

Comparison of different methods to correct artefacts in diffusion weighted MRI data

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Introduction

Data from diffusion weighted MRI (dMRI) often show artefacts from multiple sources including subject motion, eddy currents (EC) and inhomogeneities in the magnetic field. Especially the non-linear susceptibility artefacts make it difficult to establish a precise correspondence between diffusion and anatomical data. The gold standard for correcting these distortions in anterior-posterior direction is to acquire a field map that quantifies the field inhomogeneities, which allows computing a deformation field to rectify the data. Recently, methods have been published and implemented that process dMRI data with reversed phase-encoding direction [1,2,3,4]. Correcting deformation fields can be computed from these pairs of images. The purpose of this study is to compare two methods of susceptibility correction with field maps and data without non-linear correction.

All datasets were processed with the following pipeline:

1. Brain extraction from T1 image, rigid alignment to MNI coordinate system (FLIRT) and interpolation to 1mm³ voxel size.
 2. Correction for subject motion and EC by affine registration to the first b0 image using FSL [6].
 3. Computation of non-linear deformations from field maps, HySCO (SPM Toolbox) and TopUp (FSL). Additional shiftmap containing only zero values was created (MoCor) to see the effect of the non-linear methods.
 4. Linear alignment of corrected first b0 image with the anatomical T1 dataset to obtain the transformation from diffusion to anatomical space.
 5. Combination of shiftmaps with linear transformations from motion and EC correction and from alignment with T1 dataset. This resulted in one warp field for every diffusion volume that was used to warp the corresponding volumes of the dMRI dataset.
 6. Computation of diffusion tensor and fractional anisotropy (FA).
 7. Computation of cross-correlation of uniform T1 images and FA maps. Cross-correlation values were computed for the whole brain area and afterwards also for different regions in the brain (left Wernicke's area, BA44 and BA45, non-linearly warped from MNI space) to check for regional differences.
 8. Non-parametric randomisation test to assess if the differences between the methods in every subject are significant.
- Steps 2 to 5 are visualised in a flow-char in Fig. 1.

Methods

Data of 5 year old children were acquired on a Siemens Tim TRIO scanner at 3T using a 12 Channel head coil. The following datasets were acquired: a uniform T1 image using the MP2RAGE sequence [5] (1.3mm iso; GRAPPA 3), a field map (TR: 400ms; TE1 4.92ms; TE2: 7.38ms; 2.9x2.9x3.8mm³; acquisition: 90s) and 2 monopolar EPI sequences (b-value: 1000s/mm²; TR: 8000ms; TE: 83ms; 1.9mm iso; GRAPPA 2; acquisition: 48s/9:29min). 7 b0 images and 60 encoding directions have been acquired in the anterior-to-posterior direction while 1 b0 image and 1 encoding direction were acquired in the reversed phase direction. All data were scanned in the same order: MP2RAGE, field map, 2 dMRI (PA), 67 dMRI (AP). 22 datasets with the least motion artefacts were selected from a larger study.

