

An Effective Similarity Measure Via Genetic Algorithm for Content Based Image Retrieval with Extensive Features

Baddeti Syam¹ and Yarravarapu Rao²

¹Department of ECE, Mandava Institute of Engineering and Technology, India

²Instrument Technology Department, Andhra University, India

Abstract: Recently, the construction of large datasets has been facilitated by the developments in data storage and image acquisition technologies. In order to manage these datasets in an efficient manner development of suitable information systems are necessary. Content-Based Image Retrieval (CBIR) is commonly utilized in most of the systems. Based on image content, CBIR extracts images that are relevant to the given query image from large image databases. Most of the CBIR systems available in the literature extract only concise feature sets that limit the retrieval efficiency. In this paper, extensive features are extracted from the database images and stored in the feature library. The extensive features set is comprised of shape feature along with the color, texture and the contourlet features, which are utilized in the previous work. When a query image is given, the features are extracted in the similar fashion. Subsequently, GA-based similarity measure is performed between the query image features and the database image features. The Squared Euclidean Distance (SED) aids the similarity measure in determining the Genetic Algorithm (GA) fitness. Hence, from the GA-based similarity measure, the database images that are relevant to the given query image are retrieved. The proposed CBIR technique is evaluated by querying different images and the retrieval efficiency is evaluated by determining precision-recall values for the retrieval results.

Keywords: CBIR, GA, SED, shape feature, similarity measure.

Received October 4, 2010; accepted May 24, 2011

1. Introduction

Recently, because of the availability of enormous amount of storage spaces, plenty of images have been produced and stored throughout the world [31]. But to utilize it, an efficient searching and retrieval process is required. A text based retrieval system for organizing image collections was initially attempted by annotating each image with its description. But annotation has become both ambiguous and laborious because of diversity in content and increase in the size of the image collections. Hereby, the focus has been shifted to Content Based Image Retrieval (CBIR) [28]. The subject of a crucial amount of research in the past decade has been CBIR or the issue of searching for images by analyzing the content of the images stored in huge image repositories [4]. Since the early 1990s, CBIR has been an exceptionally active research area in the multimedia community [36]. Determining the concerned images that are relevant to an arbitrary query in a database is the objective of a CBIR algorithm [2]. "Query by example" is one of the types of user query technique used by CBIR systems in which the task of the system is to determine other images like the input query image. Without manual descriptive or indexing labor from humans, CBIR systems search for collections of images based on the

features that can be extracted from the image files themselves [6].

CBIR indicates an image traditionally by computing a feature vector. Initially a feature vector is computed for the given query image and it is then compared with that stored for each image in the database. Moreover, images most similar to the query image are returned by the system [34]. Hence, feature extraction and similarity measurement can be considered as two fundamental stages of CBIR systems [27]. In several CBIR systems, by implementing a segmentation algorithm the image is either classified into predefined blocks, or more generally partitioned into various significant regions. In both the case, each image region is represented by extracting a vector of feature values from it. Salient points, which are points that vary considerably in the local pixel neighborhood characteristics, are removed by certain other CBIR systems. A feature vector is created for each salient point, assisted by a salient point-based technique [21]. The image is represented and indexed in CBIR utilizing the visual contents of an image such as color, shape, texture, and spatial layout [18]. Though semantic information cannot be captured by these visual features, they are useful in characterizing an image [3].

Large amount of visual data in the form of images are utilized by applications like medicine, entertainment, education, manufacturing and more. This predicts the necessity for economical retrieval mechanisms which are fast as well as effective [19]. Bridging the gap between low level feature layout and high-level semantic concepts is the most difficult task in CBIR [9]. Both industry and academia have built numerous CBIR systems. IBM's QBIC [16], Virage [1], MIT's Photobook [17], VisualSEEK [29], and MARS [13], and much more are encompassed by several prominent CBIR systems [36]. However, for a user supplied query image, similarity based retrieval of the most excellent match in a dataset remains as an unresolved problem [11]. The adopted features for representing images in the database inherently influence the performance of a CBIR system [38, 39]. In CBIR, identification of such features for representing original image contents and extraction techniques for such features [8] are open areas of research [6].

