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Automatic Brain Tumor Extraction for MRI-T1 and T2 using Geodesic Distance and Statistical Methods

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Abstract— In this paper, we present a new approach that allows the detection of brain tumors. The approach is based on mathematical methods such as correlation, covariance and geodesic distance. Before proceeding to the segmentation and automatic extraction, the detection of central indices of abnormal tissues is based on the method of correlation and covariance. From these indices, segmentation of brain tumor area using geodesic distance in T1 and T2 magnetic resonance images (MRI-T1 and T2). The ultimate objective is to retrieve the attributes of the tumor observed on the image; these attributes form a characterizing vector, which is used latter in the extraction and classification steps to get a better diagnosis.
The proposed method yielded fruitful results and has shown a better performance in the analysis of biomedical images of modality MRI-T1 and T2.

Keywords— Biomedical Images Processing, Detection, Segmentation, Correlation, Covariance, Geodesic Distance.

I. INTRODUCTION

Recently, the medical image analysis has boomed. Various approaches have been proposed to develop an image analysis system. Detection, segmentation and extracting abnormal areas in the image are the main objectives for a better diagnosis. The also offer new hope for treatment of many diseases.
There are several methods and techniques that allow the detection and segmentation of abnormal cells in the different modalities of medical imaging (MRI, Ultrasound, X-ray, etc). The proposed methods are used to:
- Obtain the desired information from biomedical images.
- Determine the existence and type of tumors.
- Develop automated systems.

Many efforts have been made to use mathematical models to detect and to segment automatically tumor cells and analyze a large amount of medical images [1] accurately and in an appropriate time. According [2], these approaches are based on the Riemannian manifold to segment glioma cells and tumor-growth. Recent studies have introduced two major types of segmentation; brain and brain tumor cells; automatic [3-4] and semi-automatic, [5] and [6] propose the algorithm based on Spatial accuracy-weighted Hidden Markov random field and Expectation maximization approach for both automated tumor and enhanced-tumor segmentation. Other approaches used to evaluate the MRI brain tumor segmentation methods include the use of modified gradient magnitude region growing, Level set and marker-controlled watershed [7].
The detection of the tumor is an essential preliminary step to solve the problems of segmentation, [8] use symmetric analysis for automatic detection of brain tumors. 2D continuous wavelet transform (CWT) is applied to reveal the characteristics of tissues in MR brain images, [9] use Zernike moments to segmentation, it is observed that different transforms are used to extract desired information from biomedical images. Image intensities at the neighboring pixels [10] are utilized to represent the tissues in magnetic resonance and computed tomography images. Wavelet transform [9, 11], co-occurrence matrix [12], Fourier transform [13], spatial gray-level dependence matrices [14] and Law's micro-texture energies [15] are used to extract tissues in ultrasound images.
The objective of this work is the detection, segmentation and contour extraction of MRI-T1 and T2 brain tumors in biomedical images.
It is meant to:
- Reduce the complexity of medical images
- Simplify the segmentation and classification
- Characterize the region of interest using statistical methods and Riemannian descriptors which represent powerful tools for extracting attributes that characterize a medical image, represented by a characteristic vector.

Many techniques have been proposed to automate the brain tumor detection and segmentation in recent Years. The proposed methods can be broadly classified into two types, intelligent based and non-intelligent based. The notable

intelligent based systems are artificial neural network [10,16], fuzzy c-means, support vector machine and hybrid methods. On the other hand, most notable non-intelligent methods include thresholding [17] and region growing [18].

Our work include 4 sections, section 1 based on the correlation to detect and extract indices of abnormal region, in section 2 we present the covariance method to obtain automatically the coordinates of abnormal area, these coordinates that will be used in Section 3 to segment and extract the tumor cells using the geodesic distance. Implementation details and obtained results are presented in section 4.

II. CORRELATION

Correlation is the basic operation that we will perform to extract information from images. It is in some sense the simplest operations that we can perform on an image, it can be analyzed and understood very well, and it is also easy to implement and can be computed very efficiently [19] .

We use related methods to find locations in an image that resemble a template. To do this, we think of a tumor as a texture template, we are sliding it around the image looking for a location where the template overlaps the image, so that values in the template are aligned with similar values in the image [20].