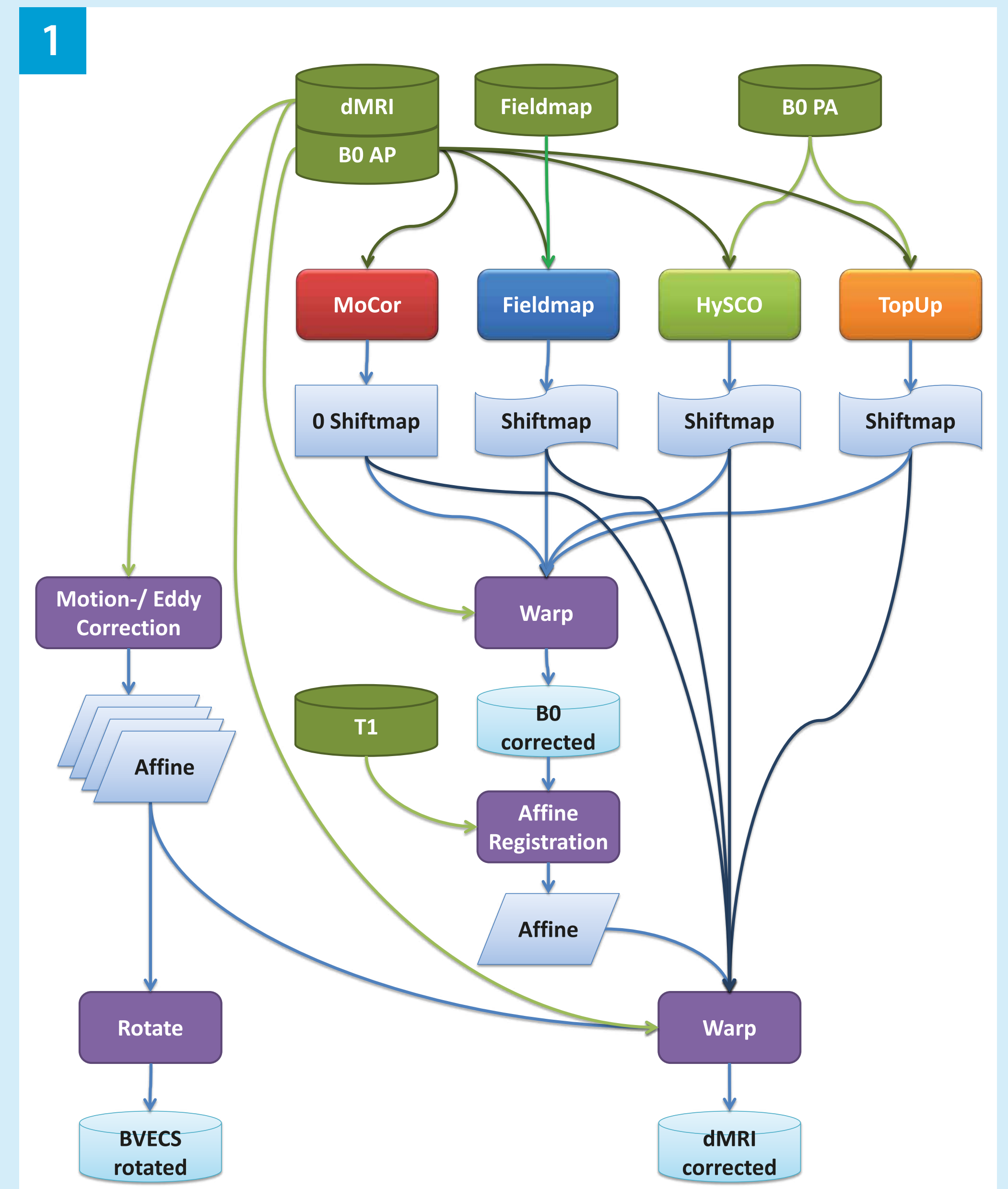


Fig. 1.: Flow-chart of the processing pipeline. Green and blue disks represent input and output data, respectively. Supporting processes are coloured purple. Affine transformations are depicted as light blue diamonds and shiftmaps as flag.

Results

HySCO and TopUp achieved highest correlations between uniform T1 and FA followed by the correction with field maps. Fig. 2 shows an axial and sagittal T1 slice through the inferior frontal gyrus (IFG) of a representative participant (subject 1) overlaid by FA outlines thresholded at 0.2. The FA map without correction (MoCor) (red) shows a strong misalignment with the white matter boundaries of the T1 dataset. The alignment was improved by field map correction (blue). HySCO (green) and TopUp (yellow) further improved the results and show comparable results in all brain regions. Fig. 3 shows the correlations between T1 and FA within the whole brain as well as in the regions of Wernicke's area, BA44 and BA45 averaged over all participants. The individual correlations for each subject are visualized in Fig. 4.

