Image Reconstruction and Processing of High Angular Resolution Diffusion Imaging

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1. INTRODUCTION

How can we get information about the human brain anatomical connectivity non-invasively? As of today, diffusion-weighted (DW) magnetic resonance imaging (MRI) is the unique non-invasive technique capable of quantifying the diffusion of water molecules in biological tissues such as the human brain white matter.[1] The great success of DW-MRI comes from its capability to accurately describe the geometry of the underlying microstructure. Diffusion tensor imaging (DTI)[2] has now proved to be extremely useful to study the normal and pathological human white matter. However, the simplified assumption of DTI has some important limitations for voxels in which there is more complex internal structure, such as fibres crossings (Figure 1). This is an important limitation, since resolution of DW images is between 1mm^3 and 27mm^3, while the physical diameter of fibres can be between 1μm and 30 μm.

The purpose of this paper is to describe how to overcome limitations of the DTI model and recover fibre crossing information. To do so, high angular resolution diffusion imaging (HARDI) is used to measure DW images along several directions. Q-ball imaging (QBI) is a recent such HARDI technique that reconstructs the angular part of the diffusion displacement probability density function (PDF) of water molecules, also called the diffusion orientation distribution function (ODF). Therefore, this paper takes the reader from local q-ball reconstruction, to fibre bundle segmentation and fibre tractography from HARDI data (Figure 1).

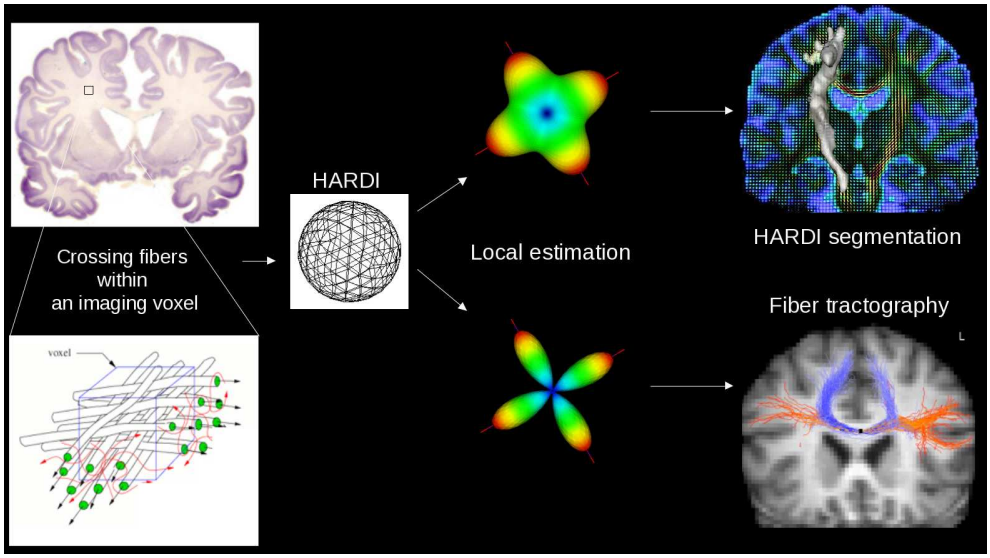


Figure 1. Sketch of this paper. Processing high angular resolution diffusion imaging (HARDI): from local estimation of water molecule diffusion phenomenon, to the segmentation and fibre tractography used to recover complex fibre crossing configurations.

