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FCM Algorithm for Medical Image Segmentation Using HMRF

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Abstract

Clustering of data is a method by which large sets of data are grouped into clusters of smaller sets of similar data. Fuzzy c-means (FCM) clustering algorithm is one of the most commonly used unsupervised clustering technique in the field of medical imaging. Medical image segmentation refers to the segmentation of known anatomic structures from medical images. Fuzzy C-means (FCM) is a method of clustering which allows one piece of data to belong to two or more clusters. Fuzzy logic is a multi-valued logic derived from fuzzy set theory. FCM is popularly used for soft segmentations like brain tissue model. And also FCM can provide better results than other clustering algorithms like KM, EM, and KNN. In this paper we presented the medical image segmentation techniques based on HMRF- FCM algorithm.

Keywords: FCM, Segmentation, Silhouette, Spatial FCM, HMRF model.

Introduction

The Fuzzy C-Means algorithm is an unsupervised fuzzy clustering algorithm. Conventional clustering algorithm finds “hard partition” of a given dataset based on certain criteria that evaluate the goodness of partition. By “hard partition” we mean that each datum belong to exactly one cluster of the partition. While the soft clustering algorithm finds “soft partition” of a given dataset. In “soft partition” datum can partially belong to multiple clusters. A soft partition is not necessarily a fuzzy partition, since the input space can be larger than the dataset. However, most soft clustering algorithms do generate a soft partition that also forms fuzzy partition. A type of soft clustering of special interest is one that ensures membership degree of point x in all clusters adding up to one, i.e.

$$\sum_j \mu_{c_j}(x_i) = 1 \quad \forall x_i \in X \quad \dots\dots\dots (1)$$

A soft partition that satisfies this additional condition is called a constrained soft partition. The Fuzzy C-Means algorithm, which is best known fuzzy clustering algorithm, produces constrained soft partition. In order to produce constrained soft partition, the objective function J1 of hard c means has been extended in two ways:

(1) The fuzzy membership degree in cluster has been incorporated in the formula.

(2) An additional parameter m has been introduced as a weight exponent in fuzzy membership. The extended objective function, denoted by Jm, is:

$$J_m(P, V) = \sum_{i=1}^k \sum_{x_i \in X} (\mu_{C_i}(x_i))^m \|x_i - v_i\|^2 \quad \dots\dots\dots (2)$$

where P is fuzzy partition of dataset X formed by C1, C2,, Ck and k is number of clusters. The parameter m is weight that determines the degree to which partial members of cluster affect the clustering result. Like hard c-means, fuzzy c-means also tries to find good partition by searching for prototype vi that minimizes the objective function Jm. Unlike hard c-means, however, the fuzzy c-means algorithm also needs to search for membership function μci that minimizes Jm. A constrained fuzzy partition {C1, C2,, Ck } can be local minimum of the objective function Jm only if the following conditions are satisfied:

$$\mu_{c_i}(x) = \frac{1}{\sum_{j=1}^k \left(\frac{\|x - v_i\|^2}{\|x - v_j\|^2} \right)^{\frac{1}{m-1}}} \quad \dots\dots\dots (3)$$

$$1 \leq i \leq k, x \in X$$

$$v_i = \frac{\sum_{x \in X} \mu_{c_i}(x)^m x}{\sum_{x \in X} \mu_{c_i}(x)^m} \quad 1 \leq i \leq k \quad \dots\dots\dots (4)$$

Few important points regarding the FCM algorithm:

- It guarantees converge for $m > 1$.
- It finds local minimum of the objective function J_m .

The result of applying FCM to a given dataset depends not only upon the choice of parameter m and c , but also on the choice of initial prototype.

Medical Image Segmentation

Segmentation of images holds an important position in the area of image processing. It becomes more important while typically dealing with medical images where pre-surgery and post surgery decisions are required for the purpose of initiating and speeding up the recovery process. Computer aided detection of abnormal growth of tissues is primarily motivated by the necessity of achieving maximum possible accuracy. Manual segmentation of these abnormal tissues cannot be compared with modern day's high speed computing machines which enable us to visually observe the volume and location of unwanted tissues. Medical imaging types mostly are ultrasound images; X-ray computed tomography, digital mammography, magnetic resonance image (MRI), and so on. MRI images have good contrast in compare to computerized tomography (CT) is shown in Figure1. Therefore, most of researches in medical image processing use MRI images. A well known segmentation problem within MRI is the task of labelling voxels according to their tissue type which include White Matter (WM), Grey Matter (GM), Cerebrospinal Fluid (CSF) and sometimes pathological tissues like tumour etc.

