



## On Improved Medical Brain MR Image Segmentation Based on Truncated Skew Gaussian Mixture model using Hierarchical Clustering and EM Algorithms

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**Abstract:** These days MRI segmentation is becoming more vital in diagnosing the cancer in the patients much effectively. There are plenty of methods available to segment the brain MR images. Among those methods, unsupervised methods are highly advised since they do not require any human interaction for segmenting with high precision. But, still there is a scope for improvement in the field of medical image segmentation. Hence, in this paper we proposed a novel approach for segmenting the MRI brain image based on Finite Truncated Skew Gaussian Mixture Model using Hierarchical Clustering algorithm. The obtained results are compared with various other techniques and the performance evaluation is performed using Image quality metrics and Segmentation metrics.

**Keywords:** Finite Truncated Skew Gaussian Mixture model, Segmentation, Image quality metrics, Segmentation metrics.

### I. INTRODUCTION

MRI segmentation plays a vital role in research and medical applications. MRI has wide range of advantages over other conventional imaging techniques as magnetization and radio waves are used instead of X-rays in making the detailed and cross-sectional images of the brain [1]. Various operations based on image processing were defined earlier on MR images. Among these, segmentation of brain images into sub-regions has enormous research and medical applications. These sub-regions are utilized in visualizing and analyzing the anatomical structures in the brain which help in neuro-surgical planning [2].

There are enormous conventional methods for MRI segmentation which require human interaction in terms of specifying the number of classes to obtain accurate and reliable segmentation. Therefore, it is essential to derive new techniques to segment effectively. Most of the emphasis has been given to the segmentation algorithm based on finite normal mixture models in which each image is assumed to be a mixture of Gaussian distributions. But, in reality it is observed that the pixels are quantized through the brightness or contrast in the gray scale level ( $Z$ ) at that point. It has been observed that the regions have a finite range of pixel intensities  $(-\infty, +\infty)$  and may not be symmetric and Mesokurtic [3]. Hence, in this paper to have an appropriate modeling of the feature vector, we considered

finite truncated skew Gaussian distribution by assuming that the pixel intensities in the entire image follow a Finite Truncated Skew Gaussian distribution [4].

Hence, in order to segment more accurately Hierarchical Clustering algorithm is widely preferred because of the additional flexibility that allows the pixel to belong to multiple classes with varying degree of membership [5].

Thus, in this paper we propose an effective Hierarchical clustering algorithm to segment the image into number of regions and derive the model parameters. The obtained parameters are refined further using the EM algorithm.

The rest of the paper is organized as follows: section-2 explains about the Hierarchical Clustering algorithm, section-3 deals with the concept of Finite Truncated Skew Gaussian distribution and section-4 handles the initialization of parameters. Section-5 shows the updation of parameters and section-6 demonstrates the proposed segmentation algorithm. In section-7 the experimental results are discussed and finally section-8 concludes the paper.

### II. HIERARCHICAL CLUSTERING

Clustering aims at partitioning the data without using the training data, hence, they are called unsupervised models. Clustering is defined as a technique where the objects of interest with similarity along the dimension of interest are kept close and the other objects are apart. The dimension of interest depends on the application [8].

A Hierarchical Clustering goes one step further by collecting similar clusters at different levels into a single cluster by forming a tree which gives better selection of clusters for further exploration and hence, in this method Hierarchical Clustering is utilized.

Given a set of N items to be segmented and an  $M \times N$  distance (or similarity) matrix, the basic process of hierarchical segmenting is as follows.

- a. First, assign each item to a segment, so that if we have N items, it implies that we have N segments, each containing just one item. Let the distances (similarities) between the segments be the same as those (similarities) between the items they contain.
- b. Find the closest (most similar) pair of segments and merge them into a single segment, i.e. we will now have one segment less.
- c. Compute distances (similarities) between the new segment and each of the old segments.

Repeat steps 2 and 3 until all items are segmented into a single segment of size N.

