

Watershed-based Segmentation of the Midsagittal Section of the Corpus Callosum in Diffusion MRI

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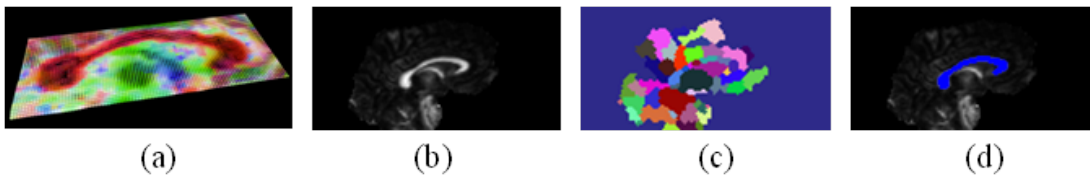


Fig. 1. The main steps of the corpus callosum segmentation: (a) the diffusion tensor image, (b) the fractional anisotropy map, (c) the watershed transform and (d) the final segmentation result

Abstract—The corpus callosum (CC) is one of the most important white matter structures of the brain, interconnecting the two cerebral hemispheres. The corpus callosum is related to several neurodegenerative diseases and, as segmentation is usually the first step for studies in this structure, it is important to have a robust method for CC segmentation. We propose here a new approach for fully automatic segmentation of the CC in the magnetic resonance diffusion tensor images. The method uses the watershed transform and is performed on the fractional anisotropy (FA) map weighted by the projection of the principal eigenvector in the left-right direction. It first computes the section of the CC in the midsagittal slice and uses it as a seed for the 3D volume segmentation. Experiments with real diffusion MRI data showed that the proposed method is able to quickly segment the CC without any user intervention, with great results when compared to manual segmentation. Since it is simple, fast and does not require parameter settings, the proposed method is well suited for clinical applications.

Keywords—corpus callosum; fractional anisotropy; diffusion tensor imaging; magnetic resonance image; segmentation; watershed transform;

I. INTRODUCTION

The corpus callosum (CC) is by far the largest fiber bundle in the human brain [1] located at the interhemispheric fissure. The largest numbers of neurons projected into corpus callosum are those found in the large pyramidal cells of cortical layers IIIIV of the contralateral hemisphere [2]. Considering its extensive function, the corpus callosum can be divided into three main parts; the genu (anterior portion), the body and the splenium (posterior portion). Thinner axons in the genu connect the prefrontal cortex between the two interhemispheres. Thicker axons in the midbody of the corpus callosum and in

the splenium interconnect areas of the premotor and supplementary motor regions and motor cortex, with proportionally more corpus dedicated to supplementary motor regions. The splenium communicates somatosensory information between the two halves of the parietal lobe and visual center at the occipital lobe [1].

As one of the functions of the corpus callosum is to connect both cerebral hemispheres, and thus to facilitate interhemispheric communication, the volume of the corpus callosum can be affected directly by lesions to the corpus callosum or indirectly by lesion occurring outside the corpus callosum. In the last case, Wallerian degeneration of projecting neurons is responsible for the corpus callosum volume loss. Independently of its etiology, corpus callosum atrophy may be considered a marker of neuronal loss and may be found in healthy elderly adults or in diseases affecting the white matter, that may be ischemic or demyelinating in nature [3] [4] [5].

Due to the advances in imaging techniques, the number of studies of the corpus callosum using different modalities of magnetic resonance (MR) scans increased considerable in the last decade.

The great majority of published studies were conducted using T1-weighted images. Among them, the majority was based on white matter segmentation, using active contours. After the segmentation, the CC could be extracted using connected components analysis with statistical information [4], or atlas-based segmentation [6]. Although T1-based segmentation methods for the corpus callosum were far more explored and well established, segmentation methods based on magnetic resonance diffusion tensor images (MR-DTI) are becoming more explored. First, because it constitutes a valuable tool to

inspect fibrous structures in a non-invasive way [7]. Thanks to its directional information, it allows not only the segmentation of the corpus callosum, but also can lead to its parcellation in some regions [1] [8]. Also, because it is desirable for the CC segmentation to be performed directly in DTI, since the final intent is to analyze the diffusion parameters within the corpus callosum.