First we must decide how to measure the similarity between the model and the image area with which it is aligned; the correlation results are calculated by aligning the center of the filter to a pixel. Then we multiply all values that overlap, and add the result. It can be written as follow:

$$F°I(x,y) = \sum_{j=-w}^{w} \sum_{i=-h}^{h} F(i,j)I(x+i,y+j) \qquad (1)$$

Where $F\ (i,j)$ the template, $I\ (x,y)$ the image to be analyzed

w: width of the image,

h: height of the image.

This system detects only tumors that are stored in the database of tumors. Any other type of tumor can't be detected. Some traditional systems require both the image with the tumor and tumor-free image. The general principle is to compare the texture of the image with the texture of all tumors in our database of tumors (Fig. 1).

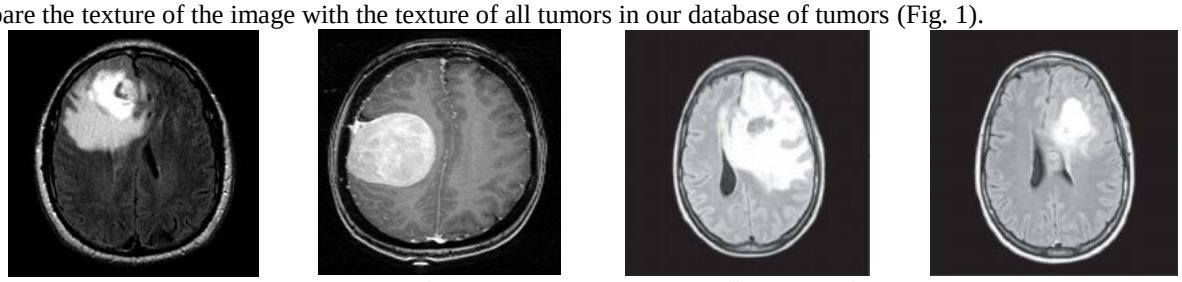


Fig. 1: MRI-T1 (left) and T2 images (right) contain different types of tumors.

The correlation is used to determine the center coordinates of tumors (Fig. 3), without any comparison with normal image following the process shown in Fig. 3. It gives good results if the texture of tumor that contains the image is already stored in database, which requires a large database of different textures.

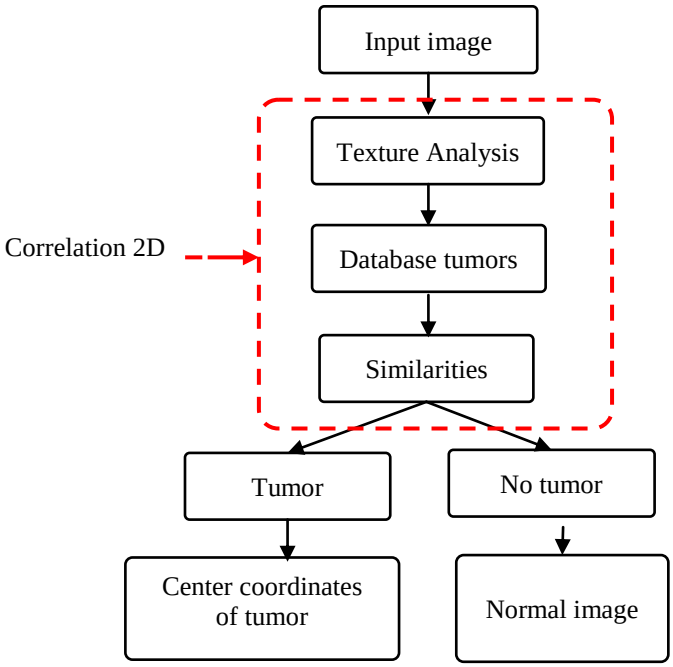


Fig. 2: Correlation steps.

Basically the images of tumor which are cropped are stored in the template folder. Then template matching algorithm is used to compare both the images and hence the tumor, if the tumor exist it can be detected. After performing template matching algorithm using correlation, tumor can be detected. If the tumor is present it will be indicated and gives the coordinates of its center, otherwise if the image would thus remain as it is.

Fig. 3: Correlation and coordinate detection of T1-MRI brain tumor region

This method has some limitations as it is sensitive to any kind of noise and change in size, thus we recommend that another method should be used to provide better results.

III. IMAGE COVARIANCE MATRIX

The medical image has more pixels and each pixel is correlated with its neighboring pixels. The covariance matrix obtained by the covariance pixel is very large and contains a lot of redundant information. Fig. 4 represents the histogram for the covariance matrix of a medical brain imaging modality MRI-T1.