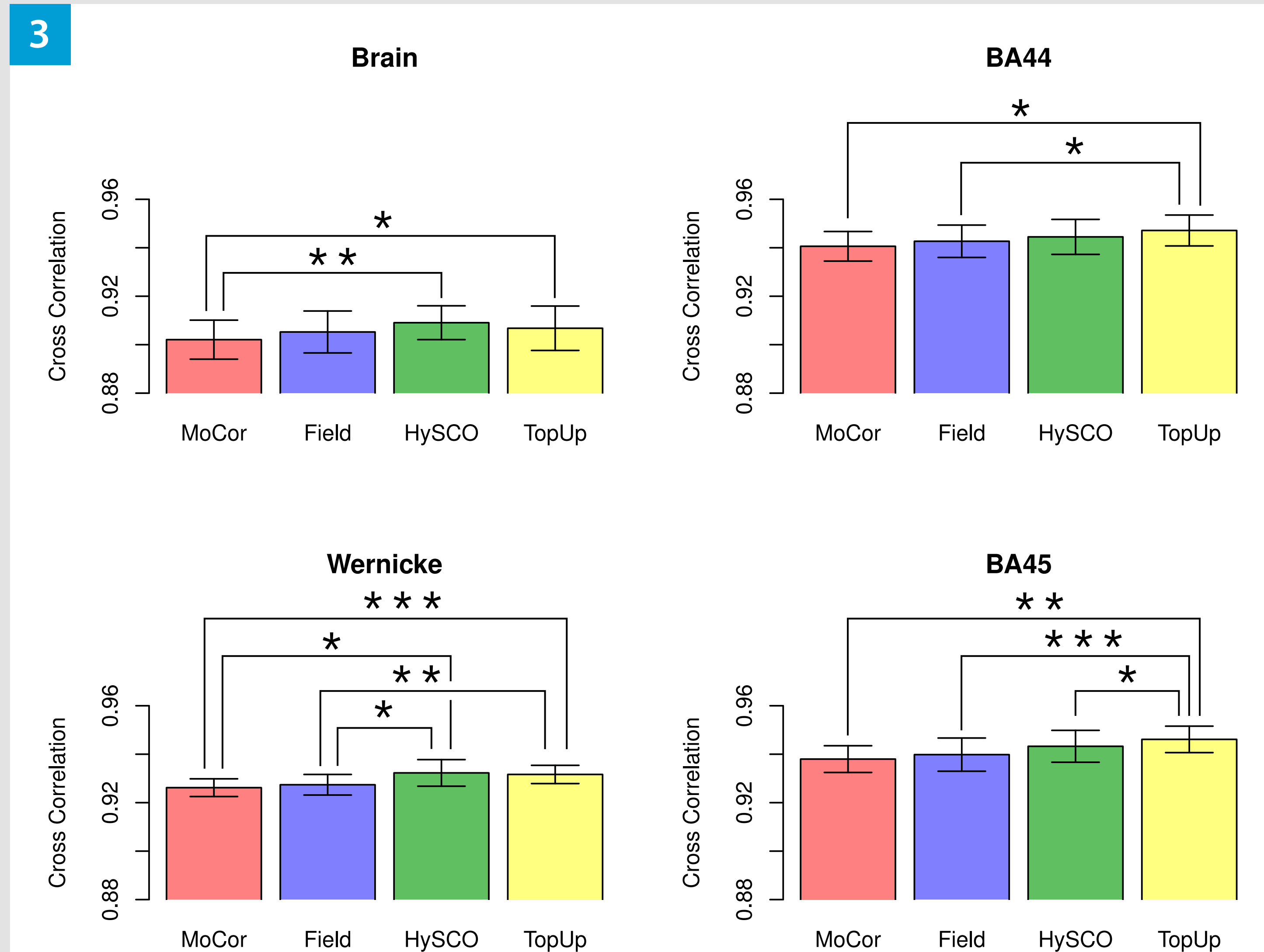


Fig. 3.: Cross-correlations between uniform T1 and FA computed in the whole brain and in different regions of the brain averaged over all participants. Values are lowest for data without non-linear correction. HySCO and TopUp improve the correlation between uniform T1 and FA more than field maps. Significant differences obtained from intra-subject comparisons are indicated above the coloured bars (* p < 0.05; ** p < 0.01; *** p < 0.001; all values corrected for multiple comparisons).

