K-mean clustering and local binary pattern techniques for automatic brain tumor detection

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ABSTRACT

Tumors in brains are caused by the unregulated emergence of tissue cells inside the brain. The early diagnosis and determining the precise location of the tumor in magnetic resonance imaging (MRI) and its size are essential for the teams of physicians. Image segmentation is often considered a preliminary step in medical image analyses. K-means clustering has been widely adopted for brain tumor detection. The result of this technique is a list of cluster images. The challenge of this method is the difficulty of selecting the appropriate cluster section that depicts the tumor. In this work, we analyze the influence of different image clusters. Each cluster is then split into the left and right parts. After that, the texture features are depicted in each part. Furthermore, the bilateral symmetry measure is applied to estimate the cluster that contains the tumor. Finally, the connected component labeling is employed to determine the target cluster for brain tumor detection. The developed technique is applied to 30 MRI images. The encouraging accuracy of 87% is obtained.

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1. INTRODUCTION

A brain tumor is an indefinite and uncontrollable growth of tissue cells in the brain. Different factors, such as position, size, shape, and region of the tumor are essential for identifying the tumor and the effective treatment [1]. Early diagnosis is the most important stage to prevent lasting damage to the brain or even patient death. Accurate data regarding the location of the tumor and its size are important issues for efficient treatment. The best method to study the structure and function of the brain by physicians and researchers is using magnetic resonance imaging (MRI). Computer technology is mainly employed to produce or display this type of imaging. The MRI image demonstrates an important component used for the detection and segmentation of the tumor region [2].

In medical imaging, the tumor brain can be characterized using various image processing operations, like image segmentation, classification, and morphological operations. In this paper, we focused on an unsupervised method for image segmentation. The K-means clustering algorithm is a popular algorithm used for brain tumor segmentation.

Bianchi *et al*. [3] improved the classification accuracy over standard intensity features using efficient gradient-based texture features. They extended texture and intensity features to symmetric texture and symmetric intensity which further improve the accuracy for all tissue classes. Anushree *et al*. [4] employed the K-means clustering algorithm to characterize the tumor in the brain MRI images. A cluster

constitutes a group of pixels with common characteristics. Clustering belongs to an unsupervised classification algorithm, in which the classification of objects is obtained using user-given criteria. In this research, the segmentation of an image for tumor detection is accomplished using a K-means clustering algorithm. Using images from an MRI scan and a support vector machine (SVM) classifier, the highest accuracy of 98.6% is obtained. The authors employed around 250 brain MRI images in the training process and 100 images for testing purposes. Haritha [1] used a local binary pattern (LBP) descriptor to eliminate the illumination effects in brain images and applied a segmentation method using threshold segmentation and morphological operations for the detection of the location of the brain tumor. Dhanalakshmi and Kanimozhi [5] integrated two algorithms to develop a computer-aided method to mark the location of brain tumors. The method achieved accuracy and reproducibility comparable to manual segmentation and in less analysis time. This method is capable of determining the position and shape of the tumor in the MRI images. The growth stage of the tumor is illustrated for the domain experts depending on the number of regions computed in the cluster. Nabizadeh and Kubat [6] developed an automated system to depict the slice that constitutes the tumor and its area. This method is based on histogram asymmetry between the two brain hemispheres for the recognition of the slice that includes tumor tissue. Afterward, the two most popular sets of feature extraction techniques are applied: Gabor wavelet and statistical texture-based, such as gray-level run length matrix (GLRLM), histogram of oriented gradient (HOG), LBP feature, and gray-level co-occurrence matrix (GLCM). These features depict the relationship among adjacent pixels based on either their intensity value or texture characteristics. The problem with the described methods is the inappropriate allocation of the proper cluster from the list of clusters that resulted from the clustering algorithm.

In this work, we explored an automatic method to allocate the tumor portion in the MRI images by integrating a K-means clustering algorithm, LBP feature, and the bilateral symmetry measure. A series of clustered images are generated using a K-means clustering algorithm. After that, the tumor portion is characterized by calculating the bilateral symmetry measure based on the LBP feature between the two brain sides to predict the inhomogeneity between these sides. If the result of the symmetry measure between the two brain sides is higher than a specific value, then the target cluster constitutes the tumor portion. Finally, the connected component labeling is employed to characterize the area that covers the location of the tumor.