Among the DTI-based segmentation methods, only a few ones were conceived to segment exclusively the corpus callosum. An atlas-based segmentation method was proposed for white matter fiber bundles in DTI [9], but it requires prior knowledge, includes registration and results are not focused on brain structures. There are also surface evolution methods using active contours applied in DTI [10] [11], based on level set function or distance of probability density functions, but they are complex and time consuming. Other method uses the orientation information of DTI and binary masking to segment white matter structures including the corpus callosum [12]. Despite being simpler, it requires user interaction and is not sufficiently robust to overcome abnormalities inside the structure. The cell-competition method [5], which uses the watershed transform, is computationally expensive and the results presented are insufficient to draw any conclusions about the generality of the method.

In this paper we propose an automatic approach method for the segmentation of the midsagittal section of the corpus callosum. The method is also based on the watershed transform but explores other concepts of mathematical morphology and includes the automatic determination of the midsagittal slice of the brain to be segmented. The method also performs the 3D volumetric segmentation, not only in the midsagittal slice.

The algorithm was developed in Adessowiki [13], a collaborative environment for development and documentation of scientific computing algorithms.

II. METHODS

The proposed approach consists of three major steps: the automatic determination of the midsagittal slice, the segmentation of the corpus callosum in the midsagittal slice and the volumetric segmentation of the corpus callosum.

This section contains a description of each one of them.

A. Automatic determination of the midsagittal slice of the brain

To perform the segmentation of the corpus callosum properly ensuring its repeatability, it is important to have an automatic method for the determination of the central slice of the brain. One of the landmarks of the central portion of the brain is the interhemispheric fissure, which is mainly composed of cerebrospinal fluid (CSF), except for some white matter structures. The objective of the proposed method is not to identify the interhemispheric fissure, which is a more complex operation, but to find the slice within a dataset that is the closest to it, here called the midsagittal slice.

The fractional anisotropy (FA) map derived from the MR-DTI reflects the scenario in the midsagittal slice: large areas,

corresponding to the CSF, with low FA values and the white matter structures, including the corpus callosum, with high FA values.

Consequently, if the average FA is calculated for each slice, discarding values above a certain limit FA_{max} , the slice with lowest average will be the midsagittal slice. That is true if not taking into account slices from extremities, with small cross-sectional area of the brain. So, slices with cross-sectional area below a certain minimum A_{min} are not considered as candidates for midsagittal slice.

B. Corpus callosum segmentation in the midsagittal slice

The automatic segmentation of the midsagittal section of the corpus callosum is performed using the watershed transform from markers [14]. Since the critical part in the watershed segmentation is the proper choice of markers, a hierarchical approach is considered in order to retain the most significant regions of the image. The extinction values of the local minima based on the volume dynamics are used to build the hierarchy [15]. Local minima with highest extinction values are then used as markers for the watershed segmentation.

Since the watershed transform is usually performed over a gradient image, the external morphological gradient is calculated. It is chosen over the morphological gradient and the internal morphological gradient due to its capacity of extracting external boundaries of objects brighter than the background [16] and is used to capture the edges of the corpus callosum. The external gradient G_e is defined as the difference between the dilated image and the original image f :

$$G_e(f) = f \oplus b - f \quad (1)$$

where \oplus denotes the dilation operation, using a structuring element b . In this case we used the elementary cross as the structuring element.

Diffusion tensor images, as tensorial images, present a variety of derived scalar maps, each one representing a particular property. The choice of a scalar map, or a combination of them, to be used in the segmentation of the corpus callosum section should consider its capacity to enhance the CC borders in the external morphological gradient computation.

To emphasize the CC features in the midsagittal slice (high FA values and preferential diffusion in the left-right direction), the fractional anisotropy map is weighted by the projection of the principal eigenvector in the left-right direction – the e_{1x} -weighted FA map ($w_{map} = e_{1x} * FA$). This combination is essential to differentiate the corpus callosum from other structures that also present high FA values but different orientation from the corpus callosum fibers, e.g., cingulum, fornix.

