Segmentation of the Human Corpus Callosum Variability from T1 Weighted MRI of Brain

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Abstract Corpus Callosum is an important part of the brain which works as major neural pathway that connects homologous cortical areas of the two cerebral hemispheres. The size of Corpus Callosum is affected by age, sex, neurodegenerative diseases and various lateralized behaviour in people. Here T1 weighted Magnetic Resonance Imaging (MRI) of brain, usually the sagittal sections is taken which is then followed by the automated segmentation of the MRI slide. This segmentation has an important application in neurology as the shape as the thickness, size and orientation of Corpus Callosum depends on the various characteristics of the person. Lobar connectivity based percolations of the corpus callosum can be computed by our proposed method which is very accurate segmentation.

Keywords Corpus callosum · Automated segmentation · MRI of brain · Quantification · Sagittal region · Bending angle · Midpoint

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1 Introduction

The human nervous system is spread throughout the human body. This system controls all the voluntary and involuntary actions in the body. It transmits signals to and from the different organs present in the body. The human brain is one of the complex structures present in the body which is responsible for the normal working of the body. If we consider the anatomy of the brain we see that the brain is majorly divided into two parts namely left and right lobes of cerebrum. These two parts are joined by Corpus Callosum (CC) through which two hemispheres communicate with each other. CC also known as the colossal commeasure is a part of the brain located in mid sagittal region. It is the largest neural pathway which connects the two hemispheres of the brain. It consists of between 200 and 800 axon fibres beneath the cortex in the ethereal brain at the longitudinal fissure. In some cases CC might be partially or completely absent in a person. This condition is known as agenesis of the CC. The nature and function of CC has been a long interest to researchers as its alteration in structure has resulted in psychiatric and developmental disorders. Magnetic Resonance Imaging (MRI) of brain is a painless test where radio waves and magnetic field is used for getting a detailed picture of brain and its associated structure. The MRI scan does not use radiation which differentiates it from CAT scan, also called a CT scan or a computed axial tomography scan. The MRI scans rather than from giving us a clearer picture also gives us the advantage of easier identification of different abnormalities of brain. In neuro-imaging, the segmentation of different parts of brain is considered to play an important role in several medical applications. This field of study has attracted much interest from the medical community and gives us crucial information that might significantly impact clinical management and practice. In the process of manual segmentation of brain like using photo editing software's is still considered the most accurate, but more time-consuming method for segmentation which includes much laborious work including detection and then extracting those parts. It is traditionally time-consuming and dependent rather than an experience. The designs of algorithms for automatic segmentation of brain are being developed to ease this task of manual segmentation. But it is usually hard to segment some parts such as the ones located at sub-cortical level. In this work, the automated segmentation was achieved by image processing algorithms and the processed images are the more refined and then compared with the manually segmented image to get accuracy using different metric algorithms. Also rather than using standard algorithms we have used morphological operation on the images to get a more refined picture of the obtained segmentation. The proposed method includes improved detection and measurement of area of CC. The proposed method includes the following phases: (1) Input of T1 weighted image and refining of the image to reduce noise. (2) Segmentation of CC using area selection and binary conversion of image. (3) Colouring of detected part in original image. (4) Detection of mid-point

and end points of segmented CC. (5) Measurement of bending angle of CC. The verification of proposed method's accuracy, reliability, robustness, and multisite consistency has been done by making comparisons with manual segmented image using randomly selected slides from the database. This proposed method has been tested on 10 data sets selected in random and has been seen that automatic segmentation gives us the most approximate result with minimum error percentage.

The preference for automated segmentation is the increasing popularization in the neuro-anatomical research area. Some of the volumetric measurements which are acquired from MRI are used to examine and quantify the impact of some brain diseases and disorders on the human central nervous system [1, 2]. In the normalization approach using voxel-based morphometry (VBM) allows us to compare different brain MRI slides on a voxel-by-voxel basis [3]. In accordance to Marchetti et al. [4], it has been seen that the time spent on manual segmentation of the hippocampus might be taking the time of 75 min. per patient for each exam. This takes up a lot of time in producing the segmented image. In [5] it was seen that using T1 slides of MRI of brain, the CC was extracted from mid sagittal section of brain. Then the threshold was used in segmentation of CC. The goal of this work is to use image-processing and using statistical models of automated segmented MRI slides as ground truth image to produce accurate segmented image with respect to ground truth image.The normalization approach used voxel-based morphometry (VBM). The VBM technique allows us to compare dissimilar brain composition stand on voxel-by-voxel examination once deformation fields have been employed to spatially standardize the images [6]. The CC is a well-known white matter bundle which is simply identifiable on MR imaging which is linking between two cerebral hemispheres in a homotopic group with orientation to the cortex illustration [7]. Besides the CC plays significant role on instructive processes of inter-hemispheric messages and specialization [8], it is of enormous significant due to its limitation to ecological poisons, white matter diseases (such as multiple sclerosis) and schizophrenia [9, 10]. The size of the CC was also investigated by neuro-biologists working in many specialized fields, including handedness [11], musical ability [12], schizophrenia [13], autism [14] and Alzheimer's disease [15]. The rest of this article is organized in three more sections. Section 2 describes the process of automatic segmentation of brain tissue. Section 3 tells us about our practical experiments and presents the CC surface area using our proposed method, and finally in Sect. 4 we conclude our methods.