Step 3 can be done using single-linkage method. In single-linkage segmenting (also called the connectedness or minimum method), we consider the between one segment and another to be equal to the shortest distance from any member of one segment to any member of the other segment. If the data consist of similarities, we consider the similarity between one segment and another to be equal to the greatest similarity from any member of one segment to any member of the other segment. The  $M \times N$  proximity matrix is  $D = [d(i, j)]$ . The segmenting is assigned sequence numbers  $0, 1, \dots, (n - 1)$  and  $L(k)$  is the level of the  $k^{th}$  segmenting. A segment with sequence number  $m$  is denoted as  $(m)$  and the proximity between segments  $(r)$  and  $(s)$  is denoted as  $d[(r), (s)]$ . The algorithm is composed of the following steps:

- a. Start with the disjoint segments having level  $L(0) = 0$  and sequence number  $m = 0$ .
- b. Find the least dissimilar pair of segments in the current  $s$ , say pair  $(r), (s)$ , where the minimum is over all pairs of segments in the current segmenting.
- c. Increment the sequence number:  $m = m + 1$ . Merge segments  $(r)$  and  $(s)$  into a single segment to form the next segmenting  $m$ . Set the level of this segmenting to  $L(m) = d[(r), (s)]$ .
- d. Update the proximity matrix,  $D$ , by deleting the rows and columns corresponding to segments  $(r)$  and  $(s)$  and adding a row and column corresponding to the newly formed segment. The proximity between the new segment, denoted  $(r, s)$  and the old segment  $(k)$  is defined as  $d[(k), (r, s)] = \min(d[(k), (r)], d[(k), (s)])$ .

If all objects are in one segment, stop. Else, go to step.2

### III. 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

$$f_{\mu, \sigma, \lambda}(x) = \frac{2}{\sigma} \phi\left(\frac{x-\mu}{\sigma}\right) \cdot \Phi\left(\lambda \frac{x-\mu}{\sigma}\right) \quad (5)$$

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

The limits and of the truncated normal distribution are  $Z_l = a$  and  $Z_m = b$ . Where  $Z_l$  and  $Z_m$  denotes the truncation limits. Truncating equation (1) between these limits, we have

$$F_{\mu, \sigma, \lambda}(x) \int_a^b = F_{\mu, \sigma, \lambda}(b) - F_{\mu, \sigma, \lambda}(a) \quad (6)$$

where,

$$F_{\mu, \sigma, \lambda}(a) = \int_{-\infty}^a F_{\mu, \sigma, \lambda}(x) dx \quad (7) \text{ and}$$

$$F_{\mu, \sigma, \lambda}(b) = \int_{-\infty}^b F_{\mu, \sigma, \lambda}(x) dx \quad (8)$$

where,

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

$$Q = \int_{-\infty}^b \frac{2}{\sigma} \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}\left(\lambda \frac{x-\mu}{\sigma}\right) dx - \int_{-\infty}^a \frac{2}{\sigma} \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}\left(\lambda \frac{x-\mu}{\sigma}\right) dx \quad (9)$$

### IV. 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  $\mu_i, \sigma_i, \lambda_i$  and  $\alpha_i$  where  $i=1, 2, \dots, k$  are estimated using Hierarchical Clustering algorithm as proposed in section-2. It is assumed that the pixel intensities of the entire image is segmented into a  $K$  component model  $\pi_i, i=1, 2, \dots, k$  with the assumption that  $\pi_i = 1/k$  where  $k$  is the value obtained from Hierarchical Clustering algorithm discussed in section-2.

### V. UPDATION OF INITIAL ESTIMATES THROUGH EM ALGORITHM

The initial estimates of  $\mu_i, \sigma_i$  and  $\alpha_i$  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  $\mu, \sigma$  and  $\alpha$  are given below.

$$\mu^{l+1} = \frac{\int_{-\infty}^b x \cdot \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\alpha(x-\mu)}{\sigma}\right) dx - \int_{-\infty}^a x \cdot \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\alpha(x-\mu)}{\sigma}\right) dx}{\int_{-\infty}^b \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\alpha(x-\mu)}{\sigma}\right) dx - \int_{-\infty}^a \phi\left(\frac{x-\mu}{\sigma}\right) \bar{\Phi}'\left(\frac{\alpha(x-\mu)}{\sigma}\right) dx} \quad (10)$$

**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 and as the limits are finite and within the specified range of values are only necessary in medical image segmentation process we have considered Truncated Skew Gaussian distribution. The initialization of parameters for each segment is achieved by using Hierarchical Clustering 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 Jacquard 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:

$$\text{Jaccard Coefficient (JC)} = \frac{|X \cap Y|}{|X \cup Y|} = \frac{a}{a+b+c} \quad (13)$$

$$\text{Volume Similarity (VS)} = 1 - \frac{||X|-|Y||}{|X|+|Y|} = 1 - \frac{|b-c|}{2a+b+c} \quad (14)$$

