Unsupervised image segmentation using finite doubly truncated Gaussian mixture model and hierarchical clustering

Srinivas Yarramalle¹ and K. Srinivas Rao^{2,*}

¹Department of Information Technology, College of Engineering, GITAM, Visakhapatnam 530 045, India

A new image segmentation method based on finite truncated Gaussian mixture model has been proposed. The truncated Gaussian distribution includes several of the skewed and asymmetric distributions as particular cases with a finite range. It also includes the Gaussian distribution as a limiting case. We used the Estimation Maximization algorithm to estimate the model parameters of the image data and the number of mixture components was estimated using hierarchical clustering algorithm. This algorithm was also utilized for developing the initial estimates of the EM algorithm. Segmentation was carried out by clustering each pixel into the appropriate component according to the maximum likelihood estimation criteria. The advantage of our method lies in its efficiency on initialization of the model parameters and segmenting images in a totally unsupervised manner. Experimental results show that this segmentation method can provide better results than the other methods.

Keywords: EM algorithm, image segmentation, image quality metrics, truncated Gaussian mixture distribution.

IMAGE segmentation is widely used in many applications. With segmentation it is possible to identify the regions of interest and objects which are highly useful to subsequent image analysis or image animation. For example, many communication tasks require high comprehensive ratio to save network resources. The common method to realize the higher comprehensive ratio is to discriminate the objects for the image and compress the necessary objects for the user. This makes image segmentation useful for providing the necessary information and image retrieval¹.

Image segmentation is defined as the process of dividing the image into different regions, such that each region is homogeneous. For intensity image segmentation there exist three popular approaches, namely (i) histogram analysis technique, (ii) region growing and (iii) edge detection. A more comprehensive discussion on image segmentation has been presented^{2–4}. There does not exist a single generic algorithm that works for all applications.

Target applications vary in the necessary degree of precession, efficiency and intensity information required from image segmentation. For applications like contentbased image retrieval and video compression, the ability to preserve the spatial relationships between objects can improve image retrieval efficiently for content-based image retrieval. Segmentation schemes can be used to extract information on the number of mixture components that can be used for initialization of model parameters. Recently, with progress in research on Gaussian mixture models, image segmentation based on Gaussian mixture models has also become popular⁵⁻⁸. In these models it was assumed that the pixel intensities inside the entire image follow a finite Gaussian mixture model distribution and the mixture parameters were estimated using the EM (Estimation Maximization) algorithm. Segmentation was completed in accordance to the maximum likelihood estimator. Experimental results showed that these methods were useful and stable in image segmentation. However, the main drawback of these methods is that the number of Gaussian mixture components (K) has to be assumed and hence these algorithms cannot be considered as totally unsupervised image segmentation algorithms. Another problem in using EM algorithm in image segmentation is that of model parameter initialization, which will affect the segmentation results. Wu¹ has utilized the K-means algorithm for solving the initialization of model parameters. However, in the K-means algorithm also it is required to assign an initial value to the number of mixture components (K) in the model. Hence this become partially unsupervised and the initial parameters are influenced by the initialization of K. Compared with the most non-hierarchical segmentation algorithm such as the Kmeans algorithm, hierarchical algorithms preserve the spatial neighbouring information among the segmented regions. The main disadvantage with the K-means algorithm is that it does not necessarily find the most optimal configuration, corresponding to the global objective function minimum. The algorithm is also significantly sensitive to the initial randomly selected segment centres. The K-means algorithm can be run multiple times to reduce this effect. To overcome these disadvantages, the hierarchical segmenting algorithm has been used.