2 Proposed Method

In the event of segmentation of corpus callosum we use 10 datasets each containing around 12–15 mid sagittal MRI slices of the brain [16, 17]. The images are entered in a bundle so as to get a 3D representation of the obtained segmented corpus

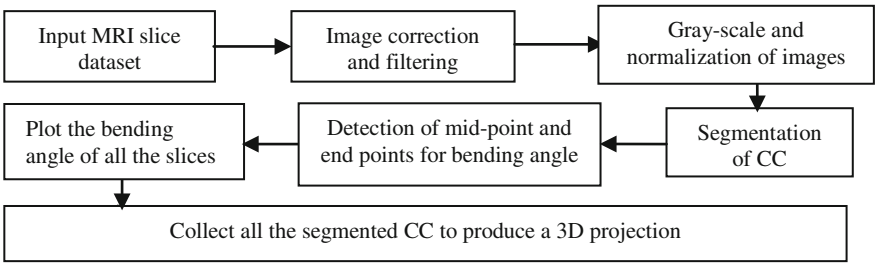

Fig. 1 Workflow of the proposed methodology

callosum. While considering each dataset we get individual result as parameters from each slice which is then plotted to analyse the result variation in each individual dataset. The work flow of our proposed methodology can be represented by Fig. 1.

2.1 Pre-processing of Slices

The T1 weighted MRI slices are chosen as input as soft tissues are clearly visible in T1 weighted MRI images. After taking the input the slices might contain many distorted element such as artefact, indistinct intensity values and uneven intensity distortion. In order to correct these defects in the slice the slice is processed through artefact removal [6] and image correction algorithm where intensity variation and other distortions are corrected. This pre-processing counts as an important step as these defects in the image gravely affects the segmentation part of our proposed methodology. The obtained image is usually a RGB image which can be represented as a 3D matrix where each 2D matrix represents Red, Green and Blue portion of the image. We convert it into gray-scale using the standard RGB to gray-scale conversion formula in which each pixel represent the intensity of images within the scale 0–255 which can be represented 8 bits of binary digit.

2.2 Segmentation of the Corpus Callosum (CC)

The segmentation of CC takes place through a series of steps. After the input and pre- processing step, we get a gray-scale image which can be represented as a 2D matrix where the image is made of intensity function done by variation of intensity in each pixel. Let us take that intensity function is X for the image I where each pixel can be given by $I[m, n]$ in which $1 \leq m \leq$ maximum number of rows (M) and

$1 \leq n \leq$ maximum number of columns (N). We need to find the threshold intensity of the grayscale image for its binary conversion. This is done by determining the threshold intensity and then putting all the pixels below the level as "0" and above it as "1". For the conversion this calculation of threshold intensity has become an important step as a slight change might even put the region of CC as "0" which is unexpected. This is done by calculating the expectation intensity $E(I)$ and then taking the expectation value in our region of interest. This expectation value is calculated by considering the principles of discrete random variable whew $E(I)$ can be given by: $(I) = I[m, n] \times P(I[m, n])$, where $P(X)$ is the probability of value X appearing in a corresponding pixel. This expectation gives us the most optimum threshold intensity to be selected and in this calculation the region of skull is not considered. Now after obtaining the threshold intensity the image is now to be sectioned to get a portion where probability of availability of CC is high. This probability is now calculated using feature extraction of CC which is present in our region of interest so that other region does not affect our extraction. Let us take rectangular distribution of probability of detection of CC in the image as it is confined in certain regions of the image. Let us divide the image into N equal divisions of rows and columns. So total number of divisions = $N * N = N^2$. Therefore the distribution can be given as:

