A Hough transform global approach to diffusion MRI tractography

Ehsan Aganj, Christophe Lenglet, Renaud Keriven, Guillermo Sapiro, Noam Harel, Paul Thompson

A Hough transform global approach to diffusion MRI tractography

I. Aganj[1], C. Lenglet[1,2], R. Keriven[3], G. Sapiro[1], N. Harel[2], and P. Thompson[4]

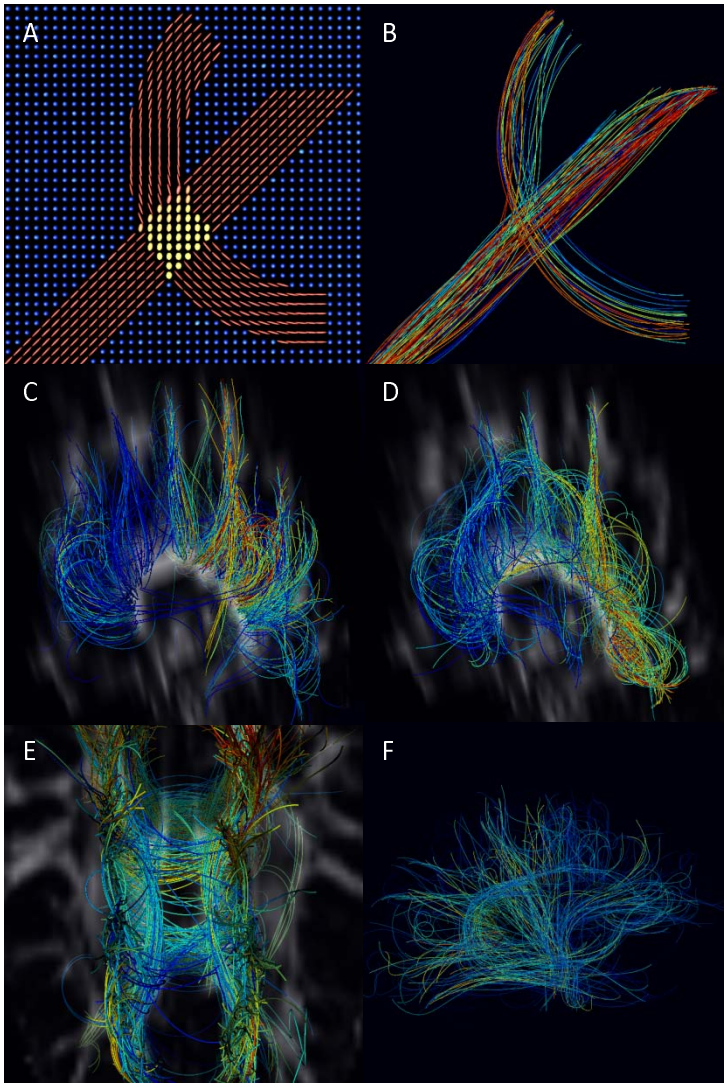
[1]Department of Electrical and Computer Engineering, University of Minnesota, Minneapolis, Minnesota, United States, [2]Center for Magnetic Resonance Research, University of Minnesota Medical School, Minneapolis, Minnesota, United States, [3]CERTIS, École Nationale des Ponts et Chaussées, Champs-sur-Marne, Marne-la-Vallée, France, [4]Laboratory of Neuro Imaging, University of California-Los Angeles, Los Angeles, California, United States

Introduction

Tractography in *Diffusion-Weighted MRI* provides a unique quantitative measurement of the brain's anatomical connectivity using information not available from other imaging techniques. Many tractography algorithms are based on local fiber orientation estimates, such as streamline methods, and are vulnerable to noise and partial volume effects; fiber crossing and kissing are also difficult to distinguish. This led to the development of probabilistic techniques [1] and global approaches relying on front propagation [2, 3] or simulation of the diffusion process [4]. In this work, we present a global approach based on the voting process provided by the *Hough transform* [5]. Our proposed tractography algorithm essentially tests all possible 3D curves in the volume, assigning a score to each of them, then selecting the curves with the highest scores, and returning them as the potential anatomical connections. We present experimental results on both artificial and real diffusion tensor images (DTI) and high-angular resolution diffusion images (HARDI).

