Can tissue segmentation improve registration? A study of 92 twins

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Introduction: Robust and automatic non-rigid registration depends on many parameters that have not yet been systematically explored. Here we determined how tissue classification influences non-linear fluid registration of brain MRI. Twin data is ideal for studying this question, as volumetric correlations between corresponding brain regions that are under genetic control should be higher in monozygotic twins (MZ) who share 100% of their genes when compared to dizygotic twins (DZ) who share half their genes on average. When these substructure volumes are quantified using tensor-based morphometry, improved registration can be defined based on which method gives higher MZ twin correlations when compared to DZs, as registration errors deplete these correlations.

Methods: T1-weighted volumetric MRIs of 23 MZ and 23 DZ same-sex twin pairs (age: 22-25 years), were aligned to the Colin27 average brain template by 9-parameter linear transformation. After preprocessing, the white matter (WM) was segmented using the modified mixture model cluster analysis technique in SPM5 [1]. Each individual's (1) whole brain volume and (2) binary WM volume were non-linearly warped to a common randomly picked subject's whole brain or binary WM volume using a Riemannian fluid algorithm [2]. For both segmented and non-segmented data, we created statistical maps from the determinants of the deformation fields using the intraclass correlation (ICC) computed independently for the MZ and DZ groups. The ICC measures the resemblance between twin pairs, and can be computed for different types of twins (MZ and DZ) with different degrees of genetic similarity. At each voxel, a p-value was also computed by randomly reassigning subject labels (5000 permutations) to determine the significance of the ICC values. To assess statistical power, the CDF plots of the p-values were created. The value at which the CDF intersects the $y = 20x$ line represents the highest statistical threshold for which at most 5% false positives are expected in the map (controlling the false discovery rate).

Results: The p-values in **Figure 1** indicate the statistical significance of the correlation ($p < 0.05$ are shown in red) for the whole brain- (top row) and WM- (bottom row) based registrations. As expected, the p-values are generally lower in the MZ twins (denoting higher intraclass correlations) who share 100% of their genes. **Figure 2** shows the CDF plots of the p-values for ICC(MZ). For a null distribution, the cumulative distribution function is expected to fall along the

x = y line. WM-based maps were more spatially coherent, although they did not offer greater statistical power than registering image intensities (Figure 2).

Conclusions: Setting the whole WM class to the same value in MRI registration is sensible, since MR intensity differences are generally not reliable inside the WM. When the WM is binarized, the effect of RF shading artifacts can be accommodated in the tissue classification, and the registration cost function has a stable gradient with a sharp global minimum. As noted by others [3], convergence is faster and CPU time is reduced, as the cost function can be set to zero in overlapping binary regions. Even so, statistical power was almost identical using both methods.

References:

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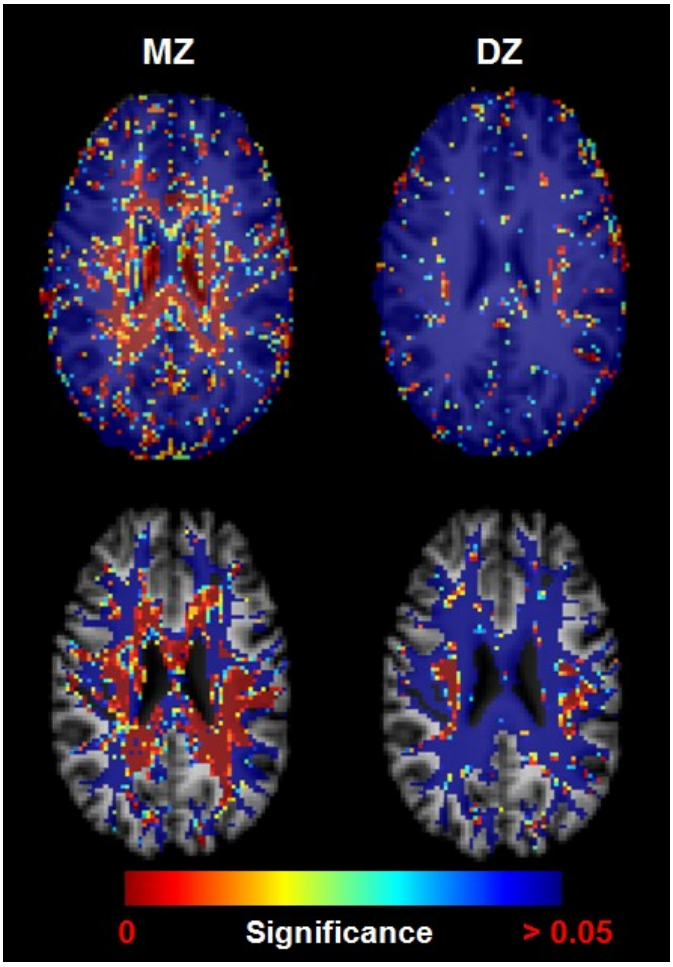

Figure 1. Significance maps for the correlations between MZ and DZ twin pairs after using registrations based on the whole brain (top row) and WM (bottom row).

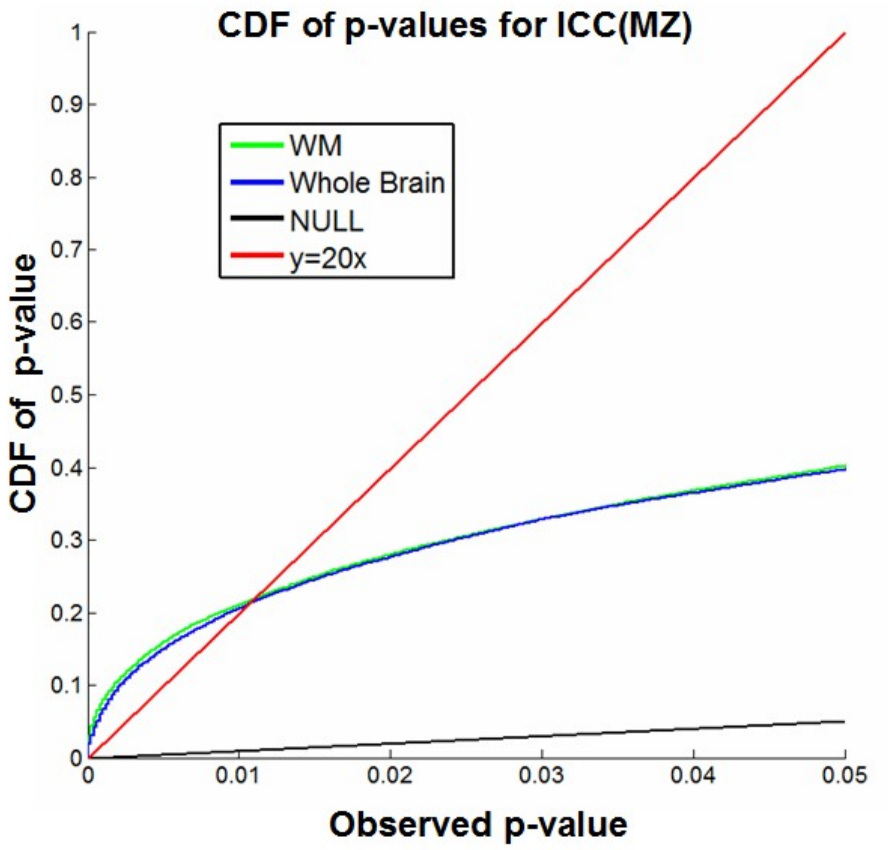

Figure 2. Cumulative Distribution Functions (CDFs) of significance maps for ICC(MZ).