Most of the CBIR techniques available in the literature utilize the narrow-downed feature set and classic similarity measure. This acts as a bottleneck for the CBIR efficiency. To overcome the issue, in this paper, we extract an extensive set of features and utilize GA for retrieving the images that are similar to the query image from the database. In the feature extraction process of the CBIR system, shape, texture, contourlet and the color histogram features are extracted. With the aid of the GA, the required optimal images is obtained that are most similar to the given query image. The rest of the paper is organized as follows: Section 2 briefly gives an introduction about the GA and section 3 reviews the recent research works related to the CBIR techniques. Section 4 details the steps involved in the proposed technique with necessary illustrations and mathematical formulations. Section 5 discusses about the simulation results and section 6 concludes the paper.

2. Genetic Algorithm (GA)

The GAs are computer programs that simulate the heredity and evolution of living organisms [7]. An optimum solution is possible even for multi modal objective functions utilizing GAs because they are multi-point search methods. Also, GAs are applicable to discrete search space problems. Thus, GA is not only very easy to use but also a very powerful optimization tool [10]. In GA, the search space consists of strings, each of which representing a candidate solution to the problem and are termed as chromosomes. The objective function value of each chromosome is called its fitness value. Population is a set of chromosomes along with their associated fitness. Generations are populations generated in an iteration of the GA [20].

Utilizing crossover and mutation techniques new generations (offspring) are generated. Crossover splits two chromosomes and by taking one split part from each chromosome combines them to create two new chromosomes. Mutation changes a single bit of a chromosome. The chromosomes that have best fitness value calculated for a certain fitness criteria are retained while others are discarded. The chromosome that has the best fitness is chosen as the solution to the problem by repeating the process until one chromosome has best fitness value [37].

In this paper, we utilize GA to obtain the most similar images from the image database, for a given query image. The generated chromosomes are the indices of the database images. For this CBIR process, the color, shape, texture and the contourlet features are extracted from the generated chromosomes and also from the query image. Then the fitness function is computed for each chromosome based on the SED. After the fitness calculation, the chromosomes are subjected to the genetic operations crossover, mutation and selection of best chromosomes. Then the most similar images, which are relevant to the given query image are retrieved from the image database.

3. Literary Works: A Brief Review

A handful of recent research works available in the literature are briefly reviewed in this section. Hiremath and Pujari [9] have proposed a method for salient point's identification on the basis of color saliency. The color and texture data close to these salient points of concern act as the local descriptors of the image. The combination of the local color, texture and the global shape features gives a strong feature set for image retrieval. The experimental results have demonstrated the effectiveness of the method.

Nandagopalan *et al.* [15] have proposed an inventive method for widespread image retrieval on the basis of semantic elements. The method has used a combination of three feature extraction approaches namely color, texture, and edge histogram descriptor. The complete system was developed utilizing AForge. imaging (an open source product), MATLAB, NET builder, C#, and Oracle 10g. The system was tested with coral image database holding 1000 natural images and obtains enhanced results.

Marwaha *et al.* [12] have offered a basic model for Content-Based Retrieval (CBR) of image data. The CBR technique is exceedingly effective and efficient than the conventional keyword search and is utilized by very few engines like alta vista. The CBR method provides more appropriate results in less time.

Sastry and Mishra [25] have proposed similarity metric for CBIR in connection with the current powerful l1-norm minimization technique, which was constructed for computing the underdetermined system of linear equations. It was verified by means of the

simulation work that the proposed similarity metric has the capability to achieve well as compared to the metric founded on the standard Euclidean distance for the CBIR of texture images.

Suhasini *et al.* [30] have achieved the color extraction and comparison utilizing the three color histograms, Conventional Color Histogram (CCH), Invariant Color Histogram (ICH) and Fuzzy Color Histogram (FCH). They have utilized the invariant ICH for attending to the issue of rotation and translation and they have utilized fuzzy linking color histogram FCH for attending to the problem of spatial relationship.

Trojacanec *et al.* [33] have proposed an extension and advancement of the present two-level CBIR architecture. Their proposed upgrading of the two-level architecture was anticipated to enhance the accuracy of the retrieval results. Castillo *et al.* [5] have detailed a CBIR system to facilitate in the diagnosis and treatment procedure of the scoliosis pathology. For performing that, the system has incorporated a module for the automatic extraction of scoliosis measures from X-rays. In addition, the system has incorporated a Fuzzy Object-Relational Database Management System (FORDBMS) to store images and its measures and to implement flexible retrieval of the images founded on its spine measures.