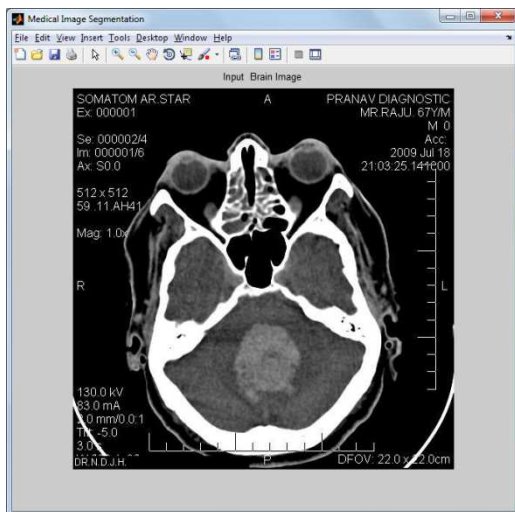


Fig 1: MRI Brain Image

Various Segmentation Methods

A) Segmentation by Thresholding

Thresholding method is frequently used for image segmentation. This is simple and effective segmentation method for images with different intensities. The technique basically attempts for finding a threshold value, which enables the classification of pixels into different categories. A major weakness of this segmentation mode is that: it generates only two classes. Therefore, this method fails to deal with multichannel images. Besides, it also ignores the spatial characteristics due to which an image becomes noise sensitive and undergoes intensity in-homogeneity problem, which are expected to be found in MRI. Both these features create the possibility for corrupting the histogram of the image. For overcoming these problems various versions of thresholding technique have been introduced that segments medical images by using the information based on local intensities and connectivity. Though this is a simple technique, still there are some factors that can complicate the thresholding operation, for example, nonstationary and correlated noise, ambient illumination, busyness of gray levels within the object and its background, inadequate contrast, and object size not commensurate with the scene. In some methods, the objective function is constructed using the divergence function between the classes, the object and the background. The required threshold is found where this divergence function shows a global minimum. The segmented output of MRI brain image is shown in Figure 2

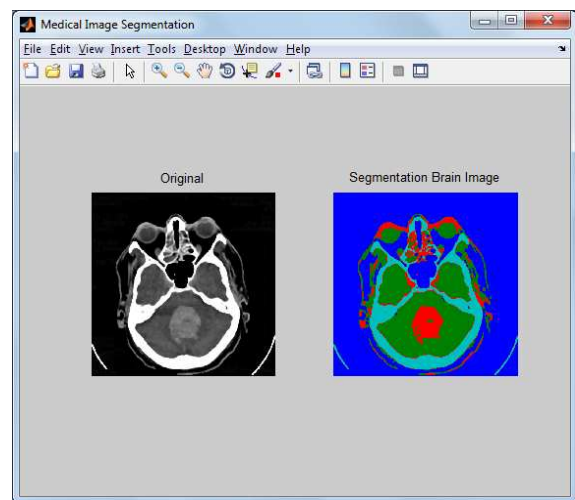


Fig 2: MRI Brain segmentation Image

B) Region Growing Method

Due to high reliability and accurate measurement of the dimensions and location of tumour, MRI is frequently used for observing brain pathologies. Previously, region growing and shape based methods were heavily relied upon for observing the brain

pathologies. Baye's based region growing algorithm that estimates parameters by studying characteristics in local regions and constructs the Bayes factor as a classifying criterion is shown in Figure 3. The technique is not fully automatic, i.e. it requires user interaction for the selection of a seed and secondly the method fails in producing acceptable results in a natural image. It only works in homogeneous areas. Since this technique is noise sensitive, therefore, the extracted regions might have holes or even some discontinuities. Shape based method provides an alternative approach for the segmentation of brain tumour. But the degree of freedom for application of this method is limited too. The algorithm demands an initial contour plan for extracting the region of interest. Therefore, like region growing approach, this method is also semi automatic. Both of these methods are error sensitive because, an improper or false description of initial plan and wrong selection of the seed image will lead to disastrous results. Statistical methods and fuzzy logic approaches seems to be reliable and are the best candidates for the replacement of the above mentioned techniques.