²Department of Statistics, Andhra University, Visakhapatnam 530 003, India

^{*}For correspondence. (e-mail: Ksraoau@yahoo.co.in)

A number of segmentation algorithms for building a hierarchical image representation have been proposed^{9–11}. In hierarchical clustering, the database was divided into various regions by multi branch tree structure and provided a more accurate number of distinct regions in the image. After obtaining the number of components in the mixture model, the efficiency of the segmentation was dependent on assignment of probability density function to the image regions. Most of the image segmentation algorithms considered that the pixel intensity in each image region followed a normal distribution, which assumed that pixel intensity in the image region has a infinite range. However, in any image the pixel intensities lie between two finite values and in some image regions the distribution may be asymmetric and skewed. Neglecting the reality of the finite range leads to serious falsification of model estimation. The probability density function of the doubly truncated normal distribution is given by:

$$g(z,\mu,\sigma) = \frac{f(z)}{\int_{Z_L}^{Z_M} f(z) dz} \quad \text{with} \quad Z_L < z < Z_M,$$

where Z_L and Z_M are the truncation points and f(z) is the probability density function of the normal distribution. The value of $1 - \int_{Z_L}^{Z_M} f(z) dz$ is significant based on the value of mean μ and Standard Deviation σ in the interval (Z_L, Z_M) . This distribution includes the skewed, asymmetric and finite range distributions as particular cases. The model also includes Gaussian distribution as a limiting case. The

various shapes of the frequency curve of the doubly truncated Gaussian distribution are shown in Figure 1.

The effect of truncation in Gaussian distribution has been discussed by several researchers 12-14. As a result of this finite range in pixel intensity, it is necessary to consider that pixel intensities in the entire image follow a finite doubly truncated Gaussian mixture distribution. However, little work has been reported in the literature regarding image segmentation based on finite doubly truncated Gaussian mixture models. Hence in this article we have developed an efficient image segmentation algorithm assuming that the pixel intensities of the entire image follow a finite truncated Gaussian mixture distribution. The number of image regions were determined by hierarchical clustering and the model parameters were estimated using EM algorithm. The EM algorithm has been extensively used to estimate the mixture parameters^{1,8,15}. The performance of the developed segmentation algorithm was compared with finite Gaussian mixture model with K-means and also with finite truncated Gaussian mixture model with K-means through image quality metrics like average distance, maximum difference, image fidelity, mean square error, signal-to-noise ratio and quality index, since the developed segmentation was efficient for image retrieval. The accuracy of the developed segmentation algorithm was also established through a comparison of misclassification rates. Six images, namely BIRD, TOWER, FLAG, LENA, FISH and TOY were used for experimentation.

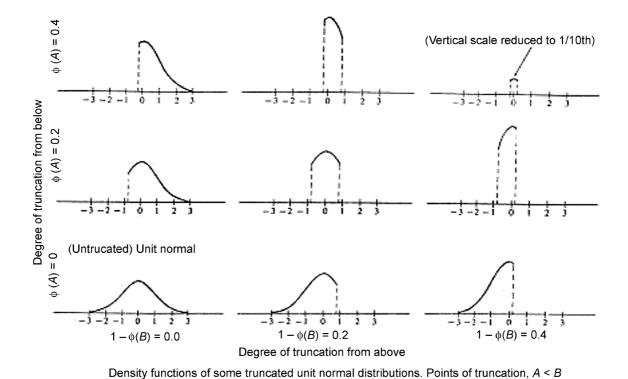


Figure 1. Some truncated normal distributions.

Truncated Gaussian mixture model

In low-level image analysis, the entire image was considered as a union of several regions. In each region the image data were quantized using pixel intensities. The pixel intensity Z = f(x, y) for a given point(pixel) (x, y) is a random variable, because of the fact that the brightness measured at a point in the image is influenced by various random factors like vision, lighting, moisture, environmental conditions, etc. To model the pixel intensities in the image region, it is customary to assume that the pixel intensity of a region in the image follows a normal distribution. However Z (pixel intensity), below some value Z_L and above some value Z_M cannot exist. Then the resulting distribution of the pixel intensities is a doubly truncated normal distribution. The lower and upper truncation points Z_L and Z_M determine the degree of truncation. It can be seen that when the truncations were large the distribution had little resemblance to a normal distribution. The case $Z_L = \mu$, $Z_M = \infty$, produced a half normal distribu-