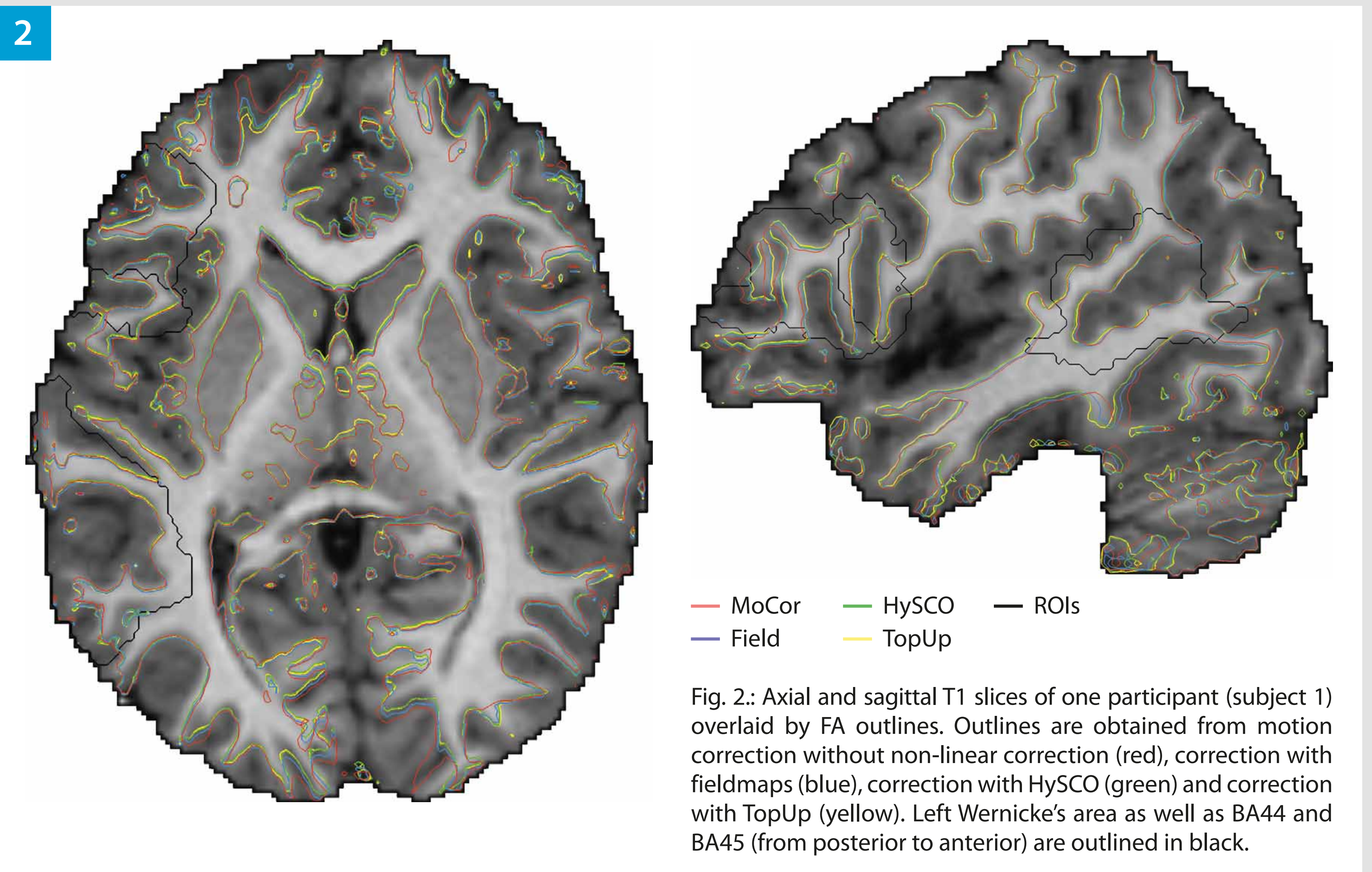


Fig. 2.: Axial and sagittal T1 slices of one participant (subject 1) overlaid by FA outlines. Outlines are obtained from motion correction without non-linear correction (red), correction with fieldmaps (blue), correction with HySCO (green) and correction with TopUp (yellow). Left Wernicke's area as well as BA44 and BA45 (from posterior to anterior) are outlined in black.

