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Unsupervised MRI segmentation with spatial connectivity

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ABSTRACT

Magnetic Resonance Imaging (MRI) offers a wealth of information for medical examination. Fast, accurate and reproducible segmentation of MRI is desirable in many applications. We have developed a new unsupervised MRI segmentation method based on k-means and fuzzy c-means (FCM) algorithms, which uses spatial constraints. Spatial constraints are included by the use of a Markov Random Field model. The result of segmentation with a four-neighbor Markov Random Field model applied to multi-spectral MRI (5 images including one T1-weighted image, one Proton Density image and three T2-weighted images) in different noise levels is compared to the segmentation results of standard k-means and FCM algorithms. This comparison shows that the proposed method outperforms previous methods.

Keywords: Unsupervised segmentation, MRI, fuzzy c-means, spatial connectivity

1. INTRODUCTION

The advantages of Magnetic Resonance Imaging (MRI) over other imaging modalities are its high spatial resolution and excellent discrimination of soft tissues. On the other hand, MRI provides a noninvasive method to get angiography and functional images and till now no side effect of MRI has been reported.

A typical MRI of a patient includes multi-model information in three dimensions. Generally, each slice has three different types of image (T1-weighted, T2-weighted and Proton Density-weighted), which have different contrast affected by selection of pulse sequence parameters. Thus, even for a single study, there are one hundred or more images to be acquired and analyzed. From computational point of view, an automated algorithm for segmentation and recognition is inevitably required. On the other hand, fast, accurate and reproducible segmentation is vital to the diagnosis, treatment and evaluation of many medical situations.

Due to the characteristics of MR images, development of automated algorithms is challenging. Because of inherent noise, partial volume effect and wide range of imaging parameters, which affect the tissue intensities, there is a significant inter-patient variation of signal intensities for the same tissue.

Unsupervised segmentation algorithms are mostly based on clustering algorithms like k-means and fuzzy c-means (FCM) algorithms. But these techniques do not consider the spatial constraints in MRI[1-3]. We use Markov Random Fields (MRF) to model the spatial constraints in MRI. The MRF has been used by other researchers to model the spatial constraints in supervised and semi-supervised segmentation algorithms[4-6]. Papas has introduced an adaptive clustering algorithm for image segmentation using MRF model[7]. In this algorithm, MRF is applied to a window around each pixel (instead of the entire image) and no specific rule is introduced for determination of MRF model parameters.

This paper is organized as follows. The proposed spatial model is presented in Section 2. In Section 3, the modified clustering algorithm is presented. In Section 4, the proposed algorithm is compared with the conventional k-means or FCM algorithms. Finally summary and conclusions are presented in Section 5.

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2. SPATIAL MODEL

Let us denote the image by S and the label set by L. In normal brain, the label set consists of background (BG), white matter (WM), gray matter (GM), CSF and skull bulk (SB), i.e.,

$$L = \{BG, WM, GM, CSF, SB\} \tag{1}$$

The intensity of pixel i in the image is denoted by s_i and its label by f_i. $f_i = l_1$ means that the pixel i belongs to region l_1. The number of tissues is denoted by K.

Because of well-designed head coils, compared to random noise, inhomogenity of brain images is not a dominant limitation in image segmentation anymore[8]. So, we assume image inhomogenity is negligible.

To find the best segmentation for pixel i (f_i) the term $P(f_i \mid s_i, F-\{f_i\})$ should be maximized in which $F-\{f_i\}$ is the segmentation of the image except the *i*-th pixel. To do this, we use the Bayes theorem:

$$P(f_i \mid s_i, F-\{f_i\}) = \frac{P(s_i \mid f_i, F-\{f_i\}) \cdot P(f_i \mid F-\{f_i\})}{P(s_i \mid F-\{f_i\})} \tag{2}$$

