A new method to quantify fiber orientation similarity in registered volumes

James Dormer, Rong Jiang, Mary B. Wagner, Baowei Fei

James Dormer, Rong Jiang, Mary B. Wagner, Baowei Fei, "A new method to quantify fiber orientation similarity in registered volumes," Proc. SPIE 10136, Medical Imaging 2017: Image Perception, Observer Performance, and Technology Assessment, 101361I (10 March 2017); doi: 10.1117/12.2255563

SPIE.

Event: SPIE Medical Imaging, 2017, Orlando, Florida, United States

A new method to quantify fiber orientation similarity in registered volumes

James Dormer [1], Rong Jiang [2], Mary B. Wagner [2], Baowei Fei [1,3 *]

[1]*Department of Radiology and Imaging Sciences, Emory University, Atlanta, GA*
[2] *Department of Pediatrics, Emory University, Atlanta, GA*
[3]*Department of Biomedical Engineering, Emory University and Georgia Institute of Technology, Atlanta, GA*
**E-Mail: bfei@emory.edu; Website: feilab.org*

ABSTRACT

Differences in fiber orientations between registered image volumes can be difficult to quantify. Angular errors between diffusion tensor imaging (DTI) volumes are often a combination of image registration errors and fluctuations of diffusion values that are used to determine the fiber orientations. In order to properly quantify the similarity between two images containing fiber orientation information, both displacement and angular fluctuation should be considered. We present a method to quantify fiber orientation similarity between registered images by allowing small pixel displacements in conjunction with minor angle differences. Adjustments to the allowed pixel displacement and degree of angle difference can help identify the major factor contributing to the error of fiber angles. The proposed method can provide a new metric for the evaluation of the fiber orientation difference.

Keywords: Fiber orientation, cardiac fiber, magnetic resonance diffusion tensor imaging (MR-DTI), similarity, image registration, gamma calculation.

1. INTRODUCTION

Magnetic resonance diffusion tensor imaging (MR-DTI) has been developed as an excellent method for fiber imaging. However, a comparison of fiber orientations between registered DTI volumes can be difficult to quantify. Normal statistical fluctuations during acquisition can cause apparent fiber orientations to vary slightly between scans of the same volume. Histological comparisons of human cardiac fiber angles found average standard deviations of approximately 5 to 12 degrees across the heart wall [1]. Registration errors also contribute to angle discrepancies. In sheep hearts, the average angle difference between two scans of the same heart was found to vary by nearly 10 degrees, mostly due to registration error [2]. Acute angle error (AAE) has been used as a common approach to quantify angle differences. AAE has been applied previously to describe fiber orientation correspondence between volumes [3-5]. However, AAE cannot differentiate between registration (displacement) errors and slight angle variations. This work introduces a new method to identify the main contributors to angle errors and to quantify the similarity between fibers in two volumes when allowing for small pixel displacements and angle variations. Our method is based on the Gamma dose evaluation metric that was originally introduced in [6] for evaluating radiation dose distributions. The proposed method applies this Gamma metric for the evaluation of fiber angular differences.

2. METHODS

Gamma Calculation Method

The workflow for the proposed method is outlined in Fig. 1. After registration, a target Volume B is sub-sampled. Each pixel in Volume A is then assigned to the corresponding pixel set of the sub-sampled Volume B. A general Euclidean

Medical Imaging 2017: Image Perception, Observer Performance, and Technology Assessment,
edited by Matthew A. Kupinski, Robert M. Nishikawa, Proc. of SPIE Vol. 10136, 101361I

distance mask is created for the local volume size of interest. The Gamma calculation is then performed on each pixel of interest (POI) in Volume A using the corresponding local region in the sub-sampled Volume B. For example, a DTI with an isotropic resolution of 1.5 mm may be resampled to pixels of a 0.1 mm resolution. Therefore, each POI in Volume A would be compared with a corresponding local grid of 15 x 15 x 15 pixels. The minimum Gamma value is found for each POI and a matrix is constructed.