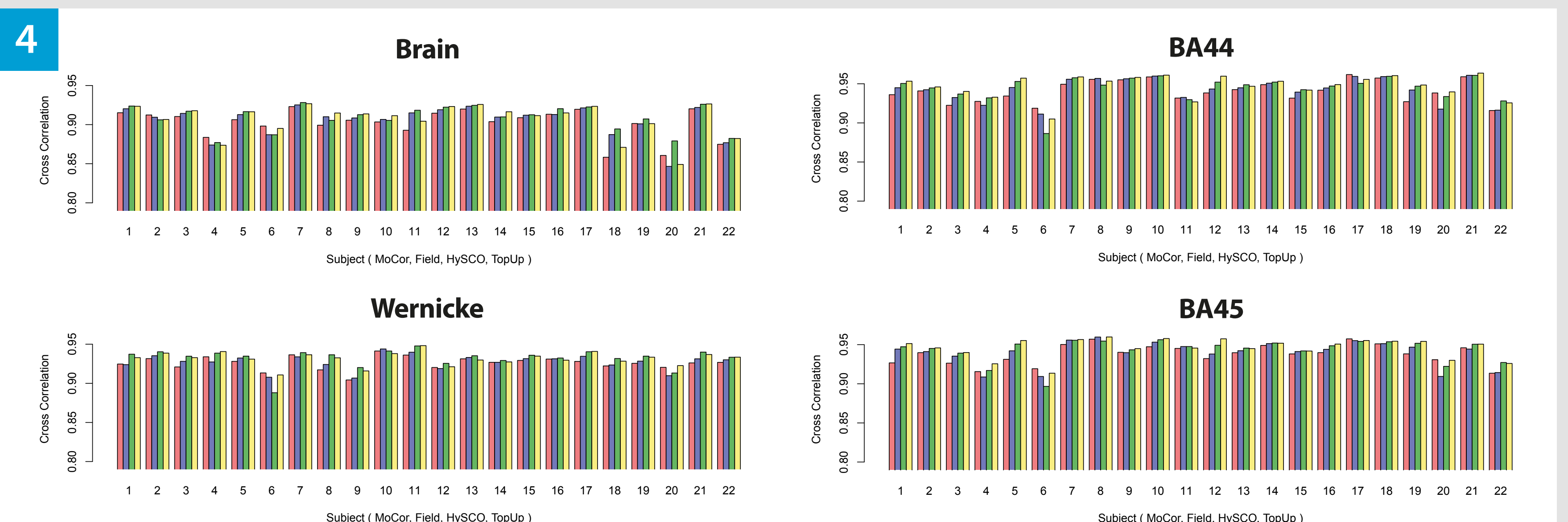


Fig. 4.: Cross-correlations between uniform T1 and FA computed in the whole brain and different regions of the brain for every participant separately. In most subjects values are lowest for data without non-linear correction (red) followed by Fieldmaps (blue) and HySCO (green) and TopUp (yellow).

Discussion

All three methods to correct for susceptibility artefacts robustly improved the alignment of the dMRI data with the undistorted T1 image. Susceptibility correction based on different readout directions seems to work more accurately than field maps and requires only half the measurement time. This distortion correction is of particular importance for surface based connectivity

mapping and multi-contrast analysis of dMRI with other quantitative MR images. In addition to the assessment of the accuracy, it would also be possible to investigate the smoothness of the shiftmaps as a criterion for quality. Note, shiftmaps were only computed using the first b0 images which preserves backwards compatibility to other processing pipelines.

References

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