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Automatic detection and segmentation of brain tumor based on an adaptive mean shift over Riemannian manifolds

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Abstract:*In this paper, we propose a fully automated approach based on the mean shift algorithm over Riemannian manifolds,for the brain tumor detection and segmentation in magnetic resonance images (MRI). This approach based on the geometricmedian, geodesic distance. We propose the median shift to overcome the limitation of mean which is not necessary a point in aset. The geodesic distance can describe data points distributed on a manifold, compared to the Euclidean distance, and produceefficient results for image segmentation. Coupled with k-means algorithm, the proposed framework can cluster the brain image intotree regions (gray matter, white matter and cerebrospinal fluid). We applied this approach to clustering the brain tissue and braintumor segmentation, and validated on a synthetic MRI.*

Keywords: Mean shift, Geometric median, Riemannian manifolds, brain image segmentation, and Geodesic distance.

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1. Introduction

Brain Magnetic resonance (MR) imaging has a broad applicationin diagnosis and detection process of different brain related diseases.MR images are usually used to study and diagnoses ofbrain related diseases such as Alzheimer, multiple sclerosis, andso forth. Accurate detection and segmentation of disease regionshas a vital role to assist physicians in the diagnosis. Which allowsto avoiding several constraints such as time of diagnosis andinaccuracy results, to save the life of patients require urgent intervention.

In order to detecting and segmenting tissue abnormalities accurately,non-brain tissues must be removed in advanced. This taskis known as brain extraction or skull stripping, which is a preliminarystage in brain MR image analysis. Brain Extraction methodsusually consider to remove skull, scalp, and dura as non-brain regions[7].

The mean shift algorithm is a non-parametric algorithm whichhas been applied to many computer vision problems, such as dataclustering, feature analysis and image segmentation. However,many works have been developed this approach in this areas tohave a sufficient results. However, this approach have some limitations[13], ineffective in clustering data and poor results of clusteringand image segmentation [2, 13], because the use of the Euclideandistance. We propose to replace the Euclidean distanceby geodesic distance, by considering the data set as residing in aRiemannian manifolds.

In medical image analysis fields, it is crucial to conduct exact segmentationto extract high-level information from images. Therefore,separating interesting image components from their backgroundseffectively is a considerable problem. The classic segmentationmethods have limitations in application to medical images.

In this paper, we propose to applied an adaptive method that employsmean shift algorithm over Riemannian manifolds. We proposean better adaptation of the mean shift algorithm to detect andsegment, accurately, the region of interest in magnetic resonanceimages of brain. This improved adaptation is a combination ofmean shift with K-means to detect and cluster the brain tumorregions; the obtained results improve the homeogene of the bothmethods.

2. Related works

Mean shift clustering has been applied to generate the segmentationof color images. The challenge facing the mean shiftalgorithm (MSA) is the adaptive specification of the bandwidthsaccording to the data statistics in the image. Furthermore, theMSA is a well-known nonparametric and unsupervised clusteringalgorithm, which is, not assume a fixed number of clusters[13].

There have been proposed many methods, range from simpleones to more sophisticated and advanced ones, for brain tissuedetection, segmentation and brain extraction during past years.Among them, there are classification-based methods such as kmeans[8], mean shift algorithm [11], adaptive mean shift basedC means clustering algorithm [12] and many other methods basedon pixel classification [5, 4, 1].

Accurate analysis of magnetic resonance (MR) images remainsa challenge due to the complexity of structures such asintensity inhomogeneity. In brain MRI data analysis, precise detectionand segmentation of normal and abnormal tissues plays apivotal role for brain diagnostic.

There are many methods proposed for brain tumor detection andbrain MRI segmentation in the past decades [6].