The number n of markers to be assigned in the watershed segmentation, and consequently the number n of regions to be segmented, must be greater than the number of labels in the final result (2 labels, corpus callosum and background) to guarantee that the external boundaries of the corpus callosum are detected.

Finally, it is necessary to group the obtained regions to achieve the final segmentation. The e_{1x} -weighted FA average

of each region is an important parameter for distinguishing between the corpus callosum and the background: all regions within the corpus callosum present a high average, in opposition to the regions outside the CC. Few voxels with high values outside the CC are not sufficient to significantly increase the average of these regions. Therefore, a single threshold T is used to classify the regions that can compose the CC, based on the e_{1x} -weighted FA average of each region. The choice of the largest connected component is enough for the corpus callosum to be correctly extracted.

C. Complete segmentation of the corpus callosum

The corpus callosum segmentation in the midsagittal slice of the brain can be considered as the final result for some studies, but it also can be the initial step for the 3D volume segmentation. The e_{1x} -weighted FA map is used because the emphasis of the CC features in this step is even more critical than in the previous one. As the corpus callosum fibers spread, they still preserve the same preferential diffusion direction, but the structures with different orientation tend to get closer.

The volumetric segmentation is accomplished using again the watershed transform from markers [9], this time with a 3D structuring element and a different choice of markers. The corpus callosum section in the midsagittal slice, after an erosion operation, is used as the internal marker for the watershed transform. The external marker is the brain mask, obtained in the beginning of the process.

The watershed transform is also performed over the external morphological gradient, as in the 2D case, and is able to differentiate the corpus callosum from the background without any further step.

III. EXPERIMENTS

The diffusion data used in our experiments were acquired on a Siemens 3T Trio MR scanner using an 8-channel phased array head coil: diffusion images with $N = 30$ diffusion encoding directions with $b = 1000s/mm^2$, $2.0mm$ isotropic voxel size, 63 slices, $TE = 95ms$, $TR = 8700ms$. The Autoalign sequence guarantees that the brain is almost aligned to image axes with the desired orientation for all datasets used. The test set consists of 15 volumes, acquired for 15 different subjects.

The first experiment was performed to evaluate the determination of the midsagittal slice of the brain, with the midsagittal slice being automatically determined by the proposed method for all images in the test set. The FA limit FA_{max} chosen was 50% of the highest FA value and the minimum area A_{min} is 80% of the maximum cross-sectional area. The slice assigned by the method for each image was compared with the slice previously assigned by a physician.

Once determined the midsagittal slice, the CC segmentation was performed in all subjects, following the steps proposed in section II.B. The chosen number of regions in the watershed transform was $n = 50$ while the threshold for region classification was set to $T = 0.2$.

After the qualitative analysis, specific tests were conducted to measure the sensibility of the proposed method to variation of the predetermined parameters (the number of regions n on the watershed transform and the threshold T for region classification). The first parameter examined was the number of regions: the threshold for region classification was fixed in $T = 0.2$ and the number of regions n ranged from 2 to 100. The second parameter tested was the threshold for region classification: the number of regions was fixed ($n = 50$) and the threshold ranged from 0.05 to 0.3. For both cases the impact of the parameter variation was observed in the final result, identifying when the CC boundaries could be extracted correctly.

The next experiment was conducted to evaluate the quality of the corpus callosum segmentation in the midsagittal slice. Because of the lack of an acceptable standard for comparison, the definition of a segmentation standard was based on manual segmentations made by specialists. Three specialists delineated the corpus callosum boundaries in the midsagittal slice and the standard segmentation for each subject was defined as the set of voxels marked as corpus callosum at least by two of them. All other voxels were labeled as background. This procedure reduces the influence of interobserver variability and human error.

