

Effects of Motion Corrupted Volumes on DTI Findings between HIV-Infected and Healthy Children

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INTRODUCTION

- Diffusion tensor imaging (DTI) is a powerful technique for the assessment of white matter structural integrity and connectivity.
- Methods for analysing DTI data with motion corruption are not standardized [1].
- Some studies do not remove corrupted volumes prior to analysis [2,3], while others do [4,5].
- The aim of this study was to investigate the differences in DTI results in a group analysis of HIV-infected versus healthy children without and with removal of corrupted volumes.

METHODOLGY

- **Participants:** 53 children (14 healthy controls, 39 HIV-infected; mean age 5.5 ± 0.4 years; age range 4.9-6.3) participating in a prospective longitudinal study were scanned on a 3T Siemens Allegra. All procedures were approved by the Institutional Review Boards; parents/guardians provided written informed consent.
- **Scanning protocol:** Children were scanned with structural T1 imaging followed by 2 DTI acquisitions with opposite phase encoding directions using the twice-refocused spin echo sequence [6]. Acquisition parameters for diffusion were: TR/TE 9500/86 ms, 72 slices, $2 \times 2 \times 2 \text{ mm}^3$, 30 diffusion directions, $b=1000 \text{ s/mm}^2$, 4 $b=0$ scans.
- **Pre-processing:** DTI data were analysed in 2 ways: (1) without elimination of corrupted DTI volumes, and (2) with removal of DTI volumes with dropout or motion corrupted slices prior to analysis. DICOM volume images were visually inspected for the presence of corrupted diffusion volumes and the diffusion encoding scheme was adjusted following the elimination of corrupted volumes. Preprocessing included susceptibility correction [7] and coregistration [8] of individual volumes to the first b_0 image using FLIRT with a mutual information cost function and 12 DOF in FSL (<http://www.fmrib.ox.ac.uk/fsl>). Outliers of each acquisition were examined by calculating z-scores based on 25 and 75 percentile limits; data points more than 3 standard deviations beyond the mean were discarded. The DTI acquisitions were averaged and FA images generated. FA images were first coregistered to corresponding structural images to achieve intra-subject alignment. Structural images of all subjects were then coregistered to a 'most representative' control image, which was subsequently coregistered to the T1-template image for children aged 4.5-8.5 years [9], using linear and non-linear coregistration algorithms in FSL. Structural and FA images were warped using the same transforms to achieve inter-subject alignment. White matter was extracted by multiplying the coregistered FAs by a white matter mask [9]. Variance smoothing of 4 mm FWHM was applied to all FA images.
- **Analyses:** Voxelwise group comparisons were performed in FSL; group differences that survived a cluster size threshold of 238 mm^3 [10] were significant at $p < 0.01$. Mean FA was determined in a $2 \times 2 \times 2 \text{ mm}^3$ region of interest (ROI) centred at the coordinate within each cluster where the difference in FA between control and infected children was maximal.

RESULTS

- Without removal of corrupted volumes (analysis 1), 22 clusters survived cluster size correction; maximum cluster size 1024 mm^3 .
- After removal of corrupted volumes (analysis 2), 17 clusters survived cluster size correction; maximum size 768 mm^3 ; average number of volumes removed 2 ± 3 (range 0-12).
- All 17 clusters in analysis (2) overlapped with clusters from (1) (Fig 1A). A number had split into multiple smaller clusters.
- 6 clusters from (1) did no longer survive cluster size correction (Fig 1B).

