



ISSN 2047-3338

An Efficient Approach for Medical Image Segmentation Based on Truncated Skew Gaussian Mixture Model Using K-Means Algorithm

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Abstract– In this paper, we proposed a novel approach for medical image segmentation process based on Finite Truncated Skew Gaussian mixture model. This approach considers various issues like skewness and asymmetric distributions with a finite range. We have utilized the Expectation-Maximization (EM) algorithm in estimating the final model parameters and K-Means algorithm is utilized to estimate the number of mixture components along with the initial estimates for the EM algorithm. Segmentation of the image is performed based on the maximum likelihood estimation criteria. The performance of the approach is evaluated using segmentation quality metrics and the image quality metrics such as Average Distance, Maximum Difference, Image Fidelity, Mean Squared Error and Signal to Noise ratio.

Index Terms– Finite Truncated Skew Gaussian Mixture Model, EM algorithm, Segmentation quality metrics, Image quality metrics, Image Segmentation

I. INTRODUCTION

THE field of medical imaging has improved significantly with the latest development of the new technologies for monitoring, diagnosing as well as treatment to patient. Many models were utilized in order to identify the disease by means of X-Ray, Magnetic Resonance (MR), Computer Tomography (CT), Positron Emission Tomography (PET), and MRI images. MRI images have gained popularity over the other images because of the non – ionizing radiation that is being used. The acquisition of huge amount of this sophisticated data led to the development and analysis of medical images into sub-regions with the basic assumption that the pixels in each region are homogeneous and no two regions share the common properties. Several segmentation techniques have been developed and utilized [1], [2], [3], [4]. Much emphasis was given to this segmentation algorithms based on Finite Normal Mixture Models and here it is considered that each image region is considered to a mixture of Gaussian distributions i.e. it is assumed that the probability density functions of the pixel intensities of the entire image follows a finite normal mixture model. However, in reality the pixels are quantized through the brightness or contrast in the

gray scale level (Z) at that point. The range of the pixel intensities in a gray scale image is always finite and hence using the infinite range $-\infty$ to $+\infty$ for pixel intensities in finite normal mixture model does seem to be unreasonable. Hence, in this paper, to have a much closer approximation to the pixel intensities in the image region, we considered Finite Truncated Skew Normal Distribution and it is assumed that the pixel intensities in entire image follow finite truncated skew normal distribution [5]. In any of the mixture models, the most predominant factor is estimating the number of image regions (K) inside a given medical image. Once, these initial estimates are obtained, one has to maximize the parameters obtained from the initial estimates. For this purpose, EM algorithm is utilized.

In this paper, to have a more accurate medical image analysis, we have developed and analyzed a finite truncated skew normal distribution with K-Means clustering technique. The basic assumption is that the pixel intensities inside each medical image region have a finite range and hence the infinite range is truncated between the limits Z_l and Z_m where, Z_m denotes the maximum level of pixel intensities of pixels in the medical image and Z_l denotes the minimum level of pixel intensities in the medical image. The number of regions and initial estimates are obtained by using K-Means algorithm. The updated estimates are obtained by utilizing the EM algorithm. The experimentation is carried out by using different brain medical images obtained from web and the performance evaluation of the segmentation process is done through Jaccard Coefficient, Volume Similarity, Variation of Information (VOI), Global Consistency Error (GCE) and Probabilistic Random Index (PRI). The medical image reconstruction is done by ascribing the pixels by using the maximum likelihood estimates. The performance of reconstructed image is evaluated by using quality metrics such as Average difference, Maximum Distance, Image Fidelity, Mean squared error and Peak Signal-to-Noise ratio.

The rest of the paper is organized as follows: Section 2 explains about the Finite Truncated Skew Gaussian distribution and the estimation of initial parameters is explained in Section 3. Section 4 discusses about the updating of initial estimates using EM algorithm and Section 5

demonstrates about the segmentation algorithm. The experimental results & performance evaluation are presented in Section 6 and Section 7 concludes the paper.

II. FINITE TRUNCATED SKEW GAUSSIAN DISTRIBUTION

In any medical image, pixel is used as a measure of quantification and the entire medical image is assumed as a heterogeneous collection of pixels and each pixel is influenced by various factors such as brightness, contrast, saturation etc. Skew symmetric distributions are mainly used for the set of images where the shape of image regions are not symmetric or bell shaped distribution and these distributions can be well utilized for the medical images where the bone structure of the humans are asymmetric in nature. To have a more accurate analysis of the medical images, it is customary to consider that in any image, the range of the pixels is finite in nature. Hence, to have a more closure and deeper approximation of the medical data, truncated skew normal distribution are well suited.