The intensity of the *i*-th pixel (s_i) only depends on f_i (the region that the *i*-th pixel belongs to) and is independant of other regions ($F-\{f_i\}$). So we have:

$$P(f_i \mid s_i, F-\{f_i\}) = \frac{P(s_i \mid F) \cdot P(f_i \mid F-\{f_i\})}{P(s_i)} \tag{3}$$

In addition, $P(s_i)$ has a defined value and does not depend on segmentation, so to maximize Equation (3) only the numerator should be maximized.

$$A = P(s_i \mid F) \cdot P(f_i \mid F-\{f_i\}) \tag{4}$$

It is assumed that each tissue type has a Gaussian distribution with the mean of μ and variance of σ^2. The mean intensity (μ) of a tissue is different from that of the other tissues. We consider that the variance (σ^2) is the same for all regions. So we can write:

$$P(s_i \mid f_i) = \frac{1}{\sqrt{2\pi} \cdot \sigma} \exp[-\frac{1}{2\sigma^2}(s_i - \mu_{f_i})^2] \tag{5}$$

in which μ_{f_i} is the mean intensity of region f_i. We also model the spatial connectivity (region process) by a Markov random field. So, if we denote the neighborhood of the pixel *i* by N_i then we can write:

$$P(f_i \mid F-\{f_i\}) = P(f_i \mid f_j, j \in N_i) \tag{6}$$

According to the Hammerley–Clifford theorem[9] the density of f is given by a Gibbs density which has the following form:

$$P(f_i \mid f_j, j \in N_i) = \frac{1}{Z} \exp\{-\sum_{C_i} V_c(f_i)\} \tag{7}$$

where C_i is the set of all possible cliques that include *i*-th pixel. So we can rewrite the term that should be maximized as follows:

$$A = \frac{1}{\sqrt{2\pi} \cdot \sigma \cdot Z} \exp\{-\frac{1}{2\sigma^2}(s_i - \mu_{f_i})^2 - \sum_{C_i} V_c(f_i)\} \tag{8}$$

This suggests that if we are using the minimum distance classifier, we should correct the distance of a pixel to its cluster center as follows:

$$d^2 = \frac{1}{2\sigma^2}(s_i - \mu_{f_i})^2 + \sum_{C_i} V_c(f_i) \tag{9}$$

We use 4-neighborhood so we have only one-point and two-points cliques. The two point clique potentials are defined as follows:

$$V_c(f) = \begin{cases} -\beta & \text{if} \quad f_i = f_j \quad \text{and} \quad i, j \in C \\ 0 & \text{if} \quad f_i \neq f_j \quad \text{and} \quad i, j \in C \end{cases} \tag{10}$$

The parameter β is positive, so that two neighboring pixels are more likely to belong to the same class than to different classes. Increasing the value of β has the effect of increasing the size of the regions and smoothing their boundaries. The one point clique potentials are defined as follows:

$$V_c(f) = \alpha_l \quad \text{if} \quad f_i = l \quad \text{and} \quad i \in C \tag{11}$$

The lower the value of α_l, the more likely that pixel i belongs to class f_i. Thus, the parameter α_l reflects our a priori knowledge of the relative likelihood of the different region types. So from a priori knowledge, we can calculate the coefficients α_l. But during the segmentation process, we do not know each region is which part of the brain and we cannot use a priori knowledge. So we assume that all region types are equally likely and set α_l =0 for all l .

Selection of β is more difficult. The Gibbs model by itself is not very useful. It is easy to see that, in the absence of an observation, the optimal segmentation is just one region. In their discussion of the Ising model, Kindermann and Snell[10] observe that the Gibbs field is ill behaved if there is no strong outside force. So to control the Gibbs force we select the parameter β as follows:

$$\beta = \xi(s_i - \mu_{f_i}) \tag{12}$$

in which $0 < \xi < 1$. By this selection, we are now sure that the potential term in Equation (9) is always a fraction of $(s_i - \mu_{f_i})$ and will never dominate it. The dominant term is always $(s_i - \mu_{f_i})$ and the Gibbs model always improves segmentation results.

