

# Tradeoffs in Supersampling of DTI Metrics

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## Introduction

This work compares several alternatives for computing diffusion tensors and derived measures at arbitrary points in a diffusion-weighted MRI volume. We find that magnifying the diffusion-weighted images before processing can significantly improve the accuracy of interpolated tensor measures and can make interpolating the diffusion tensor image unnecessary.

Most tractography methods based on diffusion tensor images (DTIs) require repeated evaluation of tensors or tensor properties at locations not on the point lattice of measurements made during imaging [1]. Furthermore, computing tractwise statistics on scalar measures [2] may also require interpolation to such locations. The process of computing tensor measures comprises two stages: first computing the DTI from the diffusion-weighted images (DWIs), and second deriving the measures from the DTI. While it is appealing to interpolate the original DWIs at the desired point and then recompute the needed values, such an operation is computationally expensive, even for simple linear tensor-fitting algorithms. Interpolation at higher levels, however, is also problematic: Euclidean interpolation of tensor elements results in “tensor swelling” and may give singular results [3], while interpolating in the Riemannian manifold prevents these artifacts at great computational cost [4].

We propose a compromise solution in which the DWIs, DTI, and fields of derived values are in turn “supersampled”, or magnified to higher resolution by interpolation, with a convolution filter. For example, to achieve 16x density in each dimension of an FA field relative to the scanning resolution, one might supersample the DWIs by 4x, then the DTI by 2x, and finally the FA field itself by 2x. Below we analyze the tradeoffs of accuracy inherent in this family of interpolation approaches.

## Methods

**Acquisition:** Our analysis is based on a cube of 8 voxels per side extracted from a DT-MRI brain scan of a healthy volunteer on a 3T system with  $b$ -value = 1000 s/mm<sup>2</sup> in 64 gradient directions and 10 non-DW images, all with 70 transverse slices of thickness 1.8mm, FOV 226mm, and acquisition matrix 128x128 voxels. Thus our sample cube has transverse side lengths of 14.1mm and axial side length 14.4mm. Figure A shows the inferior slice of the sample on a non-DW image of the brain.

**Data processing:** We co-registered all 74 DWIs using FLIRT [5], rotated the corresponding  $b$ -matrices [6], and fit tensors to the DWIs using a nonlinear sequential quadratic programming method [7]. We performed all supersampling by convolution with a sinc kernel with a positive lobe 1 voxel wide. We supersampled each component independently in the case of multi-valued images and re-normalized all interpolated eigenvectors.

**Processing cases:** We generated the trace, FA, and eigenvectors of the DTI at a 16x total supersampling (a voxel spacing of 0.11mm) in three consecutive steps: supersampling the DWIs by a factor of  $L$ , deriving the DTI and then supersampling by a factor of  $M$ , and deriving the field of measurements and then supersampling by a factor of  $N$ . We use the string  $(L,M,N)$  to indicate a particular case; the factors are powers of 2 whose product is 16, and there are 15 possible combinations.

## Results

Figure B shows the median deviation of the principle eigenvector from the  $(16,1,1)$  case for all other cases; the interquartile range was  $\sim 10^\circ$  for all except the  $(8,*,*)$  cases, where it was  $\sim 2^\circ$ . Figures C and D show the median and quartiles for percent change of, respectively, FA and Trace(D) from the  $(16,1,1)$  case for all other cases in which only the DWIs and scalar images were supersampled. Trading DTI and scalar image supersampling in these cases did not significantly affect the results.

## Discussion

Our use of the  $(16,1,1)$  case as a “gold standard” for comparison is supported by the common practice of zero-filling  $k$ -space data before reconstruction; the 16x sinc-supersampled DWIs would result from appropriate filling in  $k$ -space. The results exhibit an expected pattern of decreasing errors with increasing DWI supersampling, and Trace exhibits the expected tensor swelling. So long as the DWIs have been sufficiently supersampled, interpolating principal eigenvectors gives similar results as the more expensive operation of interpolating the DTI; interpolating FA and Trace are also similar to interpolating the DTI for all DWI supersampling factors.

## Conclusion

Orientation errors in the principal eigenvector can accrue over the length of a tract, so our results suggest supersampling the DWIs to within 2x of the desired final resolution prior to tensor-fitting. Though this drastically increases the number of tensors to be fit, the fitting process is highly parallelizable, and tractography computations are often expected to be slow. In cases where only scalar measures are the desired results, supersampling the DWIs decreases noise in the output, but the average error does not decrease significantly. In all cases, DTI supersampling has a negligible effect and should be replaced by DWI supersampling if feasible.

## References

- [1] S. Mori and P. van Zijl, NMR Biomed 15(7-8), p. 468–480, 2002. [2] Z. Ding *et al*, MRM 49(4), p. 716–721, 2003. [3] D. Tschumperlé *et al*, Proc CVPR 2001, p. 948–953. [4] X. Pennec *et al*, Int J Comp Vis 66(1), p. 41–66, 2006. [5] M. Jenkinson and S. Smith, Med Image Anal 5(2), p. 143–156, 2001. [6] A. Leemans *et al*, Proc ISMRM 2008, p. 140. [7] E. Ahrens *et al*, MRM 40(1), p. 119–132, 1998.