Where,  $a = |X \cap Y|, b = \left| \frac{X}{Y} \right|, c = \left| \frac{Y}{X} \right|, d = |\overline{X \cup Y}|$

$$\text{GCE}(S, S') = \frac{1}{N} \min\{\sum \text{LRE}(S, S', x_i), \sum \text{LRE}(S', S, x_i)\} \quad (15)$$

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.

$$\text{VOI}(X, Y) = H(X) = H(Y) - 2I(X; Y) \quad (16)$$

Where, X and Y are two clusters

$$\text{PRI}(S_t, \{S\}) = \frac{1}{\binom{N}{2}} \sum_{i,j,i < j} [I(l_i^{S_t} = l_j^{S_t})p_j + I(l_i^{S_t} \neq l_j^{S_t})(1-p_j)] \quad (17)$$

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.

$$\alpha^{l+1} = \frac{\int_{-\infty}^b \varphi' \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi} \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx - \int_{-\infty}^a \varphi' \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi} \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx}{\int_{-\infty}^b \varphi \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi}' \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx - \int_{-\infty}^a \varphi \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi}' \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx} \quad (11)$$

$$\sigma^{l+1} = \frac{\left[ \begin{array}{l} \int_{-\infty}^b \varphi \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi} \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx - \\ \int_{-\infty}^a \varphi \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi} \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx \\ \int_{-\infty}^b \varphi \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi}' \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx - \\ \int_{-\infty}^a \varphi \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi}' \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx \end{array} \right]}{2 \cdot \left[ \begin{array}{l} \int_{-\infty}^b \varphi' \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi} \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx - \\ \int_{-\infty}^a \varphi' \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi} \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx \\ \int_{-\infty}^b x \varphi \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi}' \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx - \\ \int_{-\infty}^a x \varphi \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi}' \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx \\ \int_{-\infty}^b \varphi \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi}' \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx - \\ \int_{-\infty}^a \varphi \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi}' \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx \\ \int_{-\infty}^b x \varphi' \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi} \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx - \\ \int_{-\infty}^a x \varphi' \left( \frac{x-\mu}{\sigma} \right) \bar{\varphi} \left( \frac{\lambda(x-\mu)}{\sigma} \right) dx \end{array} \right]} \quad (12)$$

**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:

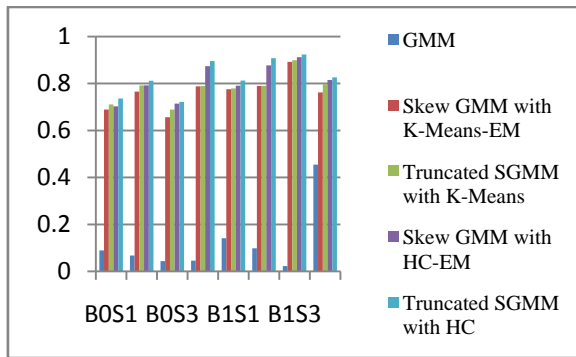
- Step-1: Obtain the initial estimates of the finite truncated skew Gaussian mixture model using Hierarchical Clustering algorithm.
- Step-2: Using the initial estimates obtained from step-1, the EM algorithm is iteratively carried out.
- Step-3: The image segmentation is carried out by assigning each pixel into a proper region (Segment) according to maximum likelihood estimates of the  $j^{\text{th}}$  element  $L_j$  according to the following equation

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

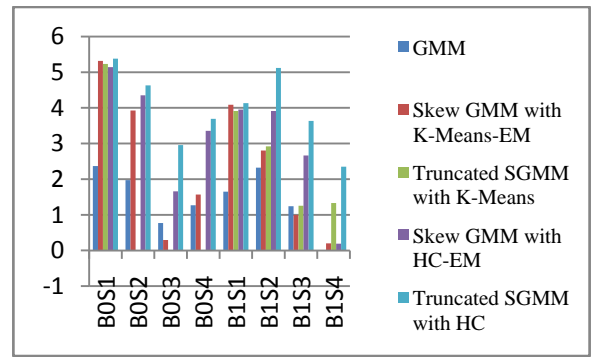
Table: I Segmentation Quality Metrics

Image	Quality Metric	GMM	Skew GMM with K-Means-EM	Truncated SGMM with K-Means	Skew GMM with HC-EM	Truncated SGMM with HC	Standard Limits	Standard Criteria
BOS1	JC	0.089	0.689	0.711	0.703	0.736	0 to 1	Close to 1
	VS	0.432	0.733	0.781	0.8799	0.887	0 to 1	Close to 1
	VOI	2.3665	5.3173	5.2323	5.142	5.381	$-\infty$ to $\infty$	Possible Big
	GCE	0.2802	0.5964	0.6088	0.561	0.626	0 to 1	Close to 1
	PRI	0.504	0.6396	0.6697	0.619	0.663	0 to 1	Close to 1

