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Segmentation of Brain MR Images using Genetically Guided Clustering

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Abstract— This paper presents a novel algorithm for fuzzy segmentation of magnetic resonance imaging (MRI) data and estimation of intensity inhomogeneities using fuzzy logic. The proposed algorithm is formulated by modifying the objective function of the standard fuzzy c-means (FCM) algorithm to compensate for such inhomogeneities and to allow the labeling of a pixel to be influenced by the labels in its immediate neighborhood. Clustering algorithms such as FCM that use calculus based optimization methods can be trapped by local extrema in the process of optimizing the clustering criterion. They are also very sensitive to initialization. The proposed algorithm uses Genetic Algorithm (GA) to optimize the modified fuzzy c-means function. The performance of the algorithm is evaluated on a series of MR images of the brain

I. Introduction

Spatial intensity inhomogeneity induced by the radio frequency (RF) coil in magnetic resonance imaging is a major problem in the computer analysis of MRI data. Such inhomogeneities have rendered conventional intensity-based classification of MR images very difficult, even with advanced techniques such as nonparametric, multichannel methods. This is due to the fact that the intensity inhomogeneities appearing in MR images produce spatial changes in tissue statistics, i.e. mean and variance.

In the last decade, several methods have been proposed that simultaneously compensate for the shading effect while segmenting the image. These methods have the advantage of being able to use intermediate information from the segmentation while performing the correction. The finite mixture (FM) model [1] is one of the most widely used models in segmentation. FM being a histogram based model has an intrinsic limitation- no spatial information is taken into account. This causes the FM model to work on well-defined images with low levels of noise. Markov random field-based algorithms [2] have been proposed that account for inhomogeneities by allowing the centroids of each class to vary independently. However, this method results only in hard segmentation.

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Recently Wells et al. [3] developed a new statistical approach based on the expectation- maximization (EM) algorithms to solve the bias–field-correction problem and the tissue classification problem. There are two main disadvantages of this EM approach. First, the EM algorithm is extremely computationally intensive, especially for large problems. Second, the EM algorithm requires a good initial guess for either the bias field or for the classification estimate. Xu et al.[4] followed Wells approach and proposed a new adaptive fuzzy c-means technique to produce fuzzy segmentation while compensating for intensity inhomogeneities. Their method however, is computationally intensive and is also very sensitive to noise.

In this paper, a different approach is proposed for fuzzy segmentation of MRI data in the presence of intensity inhomogeneities. The algorithm is formulated by modifying the objective function of the standard FCM algorithm to compensate for such inhomogeneities. This allows the labeling of a pixel to be influenced by the labels in its immediate neighborhood. The proposed algorithm uses GA to optimize the cluster centers in the modified fuzzy (J_m) c-means function to avoid local extrema.

II. Background

The observed MRI signal is modeled as a product of the true signal generated by the underlying anatomy, and a spatially varying factor called the gain field

$$Y_k = X_k G_k \quad \forall \quad k \in \{1, 2, ...N\} \tag{1}$$

where X_k and Y_k are the true and observed intensities at the kth pixel, respectively. $G_k$is the gain field at the kth pixel, and N is the total number of pixels in the MRI image. The application of a logarithmic transformation to the intensities allows the artifact to be modeled as an additive bias field [3].

$$y_k = x_k + \beta_k \quad \forall \quad k \in \{1, 2, ...N\} \tag{2}$$

where x_k and y_k are the true and observed log-transformed intensities at the kth pixel, respectively. β_k is the bias field at the kth pixel.

III. Bias Corrected FCM (BCFCM) Objective Function

The standard FCM objective function for partitioning $\{x_k\}_{k=1}^{N}$ into c clusters is given by

$$J = \sum_{i=1}^{c} \sum_{k=1}^{N} u_{ik}{}^{p} \left\| x_k - v_i \right\|^2 \quad (3)$$

where $\{v_i\}_{i=1}^{c}$ are the prototypes of the clusters and the array $[u_{ik}] = U$ represents a partition matrix, $U \in \boldsymbol{u}$, namely

$$\boldsymbol{u} \left\{ u_{ik} \in [0,1] \;\middle|\; \sum_{i=1}^{c} u_{ik} = 1 \forall k \right.$$
$$\left. \text{and} \quad 0 < \sum_{k=1}^{N} u_{ik} < \mathrm{N} \quad \forall \ \mathrm{i} \quad \right\} \quad (4)$$

The parameter p is a weighing exponent on each fuzzy membership and determines the amount of fuzziness of the resulting classification.