The structure of this paper is organized as follows: section 2 depicts the main phases of the proposed method. Section 3 clarifies the experiments and their results. Section 4 demonstrates the important conclusion points.

2.   PROPOSED METHOD

The proposed method constitutes three phases. The first phase involves segmenting the brain MRI image by utilizing the K-means clustering algorithm to generate the list of clusters. The second phase is the automatic selection of the appropriate cluster employed to detect the brain tumor region based on comparing the difference between the value of the Uniform LBP features between the left and right brain sides. After that, the bilateral symmetry measure is applied to indicate how much the two sides are symmetrical. The third phase determines the region of the tumor by employing the connected component labeling. Figure 1 depicts the three phases of the proposed system.
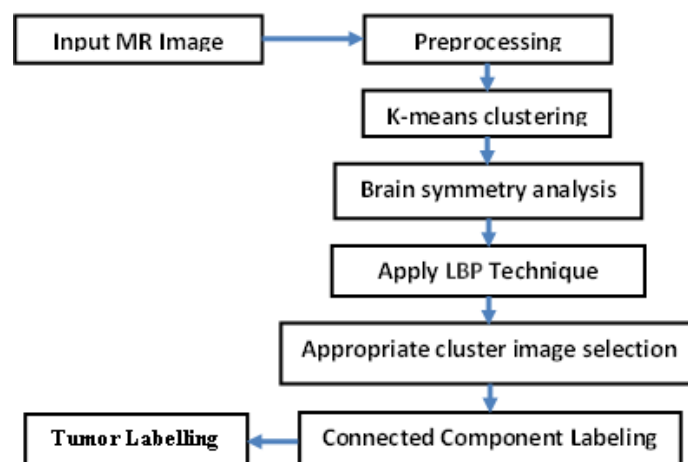

Figure 1. The phases of the adopted system

2.1. Preprocessing

Image preprocessing is an essential process in many computer vision applications. To improve the segmentation results, the preprocessing process is implemented to enhance image appearance and eliminate noise. It is also applied to eliminate the occurrence of mis-clustered regions after the segmentation phase [7]. In the current work, the preprocessing process involves image smoothing and sharpening. Image smoothing is applied to eliminate noise and improve image quality. For edge preservation under certain conditions, a median filtering technique is implemented. The sharpening filter is applied to enhance the high-frequency components [8]. This filter is utilized to magnify the fine details in the image and make the tumor boundaries clearer [9].

2.2. K-means clustering

The K-means algorithm belongs to the family of unsupervised learning techniques and is widely utilized for clustering purposes. Cluster analysis categorizes data objects in conformity with common features among them. These features can characterize the objects from their surroundings. The main aim of the clustering operation is to differentiate a set of objects that belongs to one group from objects that belong to other groups based on common characteristics. The greater the similarity (or homogeneity) within a group and the greater the discrepancy between groups, the better the clustering results can be obtained [10]-[13]. To implement the K-means clustering algorithm, the following steps are implemented: initially, the K preliminary centroids are chosen, where K denotes the number of clusters desired. The value of this parameter can be determined manually or automatically. After that, each pixel is assigned to a certain centroid in conformity with the closest distance between them. The clusters are then determined by the collection of pixels that assign to the same centroid. Next, the centroid of each cluster is updated in accordance with the pixels incorporated in each cluster. The procedure is repeatedly implemented until the centroids do not undergo any alteration. The whole process of the K-means cluster algorithm is demonstrated [14]:

Algorithm 1 basic K-means cluster algorithm.
1. Select K points as initial centroids, in a random or heuristic way.
2. Repeat
3. Form K clusters by categorizing the pixels into groups in accordance to the minimum Euclidean distance between the pixel and the K cluster centers as given in (1)
4. Re-determine the centroids of all clusters.
   Until centroids do not undergo any alteration.

$$f = \sum_{j=0}^{k} \sum_{i=1}^{n} (x_i^j - c_j)^2 \qquad (1)$$

where $x_i^{(j)}$ denotes pixel data, c_j denotes the cluster center, and n denotes the number of data points.

Figure 2 demonstrates an example of the implementation of the K-means clustering algorithm. The Figure 2(a) shown the original MRI image, Figure 2(b) depict the binary version of the brain image is first obtained. Then, the Figure 2(c)-(h) describe the six cluster images are plotted.