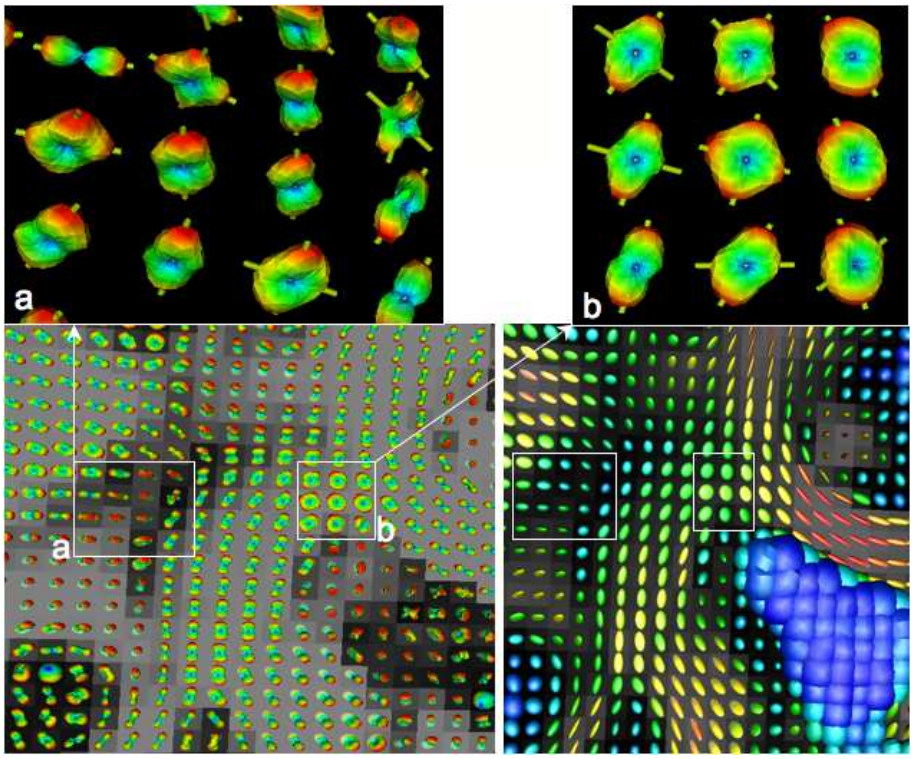


Figure 2. ODFs recovering multiple fiber crossing in a region of interest (ROI) where DTI profiles are limited. The ROI(a) shows crossing fibers between the corticalspinal tract (CST) and superior longitudinal fibers (coming out of the plane) and the ROI(b) shows crossing between the corpus callosum (in the plane) and the CST.

2. METHOD

The goal of HARDI is to capture multiple fibre directions within the same imaging voxel. Some HARDI reconstruction techniques are model dependent, some model-free, some have linear solutions whereas others require non-linear optimization schemes. A good review of these methods can be found in.[3] QBI can capture single and multiple fibre crossing information, which is an important object to better understand white matter connectivity.

2.1. Q-Ball Imaging

QBI[4] is a model-independent method that estimates the diffusion ODF from a single HARDI shell in q-space. The radius of this shell is fixed depending on the applied gradient strength of the scanner and diffusion time (also known as *b-value*[1]). The original QBI has a numerical solution[4] and more recent methods have introduced an analytical spherical harmonic reconstruction solution that is faster, more robust and require less DW measurements.[5] The spherical harmonic basis is a well-adapted mathematical tool that has powerful properties to process HARDI data on the sphere. Advantages of q-ball ODF reconstruction over DTI can be seen in the crossing regions of Figure 2.

2.2. HARDI Segmentation

The goal of HARDI segmentation is to find coherent sets of q-ball diffusion ODF that represent major fibre bundles. Very few methods exist to segment HARDI due to the complexity and high-dimensionality of the datasets. A new efficient segmentation method was developed in[6] using the fast, robust and analytical QBI solution. The approach uses a region-based statistical surface evolution defined directly on the image of diffusion ODFs represented in spherical harmonic coefficients. The solution is based on a good distance