The probability density function of the truncated skew normal distribution is given by:

$$f_{\mu, \sigma, \lambda}(x) = \frac{2}{\sigma} \phi\left(\frac{x-\mu}{\sigma}\right) \cdot \Phi\left(\lambda \frac{x-\mu}{\sigma}\right) \quad (1)$$

Where, $\mu \in \mathbb{R}$, $\sigma > 0$ and $\lambda \in \mathbb{R}$ represents the location, scale and shape parameters respectively. Where ϕ and Φ denote the probability density function and the cumulative density function of the standard normal distribution.

The limits and of the truncated normal distribution are $Z_1 = a$ and $Z_m = b$. Where Z_1 and Z_m denotes the truncation limits.

Truncating equation (1) between these limits, we have

$$F_{\mu, \sigma, \lambda}(x) \int_a^b = F_{\mu, \sigma, \lambda}(b) - F_{\mu, \sigma, \lambda}(a) \quad (2)$$

where,

$$F_{\mu, \sigma, \lambda}(a) = \int_{-\infty}^a F_{\mu, \sigma, \lambda}(x) dx \quad (3)$$

and

$$\sigma^{l+1} = \frac{\left[\begin{array}{l} \left[\int_{-\infty}^b \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx - \right. \\ \left. \int_{-\infty}^a \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx \right] \\ \left[\int_{-\infty}^b \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx - \right. \\ \left. \int_{-\infty}^a \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx \right] \end{array} \right]}{2 \cdot \left[\begin{array}{l} \left(\int_{-\infty}^b \phi'\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx - \right) \\ \left(\int_{-\infty}^a \phi'\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx \right) \\ \left(\int_{-\infty}^b x \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx - \right) \\ \left(\int_{-\infty}^a x \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx \right) \\ \left(\int_{-\infty}^b \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx - \right) \\ \left(\int_{-\infty}^a \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx \right) \\ \left(\int_{-\infty}^b x \phi'\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx - \right) \\ \left(\int_{-\infty}^a x \phi'\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx \right) \end{array} \right]} \quad (8)$$

$$F_{\mu, \sigma, \lambda}(b) = \int_{-\infty}^b F_{\mu, \sigma, \lambda}(x) dx \quad (4)$$

where,

$f_{\mu, \sigma, \lambda}(x)$ is as given in equation (1)

$$Q = \int_{-\infty}^b \frac{2}{\sigma} \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx - \int_{-\infty}^a \frac{2}{\sigma} \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx \quad (5)$$

III. INITIALIZATION OF PARAMETERS

In order to initialize the parameters, it is needed to obtain the initial values of the model distribution. The initial estimates of the Mixture model μ_i , σ_i and α_i where $i=1,2,\dots,k$ are estimated using K-Means algorithm as proposed in section II. It is assumed that the pixel intensities of the entire image is segmented into a K component model π_i , $i=1,2,\dots,k$ with the assumption that $\pi_i = 1/k$ where k is the value obtained from K-Means algorithm discussed in Section 2.

IV. UPDATION OF INITIAL ESTIMATES THROUGH EM ALGORITHM

The initial estimates of μ_i , σ_i and α_i that are obtained from Section 4 are to be refined to obtain the final estimates. For this purpose EM algorithm is utilized. The EM algorithm consists of 2 steps E-step and M-Step. In the E-Step, the initial estimates obtained in Section 4 are taken as input and the final updated equations are obtained in the M-Step. The updated equations for the model parameters μ , σ and α are given below:

$$\mu^{l+1} = \frac{\int_{-\infty}^b x \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\alpha(x-\mu)}{\sigma}\right) dx - \int_{-\infty}^a x \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\alpha(x-\mu)}{\sigma}\right) dx}{\int_{-\infty}^b \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\alpha(x-\mu)}{\sigma}\right) dx - \int_{-\infty}^a \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\alpha(x-\mu)}{\sigma}\right) dx} \quad (6)$$

$$\alpha^{l+1} = - \frac{\int_{-\infty}^b \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}\left(\frac{\alpha(x-\mu)}{\sigma}\right) dx - \int_{-\infty}^a \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}\left(\frac{\alpha(x-\mu)}{\sigma}\right) dx}{\int_{-\infty}^b \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\alpha(x-\mu)}{\sigma}\right) dx - \int_{-\infty}^a \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\alpha(x-\mu)}{\sigma}\right) dx} \quad (7)$$

