A Novel Approach for Brain MRI Segmentation using Pearson Type-IVa Mixture Model

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Abstract— Now a days, Computer-aided diagnosis plays an important role in medical image processing. Segmentation of brain tumor in magnetic resonance imaging (MRI) is a difficult task due to complexity of size and location variability. In this paper, a novel approach for segmenting the brain MRI based on Pearson type-IVa distribution using K-means algorithm is proposed. The segmentation algorithm is developed using component maximum likelihood under Bayesian frame. Experimental results are also compared with other existing techniques and the performance evaluation is done with quality metrics and segmentation metrics.

Keywords— Computer –aided diagnosis (CAD), Magnetic resonance imaging (MRI), Pearson type-IVa distribution, K-means algorithm.

I. INTRODUCTION

Throughout the most recent couple of decades, the quick improvement of noninvasive brain imaging advances has opened new horizons in analyzing and considering the brain anatomy and function. Tremendous advancement in getting to brain injury and investigating brain life structures has been made utilizing Magnetic Resonance imaging (MRI)[1]. The investigation of these enormous and complex MRI datasets has become a tedious and complex errand for clinicians, who need to physically separate significant data. Nowadays, computerized methods for MR image segmentation, registration, and visualization have been extensively used to assist doctors in qualitative diagnosis[2].

Brain MRI segmentation is an essential task in many clinical applications because it influences the outcome of the entire analysis. There are different traditional methods for MRI segmentation which require human collaboration as far as referencing number of classes for getting exact and solid division. Consequently, it is important to infer new methods for compelling division. Thus, it is necessary to derive new techniques for effective segmentation. Recently much work has been reported in literature regarding the segmentation algorithm based on finite normal mixture models where each image is assumed to be a mixture of Gaussian distributions. But actually it is observed that the pixels are quantized through the brightness or contrast in the gray scale level. It is also observed that the image regions are each region are meso-kurtic and having infinite range[3]. To overcome this drawback in image segmentation based on Gaussian mixture

model recently, Jagadesh et al [4] have developed the skin colour segmentation based on bivariate type-IVa mixture model and they assumed that each region follows Pearson type-IVa probability distributions with different parameters. The Pearson type-IVa is having the range from 0 to ∞. Hence, in this paper to have an accurate modeling of the feature vector is considered by assuming that the pixel intensities in the entire image follow a Bivariate Pearson type-IVa distribution[5].

The rest of the paper is organized as follows: section 2 explains about the Pearson mixture model, Section 3 deals with the estimation of the model parameters using EM Algorithm. Section 4 is to initialize the model parameters using moment method of estimation and K-means algorithm. In Section 5 the proposed segmentation algorithm is presented. In section 6 the experimentation and performance evaluation of the proposed algorithm is discussed. Section 7 deals with conclusion.

II. PEARSON MIXTURE MODEL

The Pearson mixture models are more versatile distributions and include different shape of the frequency curves associated with asymmetric/lepti/platikurtic distributions. The statistical observations of feature vector match closely with Pearson Type-IVa distribution as it is having non-negative and asymmetric nature of random variable [6]. Here it is assumed that the feature vector of the MR image follows a Pearson Type-IVa distribution. The Joint probability density function of feature vector is

$$f(x, y / \theta) = \frac{x^{m-1}(y-x)^{n-1}e^{-y}}{\Gamma(m)\Gamma(n)} \quad \begin{array}{l} m, n > 0 \\ 0 < x < y \end{array} \quad (1)$$

The various shapes of the bivariate frequency surfaces of Pearson type-IVa mixture model are given in Figure.1

Its Joint probability density function is

$$h(x, y) = \sum_{i=1}^{n} \alpha_i f_i(x, y / \theta_i) \quad (2)$$

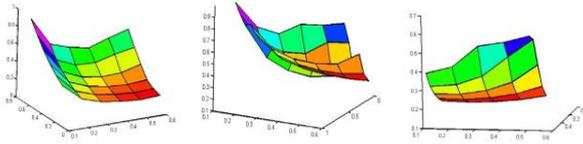where, $0 < \alpha_i < 1$; $\alpha_1 + \alpha_2 = 1$; $f_i(x, y)$ is as given shown in equation (1).

Figure 1. **shapes of bivariate Pearson type-IVa model frequency surfaces**

III. ESTIMATION OF THE MODEL PARAMETERS USING EM-ALGORITHM

The model parameters are estimated by deriving the updated equation of EM-Algorithm, and the refined estimates of the model parameters are

The updated equation of the parameter α_k is

$$\alpha_k^{(l+1)} = \frac{1}{N}\sum_{s=1}^{N}[t_k(x_s, y_s; \theta^{(l)})]$$

for k = 1,2…n

$$= \frac{1}{N}\sum_{s=1}^{N}\left[\frac{\alpha_k^l f_k(x_s, y_s; \theta^{(l)})}{\sum_{i=1}^{2}\alpha_i^l f_i(x_s, y_s; \theta^{(l)})}\right] \qquad (3)$$

The updated equation of the parameter m_K is

$$\sum_{S=1}^{N}t_k(x_s, y_s; \theta^{(l)})\log(x_s) - \sum_{S=1}^{N}t_k(x_s, y_s; \theta^{(l)})\psi(m_k) = 0$$

$$\qquad (4)$$

where, $\psi(m_k) = digamma(m_k)$

The updated equation of the parameter n_K is

$$\sum_{S=1}^{N}t_k(x_s, y_s; \theta^{(l)})\log(y_s - x_s) - \sum_{S=1}^{N}t_k(x_s, y_s; \theta^{(l)})\psi(n_k) = 0$$

$$\qquad (5)$$

where, $\psi(n_k) = digamma(n_k)$

Solving equations (3), (4) and (5) iteratively using MATLAB code we get the revised estimates of $\alpha_k, m_k \ and \ n_k$ for k=1,2…n