3. PROPOSED ALGORITHM

We may use the model discussed in the previous section in any clustering algorithm, which uses minimum distance classifier like k-means and ISODATA[11]. Also we may use the model to modify FCM algorithm. The flowchart of the algorithm to be modified remains unchanged but the part, which calculates the distance between each pixel in the feature space and cluster centers, should be modified by the Equation (9). So we need to identify the cliques of each pixel and calculate their potentials. Once the distances of each point to the cluster centers are calculated, the algorithm continues. We applied this modification to k-means and FCM algorithms and compared the segmentation result with the conventional k-means and FCM algorithms, using images with different noise levels.

4. RESULTS

Figure 1 shows a simulation study with three multi-spectral test images generated in computer with additive white Gaussian noise. Figures 2 and 3 show the segmentation result of conventional k-means and modified k-means with $\xi = 0.35$, respectively. Figure 4 shows the segmentation result of modified k-means with $\xi = 0.5$. Comparing Figures 2 and 3, the advantage of using spatial constraint in image segmentation is seen. As Figure 4 shows, if we do not control the balance between spatial constraint and minimum distance classifier, the result may not be meaningful. So the spatial constraint should only be used as an auxilary constraint to help eliminate the effect of noise and it should not be considered as the main factor for image segmentation.

Figure 5 shows five multi-spectral brain images: one T1-weighted image (TR=500, TE=25), one proton density image (TR=2500, TE=30) and three different T2 weighted images (TR_1=4200, TE_1=50, TR_2=2500, TE_2=75, TR_3=4200 TE_3=100). These images are used for brain segmentation. Four algorithms have been applied to these images: conventional k-means and FCM algorithms, Modified k-means and FCM. The segmentation of these algorithms are compared for different noise levels. Before adding more noise to the original images, we segmented them by a supervised segmentation algorithm and considered it as a true brain segmentation. Noisy images were generated by adding white Gaussian noise with different strengths. These noisy images were used to compare the percent of segmentation error of these algorithms in different noise levels. Because the number of pixels in different segments (i.e., CSF, white matter and gray matter) is not equal, the percent of segmentation error is compared individually for each segment. Figures 6-8 show the percent of segmentation error of each algorithm in different noise levels for each tissue. Figure 9 shows the percent of segmentation error for the entire image. It can be seen from Figures 6-9 that modified k-means algorithm has a better segmentation than the others. The modified FCM shows a better segmentation than FCM algorithm but it is worse than conventional k-means and modified k-means algorithms. K-means segmentation is better than FCM segmentation because the benefits of fuzzy algorithm is not used in image segmentation. Defuzzifying pixel memberships without considering the membership values eliminates the benefits of fuzzy classification. On the other hand, using spatial constraint in modified k-means and modified FCM improves the results of these algorithms compared to those of the conventional k-means and FCM.