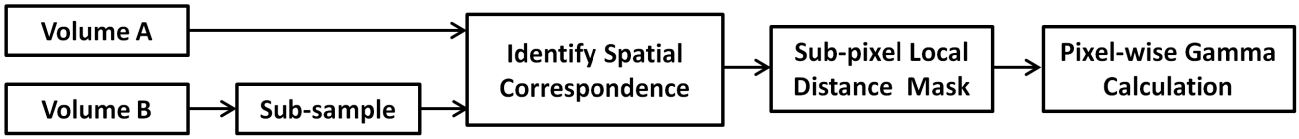

Fig. 1. Workflow for Gamma calculation between two registered DTI volumes.

Gamma values were calculated using Eq. 1, based on the work published in [6]. The importance of the difference between pixel locations for a Volume A ($\boldsymbol{r_A}$) and a Volume B ($\boldsymbol{r_B}$) is determined by a distance restriction value R. Similarly, the angle difference ϑ between pixels is weighted by an angular restriction value Θ. Gamma values less than or equal to 1 indicate similar fiber orientations between two pixels when accounting for acceptable displacement and angle variation error.

$$\Gamma = \sqrt{\frac{|r_A - r_B|^2}{R^2} + \frac{\vartheta^2}{\Theta^2}} \qquad (1)$$

Imaging Experiments

The data used to investigate the method was taken from rat hearts [5] and pig hearts. Each heart was excised and then cleaned with cold 1xPBS and fixed in formalin, 14 hours for the rat hearts and 1 week for the pig hearts. The hearts were placed individually into 2% agar phantoms for MR imaging.

T1-weighted MRI and diffusion tensor images were acquired on a 7 T Bruker Biospec MR system (Bruker Corp., MA), with a 3 cm RF coil for the rat hearts and a 7 cm coil for the pig hearts. The resolutions of the T1-weighted MRI for the rat and pig hearts were 0.078 x 0.078 x 0.156 mm^3 and 1 x 1 x 1 mm^3, respectively. DTI isotropic resolutions were 0.234 mm and 1.5 mm for rat and pig hearts, respectively. All imaging was performed using a short-axis view. Fiber orientations were estimated using the largest eigenvector from the diffusion tensor images, according to the preservation of principle direction algorithm introduced in [3].

Evaluation Methods

The method was first evaluated by comparing a DTI that was shifted by one pixel to the original. The restriction values for the distance and angle difference were adjusted. Another comparison was performed between a DTI volume with slightly altered eigenvalues compared to the original image. Gamma values were also compared between different scans of the same volume. Lastly, our approach was applied to registered volumes of different hearts.

3. RESULTS

The various components of the method are shown in Fig. 2. A local distance map (Fig. 2A) shows the separation of the sub-pixel mask from the POI while a separate map (Fig. 2B) determines the angular difference. These two maps are used to calculate the sub-pixel Gamma values (Fig. 2C). An example from a pig heart registration is shown in Fig. 2D and 2E.

Gamma results from shifting an image with an in-plane resolution of 1.5 mm x 1.5 mm by 1 pixel are shown in Fig. 3. When the distance restriction is set to 1.5 mm, all Gamma values are expected to be equal to or less than 1, as is seen in

Fig. 3A. When the distance restriction is set to 0.75, the expected maximum Gamma value is 2, as shown in Fig. 3B. For Fig. 4, the fiber directions for the first eigenvector was changed by 1.28 degrees and subsequently compared to the original image using a 0.05 mm distance restriction and 0.45 degree angle difference. The maximum gamma value was calculated to be 2.84, which corresponds to a gamma value with no displacement error and 1.28 degrees of angle error. The distribution of gamma values for these pixels indicates that the gradual change of fiber angles from neighboring subpixels could explain the fiber difference between the images as well.

An example from registration between two different pig hearts with isotropic resolutions of 1.5 mm is shown in Fig. 5, with varying restrictions. From these histograms, it is observed that by allowing more distance separation between corresponding pixels, the Gamma values decrease more than increasing the allowed angular difference.