$$P(I(m,n)) = f(x) = \frac{1}{b-a}, \text{where } 1 \leq a, b \leq N^2$$

This probability is used to determine the region of interest. The image is then resized to our findings. After resizing, the extracted part is then converts into binary matrix in accordance to our previously found threshold intensity. After binary conversion of the slide, it is then detected for maximum connected component. For calculation of maximum connected component the whole slice is broken up into different component where each component is connected. This means that each component is a bunch "1" grouped together. Now each of the components is tested for its area. This can be given by the formula

$$A = \sum_{i=m}^{M} \sum_{j=n}^{N} I(i,j),$$

where the component I ranges from $[m{:}M, n{:}N]$. This summation gives us the effective area in pixel. Using this data we find out the maximum area present in the slice and extract only the component with maximum area. CC has been seen to be a connected component with maximum area which naturally segments out from slice, thus maximum area giving us only the CC in the slice. This image might contain noise as a result of previous operation on the image. This noise is corrected using morphological operation on this image. Thus we get our required segmented part.

After this the segmented part is brought back to the original size so that they can be compared with the original MRI slide to colour the detected part.

2.3 Detection of Mid-Point and Two End Points for Calculating Bending Angle

The segmented binary image after being brought back to original size is taken as input in this step. This image is then cropped to such a size such that it satisfies the following conditions:

a. The image should contain only the segmented CC.
b. At least one pixel value in leftmost, rightmost, topmost and bottommost extreme pixel should compulsorily contain "1".

The input binary image is brought to the specified condition as stated by running nested loops by detecting all the pixels in the image and finding the extreme positions of the segmented CC. Using this figure we find the topmost which is considered as mid-point and two extreme end point of CC by running nested loops. After obtaining the end-points we use this to calculate the bending angle. Let us assume that (a_1, b_1) is the position of the pixel considered as mid-point, (a_2, b_2) as the bottom leftmost position of the pixel and (a_3, b_3) as the bottom rightmost position of the pixel which is demonstrated in Fig. 2. Then the bending angle B can be calculated as

$$m_1 = \frac{b_2 - b_1}{a_2 - a_1}, \text{ and } m_2 = \frac{b_3 - b_1}{a_3 - a_1}$$
$$\deg 1 = \tan^{-1}(m_1), \text{ and } \deg 2 = \tan^{-1}(m_2)$$
$$B = \text{abs}(\deg 2 - \deg 1),$$

where abs(x) gives us the absolute value of x. This formula of derived from the concept of the equation of a line where the slope is calculated and inverse tangent if the slope gives us the angle of inclination. Using this angle of inclination we find the difference between the two slopes which gives us the bending angle. The bending angle obtained by the stated methodology gives us an error as we had

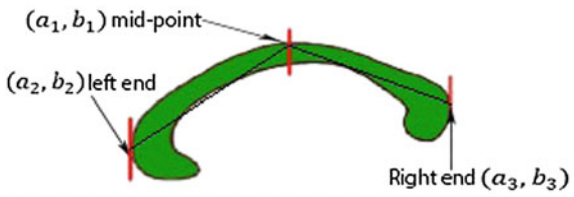

Fig. 2 Detection of mid-point and end point of CC

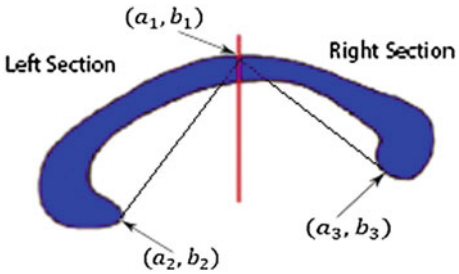

Fig. 3 Calculation of actual bending angle

aimed towards calculating bending angle between the two end points of CC. This is done by dividing the image into two parts and finding the bottom most points by applying reverse loops.

As illustrated in Fig. 3 this segmented part is divided into two parts namely left and the right section. Reverse loops are executed to find the positions of the tips from each sections. These reverse loops are useful in finding the tips using the reverse direction from the mid-point.

