Accurate tractography propagation mask using T1-weighted data rather than FA

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Introduction

dMRI tractography needs to be constrained by a white matter (WM) mask defining the 3D space within which fibers are tracked. Most techniques usually threshold the fractional anisotropy (FA) maps (typical threshold between 0.1-0.2) assuming that when FA is too small, the uncertainty of the principal diffusion direction is high. However, this criterion is rough as the FA value is not specific of a particular structural configuration and therefore constrains tracking results to region of WM with high anisotropy. In particular, FA (or GFA) can be very low in fiber crossings representing more than 2/3 of WM voxels, thus putatively discarding many valid tracts. Furthermore, because the dMRI resolution is generally coarser than standard T1-weighted MRI (on the order of 2mm isotropic), voxels at the interface between the WM and the cortex may suffer from severe partial volume effects, artificially diminishing the FA values. Therefore, many true-positive neuronal pathways may not be revealed. In this work, we propose the creation of a robust propagation mask stemming from T1 anatomy. A preliminary step consists of adequately correcting the geometrical distortions of dMRI data, and of accurately matching it to the T1-weighted data. Many post-processing pipelines already provide brain, WM or gray matter (GM) masks from T1 data relying on a robust analysis of its histogram. However, they may suffer from several limitations. First, the partial volume effect will fail at delineating some small structures like the fornix, the posterior (PC) and anterior commissures (AC). In addition, deep brain structures, commonly crossed by efferent and afferent fibers, would not be systematically well included, and the conventional millimeter resolution of T1-weighted data at 1.5T or 3.0T can cause partial volume effects in cortical regions that lead to spurious connections between neighboring gyri.

In this work we present a novel tool to create accurate anatomy-based propagation masks dedicated to tractography and calculated from T1-weighted MRI (T1) images, improving the tool presented in [1] thanks to the addition of morphological and homotopical constraints to guarantee a better definition of the WM, especially in regions close to the gray matter/white matter (GM/WM) interface. This allows a better tracking of fiber bundles, in particular of the short association subcortical U-fibers.

Material and methods

The mask calculation is based on three T1-based masks. Two masks are obtained with the T1-MRI pipeline of BrainVISA software [2]: 1) a mask of both hemispheres and the cerebellum, called the *brain mask*, and 2) a mask of the sulci skeleton, called the *sulci mask*, calculated through a homotopic multiscale erosion of a brain mask (see Figure 1A). A first processing subtracts the dilated *sulci mask* to the *brain mask* in order to prevent any connection between different gyri and to ensure that the fibers are stopped in the GM/WM interface. An *intermediate* propagation mask is thus obtained.

In order to ensure a good delineation of deep structures, of the corpus callosum (CC), of the fornix, and of AC/PC, a mask of deep nuclei and ventricles, called the *nuclei mask* is employed (see Figure 1A). The deep nuclei segmentation is obtained using a deformable model constrained with a probabilistic atlas [3]. The ventricles segmentation is calculated using a robust histogram analysis of the T1 data guided by a probabilistic atlas of the ventricles, as described in [4]. The *nuclei mask* is dilated and added to the *intermediate* propagation mask in order to fill all the deep brain regions. The ventricles are subsequently subtracted from this mask to obtain the final robust propagation mask. Last, the cerebellum can be optionally included in the final mask.

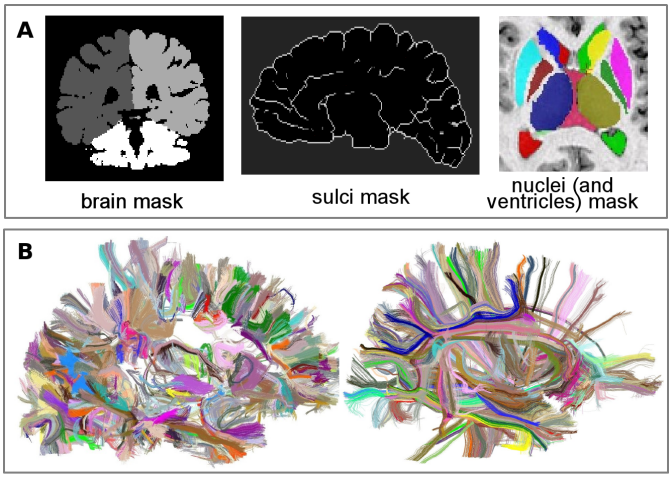

Figure 1: A: T1-based masks used for the propagation mask construction. **B:** some fiber clusters [5] obtained from a tractography dataset using the proposed propagation mask.