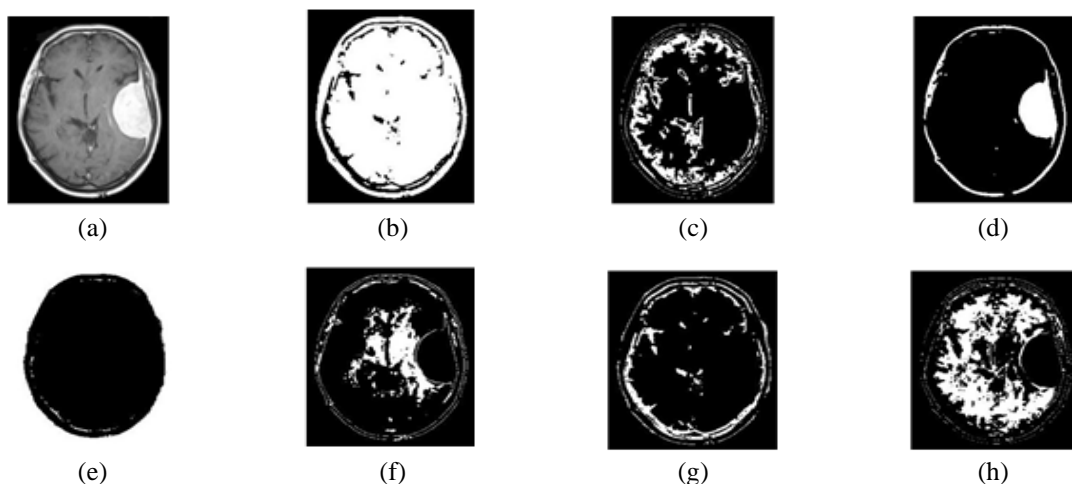(a)　　　　　(b)　　　　　(c)　　　　　(d)

(e)　　　　　(f)　　　　　(g)　　　　　(h)

Figure 2. K-Means clustering algorithm implementation (a) original image, (b) its binary version, (c) 1st cluster, (d) 2nd cluster, (e) 3rd cluster, (f) 4th cluster, (g) 5th cluster, and (h) 6th cluster

2.3. Brain symmetry analysis

The human brain exhibits nearly bilateral symmetry in a healthy state. The two hemispheres of the brain show a high degree of similarity in shape and relative location. The strokes and tumors could be characterized with the help of the symmetrical plane in brains by comparing tissue shape and areas between two sides of the mid-sagittal plane (MSP). The MSP for each brain slice provides a centre line for detecting bilateral symmetries [15], [16] as shown in Figure 3. In this figure, the MSP is indicated as a red line on the brain image (Figure 3 (a)) and as a dotted line on the brain slice (Figure 3 (b)).
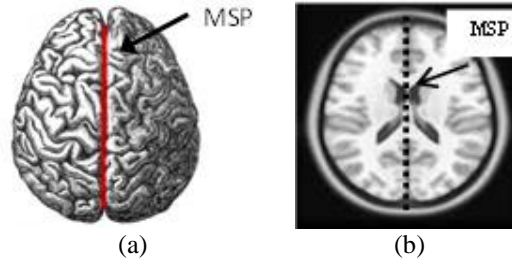

(a)   (b)

Figure 3. The MSP plotted on the human brain (a) MSP visible in the red line and (b) T1-weighted MRI brain axial slice with indicated the MSP by the red dotted line

The symmetry of the object shape can be exploited heavily in pattern analysis. In this paper, the bilateral symmetry can be realized by splitting the clustering image into two sides in accordance with the MSP of the original image. After that, the local texture feature value for each side is calculated. Finally, the asymmetry between the two sides is obtained as:

$$Asymmetry = \frac{|T_L - T_R|}{min(T_L, T_R)} \tag{2}$$

where T_L and T_R denote the local texture feature of the left and right sides respectively.