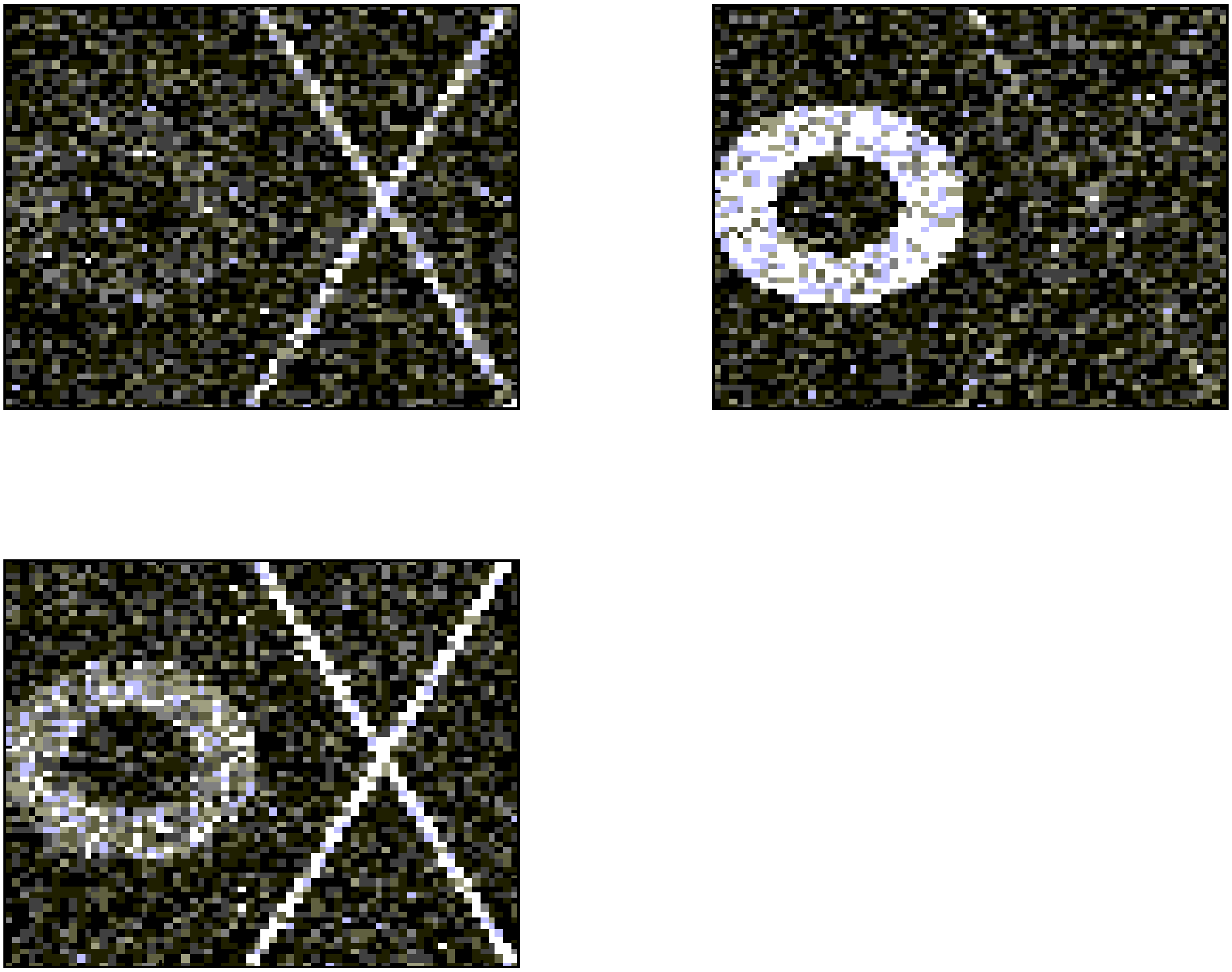

Fig. 1.Three multi-spectral test images.

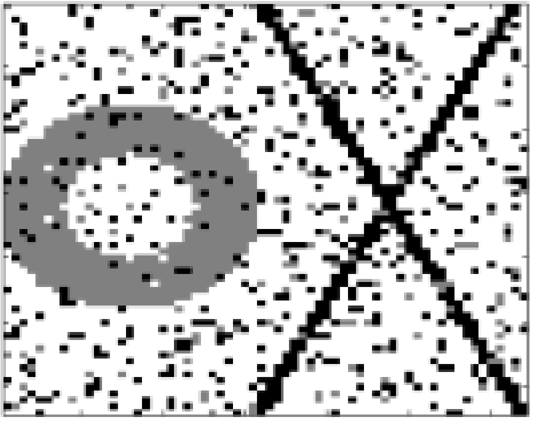

Fig. 2. Segmentation result by conventional k-means.