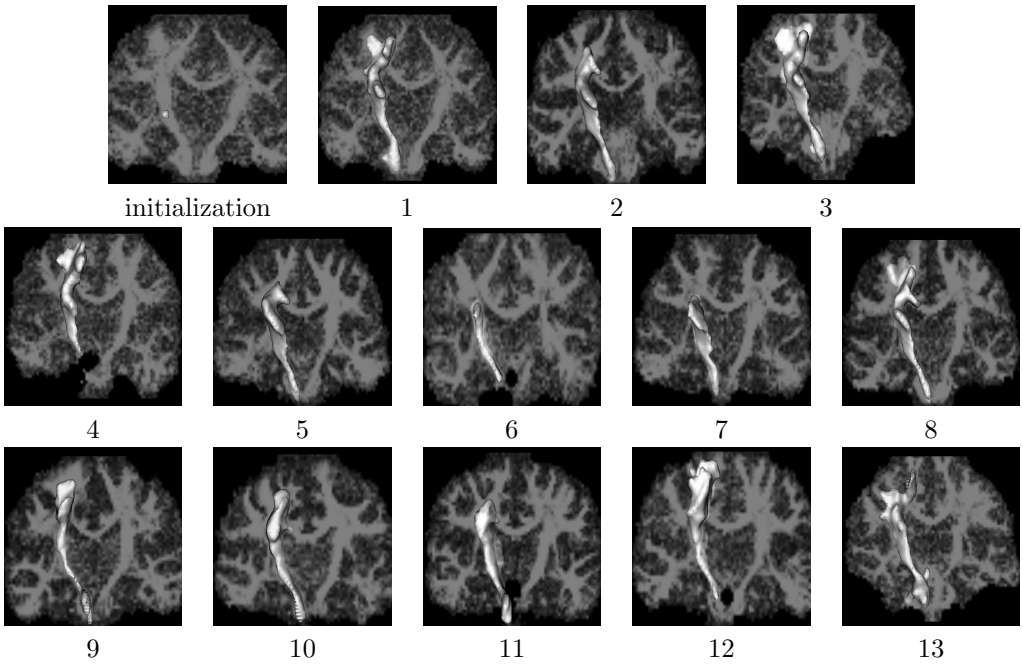


Figure 3. Automatic segmentation of the corticospinal tract (CST) using the diffusion ODF flow on the 13 subjects of the HARDI database[7] from a single seed point in the middle of the CST. Overall CSTs are similar and we observe an important variability across subjects.

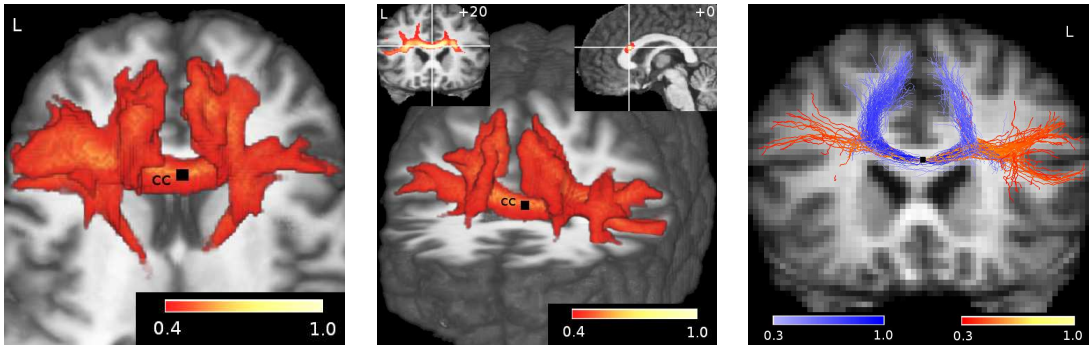
measure defined directly on the spherical harmonics so that diffusion ODFs can be compared and integrated into a level set framework. Figure 3 shows results on the corticospinal tract obtained from the 13 subjects of the public HARDI database.[7] These results show that our method is reproducible and brings a strong added value to DW-MRI segmentation.[3,8]

2.3. Fibre Tractography

One might also be interested to recover information about individual tracts and have quantitative connectivity representations of the white matter geometries. The relation between the measured diffusion ODF and the underlying fibre distribution, the fibre ODF, is still an important open question in the field.[3,4] The diffusion ODF is a blurred version of the "true" fibre ODF. Because of this blurring effect, the extracted maxima of the diffusion ODF are often used for fibre tractography. Alternativaly, one can attempt to remove this blurring effect with spherical deconvolution methods.[3,9] In,[3] an extension to streamline tractography is proposed based on the multiple maxima information of the fibre ODF so that the tracking can then propagate through crossing fibre regions. Moreover, a probabilistic algorithm based on the fiber ODF (fodf-PROBA) is proposed to account for branching and fanning fibre populations as well as fibres crossing.[10] An advantage of probabilistic tractography is that it is more robust to noise and outputs a connectivity score measuring how probable two voxels are connected to one another. Results from Figure 4 show accurate results of complex fibre bundles with crossing, fanning and branching configurations. Most current DTI-based methods neglect these fibres, which might lead to wrong interpretations of the brain functions.