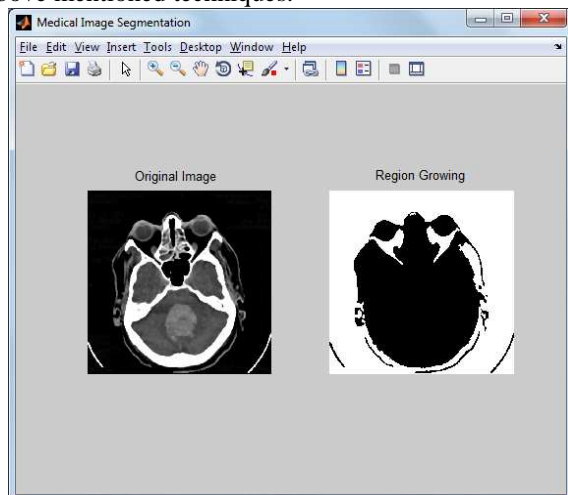


Fig 3: MRI Brain Segmentation output Image using Region Growing Method

C) Supervised and Un-Supervised Segmentation Methods

Supervised and un-supervised methods for image processing are frequently applied. Segmentation of volume using KNN and both hard and fuzzy c-means clustering methods results that there appears to be enough data non-uniformity between slices to prevent satisfactory segmentation. Supervised classification enables us to have sufficient known pixels to generate representative parameters for each class of interest. In an un-supervised classification pre hand knowledge of classes is not required. It usually employees some clustering algorithm for classifying an image data. KNN,

ML and Parzen window classifiers are supervised classification algorithm. Whereas, un-supervised classification algorithm includes: K-Means, FCM, minimum distance, maximum distance and hierarchical clustering etc. The Supervised and Unsupervised Segmentation Output for MRI Brain Image is shown in Figure 4.

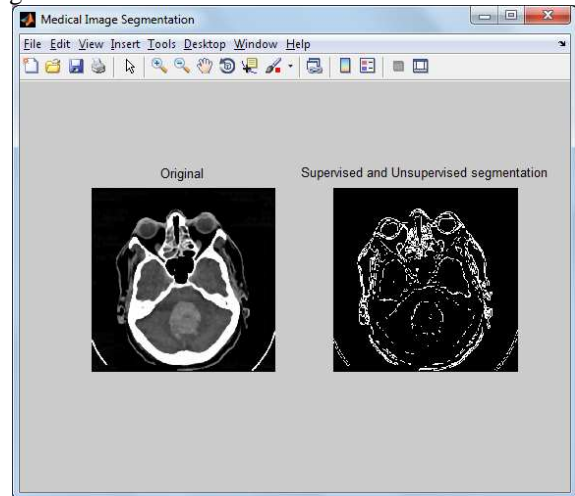


Fig 4: Supervised and Unsupervised Segmentation Output for MRI Brain Image

FCM for MR Brain Image Segmentation

Here we used some existing algorithms for MRI brain image segmentation using different types of FCM algorithms.

Silhouette Method

This method combines FCM, Silhouette Method and Programming language R. This method gives a easiest way to find appropriate structure in the data of MRI. The data of MRI T1, T2, PD images used as training set, and the new method is performed to show the ability of finding structure in the data of training set. All the data of MRI T1, T2, PD combined together, and then a combined multi MRI introduced using program in R. The steps are given below,

1. Coverts from image to data matrix, which is to be classified.
2. Separate matrices in term of Images, if more than one image to be classified.
3. Construct a new data matrix with three columns to be structured, the columns are correspond to data of T1, T2, PD.
4. Initialize the cluster centers at first time [n classes].
5. Use FCM to make partition (clusters) into data matrix.
6. If clusters Average width is ≥ 0.6 silhouette (stop algorithm) or otherwise, repeat from step 4 until the clusters average width reach 0.6. (

clusters average width may be changed according to the problem).