The standard FCM objective function given in (3) is modified by introducing a term that allows the labeling of a pixel to be influenced by the labels in its immediate neighborhood [5]. The neighborhood effect acts as a regularizer and biases the solution toward piecewise-homogeneous labeling. The modified objective function is given by

$$J_m = \sum_{i=1}^{c} \sum_{k=1}^{N} u_{ik}{}^{p} \left\| x_k - v_i \right\|^2 + \frac{\alpha}{N_R} \sum_{i=1}^{c} \sum_{k=1}^{N} u_{ik}{}^{p} \left(\sum_{x_r \varepsilon N_k} \left\| x_r - v_i \right\|^2 \right) \quad (5)$$

where N_k stands for the set of neighbors that exist in a window around x_k, and N_R is the cardinality of N_k. The effect of the neighbors term is controlled by the parameter α. The relative importance of the regularizing term is inversely proportional to the signal-to-noise ratio (SNR) of the MRI signal. Lower SNR would require a higher value of the parameter α.

Substituting (2) into (5), we have

$$J_m = \sum_{i=1}^{c} \sum_{k=1}^{N} u_{ik}{}^{p} \left\| y_k - \beta_k - v_i \right\|^2 + \frac{\alpha}{N_R} \sum_{i=1}^{c} \sum_{k=1}^{N} u_{ik}{}^{p} \left(\sum_{y_r \varepsilon N_k} \left\| y_r - \beta_r - v_i \right\|^2 \right) \quad (6)$$

Formally, the optimization problem comes in the form

$$\min_{U,\ \{v_i\}_{i=1}^{c},\ \{\beta_k\}_{k=1}^{N}} J_m, \ \text{subject to} \ U \in \boldsymbol{u} \quad (7)$$

A. Parameter Estimation

The objective function J_m can be minimized in a fashion similar to the standard FCM algorithm. Taking the first derivatives of J_m with respect to u_{ik}, v_i and β_k, and setting them to zero results in three necessary but not sufficient conditions for J_m to be at a local extrema[5].

The partition matrix is given by

$$u_{ik}{}^{*} = \frac{1}{\sum_{j=1}^{c} \left(\dfrac{D_{ik} + \dfrac{\alpha}{N_R} \gamma_i}{D_{jk} + \dfrac{\alpha}{N_R} \gamma_j} \right)^{\frac{1}{p-1}}} \quad (8)$$

where $D_{ik} = \left\| y_k - \beta_k - v_i \right\|^2$

$$\gamma_i = \left(\sum_{y_r \varepsilon N_k} \left\| y_r - \beta_r - v_i \right\|^2 \right)$$

The prototype of the cluster is obtained by

$$v_i{}^{*} = \frac{\sum_{k=1}^{N} u_{ik}{}^{p} \left((y_k - \beta_k) + \dfrac{\alpha}{N_R} \sum_{y_r \varepsilon N_k} (y_r - \beta_r) \right)}{(1+\alpha) \sum_{k=1}^{N} u_{ik}{}^{p}} \quad (9)$$

The bias term is estimated by

$$\beta_k{}^{*} = y_k - \frac{\sum_{i=1}^{c} u_{ik}{}^{p} v_i}{\sum_{i=1}^{c} u_{ik}{}^{p}} \quad (10)$$

B. BCFCM Algorithm

The BCFCM algorithm for correcting the bias field and segmenting the image into different clusters can be summarized in the following steps.

Step1**:** Select initial class prototypes $\{v_i\}_{i=1}^{c}$. Set $\{\beta_k\}_{k=1}^{N}$ to equal and very small values (e.g. 0.01).
Step2: Update the partition matrix using (8).
Step3: The prototypes of the clusters are obtained in the form of weighted averages of the patterns using (9).
Step4: estimate the bias term using (10).
Step5**:** Repeat Step2-4 till termination. The termination criterion is as follows:

$$\left\| V_{new} - V_{old} \right\| < \varepsilon \quad (11)$$

where $\|\cdot\|$ is the Euclidean norm, V is a vector of cluster centers, and ε is a small number that can be set by the user.