V. K-MEANS ALGORITHM

In order to segment the unsupervised data, K-means algorithm is used. K-means algorithm is one of the simplest partition clustering methods. The main disadvantage of K-means algorithm is to identify the initial value of K. Hence, a histogram is utilized for the initialization of K. The K-means algorithm is given below:

Inputs:

P = { 1, 2, k } (Pixels to be clustered)

K (No of Clusters)

Outputs:

C = { 1, 2, k } (Cluster Centroids)

m: P -> {1, 2...K} (Cluster Membership)

Algorithm K-Means:

Set C to initial value (e.g. Random selection of P)

For each $p_i \in P$

$$m(p_i) = \underset{j \in \{1..n\}}{\operatorname{argmin}} \text{distance}(p_i, c_j)$$

End

While m has changed

For each $j \in \{1..K\}$

Recompute c_j as the centroid of
{p | m(p) = j}

End

For each $p_i \in P$

$$m(p_i) = \underset{j \in \{1..n\}}{\operatorname{argmin}} \text{distance}(p_i, c_j)$$

End

End

End

VI. SEGMENTATION ALGORITHM

After refining the estimates, the important step is reconstruction of image. This process is carried out by performing the segmentation. The image segmentation is done in 3 steps:

Step-1: Obtain the initial estimates of the truncated skew Gaussian 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: The image segmentation is carried out by assigning each pixel into a proper region (Segment) according to maximum likelihood estimates of the j^{th} element L_j according to the following equation:

$$L_j = \underset{j}{\operatorname{Max}} \left\{ \int_{-\infty}^b \frac{2}{\sigma} \varphi\left(\frac{x-\mu}{\sigma}\right) \bar{\varphi}\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx \int_{-\infty}^a \frac{2}{\sigma} \varphi\left(\frac{x-\mu}{\sigma}\right) \bar{\varphi}\left(\frac{\lambda(x-\mu)}{\sigma}\right) dx \right\}$$

VII. EXPERIMENTAL RESULTS & PERFORMANCE EVALUATION

In order to evaluate the performance of the developed algorithm, we have used T_1 weighted images. The input medical images are obtained from brain web images. It is assumed that the intensities of the pixels in medical images are asymmetric in nature. Hence, follow a skew Gaussian distribution. The initialization of parameters for each segment is achieved by using K-Means algorithm and the estimates are updated using the EM algorithm.

The experimentation is carried out by using the segmentation algorithm depicted in section-6 and the obtained results are evaluated using segmentation quality metrics such as Jaccard Coefficient (JC), Volumetric Similarity (VS), Variation of Information (VOI), Probabilistic Rand Index (PRI) and Global Consistency Error (GCE) and the formulas for calculating these metrics are given as follows:

$$\text{Jaccard Coefficient (JC)} = \frac{|X \cap Y|}{|X \cup Y|} = \frac{a}{a+b+c} \quad (9)$$

$$\text{Volume Similarity (VS)} = 1 - \frac{||X| - |Y||}{|X| + |Y|} = 1 - \frac{|b-c|}{2a+b+c} \quad (10)$$

$$\text{Where, } a = |X \cap Y|, b = \left| \frac{X}{Y} \right|,$$

$$c = \left| \frac{Y}{X} \right|, \quad d = |\bar{X} \cup \bar{Y}|$$

$$\text{GCE}(S, S') = \frac{1}{N} \min\{\sum \text{LRE}(S, S', x_i), \sum \text{LRE}(S', S, x_i)\} \quad (11)$$

Where, $\text{LRE} = \frac{|C(S, x_i) \setminus C(S', x_i)|}{|C(S, x_i)|}$ S and S' are segment classes and x_i is the pixel.

$$\text{VOI}(X, Y) = H(X) + H(Y) - 2I(X; Y) \quad (12)$$

Where, X and Y are two clusters

$$\text{PRI}(S_t, \{S\}) = \frac{1}{\binom{N}{2}} \sum_{i, j, i < j} [I(l_i^{S_t} = l_j^{S_t}) p_j + I(l_i^{S_t} \neq l_j^{S_t}) (1 - p_j)] \quad (13)$$

Where, $p_j = P(l_i = l_j) = \frac{1}{K} \sum_{k=1}^K I(l_i^k = l_j^k)$ and the values range from 0 to 1. The value 1 denotes the segments are identical.