Two different metrics were used in the comparison with the standard: kappa and overlap. The kappa coefficient measures the agreement of the segmentations considering the probability of the random agreement to happen. Overlap is defined as the percentage of voxels classified as CC by both the method and the standard with respect to the number of voxels classified as CC by at least one of them. They are defined as follows:

$$Overlap = \frac{N_{TP}}{N_{TP} + N_{FP} + N_{FN}} \quad (2)$$

and

$$kappa = \kappa = \frac{2(N_{TP}N_{TN} + N_{FP}N_{FN})}{(N_{TP} + N_{FN})(N_{FN} + N_{TN}) + (N_{TP} + N_{FP})(N_{FP} + N_{TN})}, \quad (3)$$

where N_{TP} is the number of true positive voxels (labeled as CC by both the method and the standard), N_{TN} is the number of true negative voxels (labeled as background by both), N_{FP} is the number of false positive voxels (labeled as CC by the method but labeled as background by the standard), and N_{FN} is the number of false negative voxels (labeled as background by the method but labeled as CC by the standard).

Other metrics, such as accuracy and specificity, were not used in the comparison of segmentations because their value is highly influenced by the voxels labeled as background by both the method and the standard. As the background area is significantly larger than the corpus callosum, high values do not necessarily reflect good performance of the proposed method.

Finally, experiments were conducted using the midsagittal slice of the corpus callosum as internal marker in the water-

shed transform to accomplish the volumetric segmentation of CC. The same 15 datasets were used.

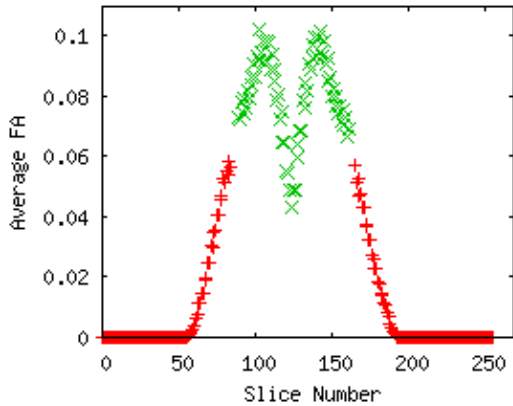


Fig. 2. The average FA for each slice of a given volume: the midsagittal is the slice with lowest average between the candidates (green ‘X’), the discarded slices (red ‘+’) are not considered.

IV. RESULTS AND DISCUSSION

As mentioned previously, the midsagittal slice of the brain had to be determined before the CC segmentation. Fig. 2 presents an example of the midsagittal slice determination. The average FA was computed for each slice of a given data set. Once extremity slices were discarded (red ‘+’), the midsagittal slice could be easily determined by its low average FA. For all datasets used in the experiment, the correct slice was identified by the method.

After determining the midsagittal slice, the segmentation of the corpus callosum was performed. The proposed segmentation method showed consistent results for all datasets, being able to identify the desired structure. In order to illustrate the proposed method, Fig. 3 contains the result of each step of the method for one subject.

Fig. 3a shows one slice of the original diffusion tensor image cropped around the corpus callosum. As can be seen, the DTI data contains complex information and its segmentation is not a trivial task.

The e_{1x} -weighted FA map (Fig. 3c) allows the corpus callosum to be distinguished from other structures with different fiber orientation, what cannot be done from the FA map (Fig. 3b) only. The external morphological gradient (Fig. 3d) was calculated from the weighted map and captured the edges of the corpus callosum. The watershed transform (Fig. 3e) was then computed from the gradient, for $n = 50$ regions. The e_{1x} -weighted FA average of each region was calculated and a threshold was used to identify the regions that could be part of the corpus callosum (Fig. 3f). The largest connected component (blue) was extracted to obtain the final result (Fig. 3g).

Although the watershed segmentation sometimes divided the CC in a different number of regions depending on the chosen value of n , the proposed method was always able to

group them correctly in the final result. First, because the e_{1x} -weighted FA average for each region within the corpus callosum is always significantly higher than the value for the majority of regions in the background. Second, because small regions with some high value voxels outside the CC can be discarded when considering only the largest connected component as CC.

It is important to point out that no prior knowledge of the shape of desired structure is necessary for the method, only the fact that the corpus callosum presents high FA values and preferential diffusion in the left-right direction. This is an indication that the proposed method would work also with patients, despite any atrophy or abnormality of the corpus callosum.