4. The GA-Based CBIR Technique

It is well known that, CBIR has been an active area of research for long due to its applications in various fields like satellite imaging, medicine etc., [26]. In order to determine which images must be retrieved, content representations of all stored images are compared with the representation extracted from the query image. The most important considerations in the design and implementation of CBIR systems are: image feature extraction, features representation, features matching, database organizing and querying mechanisms [24]. Here, we broadly classify the CBIR process as feature extraction and GA-based similarity measure.

4.1. Feature Extraction

The proposed CBIR utilizes the visual contents of an image such as color, shape, texture and utilizes CT to determine the features in Contourlet domain. CT has shown better performance in terms of computational complexity and retrieval efficiency [22]. In image similarity retrieval one of the most extensively used features is color. Color retrieval yields the best results, in that the computer results of color similarity are similar to those derived by a human visual system that is capable of differentiating between infinitely large numbers of colors [14]. Roughness or coarseness of object surface is denoted by the term 'texture'. Texture

creates intensity variation from pixel to pixel in an intensity image. We have extracted the aforesaid features in our previous work [32] and in addition to this in our present work we have included the shape feature.

4.1.1. Shape Feature Extraction

Shape representation generally looks for effective ways to capture the essence of the shape features that make it easier for a shape to be stored, transmitted, compared against, and recognized. These features must also be independent of translation, rotation, and scaling of the shape [24]. To extract the shape feature from the image, initially, the image in RGB color space is converted to gray scale image. Let I be the image of size $M \times N$ from the database D , which comprises lot of images, and I_r , I_g and I_b be the R , G , B weights of the image I respectively.

$$I_{gy} = 0.2989 * I_r + 0.5870 * I_g + 0.1140 * I_b \quad (1)$$

The above equation is the Craig's formula for converting RGB color image to gray scale image. The image I is converted to gray scale image I_{gy} , because the median filter can act on only one color channel. Particularly median filter is useful for reducing speckle noise and salt and pepper noise. It is also useful in cases where edge blurring is undesirable because it has edge-preserving nature. Hence, median filter is applied to the converted grayscale image I_{gy} to remove the noises. The filtering operation by the median filter is detailed in the following pseudo code.

```

 $E_w \leftarrow w_w/2$ 
 $E_h \leftarrow w_h/2$ 
For  $X = E_w, \dots, (M - E_w)$ 
  For  $Y = E_h, \dots, (N - E_h)$ 
    Initialize vector  $C[][]$  with size  $M \times N$ 
    For  $f_x = 0, \dots, w_w$ 
      For  $f_y = 0, \dots, w_h$ 
         $C[f_x][f_y] \leftarrow P[X + f_x - E_w][Y + f_y - E_h]$ 
        Sort  $C$  in asc;
         $P[X][Y] \leftarrow C[w_w/2][w_h/2];$ 
      End for
    End for
  End for
End for

```

where,

w_w : Width of window.

w_h : Height of window.

The noise-free image's pixels form a 2D vector P ; this 2D vector is subjected to clustering to detect different shapes present in the image. Clustering refers to the process of grouping samples so that the samples are similar within each group. The groups are called clusters [23]. Various regions in the image can be discovered by identifying groups of pixels that have similar gray levels, colors or local textures utilizing

clustering in the image analysis. Various clustering techniques exist. In our work, we make use of the K-means clustering algorithm for image segmentation for the further process.

K-means clustering treats each object as having a location in space. It finds partitions such that objects within each cluster are as close to each other as possible, and as far from objects in other clusters as possible [23]. The number of clusters to be partitioned and a distance metric for quantifying the distance between two objects are necessary for K-means clustering. Prior to the application of K-means clustering, the image, which is in the form of 2D vector, is rescaled to a 1D vector as follows:

$$P(Z) = ((X-1) * \sqrt{|P|}) + Y; Z = 1, 2, \dots, \sqrt{|P|} \quad (2)$$

Subsequently, the k means algorithm is applied, to cluster the image. The k means algorithm is briefed here.