Here it is assumed that the pixel intensity in the entire image follows a *K*-component finite mixture of doubly truncated Gaussian distribution. Its probability density is of the form

$$h(z) = \sum_{i=1}^{K} \alpha_i g(z \mid \mu_i, \sigma_i^2),$$

where *K* is the number of regions, $\alpha_i > 0$ are weights such that $\sum_{i=1}^{K} \alpha_i = 1$, and

$$g(z \mid \mu_i, \sigma_i^2) = \frac{e^{\left(\frac{-1}{2}\left(\frac{z-\mu_i}{\sigma_i}\right)^2\right)}}{\sqrt{2\pi\sigma}(A-B)}$$
$$-Z_L < z < Z_M, \quad 0 < \sigma_i, Z_L < \mu_i < Z_M,$$

where

$$A = \int_{-\infty}^{Z_L} \frac{e^{\left(\frac{-1}{2}\left(\frac{z-\mu_i}{\sigma_i}\right)^2\right)}}{\sqrt{2\pi\sigma_i}} dz \quad \text{and} \quad B = \int_{-\infty}^{Z_M} \frac{e^{\left(\frac{-1}{2}\left(\frac{z-\mu_i}{\sigma_i}\right)^2\right)}}{\sqrt{2\pi\sigma_i}} dz.$$

The mean pixel intensity of the *i*th region is

$$E(Z) = \mu_i + \frac{\sigma^2 [f(Z_L) - f(Z_M)]}{\phi(Z_L) - \phi(Z_M)}$$

The variance of the pixel intensities in the region is

$$V(z) = 1 + \frac{\left[\left(\frac{Z_L - \mu_i}{\sigma_i} \right) Z_L - \left(\frac{Z_L - \mu_i}{\sigma_i} \right) Z_M \right]}{B - A} \sigma_i^2.$$

Estimation of the model parameters by expectation maximization algorithm

The likelihood function of sample observations $z_1, z_2, ..., z_N$, drawn from an image with probability function $h(z, \theta) = \sum \pi_i g_i(z_s, \theta)$, where $g_i(z_s, \theta)$ is the probability density function of a truncated Gaussian distribution and is given by

$$L(\psi) = \prod_{s=1}^{N} \left(\sum_{l=1}^{K} \alpha_{i} g_{i}(z_{s}, \theta) \right).$$

This implies that

$$\log L(\psi) = \log \left(\sum_{i=1}^K \alpha_i g_i(z_s, \theta) \right) = \sum_{i=1}^N \log \left(\sum_{i=1}^K \alpha_i g_i(z_s, \theta) \right).$$

The first step of the EM algorithm requires reasonable initial estimates for both parameters $\mu_i^{(0)}$, $\sigma_i^{(0)}$, i = 1, 2, ..., K and component weights $\alpha^{(0)}$ from the observed sample. The EM algorithm then iteratively calculates maximum likelihood estimate of the unknown parameter ψ .

E-step

In the expectation (E) step, the expectation value of $\log L(\psi)$ with respect to the initial parameter vector $\Psi^{(0)}$ is calculated given the observed data Z as:

$$\begin{split} Q(\Psi, \Psi^{(0)}) &= E_{\Psi^{(0)}} \{ \log L(\Psi) \mid \overline{z} \} \\ &= \int_{z} (\log L(\Psi) \mid \overline{z} \mid) g(\Psi, \Psi^{(0)}) \, \mathrm{d}z \\ &= \sum_{s=1}^{N} \int_{z} g(\Psi, \Psi^{(0)}) \log g(z_{s}, \Psi) \mathrm{d}z \\ &= \sum_{s=1}^{N} \log g(z_{j}, \Psi) \int_{z} g(\Psi, \Psi^{(0)}) \, \mathrm{d}z \\ &= \sum_{s=1}^{N} \log g(z_{s}, \Psi) = \log L(\Psi). \end{split}$$

