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AN AUTOMATED SEGMENTATION FRAMEWORK FOR BRAIN MRI VOLUMES BASED ON ADAPTIVE MEAN-SHIFT CLUSTERING

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ABSTRACT

Automated magnetic resonance imaging (MRI) segmentation systems classify brain voxels into one of three main tissue types: gray matter (Gm), white matter (Wm), and Cerebro-spinal fluid (Csf). In the existing methods segmentation was done based on the intensity value of the voxels. Local signal perturbations caused by additive noise and multiplicative bias-fields are responsible for cluster overlaps in the intensity feature space resulting in poor tissue-class separability. Hence an adaptive mean-shift methodology is utilized in order to classify brain voxels where the MRI image space is represented by a high-dimensional feature space that includes multimodal intensity features as well as spatial features. This proposed method clusters the joint spatial-intensity feature space, thus extracting a representative set of high-density points within the feature space, otherwise known as modes. Due to its nonparametric nature, adaptive mean-shift can deal successfully with nonconvex clusters and produce convergence modes that are better candidates for intensity based classification than the initial voxels.

1. INTRODUCTION

Image segmentation is one of the most important steps leading to the analysis of processed image data. The result of the image segmentation is a set of regions that collectively cover the image, or a set of contour extracted from the image. Each of the pixels in the region are similar with respect to some characteristics or computer property such as colour, intensity or texture.

MRI is primarily used in medical imaging to visualize the structure and function of the body. In our project an automated scheme for magnetic resonance imaging (MRI) Brain segmentation is proposed. An adaptive mean shift methodology is utilized in order to classify brain voxels into one of the three main tissue types: Gray matter, White matter, Cerebrospinal fluid.

2. EXISTING TECHNIQUES

Both supervised and unsupervised approaches have been used for this task.

2.1 Supervised Approach

In the supervised approach, intensity values of labeled voxel samples from each tissue (prototypes) must be provided during the learning phase. In a subsequent classification phase, unlabeled voxels are classified using a selected classifier. This method requires human interaction to select the prototypes and is therefore semi-automatic. To avoid re-training the classifier for each new scan, methods are required to normalize the intensity between MRI scans.

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2.1 Unsupervised approach

Unsupervised approaches often rely on a Gaussian approximation of the voxel intensity distribution for each tissue type. This is due to the Rican behavior of the noise present in the MRI intensity signal. In this technique, a Gaussian mixture model (GMM) is fitted to the voxels intensity using the expectation-maximization (EM) algorithm , following which every voxel is assigned to the tissue class for which it gives the highest probability.

Disadvantages

However, using intensity information alone has proven to be insufficient for a reliable automated segmentation of the brain tissues. Local signal perturbations caused by additive noise and multiplicative bias-fields, are responsible for cluster overlaps in the intensity feature space, resulting in poor tissue-class separability.

3. PROPOSED ALGORITHM

3.1 Adaptive mean shift algorithm

Our proposed algorithm is based on a variation of the mean-shift algorithm, termed the adaptive mean-shift algorithm. By assigning a distinct bandwidth to every data point, the adaptive mean-shift allows for increased sensitivity to local data structure even in a higher dimensional feature space corresponding to multimodal MRI.

Let,

$x_i \in \Re^d, i = 1, \ldots, n$, be the set of feature vectors in a -dimensional feature space. The density at point x can be estimated by the Parzen window Kernel density estimator

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

where function k, $0<=x<=1$, is called the profile of the spherically symmetric kernel K with bounded support, that satisfies

$$K(x) = c_{k,d}k\left(\|x\|^2\right) > 0 \quad \|X\| \le 1 \quad (2)$$

$C_{k,d}$ is a normalization constant that makes $K(x)$ integrate to one. In (1), h_i >0 is called the kernel bandwidth or window size, and determines the range of influence of the kernel located x_i. In this work, the following kernel is used

$$K(x) = \begin{cases} \frac{1}{2}c_d^{-1}(d+2)(1-x^Tx), & \text{if } x^Tx < 1 \\ 0, & \text{otherwise} \end{cases} \quad (3)$$