7. Separate the elements of Matrix according to clusters.
8. Get segmented MR image using data matrices of Step 7.

Spatial FCM

One of the important characteristics of an image is that neighbouring pixels are highly correlated. In other words, these neighbouring pixels possess similar feature values, and the probability that they belong to the same cluster is great. This spatial relationship is important in clustering, but it is not utilized in a standard FCM algorithm. To exploit the spatial information, a spatial function is defined as

$$h_{ij} = \sum_{k \in NB(x_j)} u_{ik} \quad \text{----- (5)}$$

where NB (xj) represents a square window centered on pixel xj in the spatial domain. A 5x5 window was used throughout this work. Just like the membership function, the spatial function hij represents the probability that pixel xj belongs to ith cluster. The spatial function of a pixel for a cluster is large if the majority of its neighbourhood belongs to the same clusters. The spatial function is incorporated into membership function as follows:

$$u'_{ij} = \frac{u^p_{ij} h^q_{ij}}{\sum_{k=1}^c u^p_{kj} h^q_{kj}} \quad \text{----- (6)}$$

where p and q are parameters to control the relative importance of both functions. In a homogenous region, the spatial functions simply fortify the original membership, and the clustering result remains unchanged. However, for a noisy pixel, this formula reduces the weighting of a noisy cluster by the labels of its neighbouring pixels. As a result, misclassified pixels from noisy regions or spurious blobs can easily be corrected. The spatial FCM with parameter p and q is denoted sFCMp,q. Note that sFCM1,0 is identical to the conventional FCM.

The clustering is a two-pass process at each iteration. The first pass is the same as that in standard FCM to calculate the membership function in the spectral domain. In the second pass, the membership information of each pixel is mapped to the spatial domain, and the spatial function is computed from that. The FCM iteration proceeds with the new membership that is incorporated with the spatial function. The iteration is stopped when the maximum difference between two cluster centres at two successive iterations is less than a

threshold (=0.02). After the convergence, defuzzification is applied to assign each pixel to a specific cluster for which the membership is maximal. The spatial function modifies the membership function of a pixel according to the membership statistics of its neighbourhood. Such neighbouring effect biases the solution toward piecewise-homogeneous labelling. This technique reduces the number of spurious blobs, and the segmented images are more homogeneous. The SFCM algorithm with a higher q parameter provides a better smoothing effect is shown in Figure 5. The possible disadvantages of using higher spatial weighting are the blurring of some of the finer details.

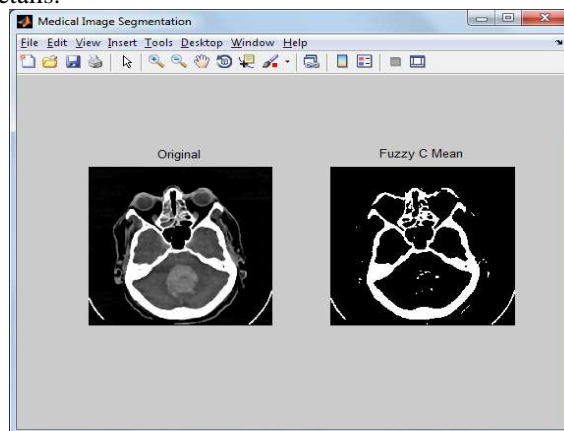


Fig 5: MRI Brain segmentation FCM Output Image

Proposed Method

Hidden Markov Random Field Model (HMRF)

The concept of a hidden Markov random field model is derived from hidden Markov models (HMM), which are defined as stochastic processes generated by a Markov chain whose state sequence cannot be observed directly, only through a sequence of observations. Each observation is assumed to be a stochastic function of the state sequence. The underlying Markov chain changes its state according to a transition probability matrix, where l is the number of states. HMMs have been applied successfully to speech recognition and handwritten script recognition. Since original HMMs were designed as 1D Markov chains with first order neighbourhood systems, it cannot directly be used in 2D/3D problems such as image segmentation. Here, we consider a special case of a HMM, in which the underlying stochastic process is a Markov random field (MRF), instead of a Markov chain, therefore not restricted to 1D. We refer to this special case as a hidden Markov random field (HMRF) model. Mathematically, an HMRF model is characterized by the following:

- Hidden Random Field (MRF)

$$X = \{X_i, i \in S\}$$

The Random field is an underlying MRF assuming values in a finite state space \mathcal{L} with probability distribution. The state of X is unobservable.