Evaluating the expectation value of $L(\psi)$, we get

$$\begin{split} \mathcal{Q}(\Psi, \ \Psi^{(l)}) &= E_{\Psi^{(l)}} \{ \log L(\Psi) \} \\ &= \sum_{i=1}^K \sum_{s=1}^N E^{(l)} \{ t_i(z, \Psi^{(l)}) (\log \ g_i(z, \Theta) + \log \pi_i \}, \end{split}$$

where

$$t_k(z_s, \Psi^{(l)}) = \frac{\alpha_k^{(l)} g_k(z_s, \theta^{(l)})}{\sum_{i=1}^K \alpha_k^{(l)} g_i(z_s, \theta^{(l)})}.$$

Thus

$$\begin{split} Q(\Psi, \Psi^{(l)}) &= \sum_{i=1}^K \sum_{s=1}^N E^{(l)} \{ t_i(z, \Psi^{(l)}) (\log \ g_i(z, \theta) + \log \alpha_i) \} \\ &= \sum_{i=1}^K \sum_{s=1}^N E^{(l)} \{ t_i(z, \Psi^{(l)}) [\log f(z, \theta) \\ &- \log [F(B) - F(A)]] + \log \alpha_i \}, \end{split}$$

where

$$f_i(z,\theta) = \frac{1}{\sqrt{2\pi} \sigma} e^{\frac{-1}{2} \left(\frac{z_i - \mu_i}{\sigma_i}\right)^2},$$

$$F(B) = \int_{-\infty}^{B} \frac{1}{\sqrt{2\pi} \sigma} e^{\frac{-1}{2} \left(\frac{t - \mu_i}{\sigma_i}\right)^2} dt.$$

M-step

The problem of calculating the maximum likelihood estimates of the segment weights α_k , under the additional condition $\sum_{i=1}^k \alpha_i = 1$, can be solved by applying the standard solution method for constrained maxima. We construct the first-order Lagrange-type function

$$L = E^{(l)} \left[\log L(\Psi^{(l)}) + \lambda \left(1 - \sum_{i=1}^{k} \alpha_i^{(l)} \right) \right],$$

where λ is a Lagrangian multiplier combining the constraint with the log likelihood functions to be maximized. The derivative of L with respect to a particular α_k gives

$$\frac{\partial L}{\partial \alpha_k} = 0, \quad \alpha_k^{(l+1)} = \frac{\alpha_i^{(l)}}{\phi(z_m, \boldsymbol{\psi}^{(l)}) - \phi(z_l, \boldsymbol{\psi}^{(l)})}. \tag{1}$$

Updating μ : For updating the parameters μ_k , we consider the derivative of $Q(\Psi, \Psi^{(l)})$ with respect to μ_k and equate it to zero,

$$\frac{\partial Q(\Psi, \Psi^{(l)})}{\partial \mu_{k}} = 0.$$

This implies

$$\mu_k^{(l+1)} = \mu_i^{(l)} + 2\sigma^{2(l)} \left(\frac{f(A) - f(B)}{\Phi(B) - \Phi(A)} \right), \tag{2}$$

where $A = Z_L$ and $B = Z_M$.

Updating σ_k^2 : For updating σ_k^2 , we consider the derivative of $Q(\Psi, \Psi^{(l)})$ with respect to σ_k^2 and equate it to zero,

$$\begin{split} \frac{\partial}{\partial \sigma_{k}^{2}} Q(\Psi, \Psi^{(l)}) &= 0. \\ \sigma_{k}^{2(l+1)} &= \mu_{i}^{2(l)} + (1 - \mu_{i}^{(l)}) \frac{\pi_{i}^{(l)}}{B} \\ &\times \left(\frac{\sigma_{i}^{2(l)}}{F(z_{m}, \theta^{(l)}) - F(z_{l}, \theta^{(l)})} \right) \\ &- \sigma_{i}^{2(l)} \frac{\pi_{i}^{(l)}}{B} \left(\frac{z_{m} f_{i}(z_{m}, \theta^{(l)}) - z_{l} f_{i}(z_{l}, \theta^{(l)})}{F(z_{m}, \theta^{(l)}) - F(z_{l}, \theta^{(l)})} \right) \\ &- \frac{\pi_{i}^{(l)}}{B} \left(\frac{2\mu_{k} \mu_{i}^{(l+1)}}{F(z_{m}, \theta^{(l)}) - F(z_{l}, \theta^{(l)})} - \mu_{i}^{2(l+1)} - 2\mu_{k} \sigma_{i}^{2(l)}}{F(z_{m}, \theta^{(l)}) - F(z_{l}, \theta^{(l)})} \right) + \mu_{i}^{2(l+1)}. \end{split}$$
(3)