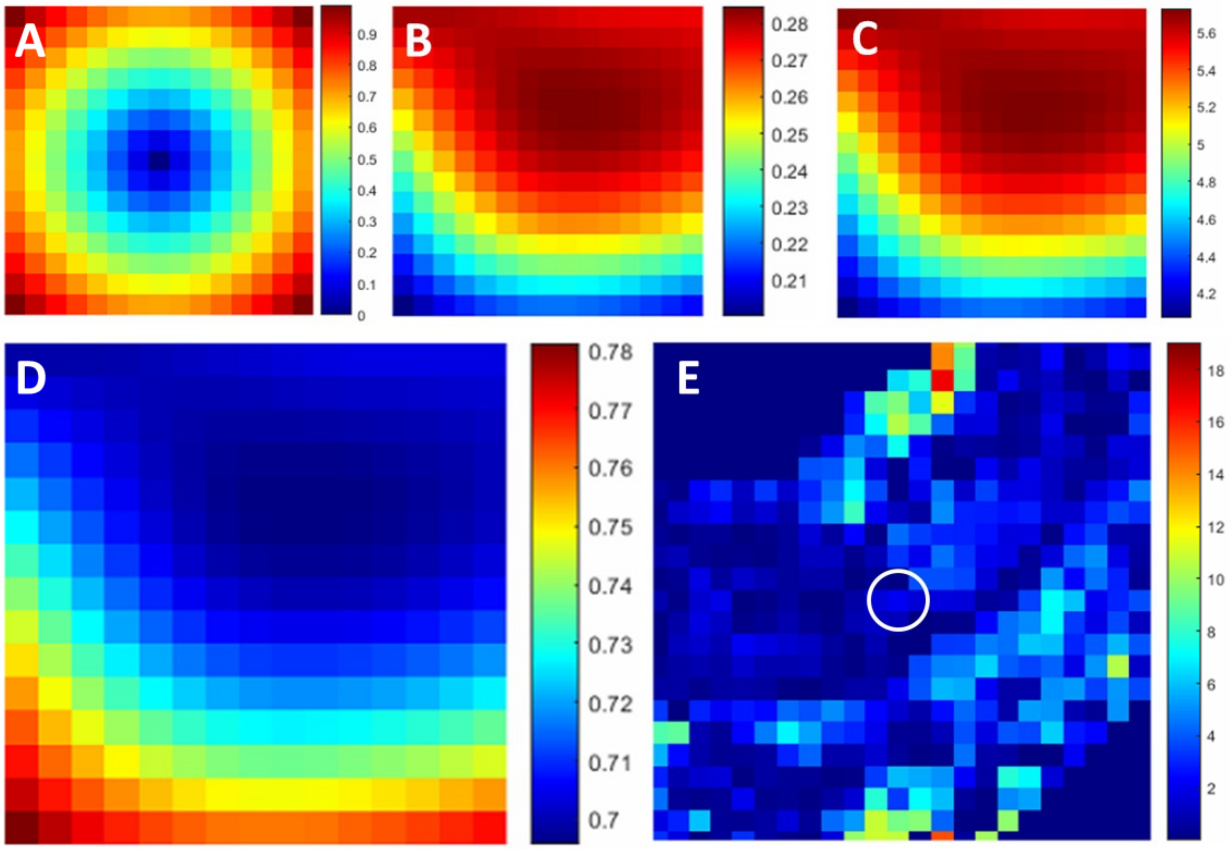

Fig. 2. **A:** Local distance map of the 15 x 15 x 15 pixel region corresponding to the current POI. **B:** The angular difference between the POI and the sub-sampled volume. **C:** The Gamma calculation for the POI. **D:** The calculated sub-pixel grid which is compared with the POI shown within the white circle in **E**.