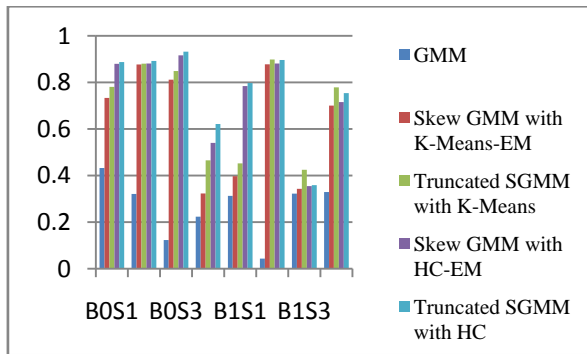
B0S2	JC	0.0677	0.7656	0.7921	0.7921	0.812	0 to 1	Close to 1
	VS	0.3212	0.8767	0.8801	0.8814	0.892	0 to 1	Close to 1
	VOI	1.9724	3.924	0	4.35	4.63	$-\infty$ to $\infty$	Possible Big
	GCE	0.2443	0.4741	0	0.419	0.5013	0 to 1	Close to 1
	PRI	0.416	0.5016	1	0.514	0.542	0 to 1	Close to 1
B0S3	JC	0.0434	0.6567	0.689	0.7143	0.722	0 to 1	Close to 1
	VS	0.123	0.812	0.849	0.916	0.932	0 to 1	Close to 1
	VOI	0.7684	0.2916	0	1.659	2.956	$-\infty$ to $\infty$	Possible Big
	GCE	0.089	0.031	0	0.107	0.02	0 to 1	Close to 1
	PRI	0.576	0.5853	1	0.632	0.661	0 to 1	Close to 1
B0S4	JC	0.0456	0.7878	0.7891	0.874	0.896	0 to 1	Close to 1
	VS	0.2233	0.3232	0.465	0.54	0.621	0 to 1	Close to 1
	VOI	1.268	1.569	0	3.354	3.693	$-\infty$ to $\infty$	Possible Big
	GCE	0.056	0.091	0	0.157	0.199	0 to 1	Close to 1
	PRI	0.189	0.191	1	0.496	0.519	0 to 1	Close to 1
B1S1	JC	0.141	0.776	0.779	0.791	0.8123	0 to 1	Close to 1
	VS	0.313	0.397	0.452	0.784	0.797	0 to 1	Close to 1
	VOI	1.6499	4.0874	3.9136	3.951	4.13	$-\infty$ to $\infty$	Possible Big
	GCE	0.1874	0.4487	0.4651	0.418	0.4468	0 to 1	Close to 1
	PRI	0.9256	0.6678	0.7578	0.6258	0.6692	0 to 1	Close to 1
B1S2	JC	0.098	0.7892	0.7902	0.877	0.908	0 to 1	Close to 1
	VS	0.0433	0.878	0.898	0.881	0.896	0 to 1	Close to 1
	VOI	2.3215	2.8047	2.921	3.91	5.122	$-\infty$ to $\infty$	Possible Big
	GCE	0.2838	0.3407	0.348	0.339	0.3695	0 to 1	Close to 1
	PRI	0.3807	0.369	0.429	0.485	0.561	0 to 1	Close to 1
B1S3	JC	0.0222	0.8926	0.899	0.9124	0.9236	0 to 1	Close to 1
	VS	0.3223	0.3429	0.425	0.3543	0.359	0 to 1	Close to 1
	VOI	1.2411	0.9988	1.252	2.665	3.6351	$-\infty$ to $\infty$	Possible Big
	GCE	0.1466	0.1157	0.227	0.398	0.424	0 to 1	Close to 1
	PRI	0.9576	0.9662	0.856	0.652	0.698	0 to 1	Close to 1
B1S4	JC	0.455	0.762	0.797	0.815	0.826	0 to 1	Close to 1
	VS	0.329	0.7001	0.779	0.7158	0.754	0 to 1	Close to 1
	VOI	-8.8e-16	0.201	1.332	0.19	2.35	$-\infty$ to $\infty$	Possible Big
	GCE	0.119	0.112	0.176	0.212	0.265	0 to 1	Close to 1
	PRI	0.065	0.1001	0.129	0.27	0.353	0 to 1	Close to 1