IV. INITILIZATION OF THE MODEL PARAMETERS USING K-MEANS

In the section, we briefly discuss the methods for initialization of the model parameters to run the Expectation-Maximization algorithm[7-8].The likelihood function contains 'n' components. The pixels of the whole image are initially divided into 'n' parts by using the K-means algorithms[9-10]. We obtain the initial estimates of the parameters m and n for each image region using the method of moment estimators for

bivariate Pearson type-IVa distribution and for the parameters α_i as $\alpha_i = \dfrac{1}{n}$ for i = 1, 2,..n

V. SEGMENTATION ALGORITHM

After refining the estimates, the important step is to convert the heterogeneous data into homogenous data or group the related pixels. This process is carried out by performing the segmentation. The image segmentation is done in 4 steps:

Step-1: Obtain the initial estimates of the bivariate Pearson type-IVa mixture model using K-Means algorithm.
Step-2: Using the initial estimates obtained from step-1, the EM algorithm is iteratively carried out.
Step-3: Substitute the estimated parameter values in the image joint probability density function

$$h(x, y) = \sum_{i=1}^{K}\alpha_i f_i(x, y; \theta_i)$$

where $f_i(x, y / \theta_i)$ is as given equation (1).
Step-4: The image segmentation is carried out by assigning each pixel into a proper region (Segment) using a threshold (t) and the likelihood function such that $L(x/\theta) \geq t$ or $L(x/\theta) < t$ respectively for 0 < t < 1.
The optimal threshold value of 't' is determined computing true positive and false positive over the segmented regions and plotting the ROC Curve.

VI. EXPERIMENTAL RESULTS AND PERFORMANCE EVALUATION

After developing the segmentation algorithm, the algorithm is applied on T1-weighted brain MRI images and the images are collected form brain web database. We have taken two sample images namely MI1, MI2 are shown in Figure. 2

MI-1   MI-2
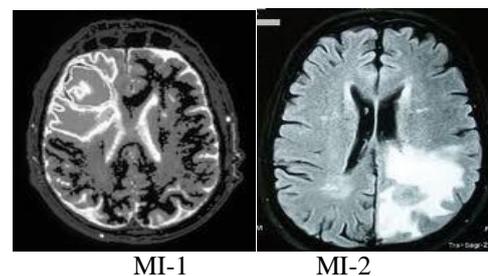
The segmentation performance is evaluated using segmentation quality metrics such as Jacquard Coefficient(JC), Volumetric Similarity (VS) [11][12][13]. The obtained results of the proposed algorithm is presented in table.1

Image	Quality Metric	GMM	PMM
MI-1	JC	0.0432	0.8652
	VS	0.3262	0.8912
MI-2	JC	0.0341	0.8713
	VS	0.4391	0.8612

Table.1 Quality Metrics of GMM and PMM

In order to evaluate the performance of the reconstructed image, we have used image segmentation metrics such as Average Difference (AD), Maximum Distance (MD), Mean Square Error (MSE). Experimental results of reconstructed image segmentation metrics are presented in Table.2

Reconstructed Image	Segmentation Quality Metric	GMM	PMM
MI-1	AD	0.4917	0.8391
	MD	0.4310	0.7962
	MSE	0.0420	0.0081
MI-2	AD	0.5160	0.8409
	MD	0.4712	0.8901
	MSE	0.0219	0.0090

Table.2 Performance of Reconstructed Image

The developed algorithm's performance is evaluated by comparing segmentation algorithm with the Gaussian mixture model (GMM). Figure.3 presents the misclassification rate of the skin pixels of the sample image using proposed model and GMM.
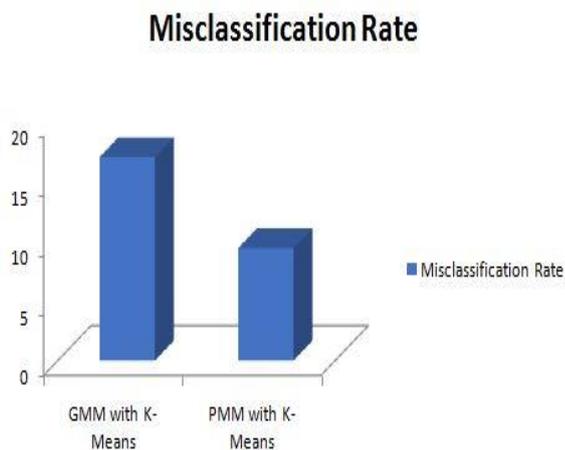

Figure.3 Misclassification Rate

From Figure.3, it is seen that the misclassification rate of the classifier with PMM is less compared to that of GMM.

VII CONCLUSION

This paper addresses a novel approach for Brain MRI segmentation in using a Pearson mixture model. The PMM includes bivariate Pearson type IVa mixture model which represent the MRI . This segmentation algorithm is capable of indentifying different abnormalities in brain MRI . The model parameters are estimated by using EM-algorithm. The initialization of the parameters is done with K-means and moment method of estimation. The performance of the algorithm is evaluated by conducting an experiment with MRI images from brain web database. The experimental results revealed that the proposed segmentation algorithm is much superior to that of GMM.

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