which is the Epanechnikov kernel that minimizes the mean integrated square error (MISE) between the underlying probability density function of the data and the kernel density estimation. Provided that the $k'(x)$ derivative of $k(x)$ exists, the function $g(x) = -k'(x)$ can be defined with the associated kernel

$$G(x) = c_{g,d}\, g(\|x\|^2)$$

It can be shown that taking the gradient of (1) leads to the following expression

$$C\frac{\nabla\hat{f}_K(x)}{\hat{f}_G(x)} = \frac{\sum_{i=1}^{n}\frac{1}{h_i^{d+2}}x_i g\left(\left\|\frac{x-x_i}{h_i}\right\|^2\right)}{\sum_{i=1}^{n}\frac{1}{h_i^{d+2}}g\left(\left\|\frac{x-x_i}{h_i}\right\|^2\right)} - x \quad (4)$$

Where C is a positive constant and the right-hand side is the mean-shift vector. From (4) we see that the mean-shift vector is proportional to the normalized gradient of the density estimate computed for kernel K. Starting from point $x^{(j)}$ in feature space, moves the mean-shift vector to a point $x^{(j+1)}$ that lies in a higher density region than $x^{(j)}$, computed as follows

$$x^{(j+1)} = \frac{\sum_{i=1}^{n}\frac{1}{h_i^{d+2}}x_i g\left(\left\|\frac{x^{(j)}-x_i}{h_i}\right\|^2\right)}{\sum_{i=1}^{n}\frac{1}{h_i^{d+2}}g\left(\left\|\frac{x^{(j)}-x_i}{h_i}\right\|^2\right)}. \quad (5)$$

From (4) that the mean-shift vector length is modulated by the inverse of the

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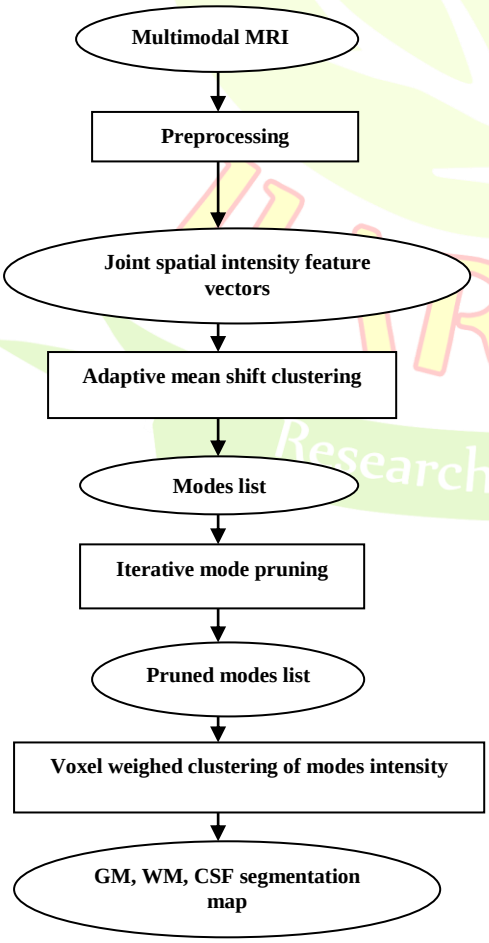
kernel density estimation with kernel G. Therefore, as we move towards higher density regions along the mean-shift vector, its length gradually decreases. By repeating iteratively for j=1, 2…., we progressively climb to the nearest stationary point of the probability density function which is usually also one of its local maxima or "modes."