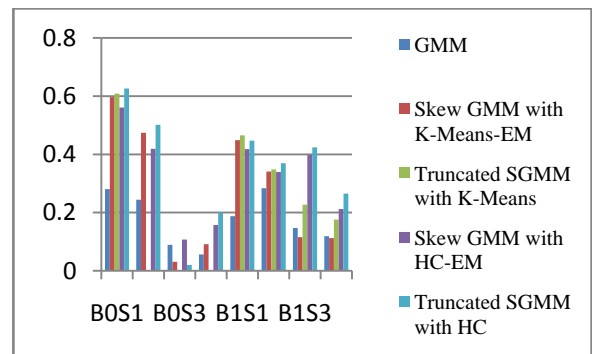
a. Jacquard Coefficient



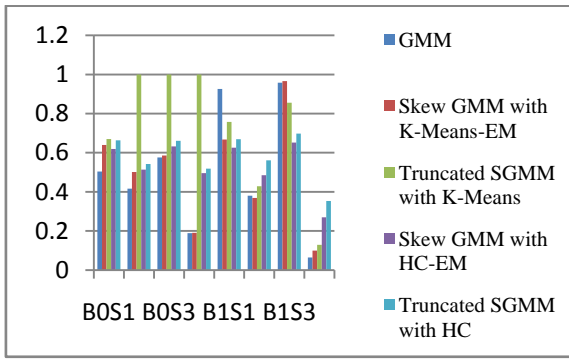
c. Variation of Information



b. Volume Similarity



d. Global Consistency Error



e. Probabilistic Rand Index

Graph: 1 Segmentation Quality Metrics

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:

Quality metric	Formula to Evaluate
Average Difference (AV)	$\frac{1}{MN} \sum_{j=1}^M \sum_{k=1}^N [F(j, k) - \hat{F}(j, k)]$ Where M,N are image matrix rows and columns

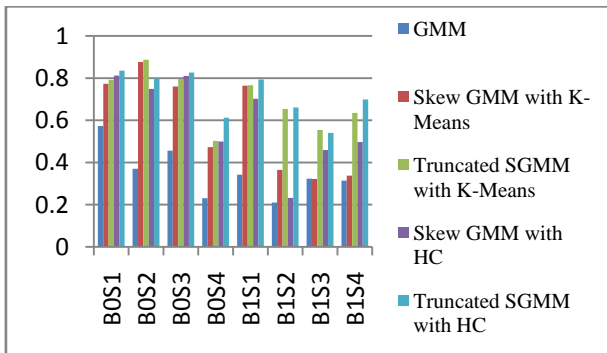
Maximum Distance (MD)	$\text{Max}\{ F(j, k) - \hat{F}(j, k) \}$
Image Fidelity (IF)	$1 - \frac{\sum_{j=1}^M \sum_{k=1}^N [F(j, k) - \hat{F}(j, k)]^2}{\sum_{j=1}^M \sum_{k=1}^N [F(j, k)]^2}$ Where M,N are image matrix rows and columns
Mean Squared error (MSE)	$\frac{1}{MN} \sum_{j=1}^M \sum_{k=1}^N [O\{F(j,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

The Developed algorithm is compared with Skew Gaussian mixture model with K-Means, Hierarchical Clustering Fuzzy C-Means, Truncated Skew Gaussian Mixture model with K-Means and Hierarchical Clustering algorithms and the results obtained are tabulated in table-1, Table-2. Graphs-I, Graphs-II and Fig.-1