Results and discussion

Figure 2 shows the final propagation mask obtained with our pipeline, compared to a FA-based mask. A better delineation of WM+GM, especially in regions close to the cortical surface was observed. Also the fornix, the AC and the PC were successfully included. As an example of tracked bundles, Figure 1B shows some fiber clusters obtained using the fiber clustering method described in [5], from a tractography dataset calculated using the propagation mask. Note, that a good registration between T1 and T2 images is needed, which implies a good correction of the susceptibility induced geometrical distortions of T2 images. Such a mask is more suitable when using diffusion models/tracking algorithms with regularization in order to resolve the trajectory direction in low anisotropy locations that are discarded using conventional FA-based masks.

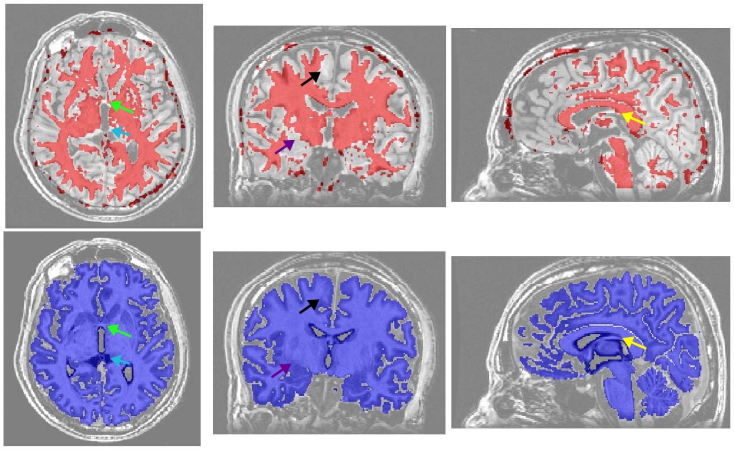

Figure 2: Axial, coronal and sagittal views for the propagation masks. **red**: FA mask (th = 0.1). **blue**: our propagation mask **(**DW data first denoised using method described in [6], orientation distribution functions calculated from the analytical q-ball model [7]). Note the good delineation in our mask of the AC (green arrows), the PC (cyan arrows), the subcortical WM (black arrows), the deep nuclei (violet arrows) and the fornix (yellow arrows).

Conclusion

We presented an improved propagation mask built from T1 data and dedicated to dMRI tractography. This mask allows a better tracking of fibers until the GM/WM interface, which is of particular interest for the study of short association U-fibers. Contrary to usual FA-based masks failing at including low FA regions such as AC/PC, the fornix or crossings, this novel technique provides an accurate mask of the brain WM+GM independent of the DW data quality. Consequently, its use in conjunction with tractography techniques improves the accuracy of the anatomical connectivity of the brain by reducing false positives and increasing the detection of the subcortical connectivity. We think that our mask can be useful for any dMRI study requiring a detailed and accurate tracking of fiber bundles.

References [1] Perrin et al., Int J Bio. Imag., 368–406, 2008. [2] Cointepas et al., HBM 2010, http://brainvisa.info. [3] Marrakchi-Kacem et al., ISBI 2010, 61-64, 2010. [4] Marrakchi-Kacem et al. HBM 2010. [5] Guevara et al., Neuroimage 2010, in press. [6] Descoteaux et al., MICCAI 2008. [7] Descoteaux et al., MRM 58:497-510.