IV GENETICALLY GUIDED CLUSTERING

Initialization has a significant effect on the final partitions obtained by the iterative c-means clustering approaches. The genetically guided clustering attempts to achieve both avoidance of local extrema and minimal sensitivity to initialization. On datasets with several local extrema, the GA approach always avoids the less desirable solutions. In any generation, element *i* of the population is V_i, a *c x s* matrix of cluster centers in FCM. The cluster centers and features are represented by *c* and *s* respectively. The initial population of size *P* is constructed by random assignment of real numbers to each of the *s* features of the *c* cluster centers. The initial values are constrained to be in the range of the feature to which they are assigned, but are otherwise random. Since only the *V's* will be used within the GA it is necessary to reformulate the objective functions (3) and (6) for optimization.

Case 1: FCM: To work only with *V*'s in FCM, (3) can be rewritten by substitution for *U* using the first order necessary condition for *U*.

Specifically, for $p>1$ as long as $D_{jk} > 0 \ \ \forall \ j,k$, we can substitute

$$u_{ik} = \left(D_{ik}^{\ 1/(1-p)} \right) \Big/ \left(\sum_{j=1}^{c} D_{jk}^{\ 1/(1-p)} \right) \qquad (12)$$

where $D_{ik} = \left\| x_k - v_i \right\|^2$ for $1 \le i \le c$ and $1 \le k \le N$

Substituting (12) into (3) and rearranging gives the reformulated FCM functional [6]

$$R_1(V) = \sum_{k=1}^{N} \left(\sum_{i=1}^{c} D_{ik}^{\ 1/(1-p)} \right)^{1-p} \qquad (13)$$

Case 2: BCFCM: To work only with V's in BCFCM (6) can be rewritten by substitution for U. We can substitute (8) into (6), resulting in the reformulated BCFCM functional

$$R_m(V) = \sum_{k=1}^{N} \left\{ \sum_{i=1}^{c} \left(D_{ik} + \frac{\alpha}{N_r} \gamma_i \right)^{\frac{1}{(1-p)}} \right\}^{1-p} \qquad (14)$$

The local (V) minimizers of R_m and U at (6) produce local minimizers of J_m and conversely, the V part of local minimizers of J_m yields local minimizers of R_m. The function R_m is optimized with genetically guided algorithm.

V. Results and Discussion

The MR brain images created by brain web simulator [7] are used for validating segmentation methods. This site also provides the ground truth that enables one to obtain a quantitative assessment of the performance of the algorithm. The images have the dimension of 129*129. The cerebrum is extracted from the brain image before applying the clustering algorithm. In the implementation of BCFCM, parameter α is set as 0.42, p=2, N_R =9 (3 x 3 window centered around each pixel) and ε =0.01.

FCM/BCFCM algorithm is run for 50 random initialization of cluster centers for image corrupted with 40% intensity inhomogeneity and 9% Gaussian noise. Fig 1 and Fig 2 shows that both FCM and BCFCM are sensitive to initialization of cluster centers. FCM/BCFCM finds the best partitions when the initial centers are near to the optimum. When the initial clusters centers are not properly chosen, the resulting partitions yield lower segmentation accuracy. Fig 1 shows the maximum segmentation accuracy of 85% is obtained with FCM when the initial cluster centers are close to the optimum. Fig 2 shows the maximum segmentation accuracy of 93.22% is obtained with BCFCM. The performance of BCFCM is better. FCM/BCFCM, if given enough random initializations will yield the segmentation accuracy obtained by genetically guided FCM (GGFCM) and genetically guided BCFCM (GGBCFCM).

The GGA is used to optimize FCM and BCFCM. The genetic clustering approach provides the best overall partitions and always yields a reasonably good partition when FCM and BCFCM are initialized by optimal centers.

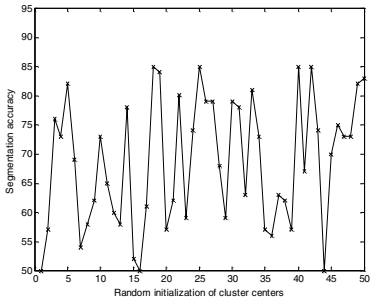

Fig 1: Plot of Segmentation accuracy of MR brain image corrupted with 40% intensity inhomogeneity and 9% Gaussian noise for 50 random initialization of cluster centers using FCM.

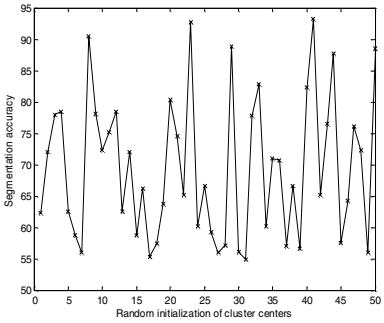

Fig 2: Plot of Segmentation accuracy of MR brain image corrupted with 40% intensity inhomogeneity and 9% Gaussian noise for 50 random initialization of cluster centers using BCFCM.