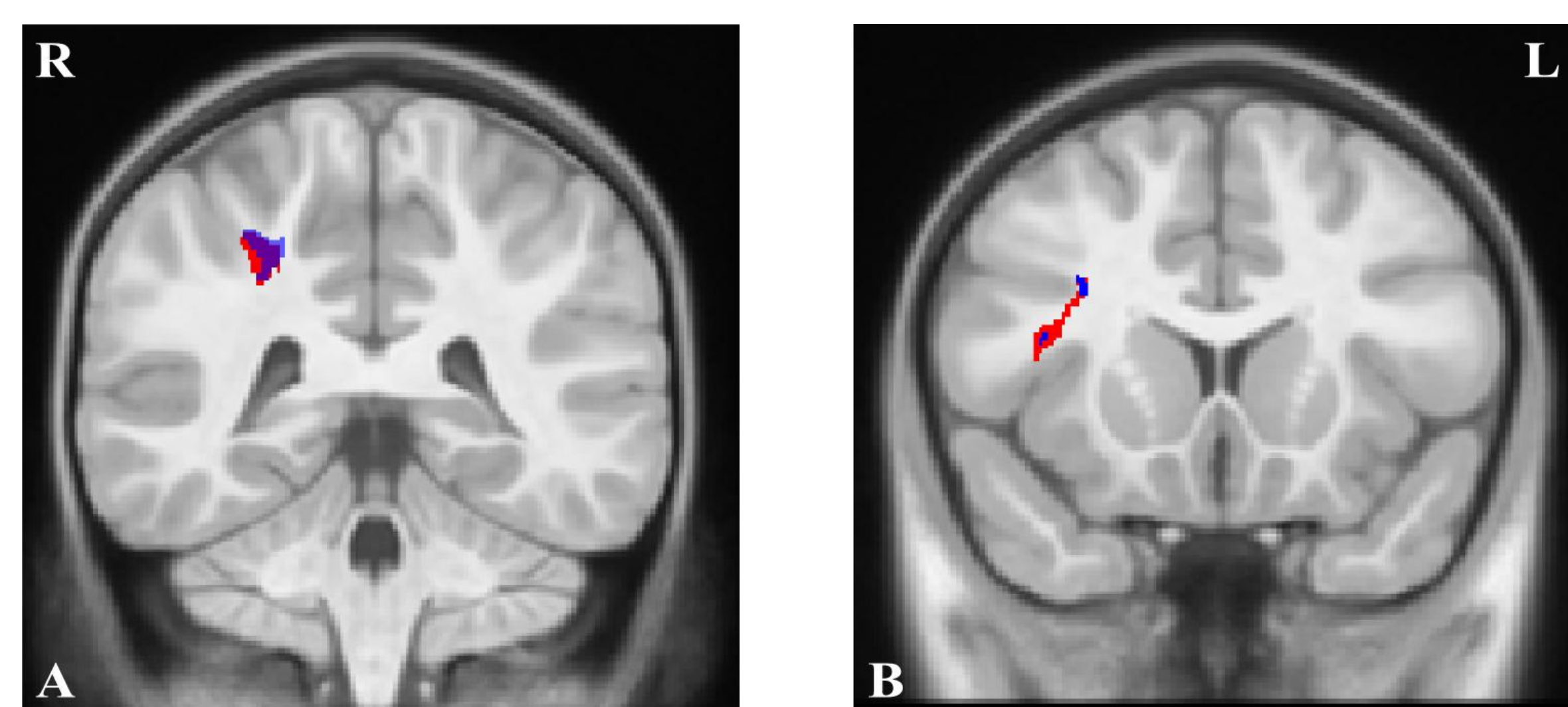


Figure 1: (A) Overlapping clusters from analysis (1) (red) and (2) (blue), and (B) an example of a cluster from analysis (1) (red) that splits into multiple small clusters in (2) (blue) that do not survive cluster-size correction.

- Mean FA values from overlapping clusters that survived cluster size correction did not differ and were highly correlated ($r=0.73$; $p < 0.01$). Bland-Altman analysis of FA values revealed 95% confidence intervals of -0.17 and 0.14 (Figure 2).