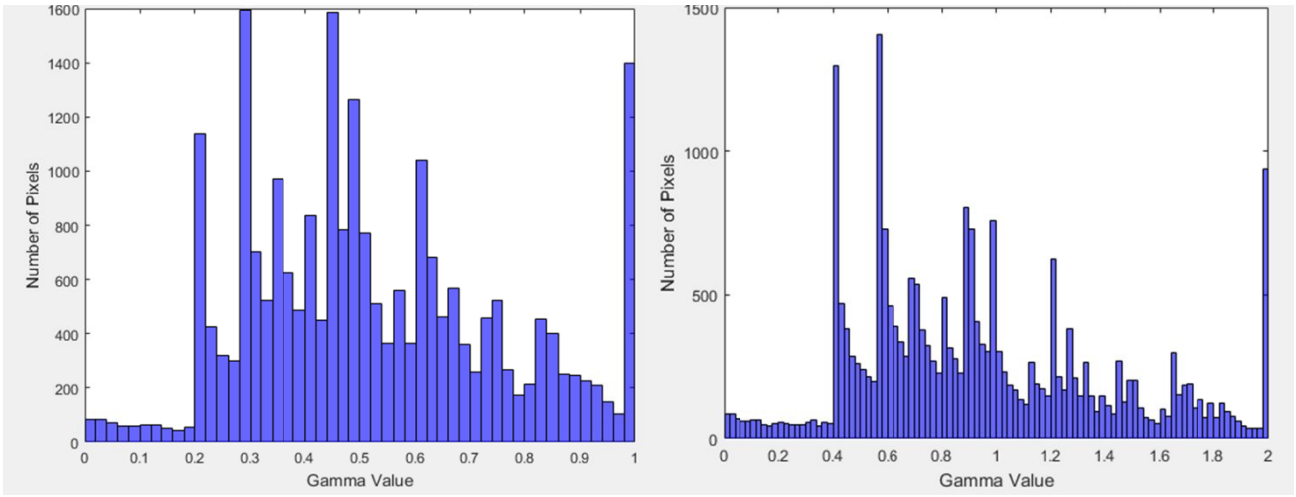

Fig. 3. Results from comparing an image shifted by 1 pixel to the original image. Left: Distance restriction set to 1.5 mm and 1 degree angle restriction. Right: Distance restriction set to 0.75 mm and 1 degree angle restriction.