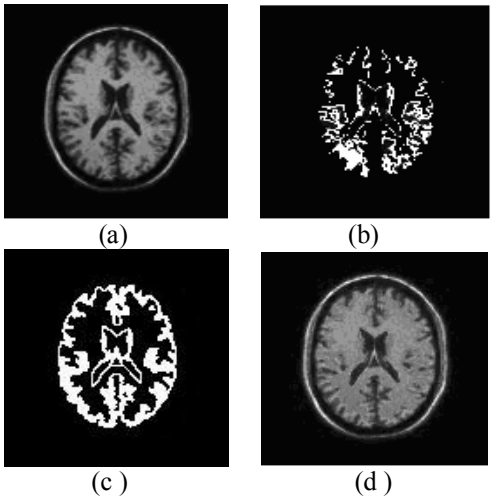

Fig 3. Comparison of segmentation results on MR image (a) Original image corrupted with 40%intensity inhomogeneity and 9% Gaussian noise (b) gray matter using GGFCM (c) and (d) gray matter and bias field estimate using GGBCFCM.

A population of twenty chromosomes is randomly generated. Each center is represented in 8 bits. Roulette wheel selection method is used to select the mating pool. Two point crossover is applied to the cluster centers with a crossover probability p_c=0.9.After every crossover, each bit

of the children is considered for mutation with a mutation probability p_m=0.01. The number of generations is used as the stopping criteria for GGA.

TABLE I
SEGMENTATION ACCURACY OF DIFFERENT ALGORITHMS WHEN APPLIED ON MR IMAGE CORRUPTED WITH 40% INTENSITY INHOMOGENEITY AND 9% GAUSSIAN NOISE

Algorithm	Segmentation accuracy
GGFCM	86.24
GGBCFCM	96.3

TABLE II
SEGMENTATION ACCURACY OF DIFFERENT ALGORITHMS WHEN APPLIED ON MR IMAGE CORRUPTED WITH SALT AND PEPPER NOISE

SNR dB	GGFCM	GGBCFCM
6.5	97.5	97.9
6	97.3	97.5
5	96.09	96.29
4.5	83.95	94.78
4	83.83	94.5
3.5	83.75	93.61

TABLE III
SEGMENTATION ACCURACY OF DIFFERENT ALGORITHMS WHEN APPLIED ON MR IMAGE CORRUPTED WITH GAUSSIAN NOISE

SNR dB	GGFCM	GGBCFCM
7.5	97.12	97.72
7	91.31	96.32
6.5	88.48	95.86
6	86.69	93.5
5.5	85.42	92.78
5	83.98	92.66
4	81.92	92.05
3.5	80.95	91.2

Fig 3 shows the result of applying the GGFCM and GGBCFCM algorithm to segment a MRI image. Strong intensity inhomogeneities are apparent in the image. Both GGFCM and GGBCFCM segments the image into four classes corresponding to gray matter, white matter, cerebrospinalfluid, and background. Fig 3(d) shows the estimate of the multiplicative gain. This image was obtained by scaling the values of the bias field from one to 255. The segmentation accuracy (SA) of GGFCM and GGBCFCM are presented in Table I. GGBCFCM is found to be more accurate than GGFCM. SA is measured as follows

$$SA = \frac{Number\ of\ correctly\ classified\ pixels}{Total\ number\ of\ pixels} * 100\% \quad (15)$$

Table II and Table III depicts the segmentation accuracy of MR images corrupted with salt and pepper noise and Gaussian noise for various SNR respectively. GGFCM and GGBCFCM produces almost similar results for high SNR. The GGBCFCM outperforms GGFCM for lower SNR.

VI. CONCLUSION

The BCFCM algorithm is demonstrated for adaptive segmentation and intensity correction of MR images. FCM and BCFCM are sensitive to initialization of cluster centers. The genetic guided algorithm is used to optimize FCM and BCFCM. The GGFCM and GGBCFCM are applied to images corrupted with intensity inhomogeneity, Gaussian noise and salt and pepper noise. The results indicate that the GGA provides good partitions by settling in one of the most desirable extrema and never in an extremum representing a degenerate partition. The GGFCM and GGBCFCM produce almost similar results for high SNR. In noisy images, the GGBCFCM technique produces accurate segmentation results than GGFCM algorithm.

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