Input: $P = \{p_1, p_2, p_3, p_4, \dots, P_{m \times n}\}$
K-number of clusters

Output: set of K clusters

Step 1: Arbitrarily select K data items from P as initial centroids.

Step 2: Repeat

- Assign remaining P apart from the selected initial centroids to the cluster K , which has the closest centroid.
- Calculate the new centroid for each cluster until convergence occurs.

After the k means algorithm is applied, again the 1D vector is converted to 2D vector and then the canny algorithm is used for the detection of different edges present in all the clustered sets of the image I_{gv} . The canny algorithm [35] consists of five steps, they are smoothing, finding gradients, non-maximum suppression, double thresholding and edge tracking by hysteresis. The above steps are explained below:

- *Smoothing*: Here, noise is removed by applying Gaussian blur to each clustered set of the image I_{gv} .
- *Finding gradients*: After smoothing, the edge strength is calculated by measuring the gradient of the segmented image I_{gv} . A 2-D spatial gradient measurement is performed on the clusters of the image utilizing the Sobel operator and the approximate absolute gradient magnitude (edge strength) at each point is determined. For estimating the gradient of the cluster, the sobel operator utilizes a pair of $m \times n$ convolution masks, one for the x -direction (columns) and the other for the y -direction (rows). Edges are marked in the segmented image where the magnitude of the gradient is large. Then the approximate magnitude of the gradient, or Edge Strength, is calculated using the formula:

$$|g_r| = |g_x| + |g_y| \quad (3)$$

where, g_x and g_y are the gradients of the clusters, in the x and y directions respectively. But, it may not indicate the exact location of the edges because the edges are typically broad. The directions of the edges are determined using the following formula:

$$\theta = \arctan^{-1} \left(\frac{|g_y|}{|g_x|} \right) \quad (4)$$

- *Non-maximum suppression*: In this step the “blurred” edges of the gradient magnitudes in the segmented image is converted to “sharp” edges.
- *Double thresholding*: Potential edges of the clustered regions of the image are determined by means of a thresholding operation.
- *Edge tracking by hysteresis*: Finally, the strong edges are immediately included in the final edge image because they are interpreted as “certain edges” and weak edges are included only if they are connected to strong edges. Hence the edges are tracked and then again the edge is smoothed to remove the number of connected components which are unused. Then we can get the different shapes that are present in the image I_{gv} and then the indices of the shaped content are extracted. Now the shape features of the image I_{gv} from the database D are combined and grouped with the other features and the featureset is created. In a similar manner, the features of the rest of the images in the database are also extracted and stored in a feature library. After extracting the featureset from the database images, it is necessary to compare the featureset with the given query image’s featureset. This can be accomplished by GA and the required equivalent images can be retrieved from the database.

4.2. GA-Based Similarity Measure

In GA-based similarity measure, initially, chromosomes are generated in which genes are the indices of the database images. These genes are generated without any repetition within the chromosome and the values of the genes depend on the number of images in the database to be queried. The extracted features of each image are grouped as a featureset and the featureset of the query image Q is also extracted. Then the chromosomes are subjected to the genetic operators, crossover and mutation, and hence the new chromosomes are generated. Then the fitness is determined for the newly generated chromosomes. Here the fitness is based on the SED between the query image and the generated chromosome’s featuresets (generated chromosomes containing the indices of the images). The optimal chromosomes are obtained which are having minimum SED, when compared to the query image Q . The genes of the obtained optimal chromosome are the indices of the similar images based on the given query image Q . The process is repeated until a required number of

similar images are obtained. The process of similarity measure using the GA is shown in the Figure 1.

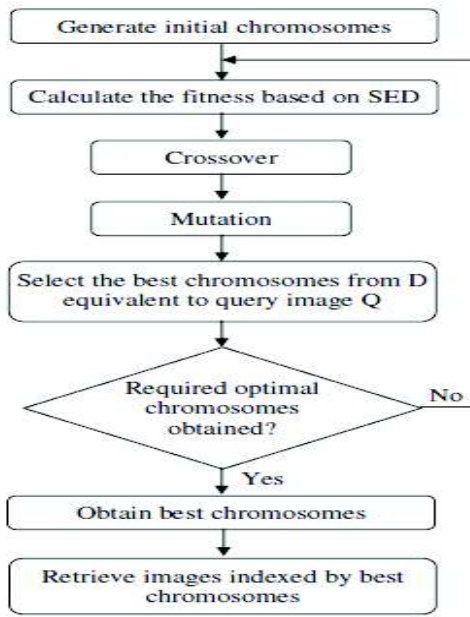


Figure 1. GA-based similarity measure for the proposed CBIR technique.