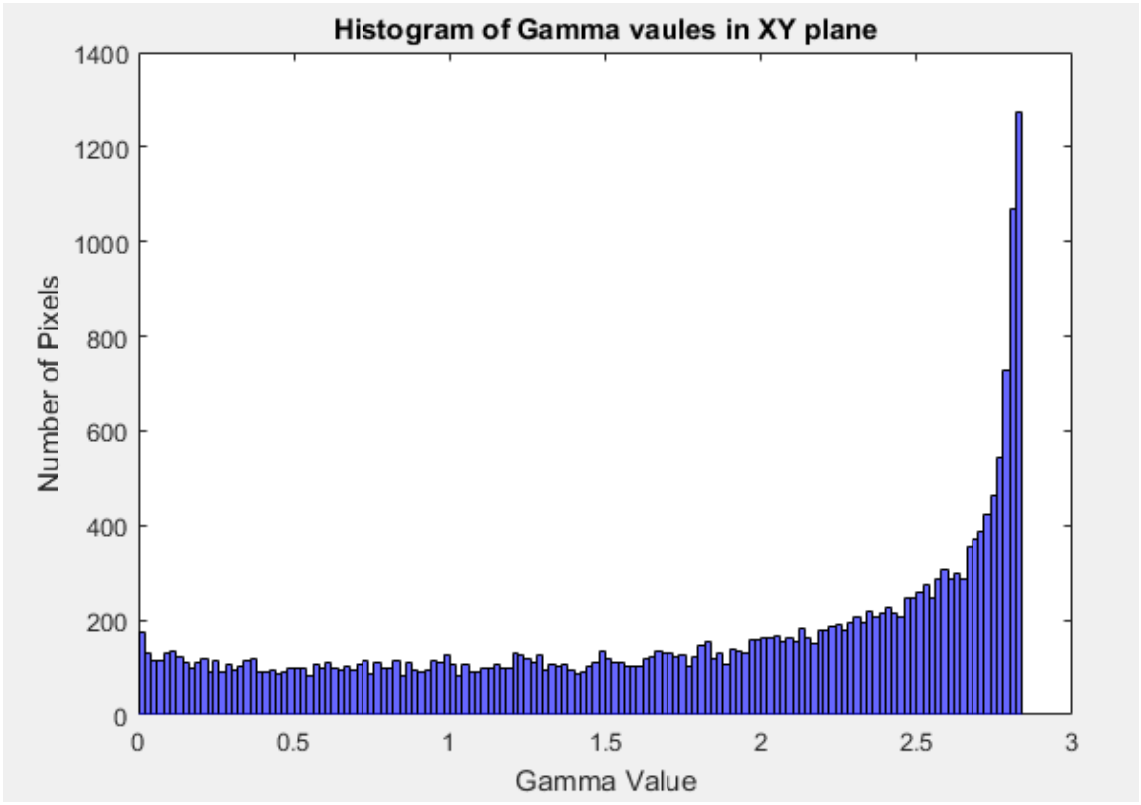

Fig. 4: Gamma histogram when a 1.28 degree angle difference is introduced into the first two eigenvalues. The restrictions were set to 0.05 mm distance and 0.45 degrees.

