Correcting spatial misalignment between fiber bundles segments for along-tract group analysis

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Introduction

While it is acknowledged that diffusion MRI datasets should be corrected for artifacts in population studies [1], the same is also recommended for fiber bundle group analyses. As shown by [2], along-tract based statistics offer a more realistic estimation than using a single averaged value from the entire studied fiber bundle. [3, 4] have previously proposed bundle-based registration algorithms, but most statistical analysis are done at the single tract level, as for example by extracting the mean representative pathway [5, 6]. In this context, the mean fiber may not be optimally aligned between various subjects as opposed to the bundles themselves, which may lead to an increased bias in the subsequent statistical analysis. To alleviate this caveat, we propose a fast and straightforward 1D rigid registration algorithm for metrics extracted along tracts based on the fast Fourier transform (FFT) and the cross-correlation theorem [7]. The algorithm works directly in the metric space by considering the extracted values as a 1D signal, thus making it perfectly suited for usage in population studies using any metric of interest.

Theory

The cross-correlation of two signals x and y can be computed with the FFT using $F^{-1}\big(F(x) \odot F^{*}(y)\big)$, where F is the Fourier transform, F^{*} is the complex conjugated Fourier transform and $\odot$ is the pointwise product**.** The cross-correlation theorem thus provides a computationally cheap way to find the maximum overlap between two 1D signals as shown on **Figure 1**. Using this idea, extracted fiber bundles metrics from different subject can be viewed as a 1D signal, which can then be realigned directly in the metric space by finding the maximum value of the FFT based cross-correlation.

Figure 1*:* A random signal can be realigned with a shifted version of itself (of a different amplitude) by maximizing the cross-correlation function. The optimal shift given by the cross-correlation also maximize the Pearson's correlation coefficient.