Table 1: Segmentation Quality Metrics

Image	Quality Metric	GMM	Skew GMM with K-Means-EM	Truncated SGMM with K-Means	Standard Limits	Standard Criteria
B0S1	JC	0.089	0.689	0.711	0 to 1	Close to 1
	VS	0.432	0.733	0.781	0 to 1	Close to 1
	VOI	2.3665	5.3173	5.2323	$-\infty$ to ∞	As big as Possible
	GCE	0.2802	0.5964	0.6088	0 to 1	Close to 1
	PRI	0.504	0.6396	0.6697	0 to 1	Close to 1
B0S2	JC	0.0677	0.7656	0.7921	0 to 1	Close to 1
	VS	0.3212	0.8767	0.8801	0 to 1	Close to 1
	VOI	1.9724	3.924	0	$-\infty$ to ∞	As big as Possible
	GCE	0.2443	0.4741	0	0 to 1	Close to 1
	PRI	0.416	0.5016	1	0 to 1	Close to 1
B0S3	JC	0.0434	0.6567	0.689	0 to 1	Close to 1
	VS	0.123	0.812	0.849	0 to 1	Close to 1
	VOI	0.7684	0.2916	0	$-\infty$ to ∞	As big as Possible
	GCE	0.089	0.031	0	0 to 1	Close to 1
	PRI	0.576	0.5853	1	0 to 1	Close to 1
B0S4	JC	0.0456	0.7878	0.7891	0 to 1	Close to 1
	VS	0.2233	0.3232	0.465	0 to 1	Close to 1
	VOI	1.268	1.569	0	$-\infty$ to ∞	As big as Possible
	GCE	0.056	0.091	0	0 to 1	Close to 1
	PRI	0.189	0.191	1	0 to 1	Close to 1
B1S1	JC	0.141	0.776	0.779	0 to 1	Close to 1
	VS	0.313	0.397	0.452	0 to 1	Close to 1
	VOI	1.6499	4.0874	3.9136	$-\infty$ to ∞	As big as Possible
	GCE	0.1874	0.4487	0.4651	0 to 1	Close to 1
	PRI	0.9256	0.6678	0.7578	0 to 1	Close to 1
B1S2	JC	0.098	0.7892	0.7902	0 to 1	Close to 1
	VS	0.04334	0.878	0.898	0 to 1	Close to 1
	VOI	2.3215	2.8047	0	$-\infty$ to ∞	As big as Possible
	GCE	0.2838	0.3407	0	0 to 1	Close to 1
	PRI	0.3807	0.369	1	0 to 1	Close to 1
B1S3	JC	0.0222	0.8926	0.899	0 to 1	Close to 1
	VS	0.3223	0.3429	0.425	0 to 1	Close to 1
	VOI	1.2411	0.9988	0	$-\infty$ to ∞	As big as Possible
	GCE	0.1466	0.1157	0	0 to 1	Close to 1
	PRI	0.9576	0.9662	1	0 to 1	Close to 1
B1S4	JC	0.455	0.762	0.797	0 to 1	Close to 1
	VS	0.329	0.7001	0.779	0 to 1	Close to 1
	VOI	-8.8e-16	0	0	$-\infty$ to ∞	As big as Possible
	GCE	0	0	0	0 to 1	Close to 1
	PRI	1	1	1	0 to 1	Close to 1