Initialization of parameters

To utilize the EM algorithm we have to initialize the parameters μ_i , α_i and σ_i (i = 1 to K). Z_L and Z_M can be estimated with the values of the maximum and the minimum pixel intensities of the entire image respectively. The initial values of α_i can be taken as $\alpha_i = 1/K$, where K is obtained from the hierarchical segmenting algorithm.

Hierarchical clustering algorithm

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.

- (1) 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.
- (2) Find the closest (most similar) pair of segments and merge them into a single segment, i.e. we will now have one segment less.
- (3) Compute distances (similarities) between the new segment and each of the old segments.
- (4) 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 distance 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..., (n-1) and L(k) is the level of the kth 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:

- (1) Start with the disjoint segments having level L(0) = 0 and sequence number m = 0.
- (2) 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.
- (3) 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)].
- (4) 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 $d[(k), (r, s)] = \min(d[(k), (r)], d[(k), (s)])$.
- (5) If all objects are in one segment, stop. Else, go to step.

After obtaining the final value for the number of regions K, we obtain the initial estimates of μ_i , α_i and σ_i for the ith region using the segmented region intensities using the method given by Cohen¹² for doubly truncated normal distribution.

Segmentation algorithm

After refining the parameters, the prime step is image reconstruction by allocating the pixels to the segments. This operation is performed by segmentation algorithm. The image segmentation algorithm consists of three steps:

- (1) To obtain initial estimates of the finite doubly truncated Gaussian mixture model with hierarchical algorithm.
- (2) With the initial estimates obtained in step 1, the EM algorithm was iteratively carried out with the update equations (eqs (1)–(3)). The EM algorithm converges when the difference between the old and new estimates was less than some threshold value (0.001), and the final estimates of the finite doubly truncated Gaussian mixture model were obtained.

- The EM algorithm contributes to the segmentation algorithm by improving the parameters of the model.
- (3) The image segmentation was carried out by assigning each pixel into a proper region/segment according to the maximum likelihood estimate of the jth element, L_i according to the following equation:

$$L_{j} = \max_{i} \left\{ \frac{\exp \frac{(z_{i} - \mu_{i}^{\text{EM}})^{2}}{2(\sigma_{i}^{\text{EM}})^{2}}}{\sigma_{i}^{\text{EM}}(B - A_{l})} \right\},$$

where

$$B = \int_{-\infty}^{z_M} \frac{1}{\sqrt{2\pi} \, \sigma_i^{\text{EM}}} e^{-\frac{1}{2} \frac{(t - \mu_i^{\text{EM}})^2}{(\sigma_i^{\text{EM}})^2} dt},$$

$$A = \int_{-\infty}^{z_L} \frac{1}{\sqrt{2\pi} \, \sigma_i^{\text{EM}}} e^{-\frac{1}{2} \frac{(t - \mu_i^{\text{EM}})^2}{(\sigma_i^{\text{EM}})^2} dt},$$

where Z_i s are the input data (pixel intensities), and μ_i , σ_i are the estimated parameters respectively.