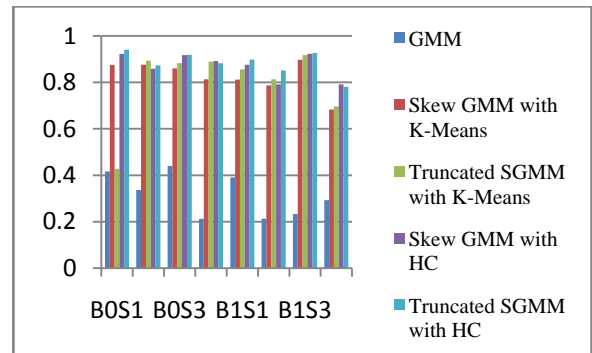
Table: II Image Quality Metrics

Image	Quality Metric	GMM	Skew GMM with K-Means	Truncated SGMM with K-Means	Skew GMM with HC	Truncated SGMM with HC	Standard Limits	Standard Criteria
BOS1	AD	0.573	0.773	0.792	0.812	0.835	-1 to 1	Closer to 1
	MD	0.422	0.922	0.941	0.9325	0.939	-1 to 1	Closer to 1
	IF	0.416	0.875	0.428	0.923	0.941	0 to 1	Closer to 1
	MSE	0.04	0.134	2.19e-005	0.094	2.92E-005	0 to 1	Closer to 0
	SNR	17.41	29.23	72.15	33.89	87.39	-∞ to ∞	Possible Big
BOS2	AD	0.37	0.876	0.887	0.749	0.798	-1 to 1	Closer to 1
	MD	0.221	0.897	0.910	0.912	0.926	-1 to 1	Closer to 1
	IF	0.336	0.876	0.894	0.859	0.873	0 to 1	Closer to 1
	MSE	0.240	0.211	0.124	0.2019	0.102	0 to 1	Closer to 0
	SNR	14.45	35.65	84.23	39.85	89.65	-∞ to ∞	Possible Big
BOS3	AD	0.456	0.76	0.796	0.81	0.826	-1 to 1	Closer to 1
	MD	0.345	0.879	0.847	0.807	0.86	-1 to 1	Closer to 1
	IF	0.44	0.86	0.883	0.917	0.919	0 to 1	Closer to 1
	MSE	0.22	0.23	0.2012	0.2123	0.267	0 to 1	Closer to 0
	SNR	19.88	37.98	77.46	39.71	82.31	-∞ to ∞	Possible Big
BOS4	AD	0.231	0.473	0.5023	0.4991	0.612	-1 to 1	Closer to 1
	MD	0.224	0.977	0.954	0.971	0.977	-1 to 1	Closer to 1
	IF	0.212	0.813	0.889	0.892	0.882	0 to 1	Closer to 1
	MSE	0.24	0.121	0.1012	0.1192	1.02E-05	0 to 1	Closer to 0
	SNR	21.42	33.28	35.6	37.41	78.8	-∞ to ∞	Possible Big

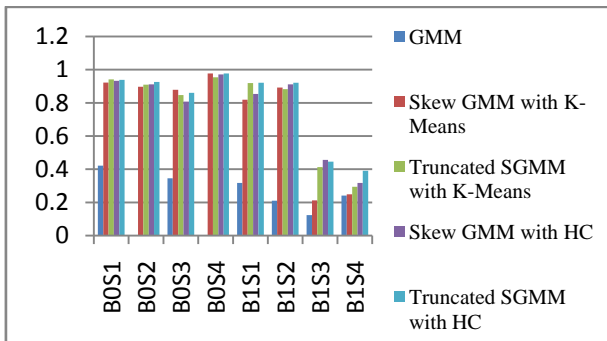
B1S1	AD	0.342	0.764	0.7661	0.7015	0.794	-1 to 1	Closer to 1
	MD	0.317	0.819	0.919	0.854	0.921	-1 to 1	Closer to 1
	IF	0.391	0.812	0.856	0.876	0.898	0 to 1	Closer to 1
	MSE	0.251	0.228	1.34e-005	0.1759	2.64E-005	0 to 1	Closer to 0
	SNR	3.241	5.514	32.154	5.68	89.31	$-\infty$ to $\infty$	Possible Big
B1S2	AD	0.21	0.3653	0.654	0.232	0.661	-1 to 1	Closer to 1
	MD	0.21	0.892	0.8825	0.912	0.921	-1 to 1	Closer to 1
	IF	0.213	0.787	0.813	0.791	0.851	0 to 1	Closer to 1
	MSE	0.06	0.145	0.096	0.594	0.024	0 to 1	Closer to 0
	SNR	13.43	49.22	99	20.39	99	$-\infty$ to $\infty$	Possible Big
B1S3	AD	0.323	0.322	0.554	0.4592	0.54	-1 to 1	Closer to 1
	MD	0.123	0.212	0.413	0.456	0.446	-1 to 1	Closer to 1
	IF	0.233	0.897	0.917	0.923	0.926	0 to 1	Closer to 1
	MSE	0.01	0.4345	0.002	0.119	1.29E-005	0 to 1	Closer to 0
	SNR	11.11	27.267	39.12	29.86	71.69	$-\infty$ to $\infty$	Possible Big
B1S4	AD	0.314	0.338	0.635	0.497	0.699	-1 to 1	Closer to 1
	MD	0.241	0.249	0.294	0.317	0.391	-1 to 1	Closer to 1
	IF	0.293	0.683	0.697	0.791	0.781	0 to 1	Closer to 1
	MSE	0.18	0.197	0.113	0.213	0.829	0 to 1	Closer to 0
	SNR	21.21	78.19	99	99	99	$-\infty$ to $\infty$	Possible Big