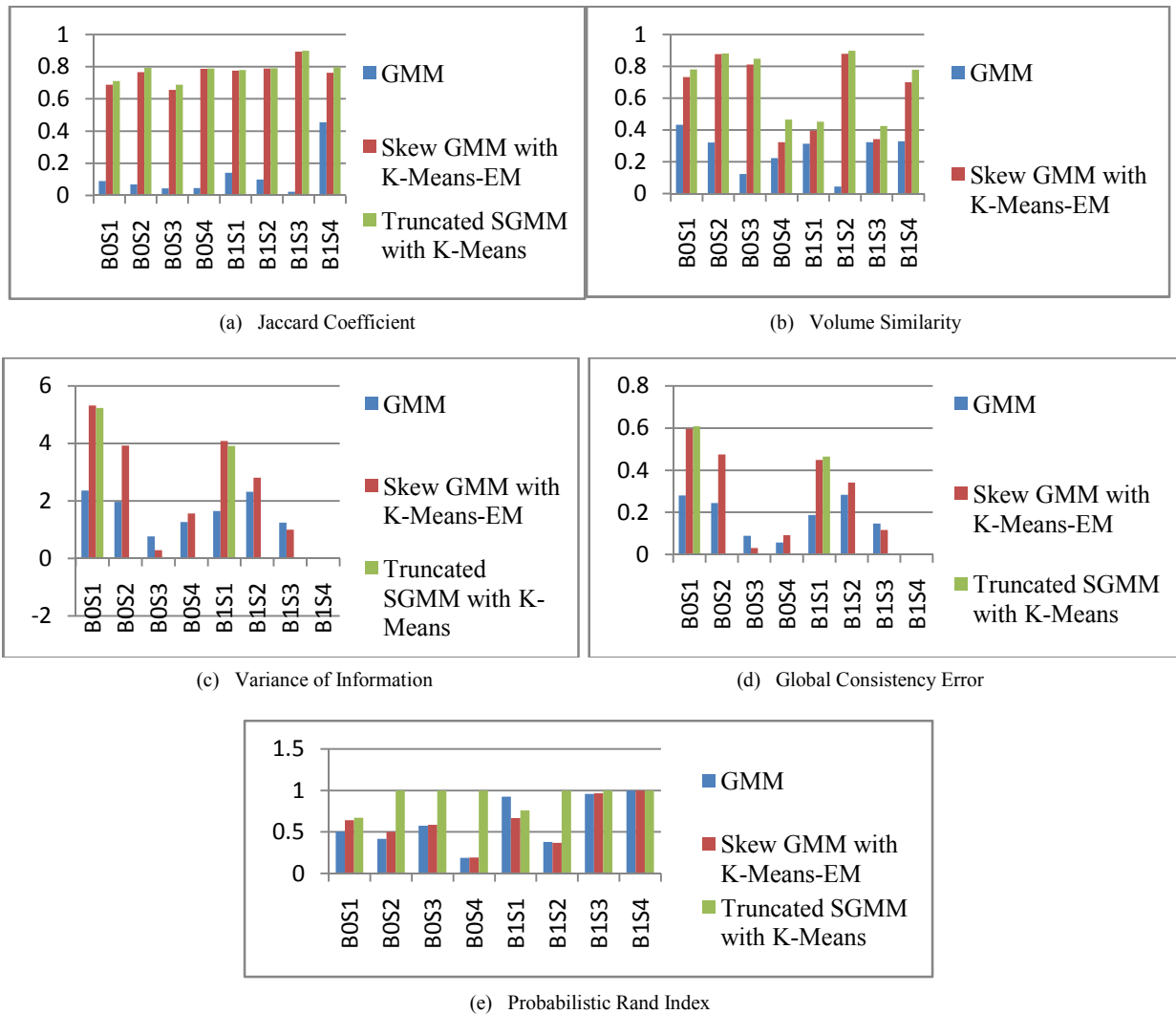


Fig. 1: Comparison of Image Segmentation Techniques









The reconstruction process is carried out by positioning each pixel into its appropriate location. The performance evaluation of the obtained output is done using the image quality metrics such as Average difference, Maximum distance, Image Fidelity, Means Squared Error and Peak Signal-to-Noise ratio. The formula for computing the above quality metrics are as follows (Table II):

Table II: Formula for Computing Quality Metrics

Quality metric	Formula to Evaluate
Average Difference	$\sum_{j=1}^M \sum_{k=1}^N [F(j, k) - \hat{F}(j, k)] / MN$ <p>Where M,N are image matrix rows and columns</p>
Maximum Distance	$\text{Max}\{ F(j, k) - \hat{F}(j, k) \}$
Image Fidelity	$1 - \left[\frac{\sum_{j=1}^M \sum_{k=1}^N [F(j, k) - \hat{F}(j, k)]^2}{\sum_{j=1}^M \sum_{k=1}^N [F(j, k)]^2} \right]$ <p>Where M,N are image matrix rows and columns</p>
Mean Squared error	$\frac{1}{MN} \sum_{j=1}^M \sum_{k=1}^N [O\{F(j, k)\} - O\{\hat{F}(j, k)\}]^2 / \sum_{j=1}^M \sum_{k=1}^N [O\{F(j, k)\}]^2$ <p>Where M,N are image matrix rows and columns</p>
Signal to noise ratio	$20 \cdot \log_{10} \left(\frac{MAX_I}{\sqrt{MSE}} \right)$ <p>Where, MAX_I is maximum possible pixel value of image, MSE is the Mean squared error</p>

The developed algorithm is compared with Skew Gaussian mixture model with K-Means and the results obtained are tabulated in Table I, Table III and Fig. 1.

