

Improved Tractography Alignment Using Combined Volumetric and Surface Registration

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Introduction

We evaluated the performance of our combined volume and surface (CVS) algorithm [1] for the purposes of fiber bundle alignment and showed that high accuracy cross-subject registration based on structural MRI images can provide improved alignment compared to methods directly aligning DWI-derived scalar volumes, such as the widely used FA volumes. For our analysis, we compared the performance of CVS to the FA-FNIRT registration (registration component from the TBSS [2] preprocessing) [3, 4] as well as linear alignment FLIRT [5] computed from either the anatomical or the DWI data. We evaluated, both qualitatively and quantitatively, the resulting alignments by analyzing the correspondence of a set of manually labeled fiber bundles.

Methods

Registration methods:

- FLIRT [5], FA-FLIRT, FA-FNIRT [2,3,4], CVS [1]

Procedure:

- use a randomly selected subject as template and register the rest of the data to it
- for FA-FNIRT, use FSL template space

Evaluation:

- align a set of manually extracted fiber bundles and compute the maximum and mean Hausdorff distance

Data sets

Data was provided by Dr. Randy Gollub and the Mental Illness and Neuroscience Discovery (MIND) Institute. Fifty-three data sets were selected; all were acquired using an identical MRI sequence on a Siemens scanner.

- Structural data: 256x256x256 size with 1 mm³ voxel resolution, TR = 12ms, TE = 4.76ms, TI = 4.76ms, flip angle = 20
- Diffusion data: single shot echo planar imaging and a twice-refocused spin echo pulse sequence, optimized to minimize eddy current-induced image distortions (TR/TE = 7400/89 ms, b = 700 s/mm², 256x256 mm FOV, 128x128 matrix, 2 mm (0 mm gap) slice thickness, 10 T2 + 60 DWI, total acquisition time 8 min 38 sec). The acquisitions also included B0 field maps that were used for further distortion correction.

Fiber Bundle Segmentation

The three fiber bundles of interest for our experiments were: the cortico-spinal tract (CST), the inferior longitudinal fasciculus (ILF) and the uncinate (UNC). They were extracted manually using the validated tract segmentation procedure defined in [6]:

1. all tract solutions are computed for the entire brain
2. regions of interest (ROIs) are used to remove fibers that are not part of the desired tract, or to restore fibers removed by previous ROIs. The ROIs interact with the full set of tract solutions using Boolean operators AND, OR and NOT.

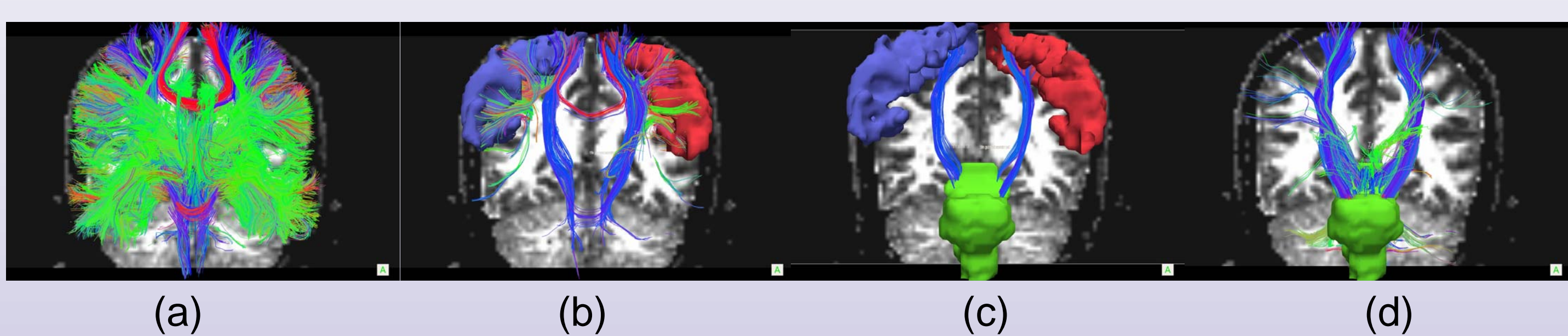


Figure 1: Labeling the CST: (a) deterministic tractography seeded in the whole brain, (b) tracts going through the precentral gyri ROIs, (c) tracts going through the brainstem ROI, (d) tracts going through both the precentral gyri and brainstem ROIs.