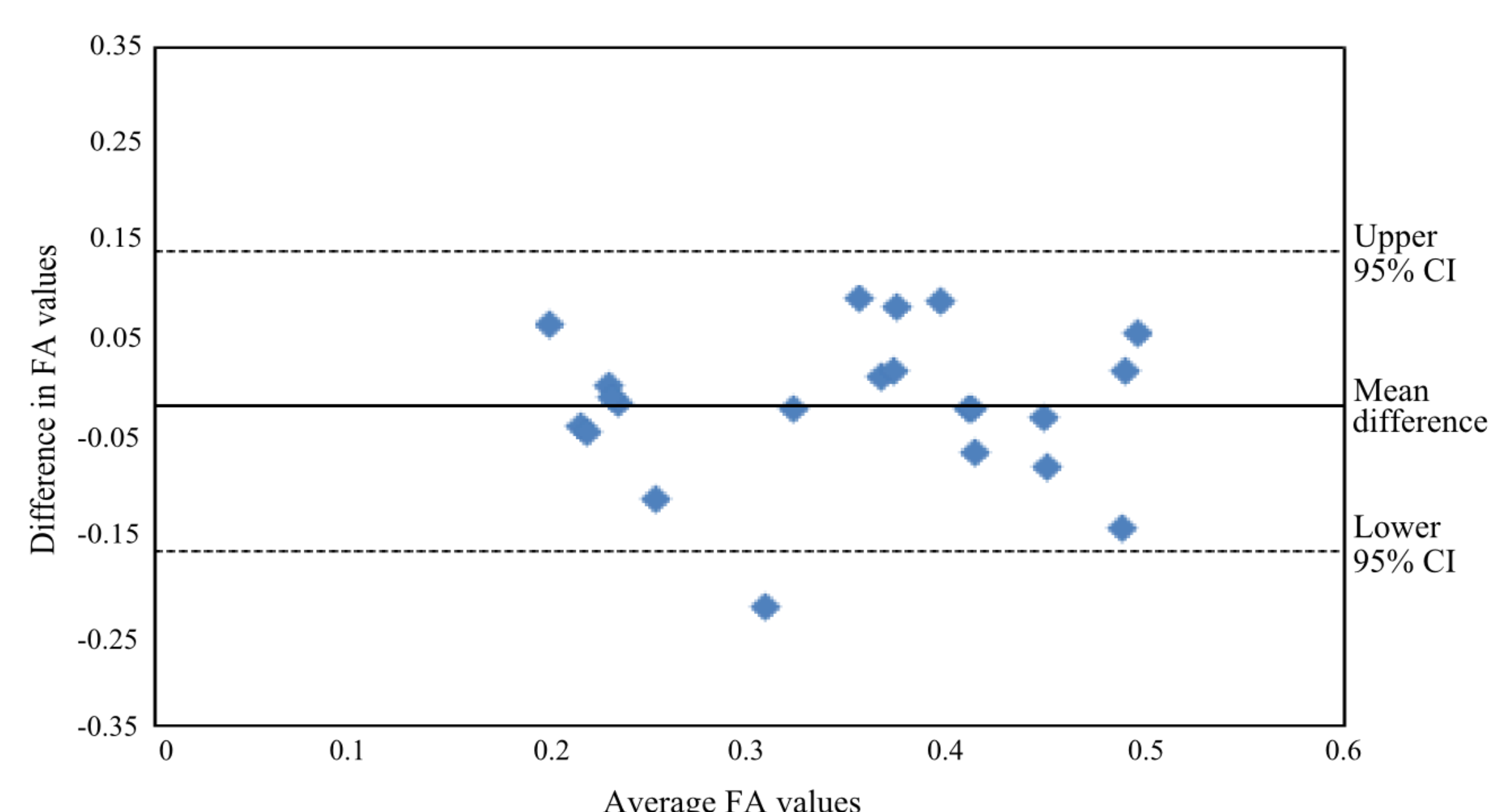


Figure 2: Bland-Altman analysis of overlapping clusters that survived cluster size correction CI: confidence interval.

CONCLUSIONS

- Eliminating vs not eliminating corrupted volumes introduces a bias in the results.
- Eliminating corrupted volumes appears to improve specificity of results.
- Although FA values were highly correlated, the 95% confidence intervals were wide, which could affect group comparisons.

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