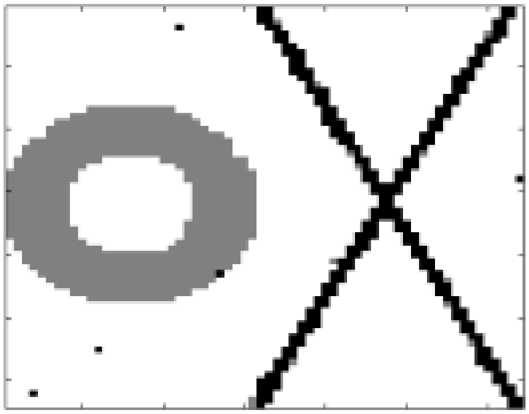

Fig. 3. Segmentation result by modified k-means with $\xi = 0.35$.

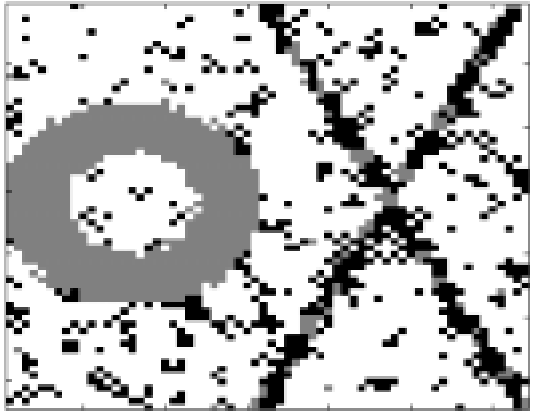

Fig. 4. Segmentation result by modified k-means with $\xi = 0.5$.