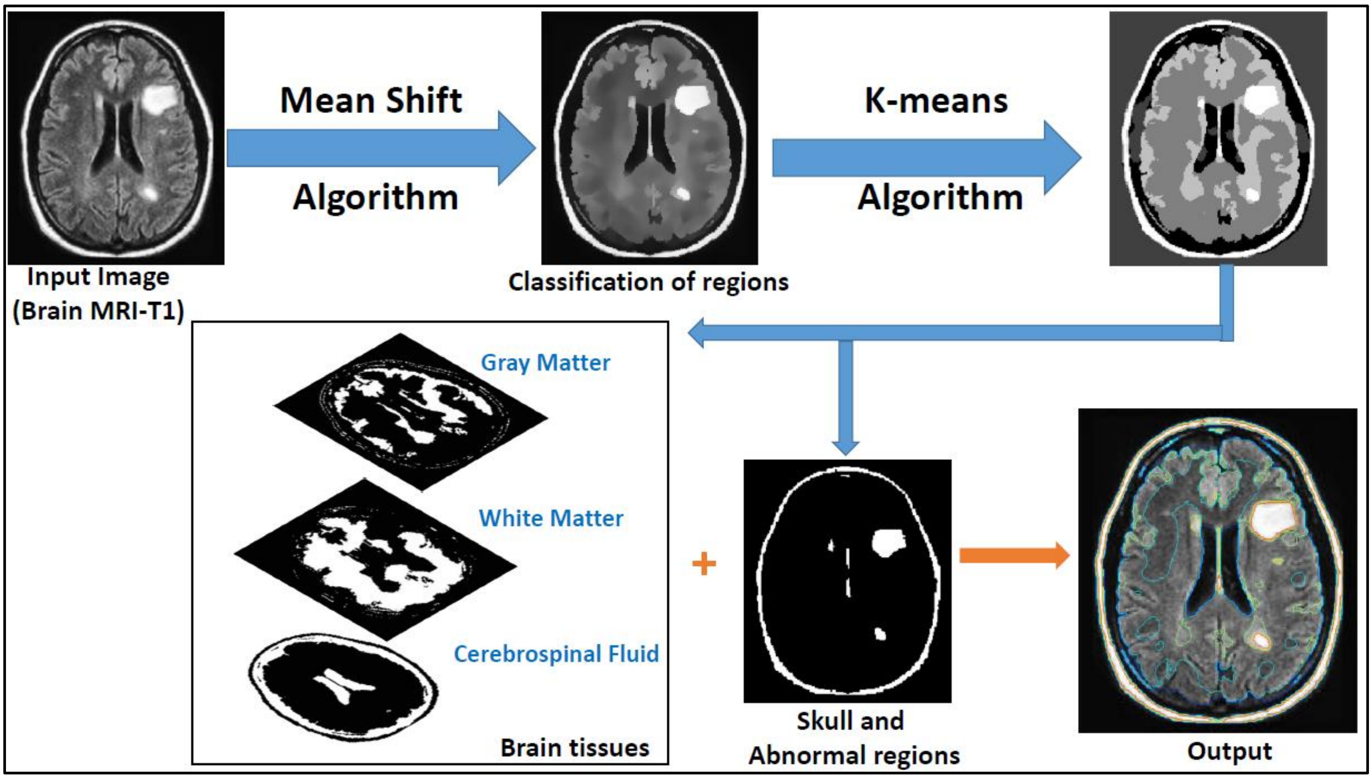

Figure 1.Overall flow of the proposed Method.

3. Preliminaries and Theory

In this section, we briefly introduce the basic theory of our method. In Section 3.1, we remained the basic mean shift and mean shift over Riemannian manifold. Then we present our contribution to detect and to segment brain tumour based on median shift algorithm in section 3.2.

3.1 Mean shift and median shift clustering

Mean shift procedure based on kernel density estimation, which is the most popular density estimation method [2]. Given a set of n points(x_i; i = 1; ...; n $\in R^d$)distributed on Euclidean space associated with a distance. The Parzen window Kernel density estimator can be estimated at point x [14]:

$$\hat{f}_k(x) = \frac{1}{n}\sum_{i=1}^{n}\frac{1}{h_i^d}k\left(\left\|\frac{x-x_i}{h_i}\right\|^2\right) \tag{1}$$

where function k is the profile of the spherically symmetric kernel K with bounded support, that satisfies, by taking the gradient of $\hat{f}_k(x)$ we obtain:

$$\nabla\hat{f}_k(x) = \frac{2}{n}\left[\sum_{i=1}^{n}\frac{1}{h_i^{d+2}}g\left(\left\|\frac{x-x_i}{h_i}\right\|^2\right)\right]\times \left[\frac{\sum_{i=1}^{n}\frac{x_i}{h_i^{d+2}}g\left(\left\|\frac{x-x_i}{h_i}\right\|^2\right)}{\sum_{i=1}^{n}\frac{x_i}{h_i^{d+2}}g\left(\left\|\frac{x-x_i}{h_i}\right\|^2\right)}-x\right] \tag{2}$$

where $g(x)=-k'(x)$ provided that the derivative of k exists. The second part of (1.2), factor in bracket, is the mean shift vector, which always points towards the direction of the greatest increase in density. The sequence of estimation points $\{y_t\}_{\{t=1,2,....,k\}}$ computed based on mean shift vector:

$$y_{t+1}=\frac{\sum_{i=1}^{n}\frac{x_i}{h_i^{d+2}}g\left(\left\|\frac{x-x_i}{h_i}\right\|^2\right)}{\sum_{i=1}^{n}\frac{x_i}{h_i^{d+2}}g\left(\left\|\frac{x-x_i}{h_i}\right\|^2\right)} \tag{3}$$

where y_1 is chosen as one of the points x_i, then y_t converges to is considered as the mode of y_1 to group the points with the same mode in the same cluster.