3. CONCLUSION

HARDI such as QBI has the advantage of being able to deal with fibre crossings, which DTI is unable to do. Hence, it is possible to obtain more accurate information about anatomical connectivity, from segmentation and tractography algorithms. The fibre ODF shows great potential for fibre tractography because it has a better angular resolution. More investigation and better characterization of crossing, kissing, fanning and



Connectivity score top view | top-left-front view | fODF-PROBA fibers

Figure 4. Tracking the projections of the corpus callosum to Broca's area. The probabilistic connectivity score is shown on a coronal and sagittal slice and as 3D rendering. The connectivity results show asymmetry with stronger connections to the left inferior and middle frontal gyrus than to the homologue area. We also show a selection of the probabilistic fibers colored differently depending on their end point projections to the lateral or medial areas.

branching fibre configurations remains to be done in the human brain.[10] Even though the classical q-ball diffusion ODF reconstruction is smooth, it can be useful for other application than fibre tractography, such as segmentation of fibre bundles and clustering.[11] It is now important to validate these results on real human brain data and, ex vivo and in vivo phantoms. Validation is an important and crucial problem that needs to be tackled at the same time as these methods are applied on specific neuroscientific applications.

REFERENCES

1. D. LeBihan and E. Breton, "Imagerie de diffusion in vivo par résonance magnétique nucléaire," *C. R. Acad. Sci. Paris* **301 Série II**, pp. 1109–1112, 1985.
2. P. Basser, J. Mattiello, and D. LeBihan, "Estimation of the effective self-diffusion tensor from the NMR spin echo," *Journal of Magnetic Resonance* **B**(103), pp. 247–254, 1994.
3. M. Descoteaux, *High Angular Resolution Diffusion MRI: from Local Estimation to Segmentation and Tractography*. PhD thesis, Université de Nice-Sophia Antipolis, 2008.
4. D. Tuch, "Q-ball imaging," *Magnetic Resonance in Medicine* **52**(6), pp. 1358–1372, 2004.
5. M. Descoteaux, E. Angelino, S. Fitzgibbons, and R. Deriche, "Regularized, fast, and robust analytical q-ball imaging," *Magnetic Resonance in Medicine* **58**(3), pp. 497–510, 2007.
6. M. Descoteaux and R. Deriche, "High angular resolution diffusion mri segmentation using region-based statistical surface evolution," *Journal of Mathetical Imaging in Vision, special issue on Mathematics in Image Analysis* –, p. in press, 2008.
7. C. Poupon, F. Poupon, L. Allirol, and J.-F. Mangin, "A database dedicated to anatomo-functional study of human brain connectivity," in *Twelfth Annual Meeting of the Organization for Human Brain Mapping (HBM)*, 2006.
8. C. Lenglet, M. Rousson, and R. Deriche, "Dti segmentation by statistical surface evolution," *IEEE Transactions in Medical Imaging* **25**(6), pp. 685–700, 2006.
9. J.-D. Tournier, F. Calamante, D. Gadian, and A. Connelly, "Direct estimation of the fiber orientation density function from diffusion-weighted mri data using spherical deconvolution," *NeuroImage* **23**, pp. 1176–1185, 2004.
10. P. Savadjiev, J. S. W. Campbell, M. Descoteaux, R. Deriche, G. B. Pike, and K. Siddiqi, "Labeling of ambiguous sub-voxel fibre bundle configurations in high angular resolution diffusion mri," *NeuroImage* **41**(1), pp. 58–68, 2008.
11. D. Wassermann, M. Descoteaux, and R. Deriche, "Diffusion maps clustering for magnetic resonance q-ball imaging segmentation," *International Journal on Biomedical Imaging, special issue on Recent Advances in Neuroimaging Methodology* **2008**, pp. –, 2008.