The objective of using this method is to have the image histogram to automatically extract the area that contains the abnormality. Consider two variables x and y, given n observations on these two variables, the sample covariance between x and y is defined as follows [21]:

$$Cov(x,y) = \frac{1}{n}\sum_{i=0}^{n}(x_i - \bar{x}\,)\,(y_i - \bar{y}\,)^T \qquad (2)$$

Let us now consider an image M composed of a number n of pixels instead of a single pixel $M = \{V_1, V_2, \dots, V_n\}$

Where V_i are columns vectors of M and n is the total number of columns. V_i a is the covariance of the image M denoted C, because V_i a are vectors of the matrix M. Then the covariance C of M corresponds to sum of pixels in V_i a calculated as follows:

$$C = \frac{1}{n}\sum_{i=0}^{n}(V_i - M\,)\,(V_i - M\,)^T \qquad (3)$$

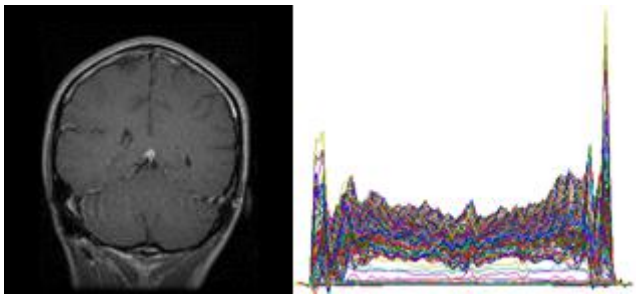


Fig. 4: Brain imaging modality MRI-T1 (left) and the representation of covariance histogram of all pixels in image M (right).

After determining the covariance C of normal image M, shown on (Fig. 4), we represent the histogram of the image that contains a tumor cells, using the same method (Fig. 5).

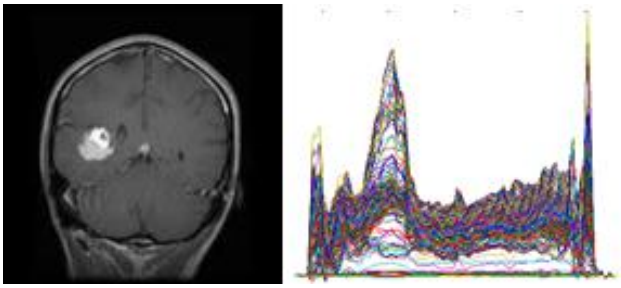


Fig. 5: MRI-T1 brain contain tumor (left) and its covariance histogram (right).

The presentation of the covariance histogram of brain image (Fig. 4 and Fig. 5) of all pixels has several redundant information, to solve this problem, the principal component analysis (PCA) is used for the histogram of MRI in order to differentiate the classes containing the image (Fig. 6).

A. *Image covariance-based PCA*

The image covariance matrix is represented as histogram of images. PCA is a statistical method based on covariance matrix to eliminate redundant information. The set of projection vectors W, which maximizes the determinant of the image covariance matrix C [21], is obtained as follow:

$$W = \arg\max(W^T C\, W) \quad (4)$$

Where W is the set of eigenvectors of C corresponding to the first largest eigenvalues. Next we proceed to represent the set of eigenvectors obtained by PCA as histogram covariance of brain image.

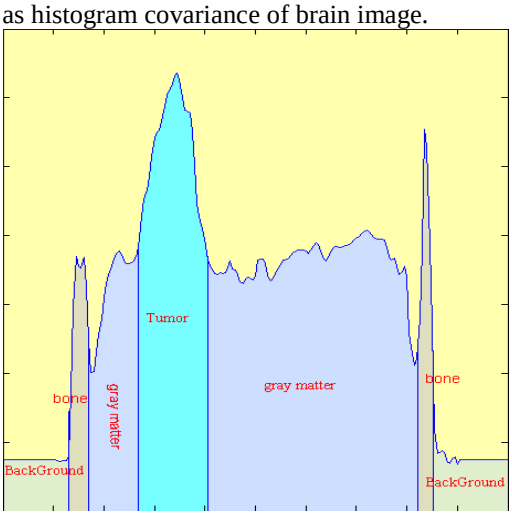


Fig. 6: Histogram and these classes by covariance.

B. *Brain tumor detection*

We then proceed to extract the brain tumor portion. For this we employ covariance matrix. The covariance histogram is based on matrix of brain image. First, we construct the vectors of image matrix that corresponds to brain regions. Next, we check the pixel values which are along to object and classify them into classes (Fig. 6). The classification of classes is done based on gray levels, the background is low, median include healthy tissues, and high contains edema and bone.

