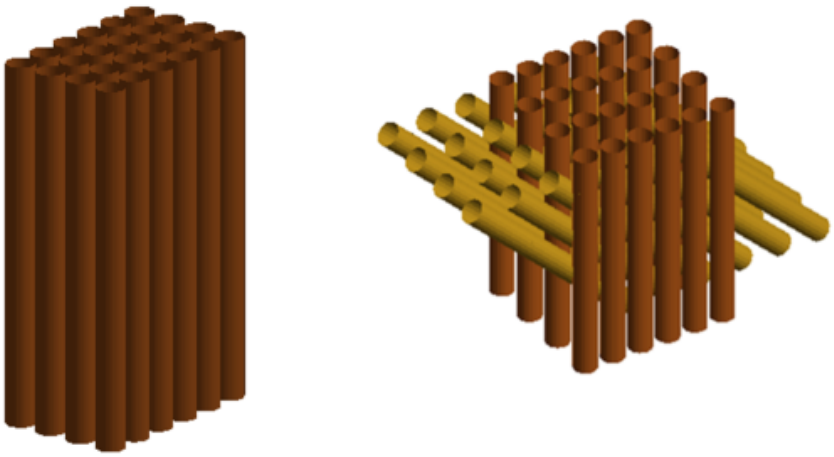
We study PGSE acquisitions with parameters $p=(g,\delta,\Delta)$ and a configuration $\Omega=(r,f,\alpha)$ of interwoven crossing fascicles (Fig. 1) with r the axonal radius, f the density, and α the crossing angle. We consider the DW-MRI signal $Int(p;\Omega)$ arising from this configuration to be well estimated by Monte Carlo simulations of the diffusion of water molecules in parallel cylinders [Rens15]. We compare this reference signal to the weighted sum

$App(p,\Omega)=0.5*Sin(p;r,f)+0.5*R[\alpha](Sin(p;r,f))$,

where Sin is the signal simulated in a single independent fascicle (Fig.1 left) and $R[\alpha](Sin)$ its rotated version.

We first look at the root-mean-square (RMS) difference between the reference interwoven-fascicle signal Int and its approximation App as a function of the acquisition parameters, here the b-value of a HARDI shell [tuch02], to test whether the validity of the approximation depends on the acquisitions (Fig. 2). In Fig. 3, we fix a clinically-realistic acquisition protocol [Alex10] and investigate whether performing the approximation using microstructural parameters close to the reference parameters leads to more similar signals. We finally perform a simple microstructural estimation experiment in an ideal noise-free setup. Given a reference signal $Int(P;\Omega_{int})$ for some protocol P of N sequences, we estimate its unknown microstructural configuration Ω_{int} by selecting the parameters Ω_{app} minimizing
$\sum_{(i=1->N)}(Int(p_i;\Omega_{int})-App(p_i;\Omega_{app}))^2$.

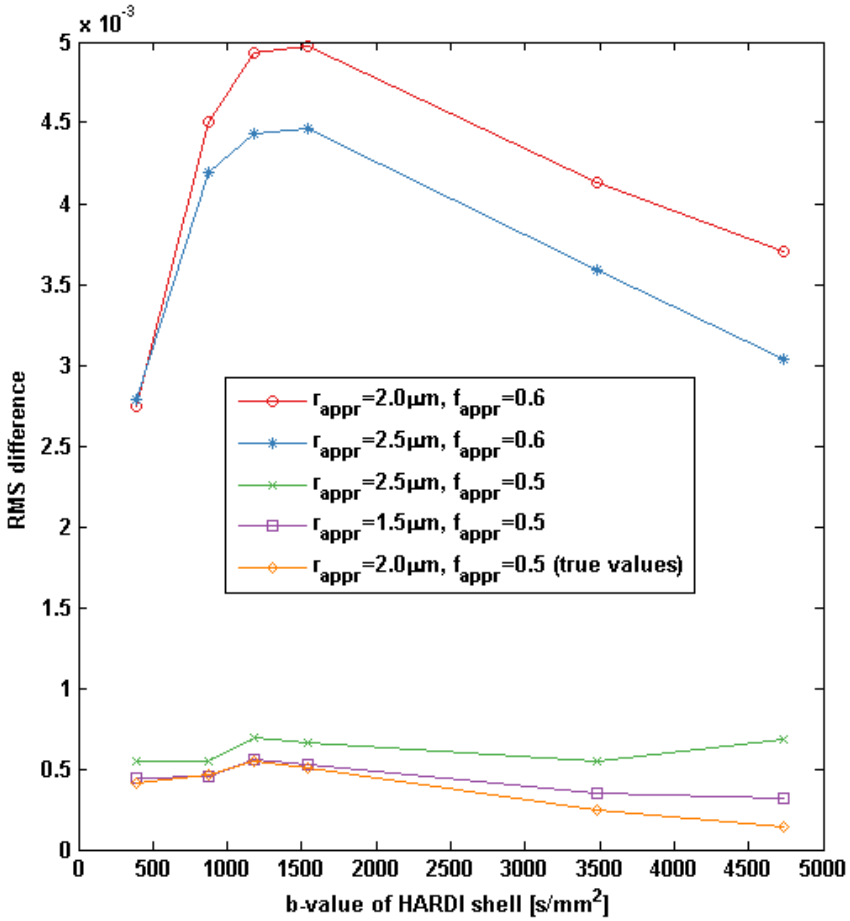
In practice we simplify this continuous minimization by performing a discrete search over a collection of 720 pre-computed signals combining 30 radii, 6 densities and 4 angles selected in realistic ranges. Fig. 4 shows the matched parameters estimating 16 configurations Ω_{int}. The rationale behind this latter experiment is that we consider the approximation to be invalid if the error made on the signal causes the underlying microstructure to be incorrectly estimated.