2.4 3D Projection of Corpus Callosum (CC)

After the segmentation and calculation of bending angle all the original size binary segmented image, the segmented image is collected. Each of the images is a 2D image with pixel containing values either "0" or "1". The images containing the CC are only considered. The 3D figure is derived considering the features of stack data structure. This structure is useful in adding another dimension for a n-D structure into $(n + 1)$-D structure. Let us consider an n-D structure. If this is pushed into the stack the total structure considering the stack becomes $(n + 1)$-D structure as stack inserts length or size of the stack as another dimension. Thus we can get a 3D figure from a 2D image using the stated proposition. We know that in MRI scan the slices are taken in an interval of some distance in millimetre. So the slides in between two consecutive slides are not taken. So the absent slides are calculated and then stored. The number of absent slice = sep × 3.779527559, where "N" is the number of absent slides and "sep" is the separation between two slides in mm. The nearest whole number is taken as the number of missing slides. The absent slides are calculated by modifying the size of an image generated by combining two consecutive slides. This modification is done by getting the values of linear interpolation of area of images. The variation is done with respect to the two areas of the consecutive slides. After getting all the sets of images the images are pushed to a top-down stack which gives us the correct orientation of the figure. This stack is then projected to give us the corresponding 3D figure of CC.

3 Results and Discussion

A number of theories have been proposed about detection and segmentation of CC such as using tensor imaging and watershed-based segmentation. But the proposed methodology uses a different approach to this problem by using statistics and feature extraction. The collected datasets each consisting sagittal plane MRI slides on which the proposed methodology has been tested obtaining different variations of output. Now as input of the algorithm we use T1 weighted MRI image as shown in Fig. 4a. Then the resizing of the image is done by the extraction algorithm to get the image as in Fig. 4b. Then the image is converted into binary image using threshold intensity as the reference intensity level as in Fig. 4c. Then extraction of maximum component executed on the resized figure to get the detected portion as in Fig. 4d. Then the extracted CC is then brought back to the original size which is the actual output as in Fig. 4e. Then this obtained output is compared with original MRI slide to get colouring on the output image showing detected CC.

The accuracy measures used to evaluate the performance [18, 19] of the proposed methods are the Relative area Error (RE) [18, 19], Kappa Index (Ki), Jacard Index (Ji), correct detection ratio (Cd) and false detection ration (Fd) has been described below. An important difficulty we have to face in developing segmentation methods is the requirement of a good benchmark for their evaluation. Although physical or digital phantasm can afford a level of known "reference or ground truth image", they are still not capable to reproduce the full range of imaging characteristics, normal and abnormal anatomical inconsistency observed in medical data. Let AV and MV denote [17, 20] the region of by design and by hand segmented region, and TP is the joint section between AV and MV. The FP can be calculated by subtracting TP from AV and FN can be calculated by subtracting TP from MV, FP and FN denote to the "true positive" and "false negative" respectively. The kappa index is determine by two multiplied by intersection of MV and AV divided by sum of AV and MV. Jacard index can be found from intersection of MV and AV divided by sum of TP, FN and FP. This metric is more susceptible to differences since both denominator and numerator varies with rising or falling overlap. Correct detection ratio or sensitivity is defined by the intersection of AV and MV divided by MV. The Relative Error [21] (RE) can be calculated by AV subtracted by MV divided by MV (Table 1).

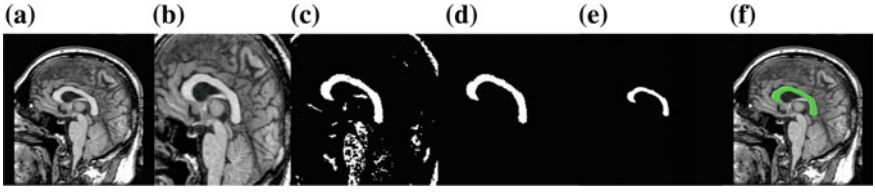

Fig. 4 **a** Original image, **b** resized image, **c** resized binary image, **d** detected CC, **e** expanding to original form, **f** actual result

Table 1 Quantification and accuracy estimation

Image name	AV	MV	RE in %	TP	FP	FN	AV +MV	Kappa index (%)	(TP +FN +FP)	Jacard index (%)
068	868	850	2.11	845	23	05	1738	97.23	873	96.79
069	920	910	1.09	901	19	09	1830	98.46	929	96.98
070	853	877	2.50	850	03	27	1730	98.26	880	96.59
071	920	893	2.93	887	33	06	1813	97.84	926	95.78
072	859	841	2.14	834	25	07	1700	98.11	866	96.30
073	868	853	1.75	848	20	05	1721	98.54	873	97.13
074	1570	1592	1.38	1563	17	29	3162	98.86	1609	97.14
075	920	908	1.32	901	19	07	1828	98.57	927	97.19
076	2418	2453	1.42	2406	12	47	2871	97.94	2465	97.60
077	2723	2749	0.945	2715	08	34	5472	99.23	2757	98.47

The above table illustrates the result of 10 T1 weighted MRI images taken as input from image database of a same person. In this table we have observed that the relative area error RE is having a mean of 1.7585 which is relatively low. The RE increases if it is difficult to distinguish between CC and its surrounding tissues. This possesses a threat to the given method as AV might differ greatly compared to MV as in image 071 with RE = 2.93 which is relatively high compared to other images. After the testing of segmentation of CC we get a set of binary images which is tested for bending angle as given by the plot in Fig. 5.