This approach applied at this stage to locate the region of brain tumor based on median gray levels (gray and white matter).

Tumor tissue of brain MRI-T1 are white gray levels, we are interested in the region that contains the white matter presented by the maximum of the histogram.

The objective of this method is to extract the coordinates of the region that represents the interests of our work (Fig. 7).

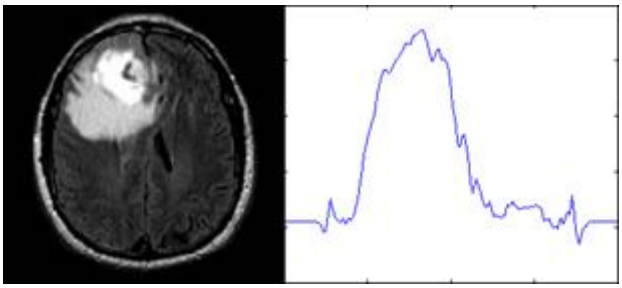


Fig. 7: Brain MRI Image (Left) And Histogram (Right).

The coordinates extracted by the histogram are the starting points of the geodesic distance that allows us to have a better automatic segmentation of tumor cells MRI-T1 and T2 images of the brain (Fig. 8).

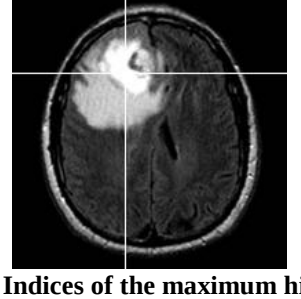


Figure 8: Indices of the maximum histogram.

Sometimes we find that the intensity of the bone is greater than that of tumors, allowing us to think of a method that segments the brain before going to the segmentation of tumors.
These two methods are the essential part of our work because they return the coordinates of the center of the region of interest and we will facilitate the step of segmentation using the geodesic distance.

IV. SEGMENTATION USING GEODESIC DISTANCE

Segmentation algorithm is based on the properties of gray level values of pixels. The different types of segmentation techniques are: (a) Edge based segmentation, (b) Threshold Based Segmentation, (c) Region Based Segmentation, (d) Clustering and (e) Matching.
Segmentation is the major step of biomedical image processing to prepare them for the classification step.
This paper outlines an efficient image segmentation technique that can distinguish the pathological tissues such as edema and tumor from the normal tissues such as White Matter (WM) and Grey Matter (GM) [2].

A. *Geodesic Distance*

x_s and x_e are two pixels in an image F That is modeled as a 2D function $F: \Omega \rightarrow \mathbb{R}$, where the image domain is usually $\Omega = [0,1]^2$. And $\gamma_{x,y}$ a path parameterized by [0,1] between these two pixels. The geodesic distance between x and y is defined by:

$$d(x,y) = \inf_{\gamma_{x,y}} \int_0^1 W\left(\gamma_{x,y}(P)\right) \left\| \gamma'_{x,y}(P) \right\| dp \qquad (5)$$

Where $\gamma'_{x,y} \in IR^2$ is the derivative of $\gamma_{x,y}(P)$, and W is the weight associated with each $\gamma_{x,y}(P)$. The use of geodesic distance is substantially defined by the W metric used. These geodesic distances can be evaluated by a Fast Marching algorithm [22].
Shortest paths are 2D curves that minimize a weighted length in a given metric $W(x)$ for $x \epsilon [0,1]^2$, the metric is usually computed from an input image F. The length of a curve $t \epsilon [0,1] \rightarrow \gamma(t) \epsilon [0,1]^2$ is

$$L(\gamma) = \int_0^1 W(\gamma(t)) \|\gamma'(t)\| dt \qquad (6)$$

Note that $L(\gamma)$ is invariant under re-parameterization of the curve γ. The geodesic curve between two points x and y has minimum length among curves joining the two points.
The process of segmentation is based on the geodesic distance using equation (6) a late predict what level up each pixel by selecting the minimum distance with the most intense regions and other less intense.

$$\min_{\gamma(0)=x;\gamma(1)=y} L(\gamma) \qquad (7)$$

A shortest curve thus tends to pass in areas where W is small. The geodesic distance between the two points is then $d(x,y) = L(\gamma)$ is the geodesic distance according to the metric W.
Finally, each pixel x is classified as a region of interest if $D_m < D_p$, where D_m is the area of less intense pixels and D_p the pixel domain is more intense.