2.4. Local binary pattern

The LBP is a commonly employed feature extractor [17] in many applications such as medical image analysis, image retrieval, phase identification, texture classification, and image segmentation. The main characteristic of the LBP is that it is computationally simple and nonparametric [1]. The LBP operator investigates the spatial relationship between a pixel and its neighbors. The image is fragmented into little equal-sized cells to calculate the LBP encoding. For a window of size 3×3, the central pixel has eight neighbors. The values of the neighbors are compared to that of the center pixel. The result of the comparison will generate the eight-bit binary representation such that the value of the neighbor is set to 1 if it is greater than or equal to that of the central pixel; otherwise, it is set to 0. After that, the binary representation is converted to its corresponding decimal digit (see Figure 4). For a neighborhood (*w, r*), the LBP operator can be demonstrated as [18], [19]:

$$LBP_{w,r} = \sum_{i=0}^{w-1} S(X_i - X_c)2^i \tag{3}$$

$$S(e) = 1 \; if \; e \geq 0 \text{ otherwise } S(e) = 0$$

where w counts of the sampling window pixels in the circle, r indicates the radius of the circle, x_c indicates the central pixel value, and x_i indicates the neighboring pixel value i.
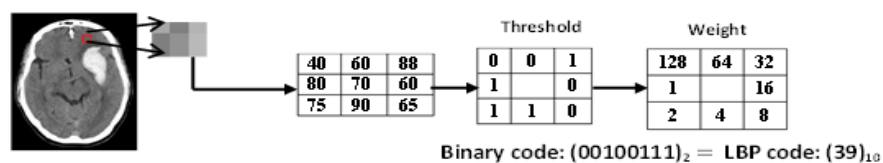

Figure 4. Example of LBP method

2.4.1. Uniform LBP

In numerous texture analysis applications, it is recommended to have features that are robust to the rotation of the input image. In order to improve and extract the texture encoding, Ojala *et al*. [17] proposed an extension to the original operator called uniform LBP patterns (ULBP). The uniformity of the LBP is an important concept to represent local primitive structural information such as edges and corners [20]. When the bit pattern is considered circular, a uniformity measure of a pattern counts the bitwise jumps from 0 to 1 and from 1 to 0. The uniform and rotation invariant $LBP_{w,r}^{riu2}$ operator is demonstrated as:

$$LBP_{w,r}^{riu2} = \sum_{i=0}^{w-1} S(X_i - X_c) \quad \text{if} \;\; U\big(LBP_{w,r}\big) \tag{4}$$

Otherwise

$$LBP_{w,r}^{riu2} = w + 1$$

where the *riu²* indicates the rotation invariant, A pattern is considered uniform if the number of jumps in the sequence is less than or equal to two ($U \leq 2$). For instance, the patterns 00000000 and 11111111 have 0 jumps, while the patterns 11100001 and 01100000 have 2 jumps (uniform patterns). Furthermore, the patterns 11011010 and 01100010 have 6 and 4 jumps respectively (non-uniform). All non-uniform patterns are considered as one pattern for the LBP^riu2. The total number of uniform patterns that encompass different output labels can be estimated as $w(w-1)+3$. The above encoding scheme produces fifty-eight different uniform patterns besides one extra pattern for the non-uniform case. Thus, the histogram of the uniform LBP encompasses fifty-nine bins [21].

2.5. Connected component labeling

The connected component encompasses a group of connected pixels that involve a common characteristic. The largest portion of the interconnected pixels is considered a connected component. To determine all the connected components or objects in a binary image, the following equation is implemented iteratively [22]:

$$T_n = (T_{n-1} \oplus S) \cap M, \quad n = 1,2,3, \ldots \tag{5}$$

where M is a test image that contains one or more connected components, and S is an appropriate structuring element. The iteration continues until $T_n=T_n\text{-}1$ and T_n encompass all the connected components of M.

The procedure is employed in our work to characterize the distinctive label of all separated objects in each binary image. A unique label is then given to all points that refer to the same object by creating a label matrix [23]. This is obtained by scanning all pixels in the binary image and characterizing all the connected portions. The obtained image will have two regions; the foreground object that is occupied by pixels with 1 value, and the background portion that is occupied by pixels with 0 value [20]. In many applications, not all the connected components are important. Some of the connected components are usually kept if their sizes are larger or equal to a pre-determined value (object of interest) [24]. The output of applying the connected component labelling on the MRI brain image is plotted in Figure 5. The original MRI image, its binary version, and the binary connected component labelling are displayed in Figure 5(a), (b), and (c) respectively. Five objects are only kept after applying the connected component labeling. In this example, objects with a size of less than 100 pixels are ignored. Table 1 illustrates each of the five objects and their size in pixels.
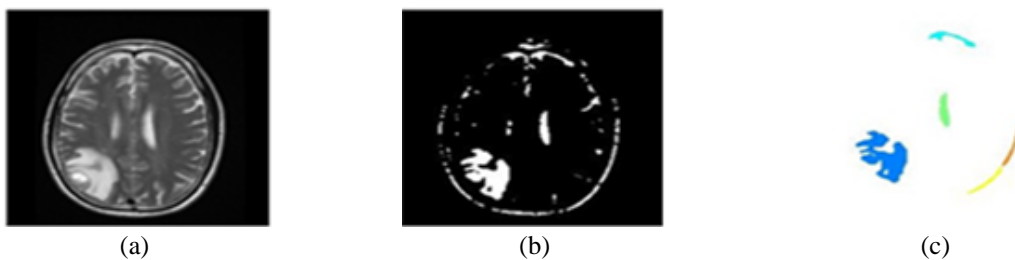

