

## Statistical Comparison of DT-MRI Interpolation Methods Using Cardiac DT-MRI Data

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### INTRODUCTION

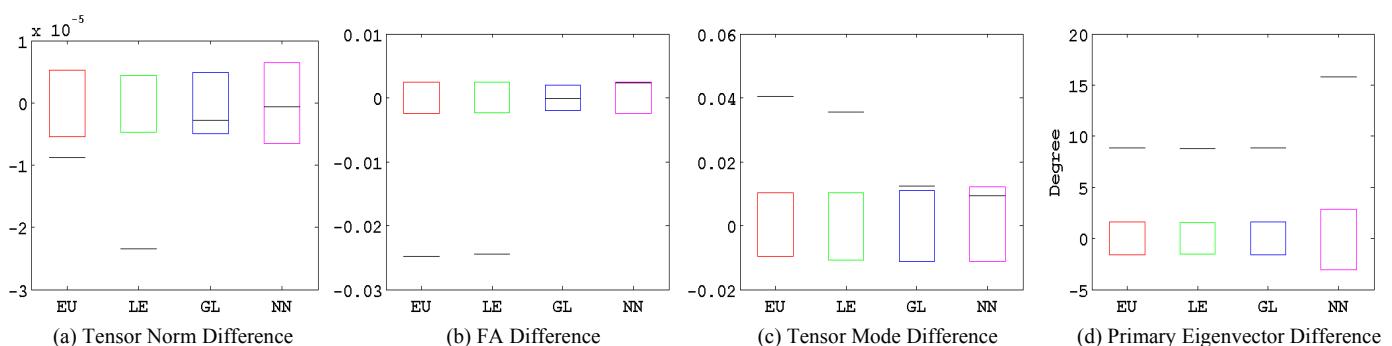
DT-MRI interpolation is the process of estimating diffusion tensors at arbitrary points in space from regularly sampled tensor data. Tensor interpolation is important for tensor-based fiber tractography, registration, volume rendering, and computational model building. The most widely used conventional DT-MRI interpolation methods are Euclidean (*i.e.* tensor component-wise linear interpolation) and nearest-neighbor. Several alternatives to the conventional methods such as Log-Euclidean [1], and geodesic-loxodromes [2] have been recently proposed, and each monotonically interpolates determinant or orthogonal invariants [3], respectively. In this work, we use bootstrap statistical methods to compare each interpolation scheme's accuracy for recovering the tensor shape (invariants) and orientation of unknown tensors from known tensor data. By using a cardiac DT-MRI dataset, we show the statistical bootstrapping results, and present recommendations for the selection of the DT-MRI interpolation method.

### METHODS

High resolution DT-MRI data was acquired in a formalin fixed rabbit heart using a 7T Bruker Biospin scanner. Twenty-five diffusion encoding gradients ( $b$ -value  $\approx 1000\text{s/mm}^2$ ) and 5 non-diffusion weighted imaging volumes were used to reconstruct the tensor data using linear regression. The imaging parameters were TE/TR = 29.1/550ms, RARE factor two, FOV = 35mm  $\times$  35mm  $\times$  38mm, 96  $\times$  96  $\times$  72 encoding matrix (365 $\mu\text{m}$   $\times$  365 $\mu\text{m}$   $\times$  528 $\mu\text{m}$ ). The original 3D DT-MRI data was segmented to identify regions of myocardium, and then to test the interpolation methods the data was down sampled by removing half the rows, columns, and slices of the data. Subsequently tensors were interpolated at the positions of the removed tensors to permit a direct comparison of the interpolated tensors to measured ("truth") tensors that were removed. According to the availability of adjacent tensors we used linear, bilinear, or trilinear interpolation weights for each missing tensor, and compared Euclidean (EU), Log-Euclidean (LE) [1], nearest-neighbor (NN), and geodesic-loxodromes (GL) [2] interpolation kernels. We computed the three orthogonal invariants ( $R_i$ : tensor norm, FA, and tensor mode) [3], and the primary eigenvector to describe tensor shape and orientation. The distributions of the orthogonal invariants of DT-MRI data are too complicated to be modeled in simple parametric forms (*e.g.* Gaussian distribution), therefore bootstrap methods, which estimate the statistical properties of an estimator without making any assumptions on the distribution of the sampled data, were used. Before applying bootstrap methods to the interpolated and original "truth" tensors, we computed the autocorrelation length of each orthogonal invariant for every dimension using the fully sampled data, and decimated the interpolated and original tensor data by a factor of the autocorrelation length for every dimension in order to uncorrelate the data. Then we performed the paired comparison of each orthogonal invariant of the uncorrelated interpolated tensors with that of the uncorrelated original "truth" tensors using bootstrap methods. We first generated a dataset of paired differences between their orthogonal invariants (interpolated minus truth values), constructed a number of resamples of the difference dataset by assigning a random sign to each difference value, and calculated the 95% confidence interval for the mean/median of the resamples. We also applied the bootstrapping technique to a dataset of paired angle differences between the primary eigenvectors of the interpolated and original "truth" tensors in order to assess the four interpolations methods in terms of tensor orientation recovery.

### RESULTS

Figure 1 shows the results of the paired comparison in term of (a) tensor norm, (b) FA, (c) tensor mode, and (d) primary eigenvector. Each black horizontal line represents the median of the orthogonal invariant or primary eigenvector differences, and each box represents the bootstrapped 95% confidence interval of the median. If these differences are not significant, it is expected that the median of the differences lies within the 95% confidence interval. As shown in Figure 1(a) and 1(b), EU and LE statistically underestimate tensor norm, and, moreover, they produce a significant decrease in FA. Figure 1(c) shows that EU, LE, and GL are all out of the 95% confidence interval, but GL is the closest to it. Finally, in the paired results of primary eigenvector shown in Figure 1(d), EU, LE, and GL are all similarly out of the 95% confidence interval, but NN shows the worst recovery of tensor orientation.



**Figure 1** Paired bootstrap comparison of DT-MRI interpolation schemes in terms of tensor norm, FA, tensor mode, and primary eigenvector. Each black horizontal line represents the median of invariant or primary eigenvector differences, and each box represents the 95% confidence interval of the median.

### CONCLUSION

First of all, we suggest not to use NN for DT-MRI interpolation largely because of the poor accuracy for recovering tensor orientation. Furthermore, there is no smoothing/denoising benefit for NN. Our bootstrap comparison results definitely show that GL outperforms EU and LE in terms of tensor shape (invariant) recovery, but GL is more expensive in computation time than EU and LE. Therefore we recommend to use GL only for the purpose of accurately recovering tensor shape and orientation, regardless of computation time.

### REFERENCES

- [1] V Arsigny *et. al.*, "Log-euclidean metrics for fast and simple calculus on diffusion tensors," *MRM*, 56:411-421, 2006.
- [2] G Kindlmann *et. al.*, "Geodesic-loxodromes for diffusion tensor interpolation and difference measurement," *MICCAI*, 2007.
- [3] DB Ennis and G Kindlmann, "Orthogonal tensor invariants and the analysis of diffusion tensor magnetic resonance images," *MRM*, 55:136-146, 2006.