For data Clustering and image segmentation this algorithm produce,sometimes, poor results in clustering data with high dimensionalmanifolds in Euclidean space because the Euclidean distance[13], and a mean may not be a point in a data set. To remedythese limitations in data ClusteringWang et al in [13] propose theuse of median, which is a point in data set, and geodesic distanceto replace Euclidean distance in manifolds.

We extend the Riemannian manifolds and median shift approachesto perform the automatic detection and segmentation ofbrain tumor in MR images.

3.2 Geometric median over Riemannian manifolds

The geodesic distance for a pair of points (x, y) distributed on a Riemannian manifold denoted $d_g(x,y)$, is the minimum length of curves connecting them. Given a set of n points $(x_1, x_2, ..., x_n \in R^n)$ distributed on a manifold associated with a Riemannian distance $d_g(x,y)$, the geometric median, of a data set, defined as $\hat{y}$ by the following equation [13]:

$$\hat{y}=\arg\min_{y\in R^n}\sum_{i=1}^{n}d_g^2(x_i,y) \tag{4}$$

Based on (1), a novel objective function for geometric median shift over Riemannian manifolds is introduced. However, the geometric median of a number of points on manifolds is indeed a true point in a data set. Based on the kernel density estimate with profile k, bandwidth h, and geodesic distance $d_g(x,y)$ [13] define a novel kernel density-estimate function for the geometric median shift on Riemannian manifolds as:

$$\hat{f}_k(y)=\frac{C_{k,h}}{n}\sum_{i=1}^{n}k\left(\frac{d_g^2(x_i,y)}{h^2}\right)\varphi(y) \tag{5}$$

where h is a bandwidth, and $C_{k,h}$ ensures $\hat{f}_k(y)$ to be density and $k(.)$ is a flat kernel function satisfying:

$$k(x)=\begin{cases}1 & \text{if } \ 0<x<1\\ 0 & \text{otherwise}\end{cases}$$

$\varphi(y)$ is another kernel function related to the sum of squaredRiemannian geodesic distances from point y to other points distributedon the manifold calculated by

$$\varphi(y)=\sum_{i=1}^{n}\exp(-d_g^2(x_i,y))$$

Finally, the kernel function for geometric median shift over a Riemannainmanifold is:

$$\hat{f}_k(y)=\frac{C_{k,h}}{n}\sum_{i=1}^{n}k\left(\frac{d_g^2(x_i,y)}{h^2}\right)\exp(-d_g^2(x_i,y) \tag{6}$$

The gradient of this equation (6) is:

$$\nabla\hat{f}_k(y)=\frac{2}{n}\sum_{i=1}^{n}\left(g\left(\frac{d_g^2(x_i,y)}{h^2}\right)\frac{\log_y(x_i)}{h^2}\exp(-d_g^2(x_i,y))+\exp(-d_g^2(x_i,y))\log_y(x_i)k\left(\frac{d_g^2(x_i,y)}{h^2}\right)\right) \tag{7}$$

where $g(x)=-k'(x)$ and $k'(x)$ is a derivative function. We denote:

$$M(y,x_i)=\left(\frac{g\left(\frac{d_g^2(x_i,y)}{h^2}\right)}{h^2}+k\left(\frac{d_g^2(x_i,y)}{h^2}\right)\right)\exp(-d_g^2(x_i,y)) \tag{8}$$

According to Eqs. ((7) , (8)), we derive the geometric medianshiftvector in tangent spaces and the shifting point on a Riemannianmanifold, we obtain:

$$MG_h=\frac{\sum_{i=1}^{n}M(y,x_i)\log_y(x_i)}{\sum_{i=1}^{n}M(y,x_i)} \tag{9}$$

The Eq. (9) represent the geometric median over Riemannianmanifolds, computed using the algorithm described in [13].The simulation results of this method presented in the nextsection 4.

4. Experimental results

In this section, we present the performance of our approach quantitativelyand qualitatively to brain extraction, and we comparethe results with the most known approach and methods cited previouslyor used in state of the art.