In order to confirm that the proposed segmentation method does not require a fine parameters tuning for each new test set, the result after region classification for different number of regions n in the watershed transform and different thresholds T in region classification is shown (Fig. 4). By observing Fig. 4 it is possible to note that if the number of regions is

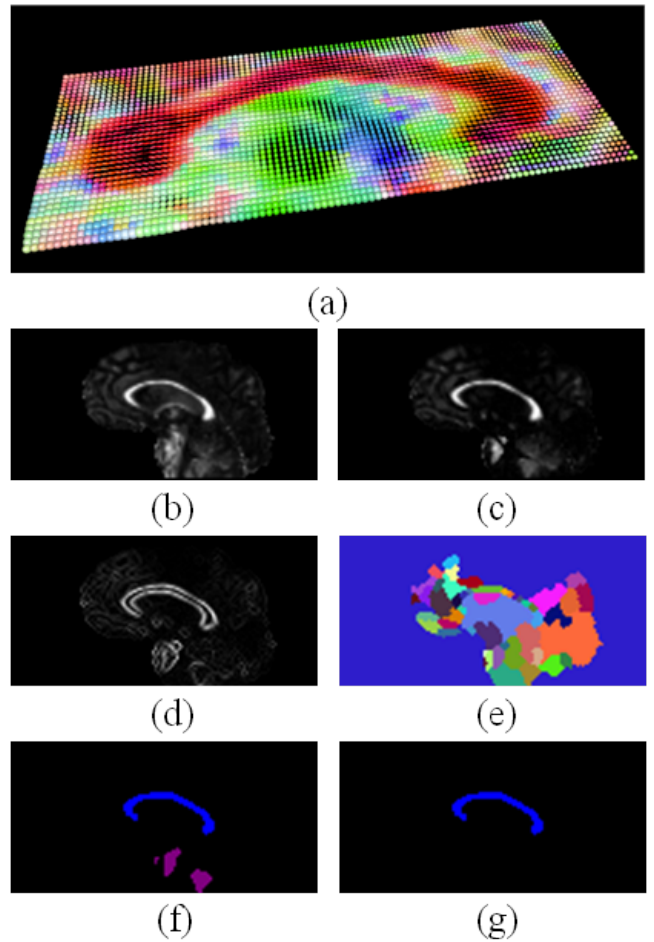


Fig. 3. Stages of the proposed method: (a) detail of the corpus callosum in a slice of the initial DTI volume, (b) the FA image, (c) the e_{1x} -weighted FA image, (d) the external gradient, (e) watershed transform, (f) the result of region classification and (g) the final result.

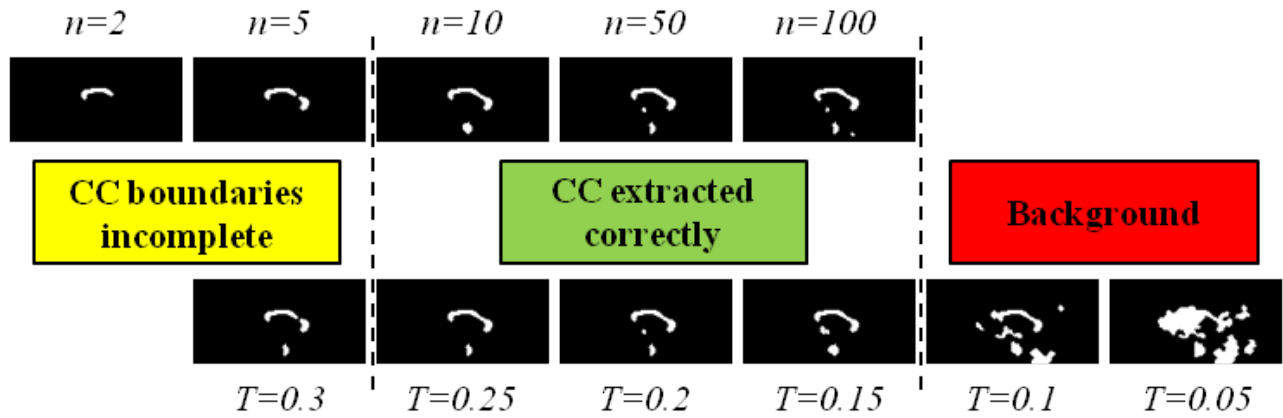


Fig. 4. Changes in the corpus callosum segmentation when modifying the number of regions of the watershed transform (n) and the threshold of the FA average (T).