Experimental results and performance evaluation

In order to evaluate the proposed model, we demonstrated our image segmentation algorithm with finite doubly truncated Gaussian mixture model with hierarchical clustering by applying it to six images, namely BIRD, TOWER, FLAG, LENA, FISH and TOY. We assumed that the pixel intensities in each segment of the image follow a doubly truncated Gaussian distribution and intensities in each image follow a finite doubly truncated Gaussian mixture distribution. Initialization of the parameters in each segment was done and the number of segments estimated using hierarchical clustering. Using the EM algorithm the parameters of the mixture model were obtained. The segmentation algorithm was used to reconstruct the image. After developing the image segmentation algorithm, it is necessary to verify the performance of the same. Performance evaluation of the retrieved image can be done by subjective image quality testing or by objective image quality testing. The objective image quality testing methods were often used since the numerical results of an objective measure are readily computed and allow a consistence comparison of different algorithms. There are several image quality measures available for performance evaluation of the image segmentation algorithm. An extensive survey of quality measures is given by Eskicioglu et al. 16. The performance of the developed algorithm was compared with the image segmentation

Table 1. Comparative study of image quality metrics

Image	Quality metric	Finite Gaussian mixture model with K-means	Finite truncated Gaussian mixture model with K-means	Finite truncated Gaussian mixture model with hierarchical algorithm	Standard limits	Standard criteria
BIRD	Average difference	0.6963	0.0863	0.45275	-1 to +1	Closest to 1
	Maximum distance	0.6708	0.9708	0.2287	-1 to $+1$	Closest to 1
	Image fidelity	1.22208	1.008	0.9001	0 to 1	Closest to 1
	Mean square error	0.9982	0.8972	0.7813	0 to ∞	Closest to 0
	Signal-to-noise ratio	23.454	32.454	65.759	0 to +∞	As big as possible
	Image quality index	-0.1254	0.2354	0.756	−1 to 1	Closest to 1
TOWER	Average difference	0.7863	0.3783	0.87817	−1 to +1	Closest to 1
	Maximum distance	-0.9708	1.3222	0.89467	-1 to $+1$	Closest to 1
	Image fidelity	0.989	0.8744	0.748	0 to 1	Closest to 1
	Mean square error	0.9982	0.1232	0.1285	0 to ∞	Closest to 0
	Signal-to-noise ratio	12.454	29.342	42.436	0 to +∞	As big as possible
	Image quality index	-0.2354	-0.023	0.723	−1 to 1	Closest to 1
FLAG	Average difference	0.0783	-0.3793	0.43808	−1 to +1	Closest to 1
	Maximum distance	-0.6708	-0.3452	0.8978	-1 to $+1$	Closest to 1
	Image fidelity	1.76208	1.2444	0.4544	0 to 1	Closest to 1
	Mean square error	0.8982	0.7432	0.5998	0 to ∞	Closest to 0
	Signal-to-noise ratio	24.454	29.342	39.734	0 to +∞	As big as possible
	Image quality index	-0.2354	-0.1733	0.980	−1 to 1	Closest to 1
LENA	Average difference	0.0543	-0.8383	0.91723	−1 to +1	Closest to 1
	Maximum distance	-0.4508	-0.3222	1.1461	-1 to $+1$	Closest to 1
	Image fidelity	1.5408	0.1124	0.678	0 to 1	Closest to 1
	Mean square error	0.7682	0.1213	0.8546	0 to ∞	Closest to 0
	Signal-to-noise ratio	36.476	35.122	47.737	0 to +∞	As big as possible
	Image quality index	-0.6354	1.023	0.5430	−1 to 1	Closest to 1
FISH	Average difference	0.0563	0.4783	0.56322	-1 to +1	Closest to 1
	Maximum distance	-0.546	-0.142	1.145	-1 to $+1$	Closest to 1
	Image fidelity	1.8978	1.2444	0.618	0 to 1	Closest to 1
	Mean square error	0.6482	0.1132	0.7058	0 to ∞	Closest to 0
	Signal-to-noise ratio	32.454	35.342	49.876	0 to +∞	As big as possible
	Image quality index	-0.4354	-0.127	0.918	-1 to 1	Closest to 1
TOY	Average difference	0.775	-0.6878	0.5621	−1 to +1	Closest to 1
	Maximum distance	-0.9543	-0.5222	1.1768	-1 to $+1$	Closest to 1
	Image fidelity	1.17608	0.5345	0.769	0 to 1	Closest to 1
	Mean square error	0.4382	0.1132	0.2255	0 to ∞	Closest to 0
	Signal-to-noise ratio	22.454	32.322	29.265	0 to +∞	As big as possible
	Image quality index	-0.3254	-0.893	1.0010	-1 to 1	Closest to 1