Table III: Image Quality Metrics

Image	Quality Metric	GMM	Skew GMM with K-Means	Truncated SGMM with K-Means	Standard Limits	Standard Criteria
	Average Difference Maximum Distance Image Fidelity Mean Squared error Signal to noise ratio	0.573 0.422 0.416 0.04 17.41	0.773 0.922 0.875 0.134 29.23	0.792 0.941 0.428 2.19e-005 72.15	-1 to 1 -1 to 1 0 to 1 0 to 1 -∞ to ∞	Closer to 1 Closer to 1 Closer to 1 Closer to 0 As big as Possible
	Average Difference Maximum Distance Image Fidelity Mean Squared error Signal to noise ratio	0.37 0.221 0.336 0.2404 14.45	0.876 0.897 0.876 0.211 35.65	0.887 0.910 0.894 0.124 84.23	-1 to 1 -1 to 1 0 to 1 0 to 1 -∞ to ∞	Closer to 1 Closer to 1 Closer to 1 Closer to 0 As big as Possible
	Average Difference Maximum Distance Image Fidelity Mean Squared error Signal to noise ratio	0.456 0.345 0.44 0.22 19.88	0.76 0.879 0.86 0.23 37.98	0.796 0.847 0.883 0.2012 77.46	-1 to 1 -1 to 1 0 to 1 0 to 1 -∞ to ∞	Closer to 1 Closer to 1 Closer to 1 Closer to 0 As big as Possible
	Average Difference Maximum Distance Image Fidelity Mean Squared error Signal to noise ratio	0.231 0.224 0.212 0.24 21.42	0.473 0.977 0.813 0.121 33.28	0.5023 0.954 0.889 0.1012 35.6	-1 to 1 -1 to 1 0 to 1 0 to 1 -∞ to ∞	Closer to 1 Closer to 1 Closer to 1 Closer to 0 As big as Possible
	Average Difference Maximum Distance Image Fidelity Mean Squared error Signal to noise ratio	0.342 0.317 0.391 0.2514 3.241	0.764 0.819 0.812 0.228 5.514	0.7661 0.919 0.856 1.34e-005 32.154	-1 to 1 -1 to 1 0 to 1 0 to 1 -∞ to ∞	Closer to 1 Closer to 1 Closer to 1 Closer to 0 As big as Possible
	Average Difference Maximum Distance Image Fidelity Mean Squared error Signal to noise ratio	0.21 0.21 0.2134 0.06 13.43	0.3653 0.892 0.787 0.145 49.22	0.654 0.8825 0.813 0 99	-1 to 1 -1 to 1 0 to 1 0 to 1 -∞ to ∞	Closer to 1 Closer to 1 Closer to 1 Closer to 0 As big as Possible
	Average Difference Maximum Distance Image Fidelity Mean Squared error Signal to noise ratio	0.3232 0.123 0.233 0.01 11.11	0.322 0.212 0.897 0.4345 27.267	0.554 0.413 0.917 0.002 39.12	-1 to 1 -1 to 1 0 to 1 0 to 1 -∞ to ∞	Closer to 1 Closer to 1 Closer to 1 Closer to 0 As big as Possible
	Average Difference Maximum Distance Image Fidelity Mean Squared error Signal to noise ratio	0.314 0.241 0.293 0.18 21.214	0.338 0.249 0.683 0.197 78.19	0.635 0.294 0.697 0.113 99	-1 to 1 -1 to 1 0 to 1 0 to 1 -∞ to ∞	Closer to 1 Closer to 1 Closer to 1 Closer to 0 As big as Possible