Data sets

To evaluate the performance of our approach, we use the followingdata sets:

1. **BrainWeb**: contains the MRI volumes for normal brain.The parameter settings are fixed to 3 modalities (T1w, T2w,and PD), 5 slice thicknesses (1mm, 3mm, 5mm, 7mm,and9mm), 6 levels of noise (0%, 1%, 3%, 5% 7% and9%), and 3 levels of intensity non-uniformity (0%, 20%,and 40%). The discrete anatomical model applied to generatethe simulated brain MRI data was used as ground truthdata. The discrete anatomical and the simulated brainswere transformed to coronal and sagittal slices before startingthe experiments.
2. **MRI Multiple sclerosis Database (MRI MS DB):** Thirty-eightpatients (17 males, and 21 females), aged 34.1 ± 10.5 (mean age ± standard deviation), with a CIS of MS andMRI-detectable brain lesions were scanned twice at 1.5 Twith an interval of 6-12 months. The transverse MR imagesused for the analysis were obtained using a T2-weightedturbo spin echo pulse sequence (repetition time=4408 ms,echo time=100ms, echo spacing = 10.8 ms). The reconstructedimage had a slice thickness of 5 mm and a fieldof view of 230 mm with a pixel resolution of 2.226 pixels/mm. Standardized planning procedures were followedduring each MRI examination [10], [9].

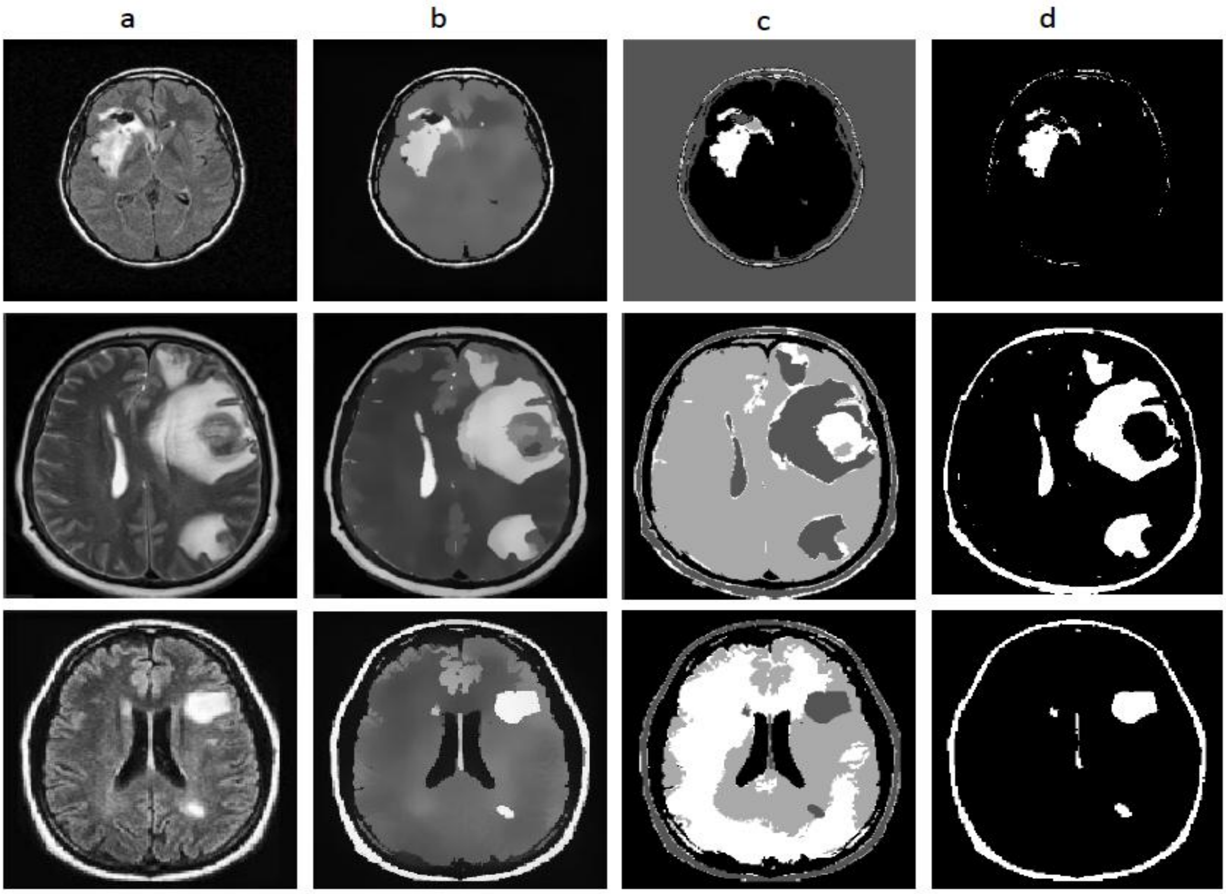

Figure 2.Segmentation steps of brain tumor of MR images. (a) Original image (b) filtered and smoothed image by geometric median,(c) regions labeled by cluster and (d) tumor regions.