4.2.1. Generation of Chromosomes

Initially generate N_p number of random chromosomes and the number of genes in each chromosome rely on the number of images required which are most similar to the given query image. As discussed earlier, the generated genes are the indices of the database images:

$$D^{(j)} = \{D_0^{(j)}, D_2^{(j)}, D_3^{(j)}, \dots, D_{n-1}^{(j)}\} \quad (5)$$

$$0 \leq j \leq N_p - 1, 0 \leq k \leq n - 1$$

n - Number of similar images to be retrieved.

In equation 5, $D_k^{(j)}$ represents the k^{th} gene of the j^{th} chromosome. The features considered in the images are shape, texture, contourlet and color histogram; these features are extracted from all the images in the database. Once the features are extracted then they are stored in a separate vector for each image. After determining all the aforesaid set of features from the database images, the individual feature sets are concatenated into a single feature set and then each feature set is normalized as shown in equation 6:

$$\{F\hat{S}_k^{(j)}\} = \left[\frac{|FS_k^{(j)}|}{\sum_{r=0}^{|FS_k^{(j)}|-1} (FS_k^{(j)}(r))^2} \right]^{1/2} FS_k^{(j)}(r) \quad (6)$$

where,

$$FS_k^{(j)}(r) = FS_k^{(j)}(r) / \sqrt{|FS_k^{(j)}|} \quad (7)$$

The normalized feature set $\{F\hat{S}_k^{(j)}\}$ obtained from the equation 6 is the definite feature set extracted for a particular database image and is stored in the feature database.

4.2.2. Fitness Function

The fitness of the generated chromosomes is evaluated using the fitness function, which is based on SED, as follows:

$$f^{(j)} = \frac{\sum_{k=0}^{n-1} SED_k^{(j)}}{|SED_k^{(j)}|} \quad (8)$$

where

$$SED_k^{(j)} = \sum_{r=0}^{|F\hat{S}_k^{(j)}|-1} (F\hat{S}_k^{(j)}(r) - FS_q(r))^2 \quad (9)$$

In equation 9, FS_q is the feature set extracted from the query image, $SED_k^{(j)}$ represents the SED for each $D_k^{(j)}$ of the j^{th} chromosome and the query image, i.e. SED of the query image and the indices of database images which are generated in the genes. Subsequently, the $f^{(j)}$ is sorted in the ascending order and $N_p/2$ number of mean distances are selected from the $f^{(j)}$. Then the corresponding $D_k^{(j)}$ of the selected $f^{(j)}$ is obtained and then the selected chromosomes are subjected to genetic operators.

4.2.3. Crossover and Mutation

Among different types of crossovers, the two point crossover is selected with the crossover rate of C_R . In the two point crossover, two points are selected on the parent chromosomes using the equations 10 and 11. The genes in between the two points c_1 and c_2 are interchanged between the parent chromosomes and so $N_p/2$ children chromosomes are obtained. The crossover points c_1 and c_2 are determined as follows:

$$c_1 = \frac{|D_k^{(j)}|}{3} \quad (10)$$

$$c_2 = c_1 + \frac{|D_k^{(j)}|}{2} \quad (11)$$

Now, we have the children chromosomes and their SED are stored separately and their corresponding indices from the $D_k^{(j)}$ are stored in $D_{newk}^{(j)}$. Subsequently mutation is done by applying equation 9 on the chromosomes obtained after crossover. Then, the mutation is accomplished by replacing N_M number of genes from every chromosome with new genes. The N_M numbers of gene are nothing but genes, which have

maximum SED value (as determined from the equation 9). The replaced genes are the randomly generated genes without any repetition within the chromosome. Then, chromosomes which are selected for crossover operation, and the chromosomes which are obtained from the mutation are combined, and so the population pool is filled up with the N_p chromosomes. Then, the process is repeated iteratively until it reaches a maximum iteration of I_{max} .