| (a) | (b) | (c) |

Figure 5. Example of the connected component labelling procedure, (a) original image, (b) binary image after applying K-means clustering, and (c) connected components labelling

Table 1. Objects size

Object No.	Size (pixel)
1	1012
2	143
3	190
4	101
5	100

3. EXPERIMENTS AND RESULTS

In this work, the detection of the tumor region in MRI images is estimated by implementing our proposed system using MATLAB programming language. The number of clusters is set to six. The adopted system has experimented on 30 brain MRI images using an axial view. The brain images are taken from the T1-weighted and T2-weighted MRI brain which are randomly selected from the database [25]. To estimate the performance of detection, the accuracy metric is employed, which illustrates the percentage rate of the number of detected tumor images to the total number of images in the database. Figure 6 illustrates an example of an MRI image (1st column), the results of clustering the image into 6 clusters (2nd column), and the results of splitting each clustered image into left and right sides (3rd and 4th column respectively) to estimate the asymmetry measure.
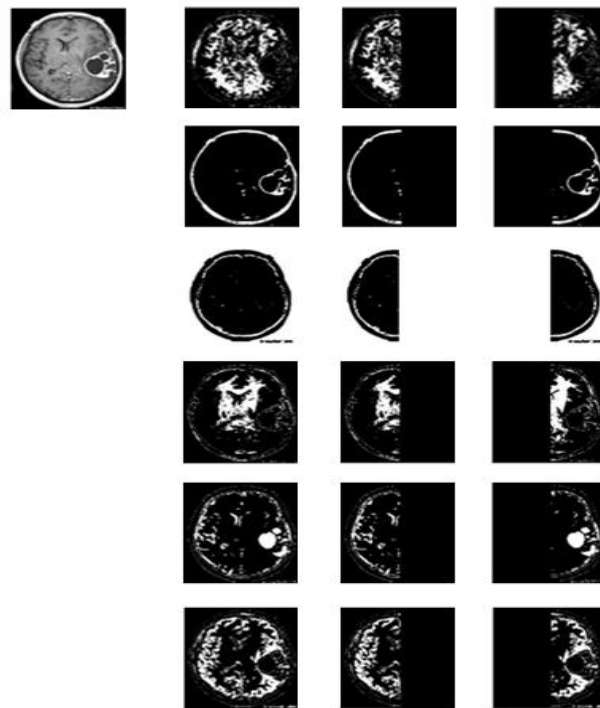

Figure 6. The results of partitioning each clustered image into left and right sides

Figure 7 illustrates the results of estimating the asymmetry measure for each cluster image to detect a brain tumor. The first column of Figure 7 indicates several MRI images of the brain slices. The 2nd to the 7th columns comprises the six clustered images and their estimated asymmetry measure value for each slice. The last (i.e. 8th) column includes the detected tumor regions after implementing the connected component labeling. In this work, the clustered image with the tumor region is identified with asymmetry values higher than 0.5 as indicated by the red tick.

After implementing our proposed system, we extract the statistical features by calculating the means (M) and standard deviation (STD) for each cluster image. Table 2 illustrates the measured values of the M and STD from the 2nd to the 7th column of the cluster images in Figure 7. According to the statistical features values, the cluster image with the white matter has the largest STD value as compared to other cluster images that have a tumor. The adopted system exhibits a high detection accuracy of 87%. More preprocessing and