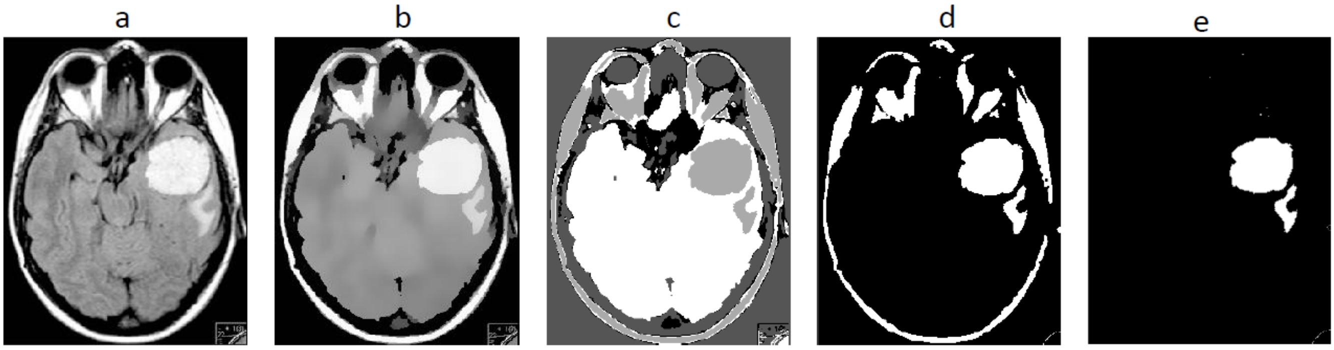

Figure 3.Segmentation results of coronal slice. (a) Original image, (b) filtered and smoothed image, (c) regions labeled by cluster, (d) skull and tumor regions and (e) extracted tumor region.

4.1.Qualitative evaluation

An example of detection and segmentation results of brain MRItumor presented by fig.2 for different modalities of brain MR images,T1-weighted and T2-weighted. The brain images presentdifferent level of noise and spatial intensity inhomogeneity forthe axial slice.

The approach shows it’s performance to labelled the regions byclusters, this allows an accurate segmentation of different regionsusing k-means algorithm. However, in (figure 2.b) the geometricmedian over Riemannian manifolds show good results of filteringand smoothing images. Then, we proceed to clustering differentregions of smoothing image (figure 2.c), the last step (figure2.d) is to separate the classified regions of brain tissues into graymatter (GM), white matter (WM), cerebrospinal fluid and abnormalitiesregions. We present in fig. 3, an example of coronal sliceof T2-weighted brain image, to evaluate the segmentation accuracyof proposed framework. The proposed method shown theefficient results to clustering brain region and to segment accuratelydifferent tissues WM, GM and CSF in a complex slice.

4.2. Quantitative evaluation

To validate the obtained results we use the Dice Similarity Coefficient(DSC)[3]. This measure indicate the amount of area overlapbetween the automatically detected and the manually delineatedbrain image. This measure calculated as follows:

$$DSC = \frac{2 \times TP}{2 \times TP + FP + FN} \qquad (10)$$

Where TP (True Positive) are the correct detections, FP (FalsePositive) are incorrect detections, and FN (False Negative) aremissing detections. The performance of our implementation isqualitatively shown in Fig.2.

Analyzing the results of the DSC, we obtained when using theT1-weighted brain MR images the better DSC (0:95%) thanwhen using T2-weighted (0:92%). This due to the complexityon T2-weighted image and high intensity inhomogeneity of tissues.

Comparing the DSC of different slice we obtained 0:98%for T1 axial slice, 0:94% for T2 axial slice.

5. Conclusion

We proposed an automatic detection and non-supervised segmentationof brain MRI tumor, the task in this method, is to automatically obtain an accuracy segmentation of tissues and check thepresence of abnormal regions in those images using Mean Shift tosmooth the images followed by K-means algorithm to cluster theregions of interest. This method applied to many images provedthat the use of this method gives better results and make it easy tocluster images after smoothing.

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