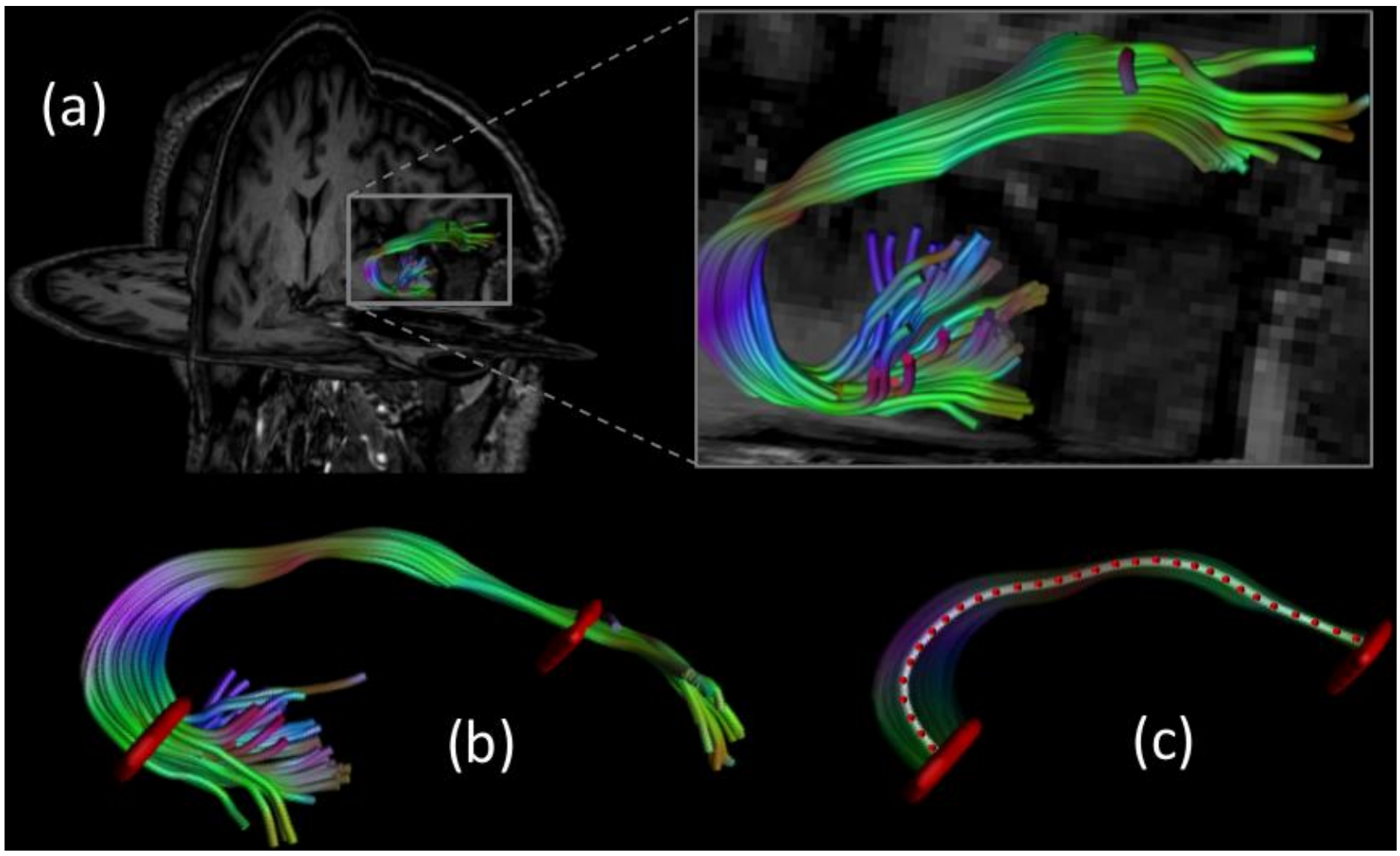

Figure 2: a) Reconstructed uncinate fasciculus (UF) for a representative subject. b) Only a straight segment of the UF (between red lines) is extracted. c) Fractional anisotropy (FA) values at each point (indicated by the red dots) along the mean fiber (white line) are extracted for subsequent statistical analysis.

Datasets

10 subjects underwent a diffusion weighted scan of 45 diffusion encoding directions at b = 1200 s/mm² and 3 b = 0 s/mm² images on a 3T Intera Philips scanner at a spatial resolution of 1.7 x 1.7 x 2.5 mm³ with TR/TE = 6638 ms / 73 ms. The data was then corrected for subject motion and eddy current distortions with ExploreDTI [8]. Whole-brain deterministic fiber tracking was made inside a mask of FA > 0.2, with one seed point per voxel distributed on a 2 x 2 x 2 mm³ grid, maximum angle deviation of 30 degrees and a step size of 1 mm. Finally, the right UF was segmented for the 10 subjects and the FA values were collected along the mean fiber of the UF for each subject as shown on **Figure 2**.

Results & Discussion

The 10 FA profiles of each subject were co-registered with our algorithm (which took less than 1 second to execute) and only the values in the region of full overlap were kept to prevent spurious effects near the endpoints. As shown in **Figure 3,** our algorithm can realign the FA values extracted along the right UF from two different subjects by maximising their cross-correlation. The maximal cross-correlation is given by a shift of 1 mm to the right, which is also the position of the maximal Pearson's correlation coefficient. **Figure 4** shows the mean and standard deviation of the FA profiles for the 10 subjects. While correcting for along-tract metric misalignment produces different estimated mean FA values than the original, misaligned metrics, the standard deviation is also lower near the left endpoint of the UF but somewhat larger for the right endpoint. The bottom graph shows that the percentage difference of the mean FA between the unaligned and realigned metrics can be as large as 14%, where percentage difference = $100\ x\ \frac{|FA_{unaligned} - FA_{realigned}|}{(FA_{unaligned} + FA_{realigned})/2}$. While we only explored translation of at least 1 mm (which is the step size used in the tracking), our algorithm could also be modified for optimal sub-millimeter realignment to yield even more accurate inter-tract correspondence for large cohorts of subjects. This can potentially reduce the standard deviation of the mean FA in group studies for increased accuracy when estimating confidence intervals. In the same way, this could also help researchers uncover relationships of interest which might have been hidden by misalignment at first, but appear as statistically significant after realigning the diffusion metrics.

References [1] Jones & al. NeuroImage 2013 [2] Colby & al. NeuroImage 2012 [3] Leemans & al. MRM 2006 [4] Garyfallidis & al. NeuroImage 2015 [5] Smith & al. NeuroImage 2006 [6] Zimmerman-Moreno & al. Hum. Brain Mapp. 2015 [7] Lewis (1995) *Vision Interface* [8] Leemans & al. ISMRM 2009