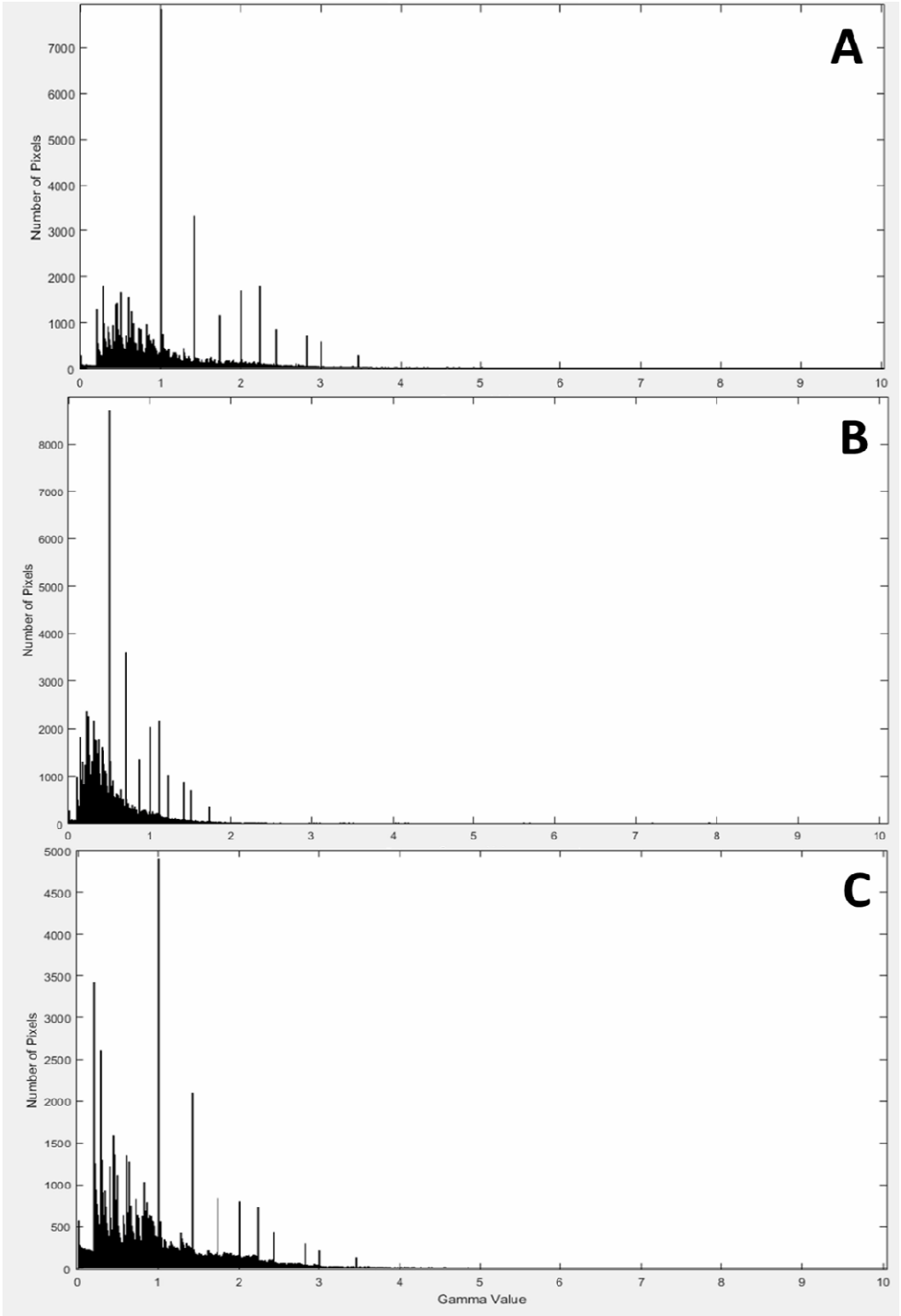

Fig. 5: Histograms of Gamma values for the registration of two pig hearts. A: 3.0 mm distance and 1.0 degree angle restrictions. B: 1.5 mm distance and 5.0 degree angle restrictions. C: 1.5 mm distance and 1.0 degree angle restrictions. A bin size of 0.02 was used. From the figure, it is observed that relaxing the restriction on pixel displacement improves the Gamma distribution more so than allowing for greater angle differences. This suggests that the registration error is the main contribution to fiber orientation differences.

4. CONCLUSIONS

We have developed a new approach to quantify the similarity of cardiac fiber orientations between two registered DTI volumes. This new metric can provide more information regarding the cause of the fiber orientation difference. The method could also be applied during registration routines to determine iteration completion.

One limitation of the work is that the fiber orientation between neighboring voxels is assumed to change in a gradual, linear fashion. This may not be the case near the wall edges of the heart. Future work will extend the procedure to include non-linear orientation changes.

ACKNOWLEDGEMENTS

This research is supported in part by NIH grants (CA176684, CA156775, and CA204254) and a pilot grant from the Children's Heart Research and Outcomes Center of Children's Healthcare of Atlanta.

REFERENCES

[1] R. A. Greenbaum, S. Y. Ho, D. G. Gibson *et al.*, "Left-Ventricular Fiber Architecture in Man," British Heart Journal, 45(3), 248-263 (1981).

[2] M. L. Milne, G. K. Singh, J. G. Miller *et al.*, "Toward 3-D Echocardiographic Determination of Regional Myofiber Structure," Ultrasound in Medicine and Biology, 42(2), 607-618 (2016).

[3] D. C. Alexander, C. Pierpaoli, P. J. Basser *et al.*, "Spatial transformations of diffusion tensor magnetic resonance images," Ieee Transactions on Medical Imaging, 20(11), 1131-1139 (2001).

[4] H. Sundar, D. G. Shen, G. Biros *et al.*, "Estimating myocardial fiber orientations by template warping," 2006 3rd Ieee International Symposium on Biomedical Imaging: Macro to Nano, Vols 1-3, 73-76 (2006).

[5] X. L. Qin, and B. W. Fei, "DTI template-based estimation of cardiac fiber orientations from 3D ultrasound," Medical Physics, 42(6), 2915-2924 (2015).

[6] D. A. Low, W. B. Harms, S. Mutic *et al.*, "A technique for the quantitative evaluation of dose distributions," Medical Physics, 25(5), 656-661 (1998).