Adaptive mean-shift (AMS) clustering has been shown to produce better results than the fixed bandwidth algorithm especially in high dimensional feature spaces. Many methods exist to determine an adaptive window size for the AMS algorithm .A simple method is to define the window size as the distance, *hi*, between x_i and its *k* -nearest neighbor xi, k

$$h_i = \|x_i - x_{i,k}\|. \quad (6)$$

4. ALGORITHM



4.1 ALGORITHM DESCRIPTION

4.1.1 Step 1:Preprocessing

The adaptive mean-shift algorithm (AMS) is utilized to analyze multimodal MRI data and provide segmentation maps of the three main tissue type's Gray matter, White matter and cerebro spinal fluid. One to four MRI modalities are available per segmentation task. Standard preprocessing steps include: Brain parenchyma extraction using the brain extraction tool (BET). The obtained brain masks were visually inspected and corrected for outliers when needed. When a binary mask was available from the dataset, it was used instead of applying BET. Christo Ananth et al. [3] discussed about Vision based Path Planning and Tracking control using Mobile Robot. This paper proposes a novel methodology for autonomous mobile robot navigation utilizing the concept of tracking control. Vision-based path planning and subsequent tracking are performed by utilizing proposed stable adaptive state feedback fuzzy tracking controllers designed using the Lyapunov theory and particle-swarm-optimization (PSO)-based hybrid approaches. The objective is to design two self-adaptive fuzzy controllers, for x-direction and y-direction movements, optimizing both its structures and free parameters, such that the designed controllers can guarantee desired stability and, simultaneously, can provide satisfactory tracking performance for the vision-based navigation of mobile robot. The design methodology for the controllers simultaneously utilizes the global search capability of PSO and Lyapunovtheory-based local search method, thus providing a high degree of automation. Two different variants of hybrid approaches have been employed in this work. The proposed schemes have been implemented in both simulation and experimentations with a real robot, and the

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results demonstrate the usefulness of the proposed concept.

4.1.2 Step 2: Extraction of feature vectors

Following the initial data processing, feature-vectors are extracted per input voxel. Intensity as well as spatial features (voxel coordinates) is used, for an overall dimensionality of 3+n, where n is the number of input intensity channels (modalities). The set of feature-vectors is input to the adaptive mean-shift clustering stage of the framework. The feature vectors used as the inout are:

The normalized color rgb

r = R/(R+G+B)

g = G/(R+G+B)

The opponent colour space

O_1 (R, G, B) =(R-G)/2

O_2 (R,G, B) = (2B-R-G)/4

The hue

$$\theta = \arctan\left(\frac{\sqrt{3}(G-B)}{(R-G)+(R-B)}\right) \quad (7)$$

The uncertainity of normalised coordinates

$$\sigma_r = \sqrt{\frac{R^2(\sigma_B^2+\sigma_G^2)+(G+B)^2\sigma_R^2}{(R+G+B)^4}}$$
$$\sigma_g = \sqrt{\frac{G^2(\sigma_B^2+\sigma_R^2)+(R+B)^2\sigma_G^2}{(R+G+B)^4}}. \quad (8)$$

The uncertainty of o_1 and o_2

$$\sigma_{o_1} = \frac{1}{2}\sqrt{\sigma_G^2+\sigma_R^2}$$
$$\sigma_{o_2} = \frac{1}{4}\sqrt{4\sigma_B^2+\sigma_G^2+\sigma_R^2}, \quad (9)$$

The uncertainty of hue

$$\sigma_\theta = \sqrt{\frac{3}{4}\frac{(B-G)^2\sigma_R^2+(B-R)^2\sigma_G^2+(R-G)^2\sigma_B^2}{(R^2+G^2+B^2-RG-RB-GB)^2}}, \quad (10)$$

4.1.3 Step 3: Adaptive mean shift clustering

The process starts by clustering the input feature vectors, which represent the multimodal MRI brain data using the AMS algorithm. The feature vectors used in this project are normalized colour, opponent colour space, and hue, uncertainity of normalized colour coordinates, uncertainity of hue and uncertainity of opponent colour space. A bandwidth value, h_i is associated with each feature vector x_i , using ,

$$h_i = \|x_i - x_{i,k}\|_{L1} \quad (11)$$

Where h_i is taken as the *L1* distance between x_i and its *k*-nearest neighbor. A constant value of K=4 is used .The adaptive mean-shift clustering is initiated from each feature point x_i using the above expression, and the convergence points are saved. An internal representation of 16 bits is used; thus, convergence points that result in the same number at working precision are assigned to the same mode. At this stage, each feature vector bears the label of its convergence mode, or cluster. Each mode obtained by the clustering process expresses the local structure of the data in a given region of the feature space. It should be emphasized that modes define clusters of arbitrary shape, without any convexity constraints. The number of obtained modes is an output of the mean-shift algorithm. It depends on the window sizes, as well as the data considered. In this project the initial voxels is reduced into eight modes.