In Fig. 5 we have shown the variation of the bending angle in a dataset with 6 slides where CC has been correctly detected. As we see in the figure the variation observed is ±0.5°−20° in the taken Fig. 5 and generally stays within this range for all the tested datasets. The calculated angle gives us the correct variation. In the event if 3D representation of CC it have been observed that there is a little variation

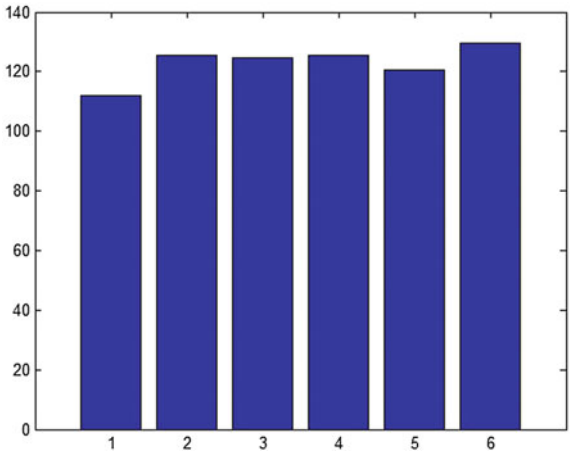

Fig. 5 Plot of the bending angle of 6 CC detected slides

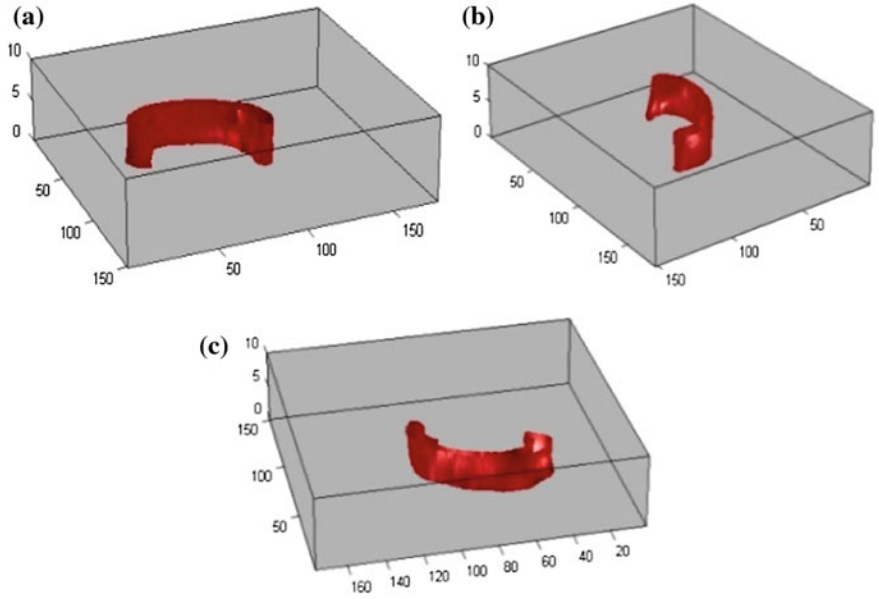

Fig. 6 Different views of the 3D figure

to consecutive slices, so the figure formed (Fig. 5) appears as a solid figure with smooth surface.

Figure 6a–c gives us the different views of the CC viewed at different angles. Using this figure we can view the actual shape of CC present in the brain. This 3D projection is observed by projecting the 3D stack of 2D images. The cracks and fissures present in the figure can be observed clearly by varying the output image.

4 Conclusion

The proposed algorithm usually works on MRI slides taken from mid sagittal section of brain. In this algorithm it is sometimes difficult to identify CC in some slides. To remove artefact we need morphological operation on binary images for correction of the result. This proposed methodology gives us the most suitable result as per T1 weighted MRI images are involved. In this proposed methodology we just highlight the detected portion of CC and keeping rest of the image untouched. This ensures us to detect other tissues in the slide with respect to CC. In the above proposed algorithm we see that the results obtained so far is promising but we need to improve on the removal of surrounding tissues which sometimes interfere with detection and extraction part of the algorithm.

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