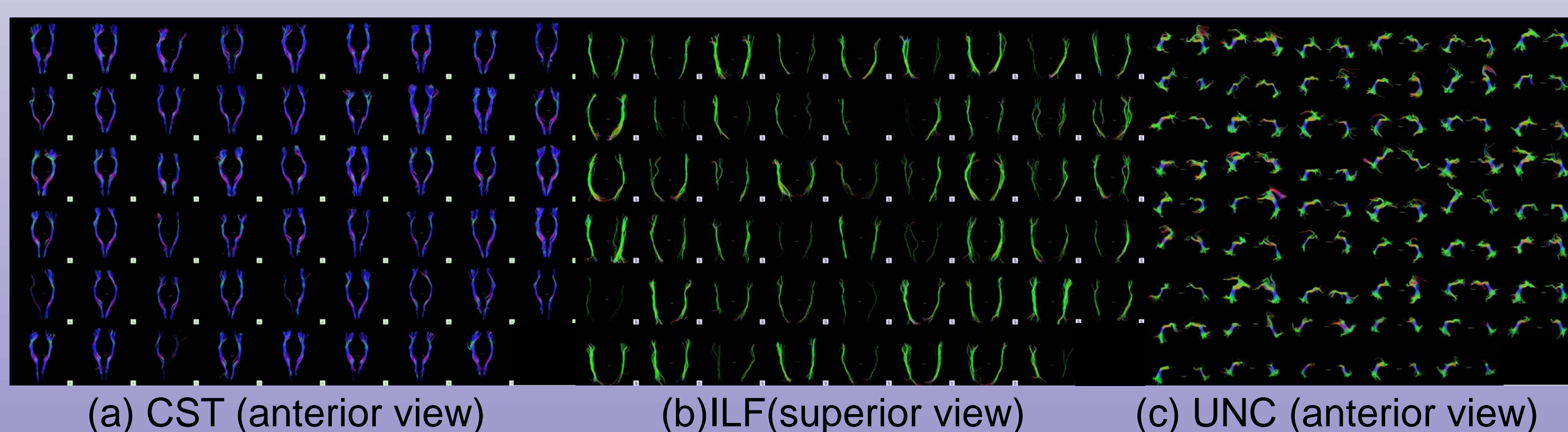


Figure 2: The three tracts of interest manually selected from 53 subjects.

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Results

Quantitative analysis: compute maximum and mean Hausdorff distance measures for each of the tracts.

Summary:

- CVS outperformed FLIRT, FA-FLIRT and FA-FNIRT for all three tracts and both hemispheres, in a statistically significant manner (p-values were computed using the Student T-test with alpha < .0025)
- FA-FLIRT was outperformed by all other three methods in a statistically significant manner
- FLIRT was outperformed also by FA-FNIRT in all cases in a statistically significant manner except for lh UNC and lh ILF where FLIRT outperformed FA-FNIRT

Note that the accuracy of the linear registration computed by FLIRT increased substantially when using the structural data (FLIRT) over the DWI data (FA-FLIRT), even though the gold standard we use for assessing accuracy is derived from the DWI data.