4.1.4 Step 4: Iterative mode pruning

The number of modes is a large compression of the initial data but it is still much larger than the targeted number of classes. A mode pruning step is therefore required. In fact, we have used the nonparametric adaptive mean-shift for clustering in the joint spatial-intensity feature space as the clusters are inherently nonconvex.

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For the pruning of the modes however an intensity-only feature space for which clusters can be conveniently approximated as convex, enabling the use of parametric models (i.e., multivariate Gaussians). For this purpose, a pruning mechanism is added as follows. A fixed-radius window is shifted across the intensity feature space (ignoring spatial features), centered on each mode. Modes that co-exist within the window are merged. Mahalanobis distance is utilized for the distance computation. For the computation of the Mahalanobis distance, a covariance matrix is computed per mode from the intensity values of its corresponding voxels. As each mode has a distinctive $(N*N)^2$ covariance matrix, the Mahalanobis distance is usually not symmetric. Therefore, for two intensity vectors, I_m and I_n , representing the intensity components for two convergence modes, m and n , respectively, m and n are merged if

$$\min\left(MD(I_m, I_n), MD(I_n, I_m)\right) < R \quad (12)$$

Where MD (I_m, In) is the Mahalanobis distance between vectors I_m and I_n, and Ris the window radius. The process is repeated iteratively with an increasing window radius R, and updated covariance matrices (for the merged modes). Empirically, the initial window size, as well as its increment between iterations, is set to 1. In theory, the pruning process could proceed until the number of pruned modes reaches the number of desired classes. In practice, as pruning proceeds, merged modes represent voxel sets with growing intensity spread. In the multimodal case, the variances of the modes for each intensity channel are extracted from the covariance matrices and tested for the same threshold.

It was chosen empirically as it is still small enough with regards to the standard deviation of Gm, Wm, Csf intensity signals in real MRI data, but large enough to allow for a significant intensity pruning.

4.1.5 Step 5: Voxel-weighted Clustering of Modes Intensity

The remaining modes are assigned to the three desired tissue classes by clustering their intensity values using the K–means clustering algorithm (*K=3).* Each mode may represent a different number of voxels. To account for this fact, the standard *K*-means updating step for each centroid, M_i *(i=1….3)*, is replaced by a weighted mean

$$M_i = \sum_{\forall m \in i} w_m \cdot I_m \quad (13)$$

where the intensity vector I_m, for each mode *m* assigned to class *I* , is weighted by w_m , the relative portion of the total number of voxels it represents. The resulting procedure is termed "voxelweighted" *K*-means. A correspondence between the three extracted clusters and the three tissue types is obtained by using prior knowledge on tissue intensity ordering in MRI modalities. For example, in Pd-weighted images Wm, Gm, and Csf correspond to the darkest, less-dark and brightest clusters, respectively. Based on the defined correspondence, each mode and its associated voxels is assigned to a tissue, thus producing the final segmentation map. The underlying idea of this second merging step is that by acting in the joint spatial-intensity domain mean-shift brings together many voxels with potentially significant intensity variations into a few modes that are located in high-density regions of the feature-space, close to cluster centers. Mode intensities can be seen as "filtered" values for the original voxels and are less contaminated by outliers. Therefore, modes can now be classified using intensity information alone. Christo Ananth et al. [4] discussed about a model, a new model is designed

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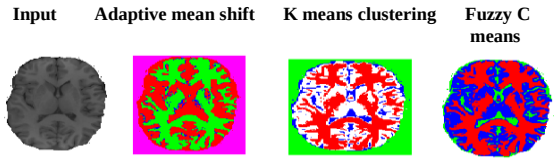
for boundary detection and applied it to object segmentation problem in medical images. Our edge following technique incorporates a vector image model and the edge map information. The proposed technique was applied to detect the object boundaries in several types of noisy images where the ill-defined edges were encountered. The proposed techniques performances on object segmentation and computation time were evaluated by comparing with the popular methods, i.e., the ACM, GVF snake models. Several synthetic noisy images were created and tested. The method is successfully tested in different types of medical images including aortas in cardiovascular MR images, and heart in CT images.