Methods

We first randomly generate a sufficiently high number of initial seed points inside a mask/ROI of the brain. The spatial probability distribution of the seed point is set to be proportional to its fractional anisotropy (FA). From each initial point, all possible curves passing through this location are estimated. A score is computed for each possible curve, and the curve with the maximum score is then chosen as the best fiber passing through that seed point. Curves are parameterized by the arc length s, and the (unit) tangent vector of the curve is identified at each point by standard polar coordinates $\theta(s)$,$\phi(s)$: $\vec{t}(s) = (\sin\theta(s)\cos\phi(s), \sin\theta(s)\sin\phi(s), \cos\theta(s))^T$. In our proposed model, we consider polynomial approximations of these two angles with respect to the arc length, $\theta(s) = \sum_{k=0}^{N-1} a_k s^k$ and $\phi(s) = \sum_{k=0}^{N-1} b_k s^k$, where the order N was chosen to be 4 in the experiments. In addition, two extra parameters L_- and L_+ determine the partial lengths of the curve at each side of the seed point ($0 \le (L_-, L_+) \le L_{\max}$, where $L_{\max}$ is a constant). Each curve initiated from the point $\vec{x}_0$ is then represented using $2N+2$ parameters $\{a_0, \dots, a_{N-1}, b_0, \dots, b_{N-1}, L_-, L_+\}$, and the curve itself can be computed by integrating the tangent vector, $\vec{x}(s) = \vec{x}_0 + \int_0^s \vec{t}(s')ds'$, $s \in [-L_-, L_+]$. The score of each possible curve passing through a seed point $\vec{x}_0$ is given by $S_{\vec{x}_0}(a_0, \dots, a_{N-1}, b_0, \dots, b_{N-1}, L_-, L_+) \coloneqq \int_{-L_-}^{L_+} \left(\log P\left(\vec{x}(s), \vec{t}(s)\right) + \lambda\right) ds$. The function $P(\vec{x}, \vec{t})$ represents the probability for a fiber to pass through $\vec{x}$ in the direction $\vec{t}$, which can be computed as $P(\vec{x}, \vec{t}) = P(\vec{t}|\vec{x})P(\vec{x})$ (see below). The positive constant λ encourages longer fibers to be chosen; without using λ, the negative value of the logarithm would give the zero-length curve ($L_- = L_+ = 0$) the maximum score. The probability of the existence of a fiber at the point $\vec{x}$, $P(\vec{x})$, was considered to be zero outside the brain mask and equal to the FA inside the brain, since we suppose that the more anisotropic a region is, the more likely a fiber bundle may be passing through that region. Finally, assuming that a fiber is actually passing through the point $\vec{x}$, the probability that it is in the direction $\vec{t}$, $P(\vec{t}|\vec{x})$, may be obtained from the orientation distribution function (ODF) [6] at each voxel in the volume. For example, in the DTI case, it is computed by integrating the 3D normal distribution function in a cone (with constant solid angle) which yields the probability of diffusion in the direction specified by the unit vector $\vec{t}$: $P(\vec{t}|\vec{x}) = \int_{-\infty}^{\infty} \frac{1}{(2\pi)^{\frac{3}{2}}|D(\vec{x})|^{\frac{1}{2}}} e^{-\frac{1}{2}r\vec{t}^T D(\vec{x})^{-1} r\vec{t}} r^2 dr = \frac{1}{2\pi|D(\vec{x})|^{\frac{1}{2}}(\vec{t}^T D(\vec{x})^{-1}\vec{t})^{\frac{3}{2}}}$, where $D(\vec{x})$ is the diffusion tensor. In the case of HARDI, the ODFs were approximated by 4th or 6th order spherical harmonic series. This allows for their sampling in any desired direction $\vec{t}$. At each seed point, the curve with the highest score is chosen in a multi-resolution approach, discretizing the $\mathbb{R}^{2N+2}$ space of parameters and computing the score for each set of parameters.



Results and Discussion

Fig. A shows an artificial DTI volume used to test our algorithm on a region with fiber crossing. We generated 200 random seed points, and the algorithm computed the best curve for each point. The top 100 curves are shown in Fig. B. We also ran the algorithm on real human brain data. Diffusion-weighted images were acquired on a 4T Bruker/Siemens MRI scanner using an optimized diffusion tensor sequence. 30 images were acquired, 3 with no diffusion sensitization and 27 diffusion-weighted images at $b = 1100\ s/mm^2$. 1000 seed points were generated inside a mask of the *corpus callosum* and fed to the algorithm to compute the corresponding curves. 600 curves out of 1000 with the highest scores are depicted overlaid on the FA map in Figs. C and D, respectively for DTI and HARDI. The color of each fiber corresponds to its computed score, increasing from blue to red. In addition, a closer axial view with a larger number of curves allows us to see the *cingulum* (Fig. E). Eventually, an overall test was performed on the entire brain DTI of a different dataset. This produced 1500 curves, out of which the 900 with the highest score, mostly corresponding to the *corona radiata*, are illustrated in Fig. F (fibers with smaller score are more transparent).

References [1] Behrens T.E.J. et al, NeuroImage 34:144-155, 2007. [2] Tournier J.D. et al, NeuroImage 20:276-288, 2003. [3] Pichon E., Proc. MICCAI 180-187, 2005. [4] Batchelor P.G. et al, Info. Proc. in Med. Img. 121-133, 2001. [5] Gonzalez R.C. and Woods R.E., Digital Image Processing, Prentice Hall, 2002. [6] Descoteaux M., PhD dissertation, INRIA, University of Nice – Sophia Antipolis, 2008.

Acknowledgments This work was supported in part by the National Institutes of Health (NIH) (P41 RR14075, P41 RR008079, P30 NS057091, R01 EB007813, RO1 HD050735, CON000000004051-3014), the National Science Foundation (NSF), and the Mental Illness and Neuroscience Discovery (MIND) Institute.