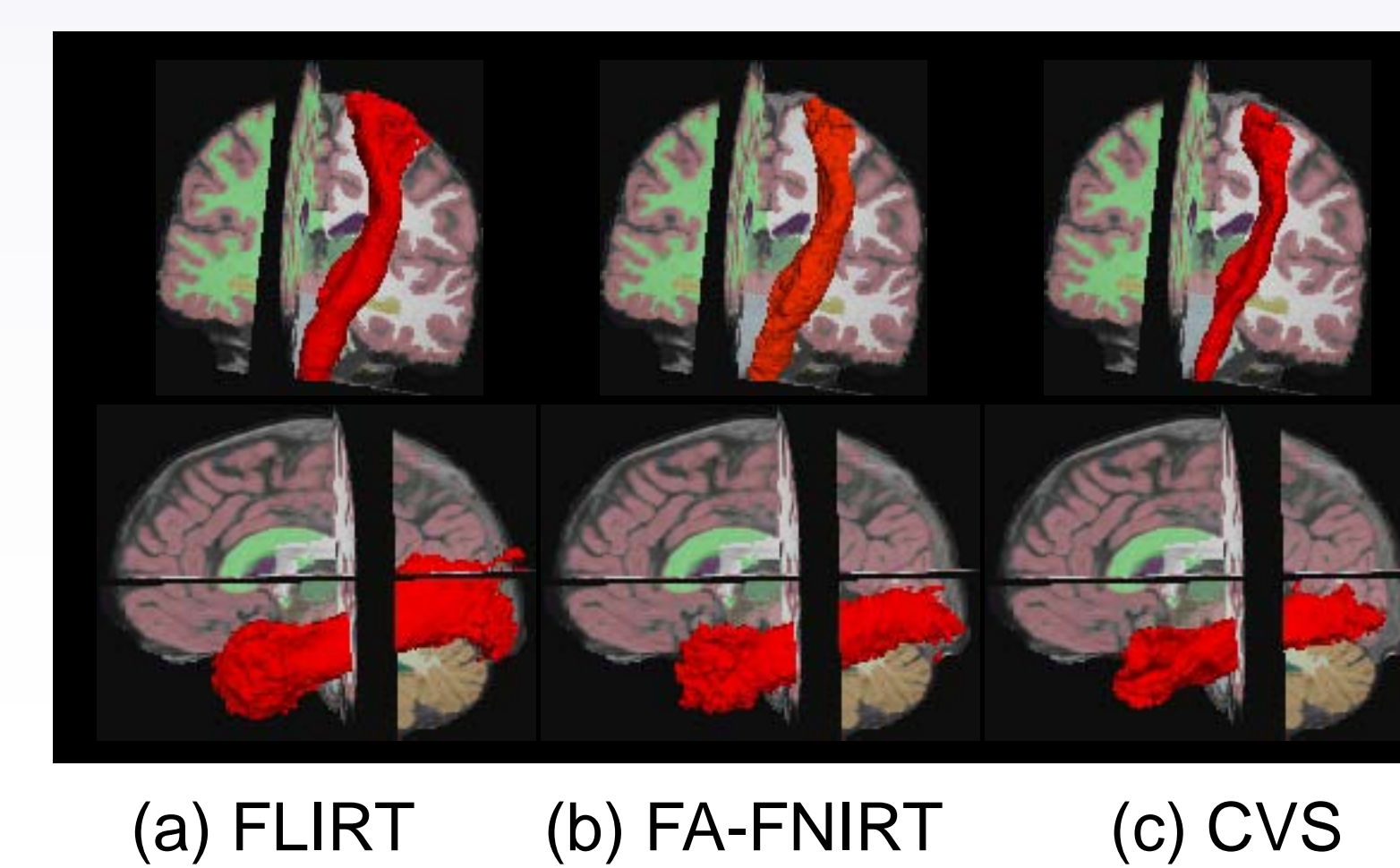
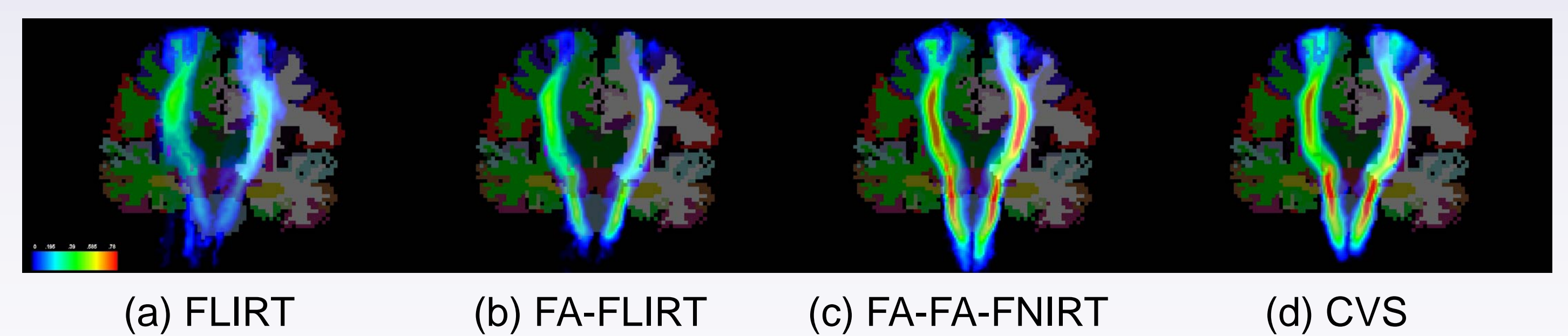