algorithms based on finite Gaussian mixture model and finite truncated Gaussian mixture model with *K*-means algorithm through image quality metrics, by evaluating average distance, image fidelity, mean square error, structural symmetry, cross correlation, maximum difference, *N*-cross correlation, quality index, structural content. The original and reconstructed images of BIRD, LENA, TOWER, FLAG, FISH and TOY are shown in Figure 2. The comparative performance of various algorithms with reference to image quality metrics is given in Table 1 and Figures 2 and 3.

From Table 1 and Figures 2 and 3, it can be observed that the developed algorithm performs much superior to

existing algorithms with respect to the image quality metrics.

The performance of the image segmentation algorithm was also studied through classifier accuracy by computing the misclassification rate. The misclassification rates of the different images, namely BIRD, TOWER, FLAG, LENA, FISH and TOY with reference to the developed segmentation algorithm and the finite Gaussian mixture model with *K*-means algorithm are computed and given in Table 2. From Table 2 it can be observed that the accuracy of the developed algorithm is superior to that of the finite Gaussian mixture model with *K*-means. It is highly desirable to develop an image segmentation algorithm

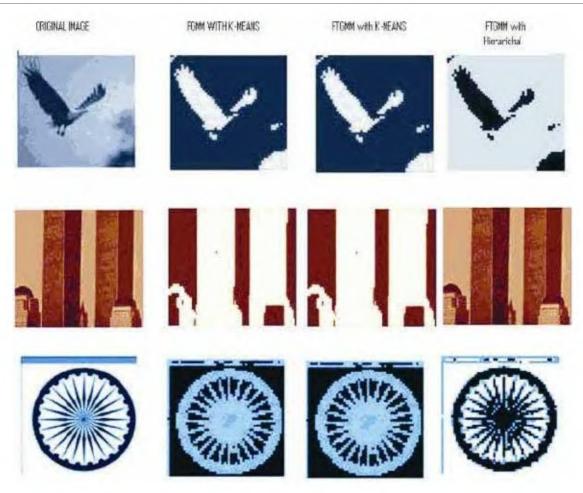


Figure 2. The original and the reconstructed images.

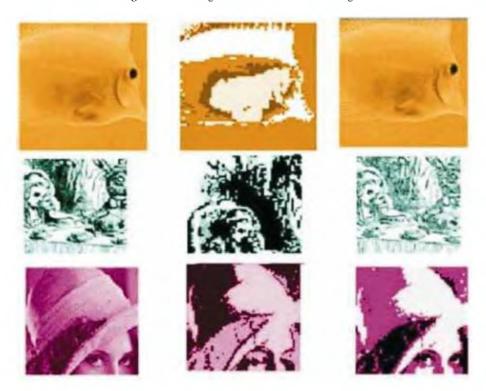


Figure 3. The original and the reconstructed images.

Table 2. Classifier accu	uracv
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Image	Finite Gaussian mixture model with <i>K</i> -means	Finite truncated Gaussian mixture model with <i>K</i> -means	Finite truncated Gaussian mixture model with hierarchical algorithms
BIRD	93.45	94.76	97.78
TOWER	96.34	97.11	97.98
FLAG	95.23	96.13	97.81
FISH	96.02	96.91	97.54
TOY	97.34	97.12	98.17
LENA	96.12	96.87	98.43

based on finite doubly truncated multivariate Gaussian mixture model with hierarchical clustering, which will serve as a generic algorithm for analysing and retrieving several images.

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