low or the threshold is high (left), the corpus callosum may not be extracted correctly. For intermediate values of both, the CC could be segmented correctly, with some smaller structures also appearing in the final result. There were subtle changes in CC boundaries as the number of regions was increased or the threshold was decreased (center). The boundaries of the corpus callosum changed considerably if the threshold chosen was too low (right).

All datasets were first used to assess the sensibility of the proposed method to the number of regions n . For each number of regions the segmentation was performed and the result was classified according to its capacity to capture the CC boundaries (Fig. 5a). The same process was used to assess the impact of the threshold T in the final result (Fig. 5b), complementing the robustness analysis.

The experiments have shown that $n = 40$ regions were sufficient for the detection of the CC boundaries for all tested images, and increasing the number of segmented regions did not affect significantly the final result. As shown in Fig. 5b, the safe range for the choice of the threshold value was not as wide as the range for the previous parameter. Nevertheless, it was still possible to segment correctly the corpus callosum in all images.

Since the segmentation result is not affected by the chosen number of regions n , if it is within the mentioned range of values (40 to 100), new images could be easily segmented by the proposed method. Also the same threshold could be used without any special adjustments, making the method more reliable and increasing its capacity to adapt to new DTI datasets.

Comparing the CC segmentation in the midsagittal slice using the proposed method and the manual segmentations for different specialists with the manual standard defined it was possible to evaluate the proposed method: the mean kappa coefficient for all 15 subjects was $91.51\% \pm 2.12\%$ (SD) using the proposed method and $96.60\% \pm 4.30\%$ with the manual segmentations, while the mean overlap was $84.64\% \pm 3.55\%$

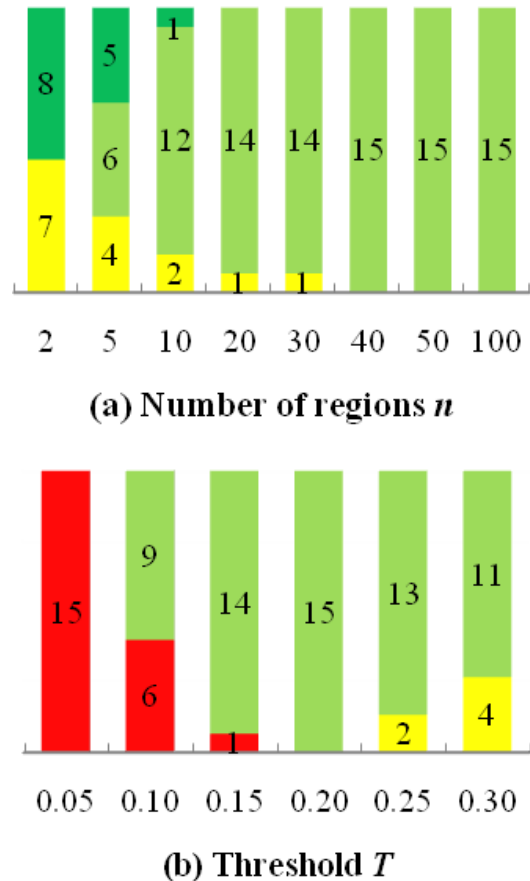


Fig. 5. Analysis of the corpus callosum segmentation obtained for a given number of regions in the watershed transform (a) and a given threshold in region classification (b). Light green indicates that the CC segmentation was successful. Dark green indicates that, besides the correct segmentation, the corpus callosum is the only connected component after region classification. Yellow represents that the CC boundaries could not be extracted and Red represents that background regions were added in the CC for the final result.