B. *Pixel values-based Geodesic Metric*

The geodesic distance map $D(x) = d(x_0, x)$ to a fixed starting point x_0 is the unique viscosity solution of the Eikonal equation [20].

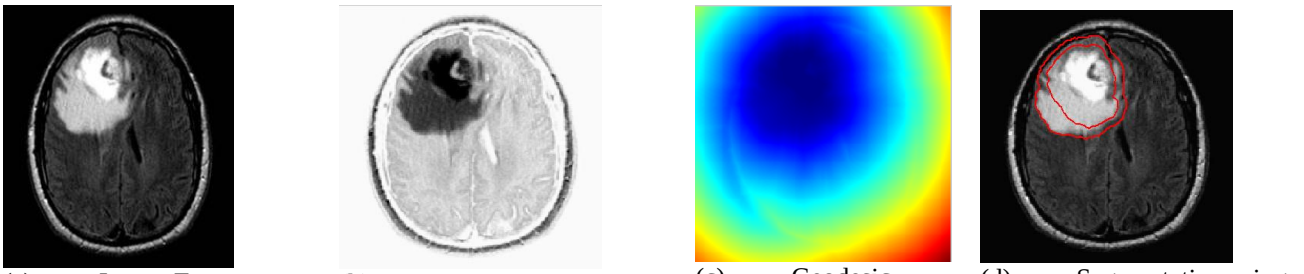
$$\|\nabla D(x)\| = W(x) \; et \; D(x_0) = 0 \qquad (8)$$

This equation can be solved numerically in $O(N\, log(N))$ operation on a discrete grid of N points. Given that tumor cells preferentially spread along nerve fibers, we propose the use of a geodesic distance on the Riemannian manifold of diffusion tensor brain to replace the Euclidean distance used in clinical practice and to correctly identify the margin of tumor invasion. These mathematical models results in a partial differential equation (PDE) of the first order which can be solved numerically in a stable and consistent. To compute the geodesic distance we use actual data from the diffusion-weighted imaging (DWI) [2].
The main idea of several methods is to assign an anisotropic distribution of gray matter and isotope diffusion of white matter with greater diffusion along the principal eigenvector of the diffusion tensor of water. We show the color of the distance map in areas where the front spread, and let black and white region where the front does not spread (Fig. 9 (c)).
Once the card geodesic distance $D(x)$ at x_0 starting point is calculated, the geodesic curve between any points x_1 and x_0 extracted by gradient descent.

$$\gamma'(t) = -\eta_t \, \nabla D\big(\gamma(t)\big) \qquad (9)$$

Where $\eta_t > 0$ controls the parameterization speed of the resulting curve. To obtain unit speed parameterization, one can use.

