Fiber Challenge -SCI Utah Solution

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1 Introduction

In this paper we describe the methods and algorithms used in the MICCAI '09 FiberCup. Given a set of diffusion weighted images (DWIs), their associated gradient directions, and a set of specific seed point for tracking fiber bundels and finally create one single fiber associated to each seed location. The phantom is a plexiglass cylindrical container filled with hydrophobix acrylic fibers in specific configurations.

2 Method description

The original data given by the FiberCup organizers is composed of three files. The first one is a set of 130 DWIs acquired with b-values of 650, 1500 or 2000 and with two sets of resolutions: 3x3x3 mm or 6x6x6 mm. For our algorithm we choose the set with a b-value of 1500 with the 3x3x3 mm resolution. To be able to estimate the tensor field we are provided with the 130 gradient directions. The last file available for this contest is an image with 16 voxels being part of the fibers embedded in the phantom. Each of them is to be used as a seed point in the tracking algorithm. As specified by the organizers, our goal is to generate only one fiber per seed point.

As a first step toward the tracking, we estimate the tensor field using the 130 DWIs and the gradient directions. This dataset is actually composed of 2 repetitions of 64 diffusion gradients plus one baseline which add up to the 130 images. The data is available in a single 4D ITK compatible NIFTI format file. The tensor estimation is done using the MedINRIA 1.8.0 software. (see details in the appendix section 4). Once we have the tensor field we save it as a Nrrd file and export it to be used with a set of tools different from MedINRIA.

Originally, the provided seed point file is one single image with 16 points each with a value from 1 to 16. Our tracking algorithm requires single file with a region of interest (ROI) where the seed is labeled 1. In order to create the adapted ROI we produced 16 images with a single voxel with the value 1 applying simple threshold operations.

The tracking itself is performed with our open source, ITK based, freely available FiberTracking tool originally developed by Pierre Fillard and later refined by Isabelle Corouge, Sylvain Gouttard and Matthieu Jomier [1,2] (see details on how to use the tool in the section 4). First the Nrrd tensor field file is loaded into the tool. The implemented algorithm is a backward tracking scheme, using source and target regions or one target region and the whole brain as source. In the latter mode, the method traces paths from each voxel backwards to the ROI point, and only fiber tracings passing through the specific point are kept.

Two main parameters need to be set for the tracking: an angle of local maximum deviation and a neighborhood coherence threshold. The first parameter keeps the angle between the main eigen vector of two consecutive points below the threshold. It prevents unrealistic tracking with jitter. The coherence threshold tests the directions of all the neighboring voxels and the next point in the fiber. If the eigenvector associated to the main eigen value of the surounding voxels have have too much variation, the tracking is stopped. In the contest for each of the 16 seeding points we tuned these two key parameters to obtain best results based on qualitative checking, similarly to our routine user-supervised tractography as done in clinical studies.

Our tracking algorithm gives us a fiber bundle where each fiber passes through the seed point. As we are asked to provide only one fiber per bundle, we chose a postprocessing that calculates a *spatial curve with the average spatial geometry of the bundle*. We use arc-length parametrization with a plane orthogonal to the seed point as origin. This assumes a high-quality bundle where streamlines are close with similar trajectories. This is achieved by optimizing the fiber tracking parameters as discussed above.

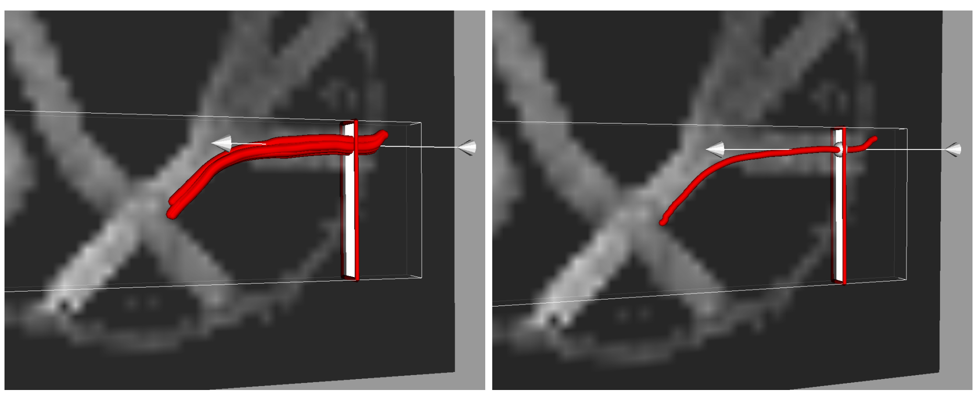

Fig. 1. Left: Fiber bundle tracked with FiberTracking. The arrow is the plane normal at the seed points, shown as spheres. Right: curve with average geometry computed from the bundle.

The averaging is done using the method described by Corouge et al. [2]. We define a fiber bundle specific, origin plane which defines a set of starting points for each fibers where they cross the plane. Then the algorithm walks along each fibers and averages the spatial positions at each arc-length position. To use a non user-guided automatic postprocessing step for this FiberCup, we developed a stand-alone tool that takes a fiber bundle, its associated seed point and then calculates the origin plane perpendicular to the seed point. The normal is calculated from streamlines close to the seed point by choosing the tangent of the fiber closest to the seed point, which showed to be stable enough for this problem. A more robust scheme would make use of all fiber directions in the vicinity of the seed. The seed point and normal thus define our plane used as origin for the geometric averaging, and the tool then calculates the average curve.