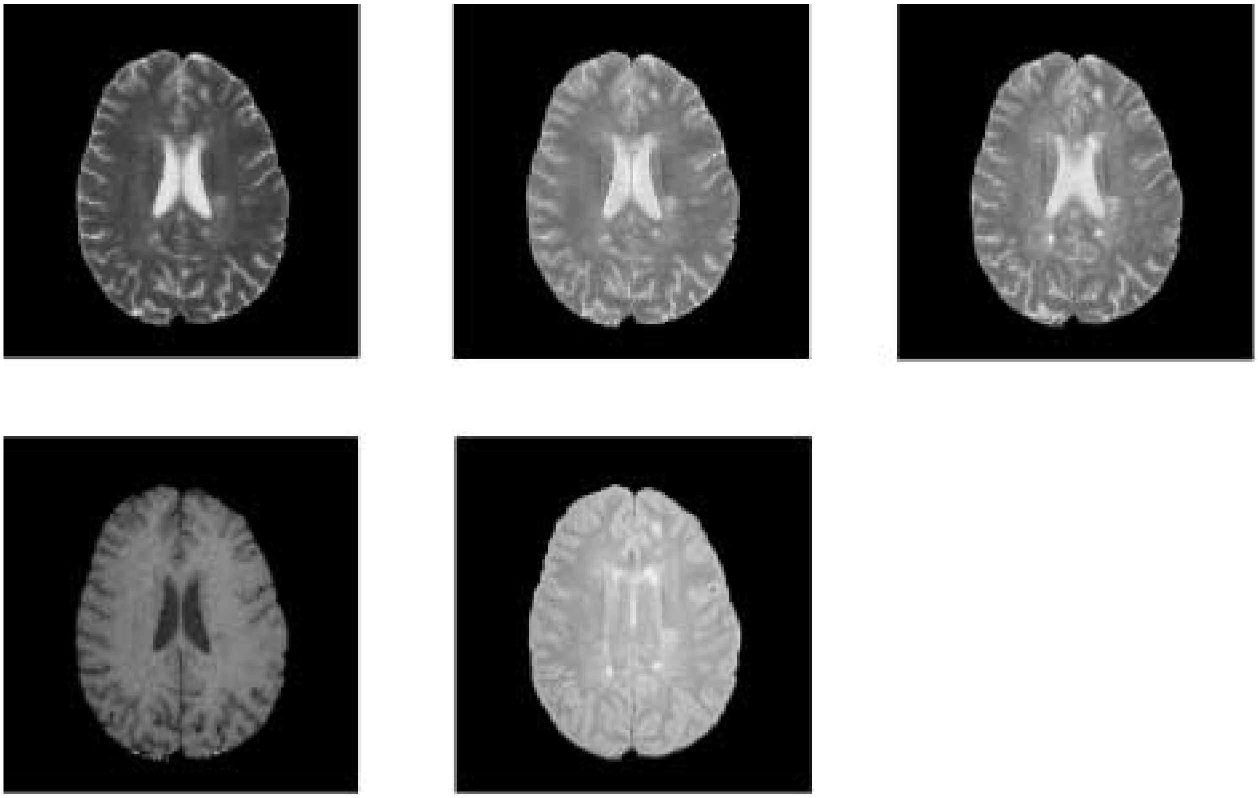

Fig. 5. Multi-spectral MRI of the brain (Three T2-weighted, one T1-weighted, and one PD-weighted).

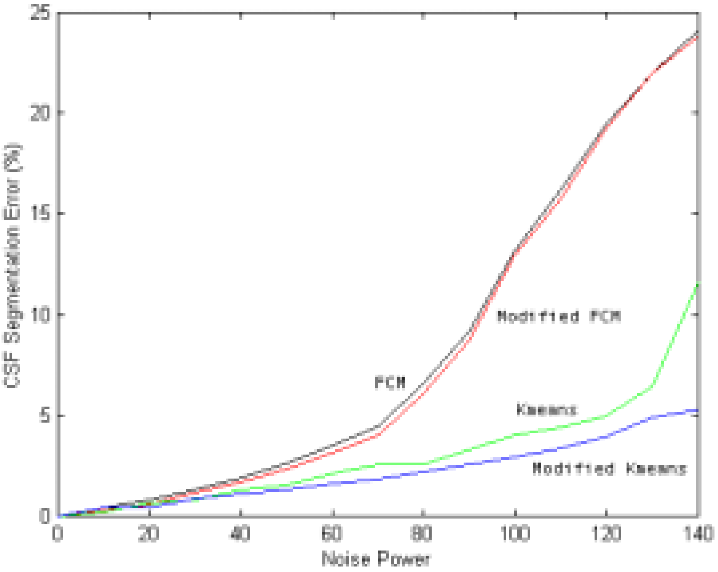

Fig. 6. Percent segmentation error in CSF for different algorithms in different noise levels.

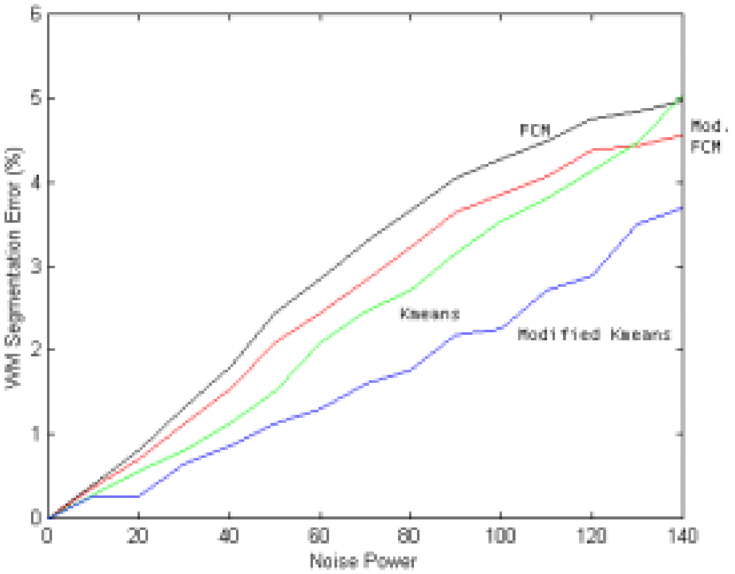

Fig. 7. Percent segmentation error in white matter for different algorithms in different noise levels.