• Observable Random Field
 $Y = \{Y_i, i \in S\}$
 is a random field with a finite state space \mathcal{D} .

Given any particular configuration \mathbf{x} , every Y_i follows known conditional probability distribution $p(y_i|x_i)$ of the same functional form $f(y_i; \theta_{x_i})$, where θ_{x_i} is the involved parameters. This distribution is called the emission probability function and Y is also referred to as the emitted random field.

• Conditional Independence For any $\mathbf{x} \in \mathcal{X}$, the random variables Y_i are conditional independent,

$$P(\mathbf{y}|\mathbf{x}) = \prod_{i \in S} P(y_i|x_i). \tag{8}$$

Based on the above, we can write the joint probability of (X,Y) as

$$P(\mathbf{y}, \mathbf{x}) = P(\mathbf{y}|\mathbf{x})P(\mathbf{x}) = P(\mathbf{x}) \prod_{i \in S} P(y_i|x_i).$$

According to the local characteristics of MRFs, the joint probability of any pair of (X_i, Y_i) , given X_i 's neighbourhood configuration \mathbf{x}_{N_i} , is:

$$P(y_i, x_i|x_{N_i}) = P(y_i|x_i)P(x_i|x_{N_i}) \tag{9}$$

Thus, we can compute the marginal probability distribution of Y_i dependent on the parameter set θ (in this case, we treat θ as a random variable) and \mathbf{x}_{N_i} ,

$$p(y_i|x_{N_i}, \theta) = \sum_{\ell \in \mathcal{L}} p(y_i, \ell|x_{N_i}, \theta) = \sum_{\ell \in \mathcal{L}} f(y_i; \theta_\ell) p(\ell|x_{N_i}), \tag{10}$$

$$\theta = \{\theta_\ell, \ell \in \mathcal{L}\}$$

where θ_ℓ . We call this the hidden Markov random field (HMRF) model. Note, the concept

of an HMRF is different from that of an MRF in the sense that the former is defined with respect to a pair of random variable families (X,Y) while the latter is only defined with respect to X. More precisely, an HMRF model can be described by the following:

$$X = \{X_i, i \in S\}$$

- hidden MRF, with prior distribution $p(\mathbf{x})$;
- $Y = \{Y_i, i \in S\}$ - observable random field, with emission probability distribution $p(y_i|x_i)$ for each y_i ;
- $\theta = \{\theta_\ell, \ell \in \mathcal{L}\}$ - the set of parameters involved in the above distributions.

If we assume the random variables X_i are independent of each other, which means that for $\forall \ell \in \mathcal{L} \quad i \in S$ and we have

$$P(\ell|x_{N_i}) = P(\ell) = \omega_\ell,$$

then equation reduces to

$$p(\mathbf{y}|\theta) = \sum_{\ell \in \mathcal{L}} \omega_\ell \cdot f(\mathbf{y}; \theta_\ell),$$

which is the definition of the finite mixture model. Therefore a FM model is a degenerate special case of an HMRF model. It is obvious from the above that the fundamental difference between the FM model and the HMRF model lies in their different spatial properties. The FM model is spatially independent whereas the HMRF model may be spatially dependent. Therefore, the HMRF model is more flexible for image modelling in the sense that it has the ability to encode both the statistical and spatial properties of an image. With a Gaussian emission distribution, the FM model is usually known as the finite Gaussian Mixture (FGM) or finite normal mixture (FNM) model. More specifically, the observable random variables have the following density function:

$$p(\mathbf{y}|\phi) = \sum_{\ell \in \mathcal{L}} \omega_\ell \cdot g(\mathbf{y}; \theta_\ell) \tag{11}$$

where

$$g(\mathbf{y}; \theta_\ell) = \frac{1}{\sqrt{2\pi\sigma_\ell^2}} \exp\left(-\frac{(y-\mu_\ell)^2}{2\sigma_\ell^2}\right) \text{ and}$$

.....(12)

Similarly, an HMRF model with a Gaussian emission distribution can be specified as:

$$p(y_i | x_{N_i}, \theta) = \sum_{\ell \in \mathcal{L}} g(y_i; \theta_\ell) p(\ell | X_{N_i}), \quad (13)$$

where g and θ_ℓ are defined. We refer to this type of HMRF as the Gaussian hidden Markov random field (GHMRF) model.