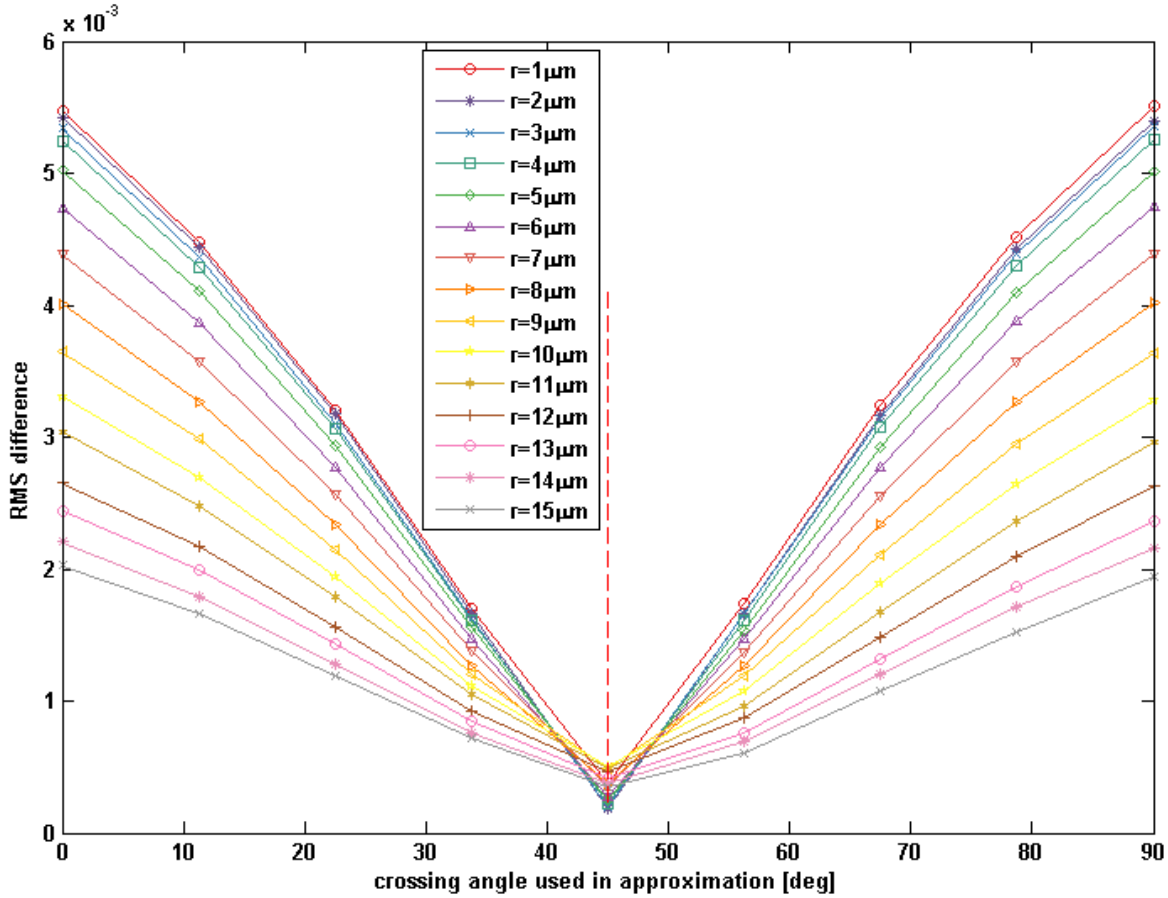
·1) Single fascicle of identical axons (left) and fascicles crossing in interleaved planes (right).