postprocessing steps are necessary to improve detection accuracy and overcome the difficulty of rotation and translation variations in the original MRI images.
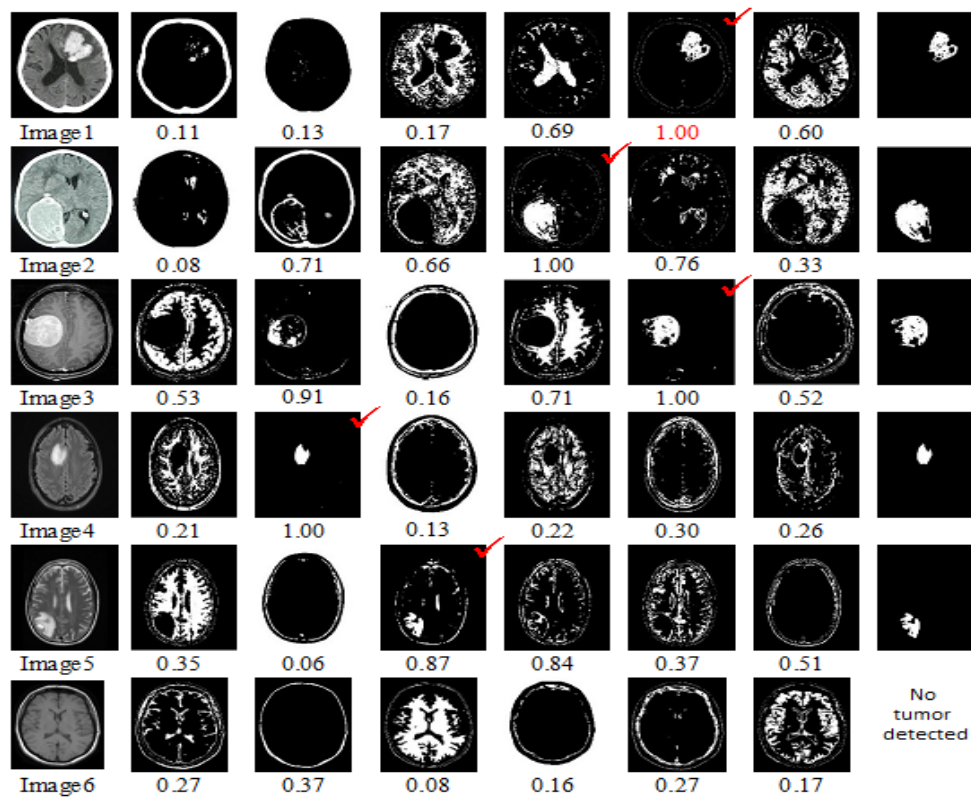

Figure 7. The tumor detection process for several MRI slice images. The 1st column indicates the original slice image, and the 2nd–7th columns indicate the clustered images. The 8th column indicates the detected tumor region

Table 2. The statical features values (means (M) and standard deviation (STD) of images in Figure 7

Features	Cluster1 M	STD	Cluster2 M	STD	Cluster3 M	STD	Cluster4 M	STD	Cluster5 M	STD	Cluster6 M	STD
Image1	0.13	0.33	0.37	0.48	0.19	0.39	0.09	0.28	0.04	0.21	0.18	0.39
Image2	0.32	0.47	0.12	0.33	0.18	0.4	0.1	0.29	0.03	0.19	0.25	0.41
Image3	0.22	0.38	0.04	0.18	0.43	0.49	0.18	0.37	0.05	0.29	0.07	0.24
Image4	0.06	0.35	0.02	0.13	0.56	0.5	0.1	0.34	0.07	0.26	0.06	0.24
Image5	0.22	0.39	0.56	0.49	0.05	0.19	0.05	0.24	0.08	0.32	0.04	0.19
Image6	0.09	0.36	0.04	0.13	0.3	0.47	0.34	0.48	0.07	0.27	0.16	0.38

4. CONCLUSION

In this paper, we proposed a new system for the automatic selection of the appropriate cluster image for the detection of brain tumors in MRI images. Several samples from the T1-weighted MRI brain axial slice images database are employed to estimate the performance of the adopted system. The K-means cluster algorithm and uniform local texture feature approach are employed to estimate the asymmetry values between the left and the right half of each clustered image. Consequently, the largest asymmetric value is employed as an indicator to select the appropriate cluster image. The results highlight that the texture features can be employed to differentiate the tissue between the left and right brain sides. The quality of the detection is highly influenced by the determination of the appropriate clustered image. The asymmetry value exhibits a high discriminatory power. Finally, the adopted system produces an encouraging detection accuracy.

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