HMRF-FCM

The hidden Markov random field model (HMRF) to model the image class labels, which takes into account the mutual influences of neighbouring sites formulated on the basis of fuzzy clustering principle. In this method the explicit assumptions of the HMRF model is incorporated into fuzzy clustering procedure, an efficient fuzzy clustering type treatment is yielded. This combines the benefits from the spatial coherency modelling capabilities of the HMRF model, and the enhanced flexibility obtained by the fuzzy clustering algorithm, i.e. fuzzy c-means algorithm (FCM). The HMRF-FCM segmentation framework is validated with noisy synthesis as well as brain MR images. This method is formulated using an HMRF-FCM algorithm which offers an FCM-type treatment of the HMRF model. This combines the benefits from the spatial coherency modelling capabilities of the HMRF model, and the enhanced flexibility obtained by the fuzzy clustering algorithm. The algorithm is given below,

Derive an estimation of $x(k)$ using

$$\hat{x}_j^{(k)} = \arg \max_{i=1}^q r_{ij}^{(k)} \quad \dots\dots\dots (7)$$

Using $x(k)$, compute the point wise prior probabilities of the MRF $\pi_{ij}(k)$ given by

$$\pi_{ij} = p(x_j = i | \hat{x}_j, \beta) = \frac{\exp(-\sum_{c \in \mathcal{E}_j} V_c(\hat{x}_j | \beta))}{\sum_{h=1}^q \exp(-\sum_{c \in \mathcal{E}_j} V_c(\hat{x}_{hj} | \beta))} \quad \dots\dots\dots (8)$$

Compute the fuzzy membership functions $r_{ij}(k)$ using

$$r_{ij}^{(k+1)} = \frac{\pi_{ij}^{(k)} \exp(-\frac{1}{\lambda} d_{ij}^{(k)})}{\sum_{h=1}^q \pi_{hj}^{(k)} \exp(-\frac{1}{\lambda} d_{hj}^{(k)})} \quad \dots\dots\dots (9)$$

Compute the estimator updates $\mu_{ij}(k+1)$ and

$\sigma_{ij}(k+1)$ by and

$$\mu_i^{(k+1)} = \frac{\sum_{j=1}^s r_{ij}^{(k)} y_j}{\sum_{j=1}^s r_{ij}^{(k)}} \quad \dots\dots\dots (10)$$

$$\sigma_i^{(k+1)} = \frac{\sum_{j=1}^s r_{ij}^{(k)} (y_j - \mu_i^{(k)}) (y_j - \mu_i^{(k)})^T}{\sum_{j=1}^s r_{ij}^{(k)}} \quad \dots\dots\dots (11)$$

In case of convergence, i.e.

$$|Q_\lambda(\psi^{(k+1)}) - Q_\lambda(\psi^{(k)})| / Q_\lambda(\psi^{(k)}) < T_c \quad \dots\dots\dots (12)$$

Where T_c is the convergence threshold, exit; otherwise $k = k + 1$ and return to 1.

Conclusion

In this work we have made a analysis about the performance of three segmentation methods Silhouette method, Spatial FCM, HMRF-FCM. The HMRF-FCM algorithm combines the advantages of HMRF model, in terms of spatially correlated data clustering effectiveness, and the increased flexibility of FCM-type method. It gives less misclassification error, faster convergence and better accuracy. Silhouette method gave a easiest way to find appropriate structure in the data of MRI. The data of MRI T1, T2, PD images combined together, and then a combined multi MRI introduced using program in R. The training set originally had large dimension of data matrix, so the program used to reduce the dimension of training set and the new algorithm method is applied to show the ability of the method. Spatial FCM that incorporates the spatial information into the membership function to improve the segmentation results. The membership functions of the neighbours centered on a pixel in the spatial domain are enumerated to obtain the cluster distribution statistics. These statistics are transformed into a weighting function and incorporated into the membership function. This neighbouring effect reduces the number of spurious blobs and biases the solution toward piecewise homogeneous labelling. This method provided that the effect of noise in segmentation was considerably less with the new algorithm than with the conventional FCM.

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