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Mapping neuronal fiber crossings in the human brain

Maxime Descoteaux and Rachid Deriche

New magnetic resonance imaging processing tools allow white-matter fiber bundles to be segmented and tracked in regions of high complexity.

Obtaining information about the anatomical connectivity of the human brain, noninvasively, is a difficult challenge facing neuroscientists. The adult human brain contains tens of billions of neuronal cells, each with multiple cell contacts that form a complex web. Moreover, higher-order structures, termed neural tracts or fiber bundles, form a complicated 3D network within and connecting different brain regions. The distinct connectivity pattern of a given brain region determines how it processes information and functions. Being able to map these complex neural patterns in vivo is essential for understanding the fundamental basis of many developmental disorders as well as defining how the brain's structure relates to its function.

Diffusion-weighted (DW) magnetic resonance imaging (MRI) is a unique, noninvasive technique capable of quantifying the flow of water molecules in biological tissues such as the human brain.[1] The success of DW-MRI comes from its unique capability to accurately describe the geometry of the underlying tissue microstructure as it constrains diffusion. From the raw DW images, diffusion tensor imaging (DTI)[2] models the 3D movement of water molecules and has proved to be extremely useful in reconstructing the principal diffusion orientation needed to obtain fiber bundles and in the study of fiber-bundle connectivity in both normal and pathological brain tissues. However, DTI is most notably limited in regions of complex fiber crossings. This becomes a significant constraint when trying to map areas of the brain with complex internal structures (see Figure 1). The limitation is an important one, since the resolution of DTI images is between 1 and 27mm^3, while the physical diameter of fibers ranges between 1 and 30μm.

Overcoming the limitations of the DTI model and recovering fiber-crossing information is essential for constructing high-resolution maps of the human brain. To do so, high angular resolution diffusion imaging (HARDI) reconstruction techniques[3] have been used to measure DW images along several directions, capturing multiple fiber routes within the same imaging voxel. Specifically, local q-ball reconstruction, fiber-bundle segmentation, and fiber tractography are all techniques that rely on HARDI data and together give us a more accurate picture of white-matter geometries within the human brain (see Figure 1).

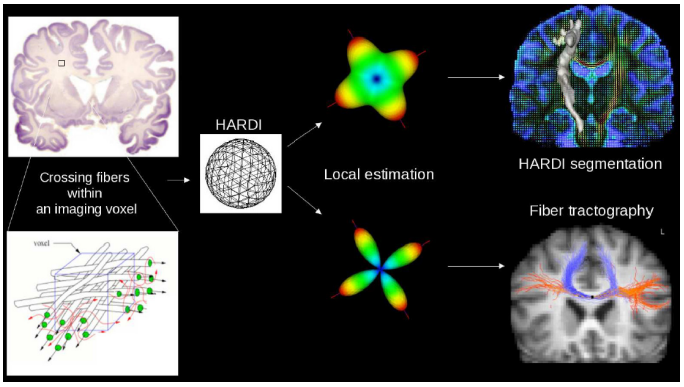

Figure 1. *Processing high angular resolution diffusion imaging (HARDI) from local estimations of water molecule diffusion phenomena to the segmentation and fiber tractography used to recover complex fiber-crossing configurations.*

Q-ball imaging (QBI)[4] is a recent HARDI technique that reconstructs the angular part of the diffusion displacement probability density function of water molecules, also called the diffusion orientation distribution function (ODF). QBI 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 the 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 requires fewer DW measurements.[5] The spherical harmonic basis is a well-adapted mathematical tool that has powerful properties for processing HARDI data on the sphere. QBI can capture single and multi-

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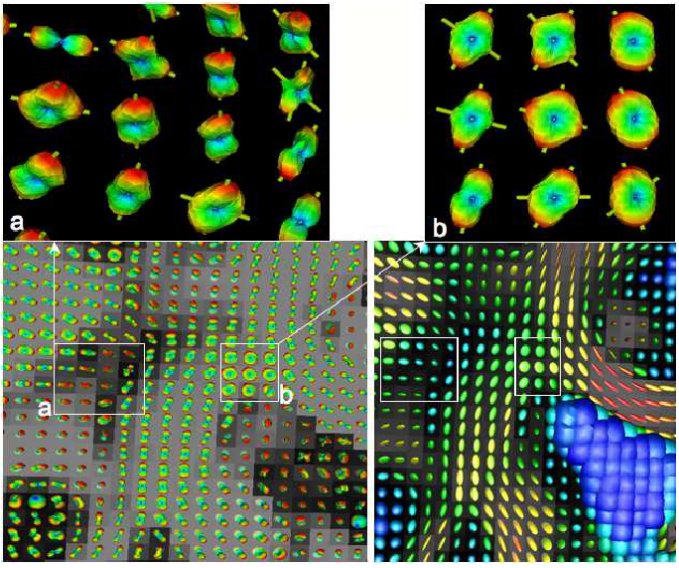

Figure 2. *ODFs recovering multiple fiber crossings in a region of interest (ROI) where DTI profiles are limited. ROI (a) shows crossing fibers between the corticospinal tract and superior longitudinal fibers (coming out of the plane), and ROI (b) shows crossing between the corpus callosum (in the plane)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