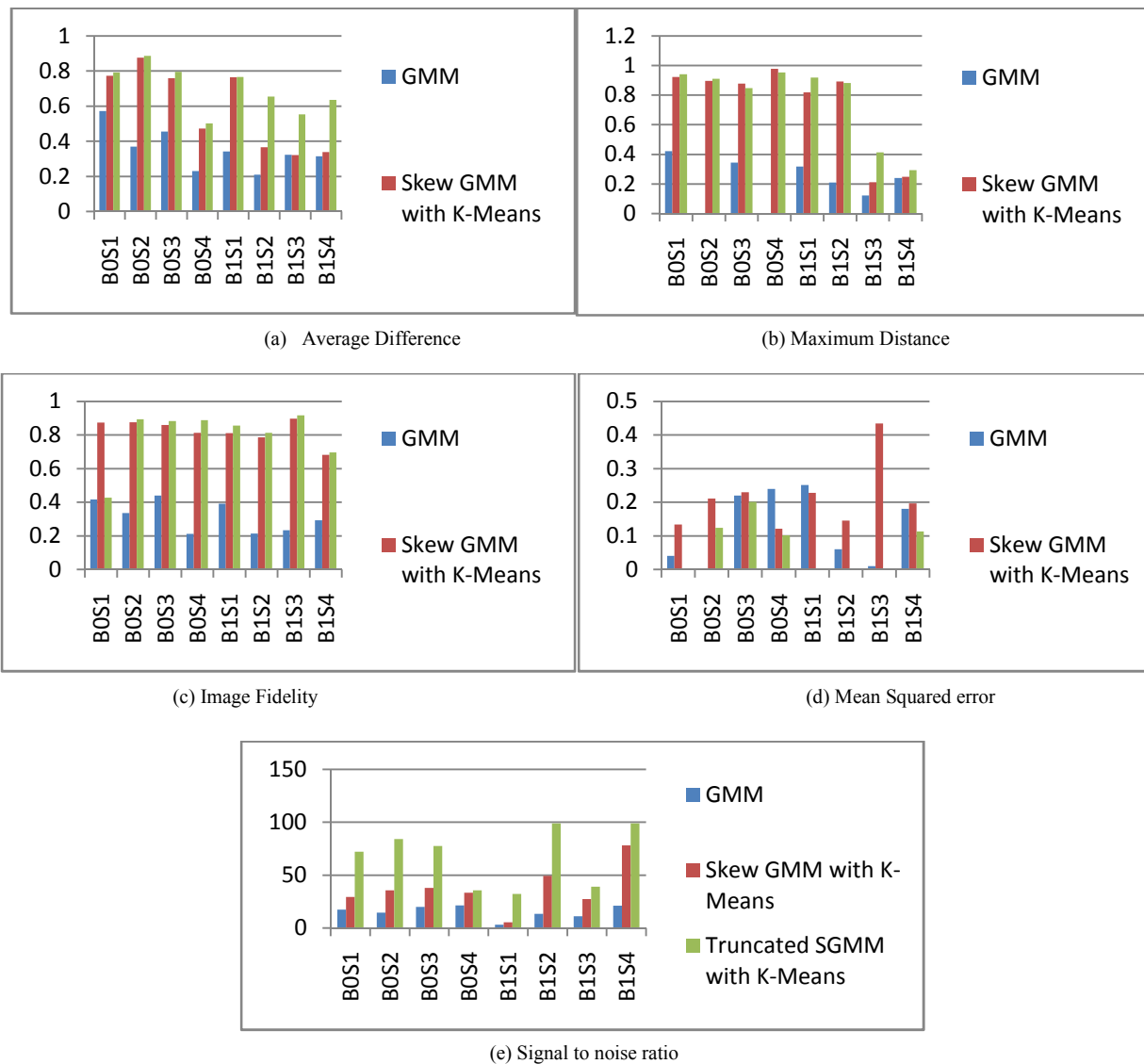


Fig. 2: Comparison of Image Segmentation Techniques

From the above Table II, Table III and Fig. 2, it can be clearly seen that the developed algorithm yields better results than the existing methods on Medical image segmentation based on Gaussian mixture model and Skew Gaussian mixture model using K-Means algorithm.

VIII. CONCLUSION

Segmentation plays an important role in the field of medical imaging. It is essential to diagnose the diseases like acoustic neuroma more accurately which help better treatment. Hence, it is needed to segment the image more accurately, which helps in identifying the damaged tissues much more efficiently. Thus, this paper suggests a new approach based on Finite Truncated Skew Gaussian distribution. The performance evaluation is carried out by using quality metrics which show that the developed algorithm is more efficient than the other algorithms.

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