Figure 3: Average CST tracts after registration mapped to the template.

(LEFT) Average CST tracts displayed with iso-surfaces. The probability threshold at 0.1.

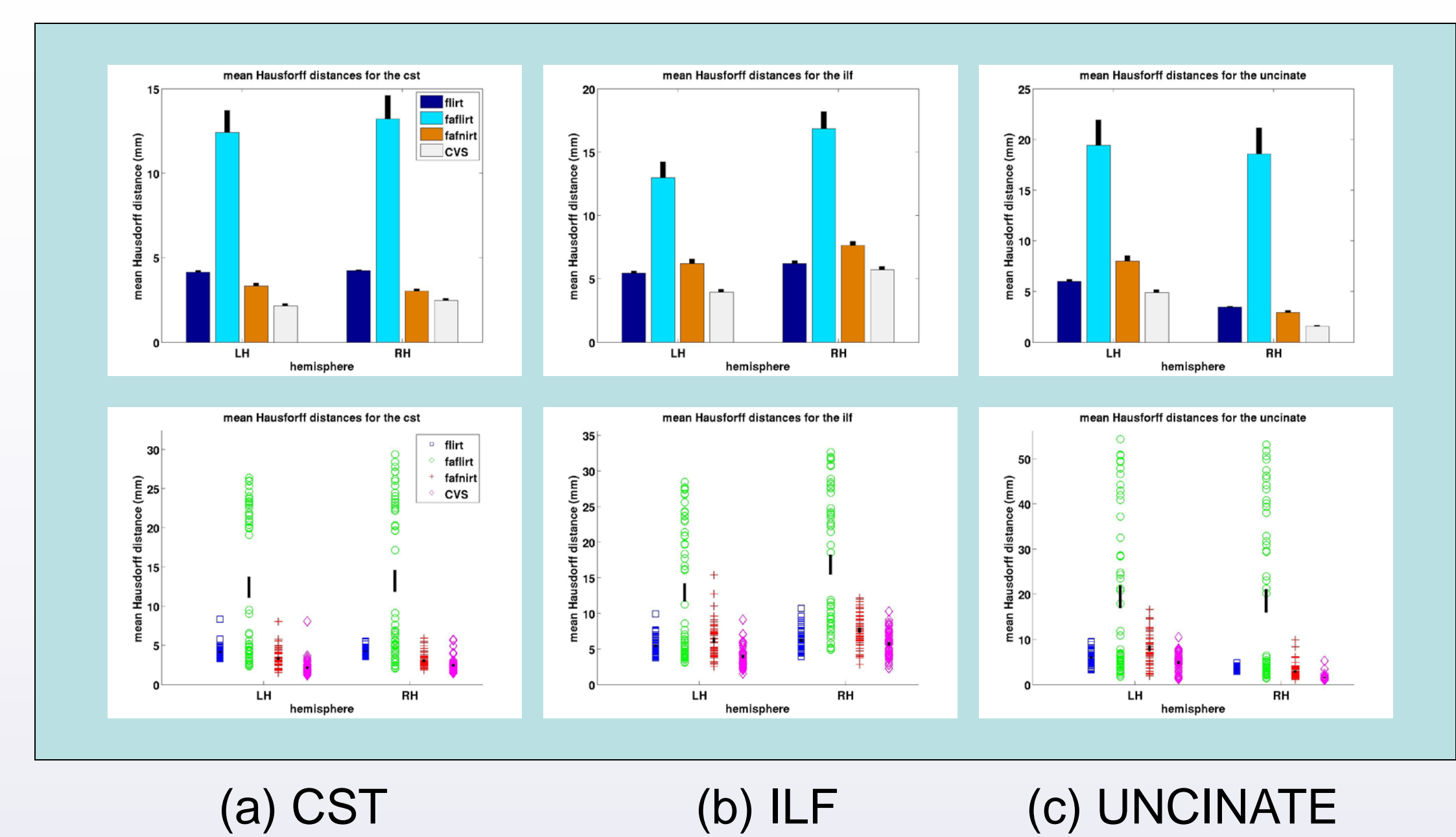
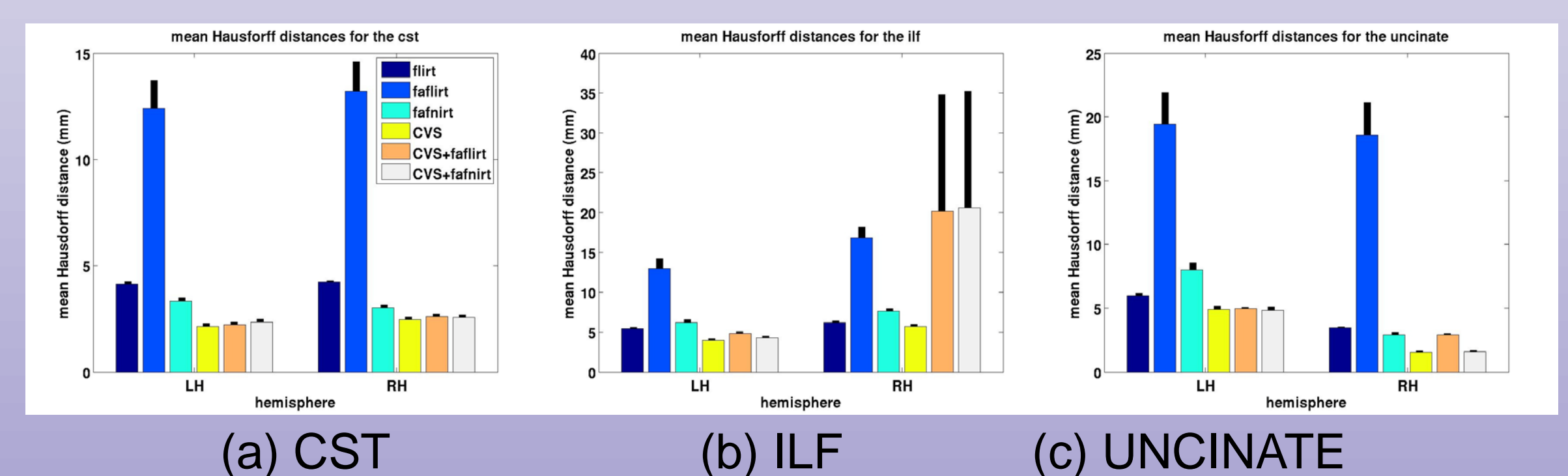


Figure 4: Mean Hausdorff distance measures for the three fiber bundles

Additional experiments:

We ran two sets of further experiments: after completing our CVS registration framework we added an additional registration step using FA information from the diffusion images.

- CVS+FLIRT-FA
- CVS+FNIRT-FA



Conclusions

The results demonstrated that there is a clear advantage to aligning the anatomy, when available, as opposed to relying only on the lower resolution, distorted diffusion information, even if the goal of the registration is the analysis of the diffusion properties of the brain.

Note, the additional diffusion-based step did not improve the alignment, but actually slightly made it worse in all three bundle cases. Therefore, we believe that relying on a combination of such multi-modal data sources will necessitate a more careful evaluation. For more details of our work, see [7].