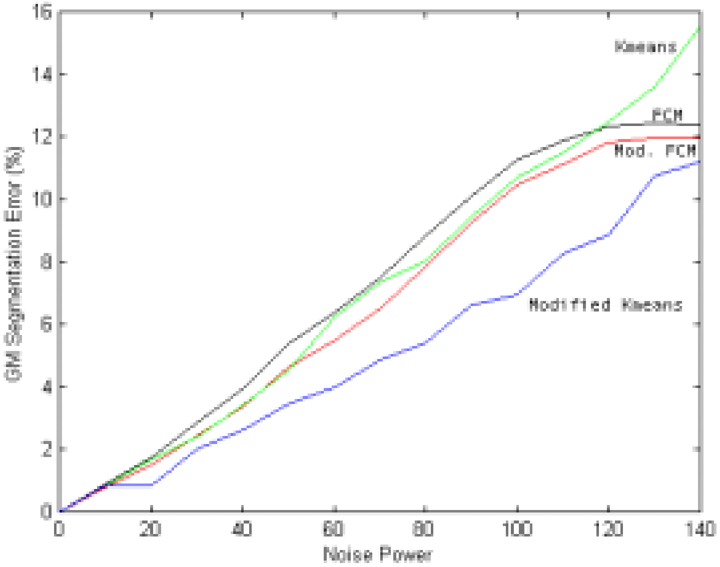

Fig. 8. Percent segmentation error in gray matter for different algorithms in different noise levels.

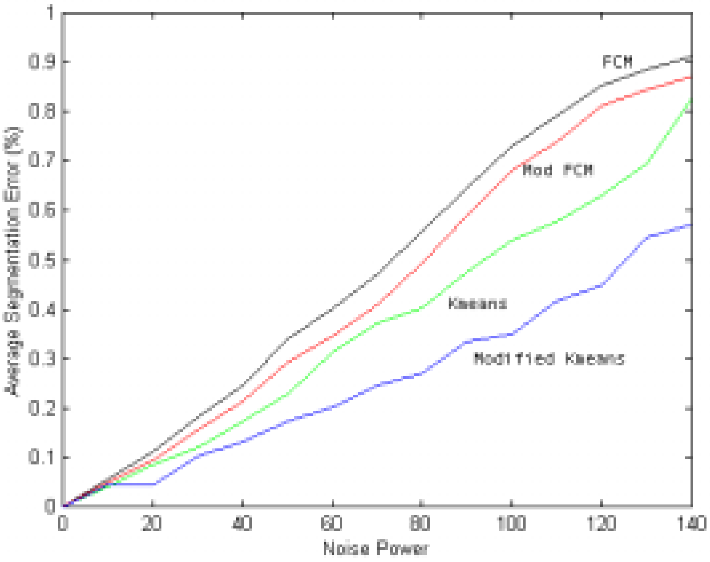

Fig. 9. Percent segmentation error of entire image for different algorithms in different noise levels.

5. CONCLUSION

Unsupervised image segmentation is desirable for fast segmentation and removing operator's reproducibility problem. Unsupervised image segmentation algorithms are mostly originated from clustering algorithms and pattern recognition. These clustering algorithms are developed for clustering data in feature space and do not use spatial constraint, which has some useful information. By modeling the spatial constraint with Markov Random Fields, we modified k-means and FCM algorithms. The amount of this spatial constraint is controlled in our modification to get a good segmentation without losing any details. Comparison of modified algorithms with conventional algorithms illustrates that proposed algorithms generate more accurate segmentation than the conventional counterparts. Among the four algorithms compared with each other, modified k-means shows the best performance.

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