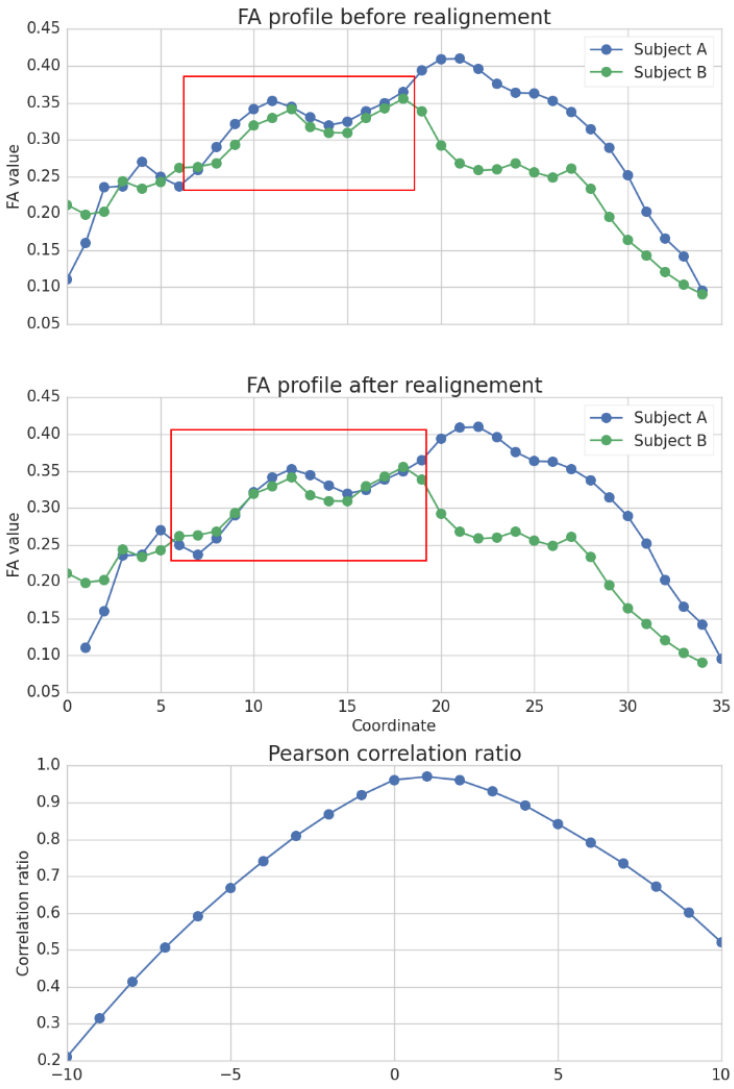

Figure 3 : FA profile along the uncinate fasciculus for two subjects. Our algorithm finds that a shift of 1 mm to the right provides the maximum overlap between the two subjects. This translation also gives the maximum Pearson's correlation coefficient as shown by the bottom graph.

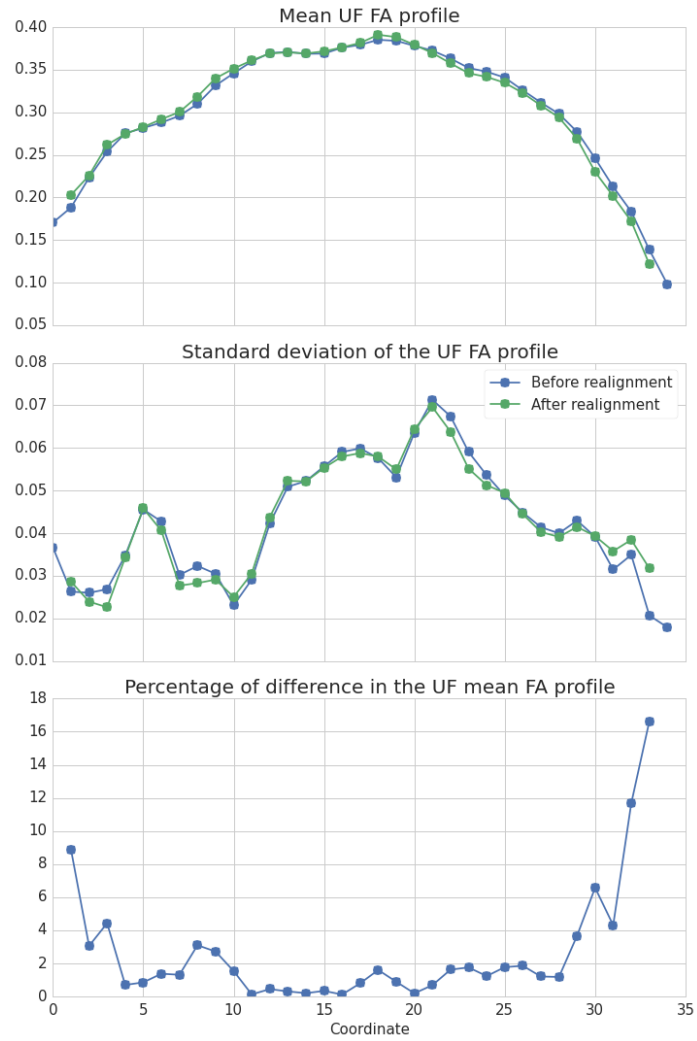

Figure 4 : Mean and standard deviation of the FA and relative percentage in the mean FA profile for the right uncinate fasciculus before and after correction. Realignment versus original can change the mean FA values by as much as 14 %.