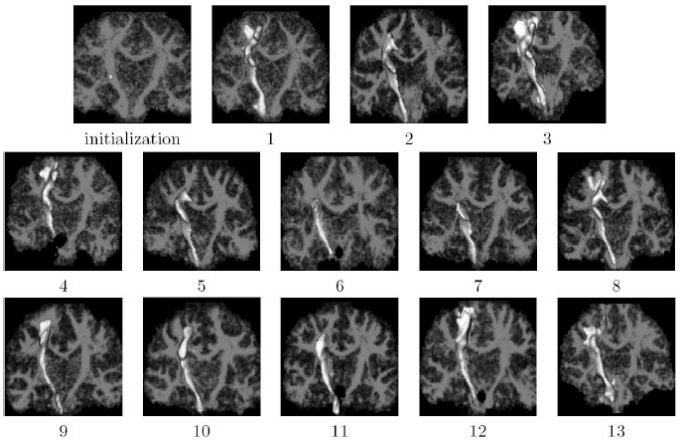

Figure 3. *Automatic segmentation of the corticospinal tract using the diffusion ODF flow on 13 subjects from the HARDI database [7] from a single seed point in the middle of the tract. Overall, corticospinal tracts are similar, and we observe important variability between subjects.*

ple fiber-crossing information, which is an important objective in better understanding white-matter connectivity. The advantages of q-ball ODF reconstruction over DTI can be seen in the crossing regions of Figure 2.

The goal of HARDI fiber-bundle segmentation is to find coherent sets of q-ball diffusion ODFs that represent major fiber bundles. Very few methods exist to segment HARDI data due to the complexity and high dimensionality of the data sets. We developed a new, efficient segmentation method using the fast, robust, analytical QBI solution.[6] 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 measure defined directly on the spherical harmonics so that diffusion ODFs can be compared and integrated into a level set framework. Figure 3 shows the results for the corticospinal tract obtained from 13 subjects in the public HARDI database.[7] These results show that this method is reproducible and brings a strong added value to DW-MRI segmentation.[3,8]

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

HARDI techniques, such as QBI, have the advantage of being able to accurately image fiber crossings, which traditional DTI is unable to do. These techniques make it possible to obtain increasingly accurate information about the anatomical connectivity of the human brain using segmentation and tractography algorithms. However, better characterization of crossing, kissing, fanning, and branching fiber configurations remain problematic for obtaining high-resolution maps of the human brain.[10] Fur-

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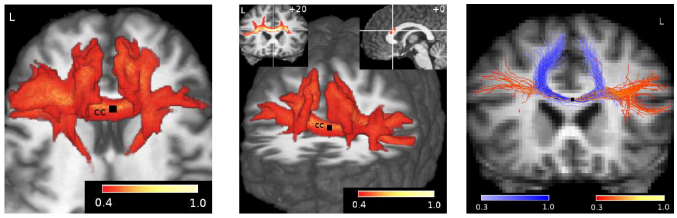

(a) Connectivity score top view (b) top-left-front view (c) fODF-PROBA fibers

Figure 4. *(a) Connectivity score top view, (b) top-left-front view, and (c) fODF-PROBA fibers.*

thermore, validation has become an important and crucial problem that needs to be tackled as these methods are beginning to be applied to specific neuroscience applications.

Author Information

Maxime Descoteaux
NMR Lab
NeuroSpin, CEA Saclay
Gif-sur-Yvette, France
http://www-sop.inria.fr/members/Maxime.Descoteaux/index.en.html

Maxime Descoteaux is currently a postdoctoral fellow at NeuroSpin working on high spatial, angular, and temporal resolution diffusion MRI sequence design for structural and functional study of the diffusion process within the human brain. He obtained his PhD in computer science and HARDI processing at INRIA Sophia Antipolis, supervised by Rachid Deriche.

Rachid Deriche
Odyssée Project Team
INRIA Sophia Antipolis–Méditerranée
Sophia Antipolis, France
http://www-sop.inria.fr/odyssee/en/rachid.deriche

Rachid Deriche is a research director at INRIA Sophia Antipolis in the Odyssée Project Team. His research interests are in brain imaging as well as computer and biological vision. He has authored and coauthored more than 150 scientific papers for conferences and journals of the computer vision and medical image communities.

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. J. Basser, J. Mattiello, and D. LeBihan, *Estimation of the effective self-diffusion tensor from the NMR spin echo*, **J. Magnet. Res. 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*, **Magnet. Res. Med. 52** (6), pp. 1358–1372, 2004.
5. M. Descoteaux, E. Angelino, S. Fitzgibbons, and R. Deriche, *Regularized, fast, and robust analytical Q-ball imaging*, **Magnet. Res. Med. 58** (3), pp. 497–510, 2007.
6. M. Descoteaux and R. Deriche, *High angular resolution diffusion MRI segmentation using region-based statistical surface evolution*, **J. Math. Imag. Vision**, in press.
7. C. Poupon, F. Poupon, L. Allirol, and J.-F. Mangin, *A database dedicated to anatomo-functional study of human brain connectivity*, **12th Ann. Meet. Org. Human Brain Mapping**, 2006.
8. C. Lenglet, M. Rousson, and R. Deriche, *DTI segmentation by statistical surface evolution*, **IEEE Trans. Med. Imag. 25** (6), pp. 685–700, 2006.
9. J.-D. Tournier, F. Calamante, D. G. 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.