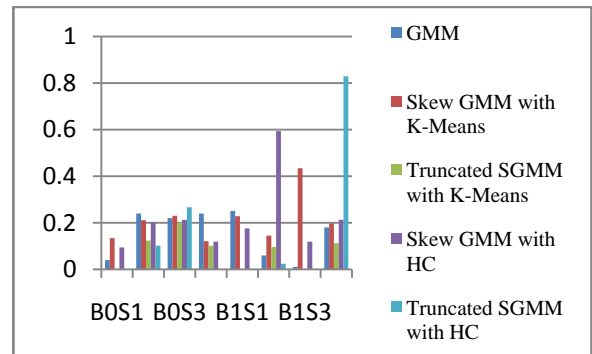
a. Average Difference



c. Image Fidelity

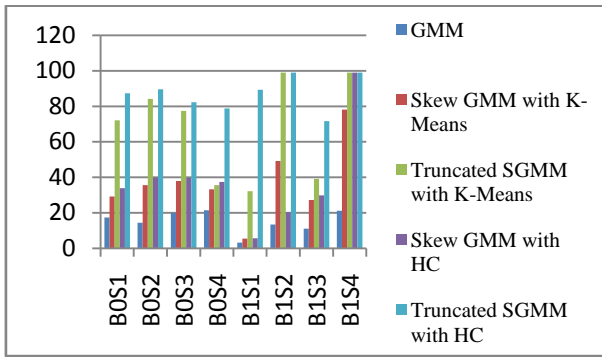


b. Maximum Distance



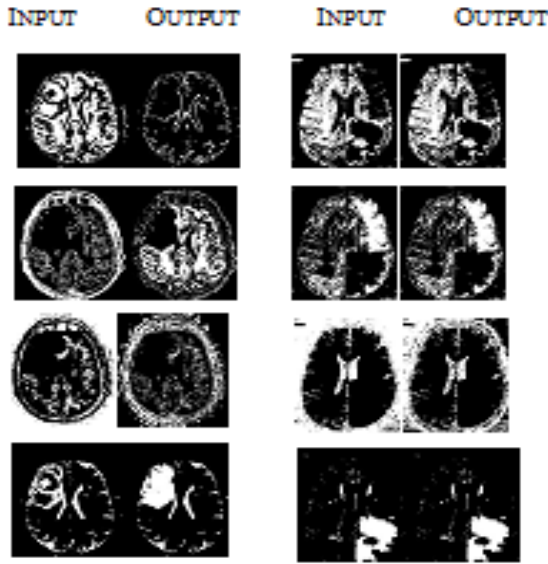
d. Mean Square Error





e. Singal to Niise Ratio

Graph: 2 Image Quality Metrics



(a) B0 Image (b) B1 Image  
Figure: 1 Input and Output Image

At the outset, from the above Table-1, Table-2, Graphs-1, Graphs-2 and figure-1 it can be clearly identified that the developed algorithm gives much better results than the existing methods on Medical image segmentation based on Gaussian mixture model and Skew Gaussian mixture models using K-Means, Hierarchical clustering and truncated skew gaussian mixture models using K-Means.

### VIII. CONCLUSION

Segmentation has an important role to play in the field of medical imaging. It is necessary to accurately identify the diseases like acoustic neuroma, Alzheimer’s, Parkinson’s etc. to provide better treatment. Therefore, it is essential to segment the image much more appropriately to help in identifying the damaged tissues with higher efficiency. Hence,

this paper suggests a new approach based on Finite Truncated Skew Gaussian Mixture Model. The experimental results also show that the suggested technique outperforms the existing models.

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