5. SOFTWARE DESCRIPTION

MATLAB is an integrated technical computing environment that combines numeric computation, advanced graphics and visualization, and a high-level programming language. MATLAB is an ambitious program. It contains hundreds of commands to do mathematics. One can use it to graph functions, solve equations, perform statistical tests, and do much more. It is a high-level programming language that can communicate with its cousins, *e.g.*, FORTRAN and C. we can produce sound and animate graphics. We can do simulations and modeling.

6. OUTPUT

6.1 Segmentation results for various inputs



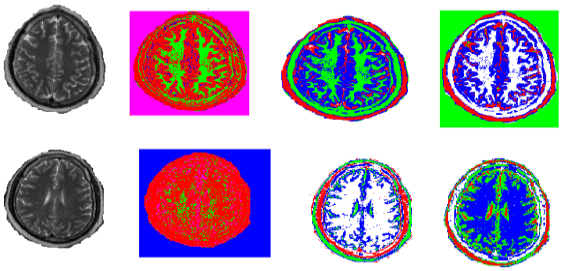
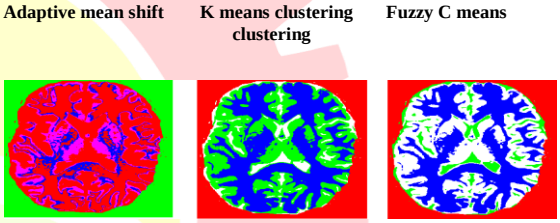


Fig 3: Segmentation results for various inputs

6.2 Bandwidth selection results

Bandwidth = 6



Bandwidth = 9

Bandwidth = 10.5

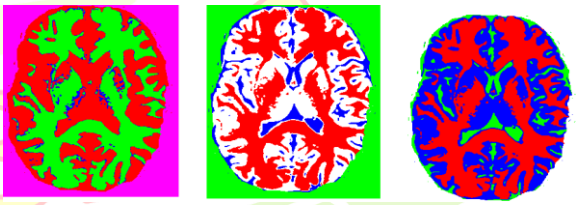


Fig 4: Bandwidth selection results

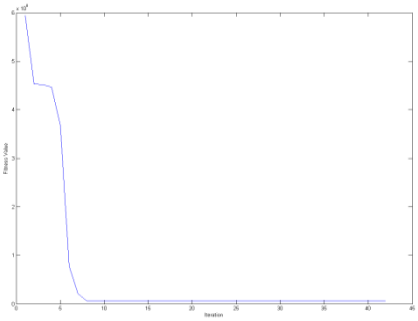


Fig 6: fitness value Vs iteration

7. CONCLUSION

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An automated segmentation framework for brain MRI volumes based on adaptive mean-shift clustering in the joint spatial and intensity feature space is presented. Mean shift algorithm alone cannot produce better result. So in this project along with mean shift K means or fuzzy C means are used in order to improve the segmentation results. The advantage over intensity based schemes has been shown in the output. Moreover, by using the adaptive mean-shift instead of the constant bandwidth algorithm, we ensure an appropriate bandwidth value for each feature point without requiring per-dataset manual tuning.

8. FUTURE WORK

The current bandwidth selection algorithm based on the k–nearest neighbor makes no use of application specific information. Edge information, for instance, could help define the region of influence of a kernel by a given point since edges generally delimit regions corresponding to different tissue types. The proposed framework will be extended to incorporate the detection of abnormal tissues such as sclerotic lesions and tumors.

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