$$\eta_t = \left\| \nabla D\big(\gamma(t)\big) \right\|^{-1} \qquad (10)$$



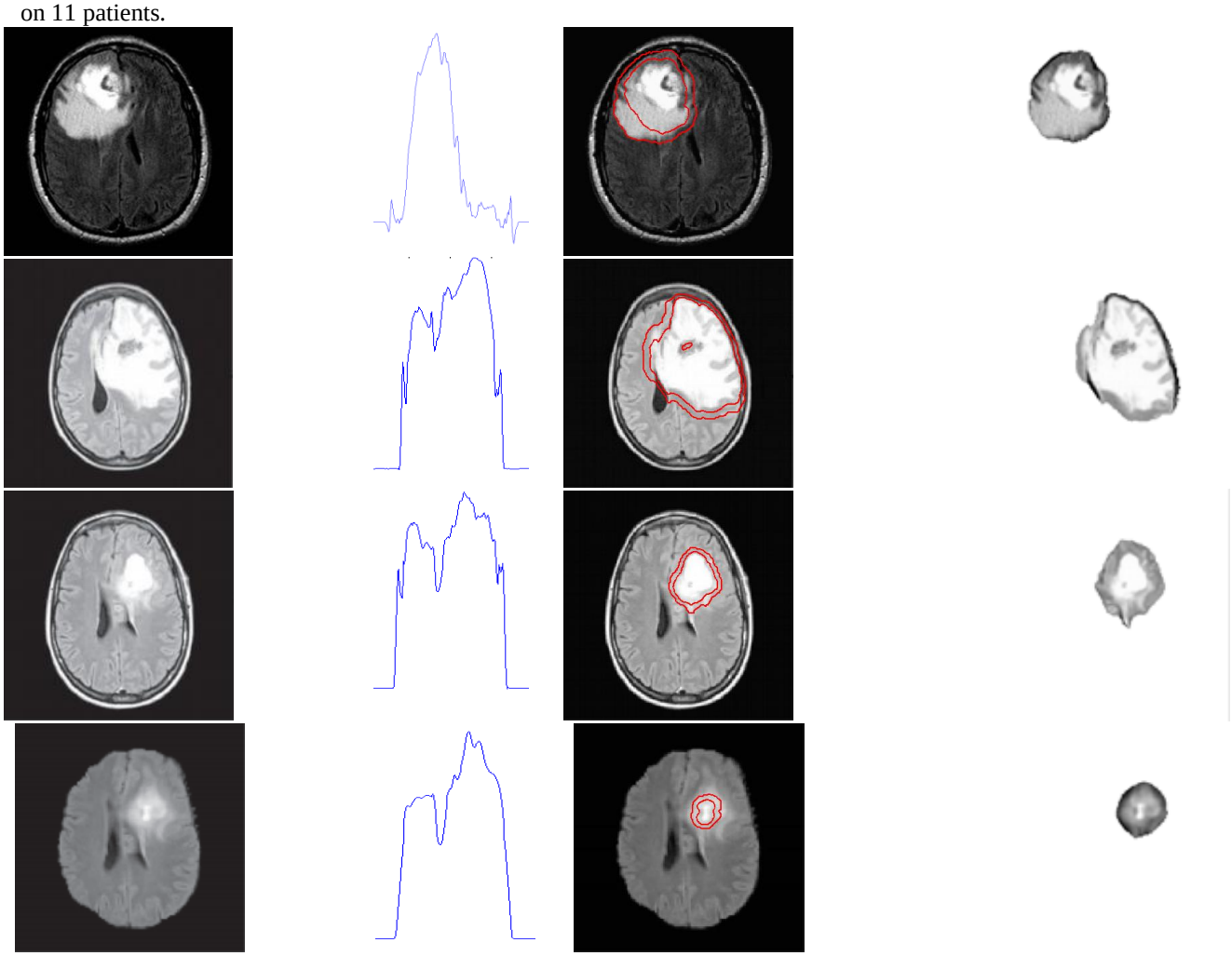
(a) Image F (b) Metric W (c) Geodesic curve (d) Segmentation using geodesic distance

Fig. 9: The results of the different phases to segment the tumor by geodesic distance: (a) test image, (b) calculating the Riemannian metric, (c) the geodesic curve color and (d) segmentation of the abnormal region of the image which represents the tumor tissue.

The curve is γ_t those edges of the geodesic balls of radius t, it can be calculated using the fast marching algorithm [21], and in fact γ_t can be approximated by the front which is the spread of fast marching during the iterations. As t increases, these balls are swollen and γ_t moves faster in the region where W is wide. We propose the use of this evolution to segment the tumor cells using the metric $W(x)$, which is low for pixels outside the region segmentation, and using the radius t chosen to match the size of region, this respect we can also recover automatically from the histogram. Fig. 4 shows the application of this method on an abnormal brain magnetic resonance image F.

V. RESULTS AND DISCUSSION

The segmentation is based on the calculation of geodesic distance from a tumor location automatically retrieved by the statistical methods used in the previous sections.The method of the geodesic distance to segment the tumor cells is a new method to be tested in real time and on a large number of images, on the other hand there are other methods based on comparison between the conventional methods which use a limited number of images. The validation of the method by [24] by monitoring the developments of tumor cells from the same person and [2] who made the validation of the method on 11 patients.



(a) (b) (c) (d)

Fig. 10: The results of 4 different MRI-T1 and T2 images: (a) test images, (b) covariance histogram for detection, (c) segmentation by the geodesic distance and (c) extracting the area of tumor cells accurately.

Since patients with cancer need immediate treatment, the strong point of this method can measure the tumor cells in real time which shows that it can be practiced clinically. This approach can be used to extract brain tumor of MRI-T1 and T2 in real time and in large dataset images.

VI. conclusion

In this paper, we proposed an automatic extraction and segmentation of MRI brain tumors, the task in this approach is to automatically detect the presence of tumors in MR images of the brain using mathematical methods, and segment the abnormal region from images using geodesic distance on the Riemannian manifolds of brains fibers. This method tested on several MRI-T1 and T2 proved that the use of geodesic distance could be having significant results.

The use of mathematic methods to locate automatically the abnormal region in brain MRI promises efficient and automatic results.

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