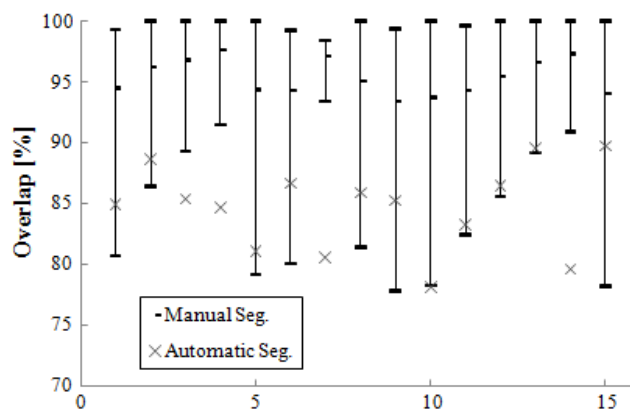


Fig. 6. Results of the overlap with the defined standard: comparison of the different manual segmentations (minimum, maximum and mean overlap value) with the proposed method.

and $93.86\% \pm 7.61\%$, respectively. Fig. 6 presents the overlap for each image.

The accuracy of the proposed method was very high ($99.71\% \pm 0.06\%$), confirming that this metric is not recommended for evaluation of the actual performance of the method in such cases, when the background area is significantly larger than the desired structure.

The kappa coefficient and the segmentation overlap for the proposed method were high and within the range of the manual segmentation variation for most of the images (10 of 15 cases). The errors with automatic brain segmentation were in part due to the low resolution of the DT images.

The experiments with the 3D segmentation of the corpus callosum were successful. The CC volume could be extracted for all datasets (Fig. 7). The evaluation of obtained boundaries is not the focus of this work, and future works will assess the quality of the 3D segmentation, mainly for the most difficult regions where the CC is merged with fiber bundles.

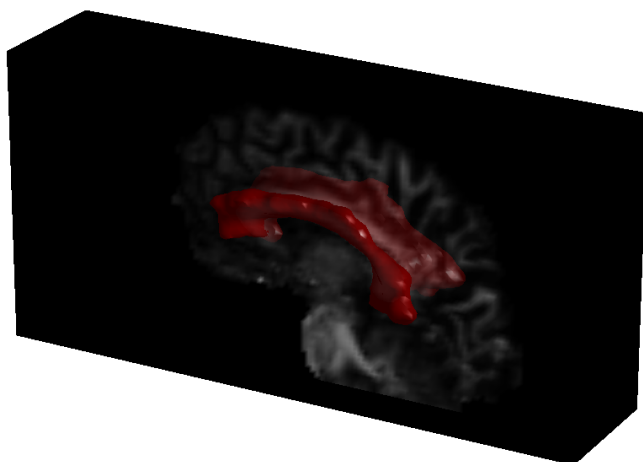


Fig. 7. Example of the 3D Volume segmentation of the corpus callosum made using the proposed method for a given dataset.

V. CONCLUSION

In this article we proposed a new approach for segmentation of the midsagittal section of corpus callosum in magnetic resonance diffusion tensor images, using the watershed transform. This approach includes the automatic determination of the midsagittal slice of the brain, which is important to allow the reproducibility of presented results.

The proposed method has shown important results, not only for the corpus callosum segmentation but also for the determination of the midsagittal slice of the brain. Experiments with real diffusion MRI data showed that the method is able to quickly segment the CC and to determine the midsagittal slice without any user intervention. It is simple and does not require parameter settings. All parameters are previously assigned.

A method for 3D volume segmentation of the corpus callosum was also proposed, with the CC section in the midsagittal slice being used as seed in this process. The results are promising and new experiments should be conducted in order to evaluate the quality of the volume segmentation.

The experiments conducted in this paper accredited the presented methods to be used for clinical applications. The safe range for the choice of pre-determined parameters demonstrates the robustness of the proposed method. It indicates that the method would work for new DTI datasets, even for patients with alterations in the corpus callosum.

Our intention is now to use the proposed segmentation methods to study the diffusion characteristics within the corpus callosum, trying to relate them to neurodegenerative diseases.

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