Results:

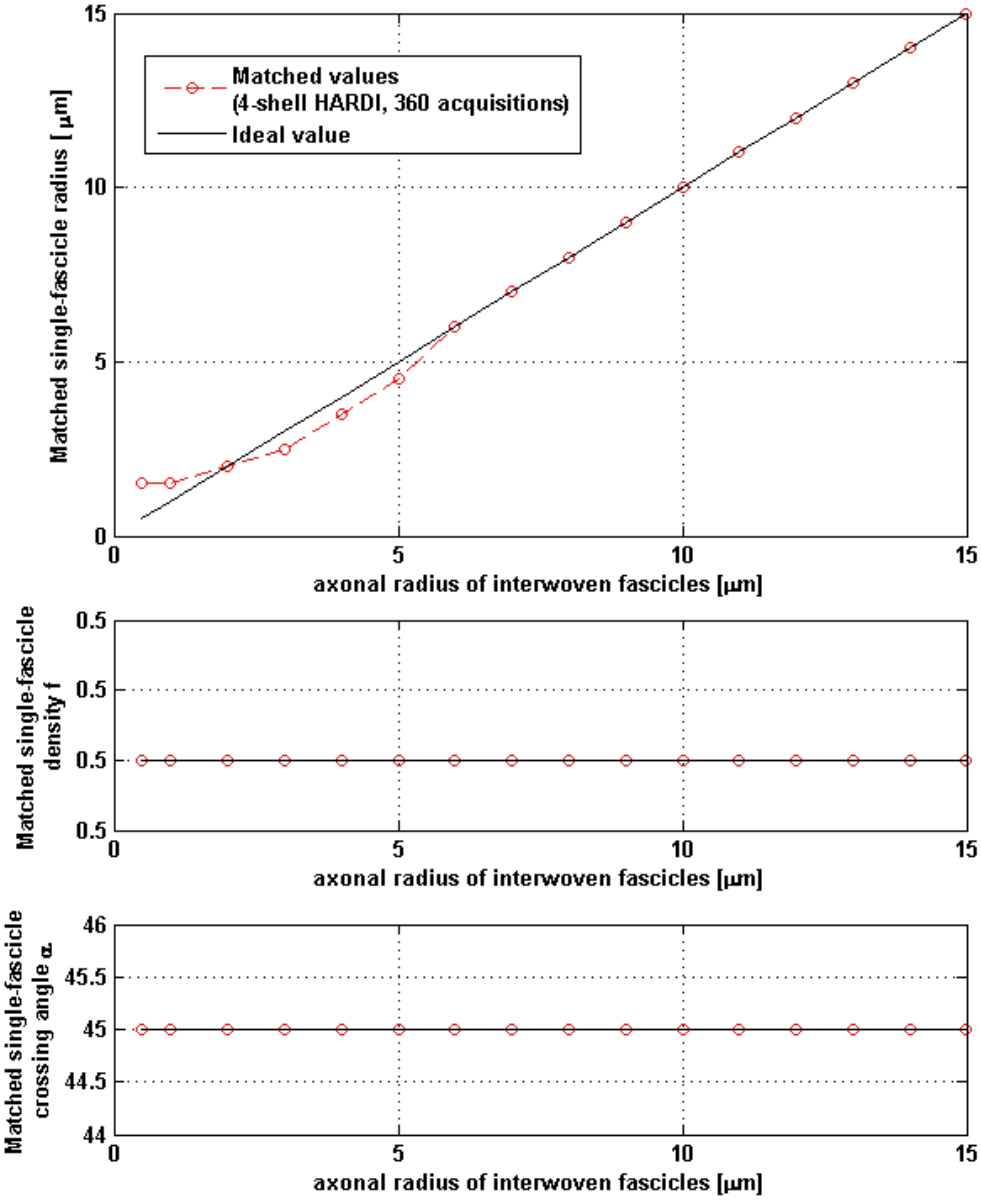
It appears from Fig. 2 that the approximation does not hold uniformly for all b-values and from Fig. 3 that it seems better for fascicles of large axonal radii, yielding lower signal difference. We also see on Fig. 3 a clear correlation between the crossing angle used in the approximation and signal similarity for a large spectrum of radii. This is confirmed on Fig. 4 where smaller radii (<5μm) fail to be accurately estimated and the best available value for α in the pre-computed collection is selected in all 16 cases, from which we infer that the error on the angle is less than 22.5°, the difference between α and the next closest angles in the collection. Similarly we conclude that the density can be estimated with an error less than 0.1.



·2) RMS signal difference vs b-value of a 90-gradient HARDI shells with δ=15ms and Δ=20ms. All the approximations use α=67.5°, the value of the reference interwoven-fascicle signal..



·3) RMS difference vs crossing angle, all other parameters kept equal. The reference angle is indicate by the red dashes. Reference density was 0.5.



·4) All 16 microstructural estimations, using the protocol from [Alex10]. The discrete search is performed over 30 radii spanning [0.5,20]μm, 6 densities in [0.1,0.9] and 4 angles in [22.5,90]°.

Conclusions:

The validity of the superposition hypothesis varies with the acquisition sequences and might not be compelling with axons of small radii as they present larger signal differences and may cause incorrect estimation of the underlying microstructure even in a noise-free setup. Accurate axonal density and crossing angle do seem to correlate with signal similarity. Further studies should investigate the validity of this approximation in more complex situations, e.g. in fascicles with different radii or densities.

Imaging Methods:

Diffusion MRI [2]

Modeling and Analysis Methods:

Diffusion MRI Modeling and Analysis [1]

Keywords:

Modeling
WHITE MATTER IMAGING - DTI, HARDI, DSI, ETC

[1|2]Indicates the priority used for review

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Not applicable

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Diffusion MRI

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