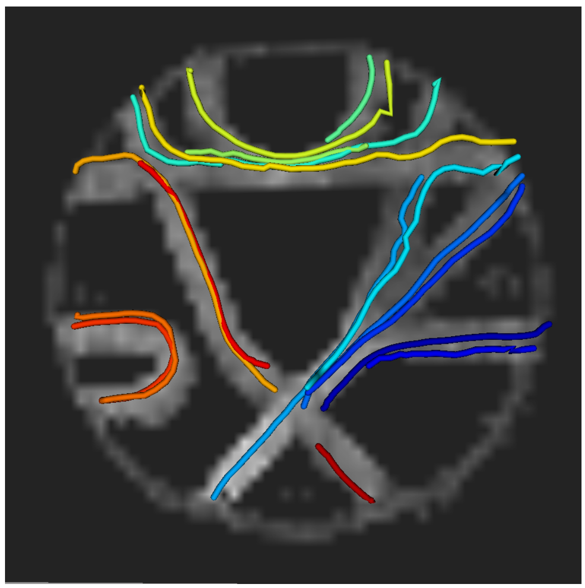

Fig. 2. All single fibers extracted from the 16 seed points.

3 Conclusion

The method described here produces the 16 single fibers asked for the FiberCup, one for each original seeding point. The main user interaction is in the tuning of the parameters in FiberTracking. Knowing these parameters (listed in the appendix section 4) and using the tools as provided in the delivered package, the results are fully reproducible and can be regenerated by everyone at any time.

4 Appendix

In this Appendix we described how to use the different tools use in our procedure. We also give the different parameters specific for the tracking of each fibers. We have made available online the 16 images with the single seeding point needed by FiberTracking and also the source code and the binary of the averaging tool. All the files are zipping in a single file that can be found here:

http://www.sci.utah.edu/~gouttard/DataSharing/fibercup_miccai09_files.zip

4.1 MedINRIA tool

As a first step to estimate the tensor field and save it as a Nrrd file format we use MedINRIA. The software is available here:

http://www-sop.inria.fr/asclepios/software/MedINRIA/

We used the version 1.8.0 where we can load the Nifti file in the DTI Track module along with the gradient direction list. Then we estimate the tensors with the default parameters: no tensor smoothing and the Background removal threshold set a 200.

4.2 Seed point images

The FiberTracking tool used in our method takes only one seed point region at a time. The image provided by the organizer is split up into 16 images with only one voxel at the value 1. The set of the 16 images can be found in the zip file described at the beginning of the Appendix (http://www.sci.utah.edu/~gouttard/DataSharing/fibercup_miccai09_files.zip)

4.3 FiberTracking

The tracking itself is performed with our FiberTracking tool available at:

http://www.ia.unc.edu/dev/download/fibertracking/index.htm.

- The first step is to open the software and load the tensor field ("File" then "Load Tensor Image").
- Then in the 3rd tab "Parameters" the "White Matter Extraction Threshold" is to be set at 0.02 (minimum FA to be used for tensor calculation.
- Back at the first tab "Pre-Processing", hit the "Compute FA_MD" button.
- In the 2nd tab "Computation" you can load the region of interest with the "Load ROIs" button for the seed image. Take one of the images you extracted in the previous section. In the fiber cup, the seed image has only one voxel set with the value 1.
- Select the "Track the whole brain" check box. (below the "Load ROIs" button).

– Before tracking the fibers for each specific seed, you have to set the tractography parameters in the 3rd tab “Parameters”. Two parameters need to be set at the bottom of the tab: “Fiber Tracking Threshold” (coherence) and “Angle of Max Deviation” (angle between consecutive vectors). The optimal values of these two parameters for each of the fiber are listed below.
– Back in the 2nd tab “Computation”, you can now press the “Compute Fibers!” button. You can see the result in the 3D bottom right corner window.
– The final step is to save the computed fiber bundles in “File” and “Save Fibers”.

Parameter list:

Seed id	Fiber Tracking th	Angle Max
seed 01	0.780	0.102
seed 02	0.804	0.102
seed 03	0.715	0.102
seed 04	0.897	0.102
seed 05	0.808	0.102
seed 06	0.724	0.102
seed 07	0.668	0.102
seed 08	0.701	0.102
seed 09	0.937	0.102
seed 10	0.741	0.102
seed 11	0.506	0.500
seed 12	0.693	0.500
seed 13	0.693	0.102
seed 14	0.813	0.898
seed 15	0.909	0.102
seed 16	0.709	0.102

4.4 Geometric averaging to calculate single fiber

The last piece of software used in our method computes the spatial average of the whole bundle. The source code along with a binary of this code can be found in the zip file described at the beginning of the Appendix (http://www.sci.utah.edu/~gouttard/DataSharing/fibercup_miccai09_files.zip) . (It compiles against ITK and VTK). The inputs needed here are the fiber bundle, the associated seed point coordinate in image space and the name of the file where the fiber (x,y,z)-coordinates in the world space are saved.

The list of each seed point in the world space and in the image space can be found on the FiberCup web site. (http://www.lnao.fr/spip.php?article109).

References

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2. Corouge, I., Fletcher, P., Joshi, S., Gouttard, S., Gerig, G.: Fiber tract-oriented statistics for quantitative diffusion tensor mri analysis. Medical Image Analysis (2006) 786 – 798