4.2.4. Selection of Optimal Solution

After the process is repeated I_{max} times, best chromosomes are selected from the obtained group of chromosomes. Here, the best chromosomes are the chromosomes which have maximum fitness. The obtained best chromosome is used to retrieve the similar images from the database. In other words, the database images that are represented by the indices, which are obtained from the genes of the best chromosomes, are the images similar to the given query image and they are retrieved in an effective manner.

5. Results and Discussion

The proposed GA based CBIR system has been implemented in the working platform of MATLAB (version 7.8). The proposed system has been evaluated with different query images and the relevant images are retrieved from the coral image database. To accomplish this, features including shape, contourlet, texture and color histogram has been extracted from every image in the system database. The step by step results attained by the proposed CBIR system are given below.

Figure 2 depicts the original image, gray scale converted image, filtered image by median filter, clustered image by k-means clustering, edge detected image by canny algorithm and the smoothed image.

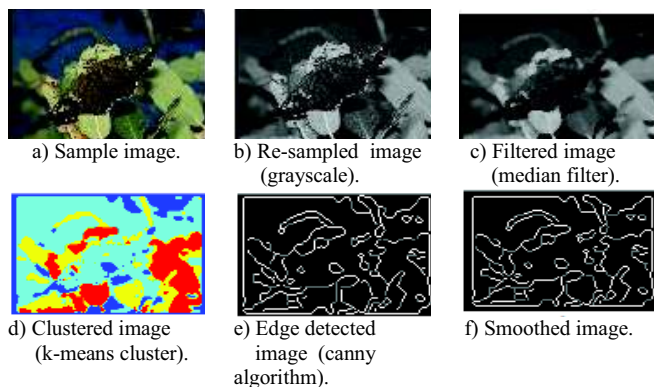


Figure 2. Depicts the original image.

Figure 3 depicts the LBP histograms for different orientations of the image. Based on these histograms, the texture pattern of the image has been extracted. Figure 4 depicts the original image, the corresponding

re-sampled grayscale image and the decomposed image in CT domain. From the decomposed image, the contourlet features have been computed in terms of energy and standard deviation. Figure 5 shows the original image and re-sampled color segmented image together with their color histograms. After the feature extraction process, GA was applied for measuring the similarity.

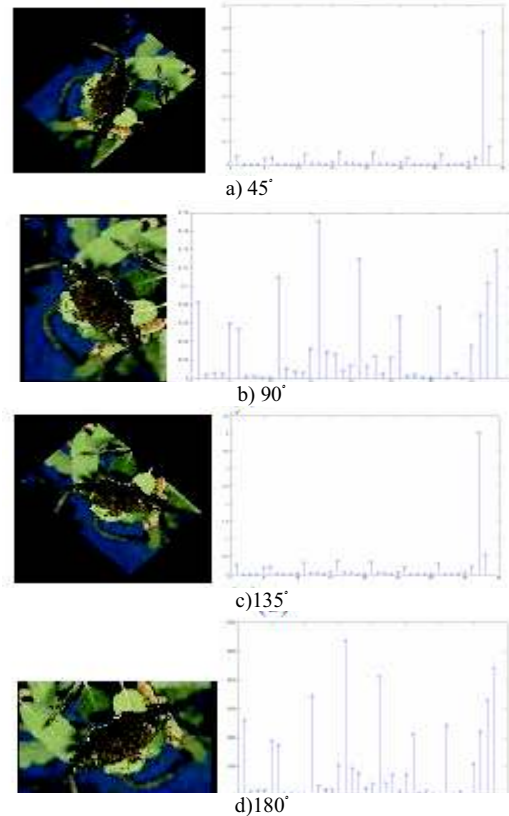


Figure 3. LBP histograms for a sample image at orientations.

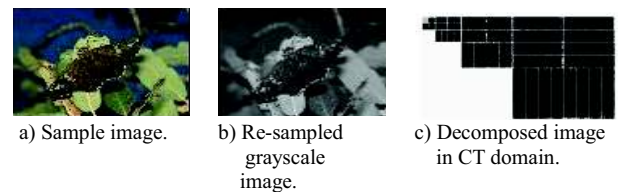


Figure 4. Depicts the original image.

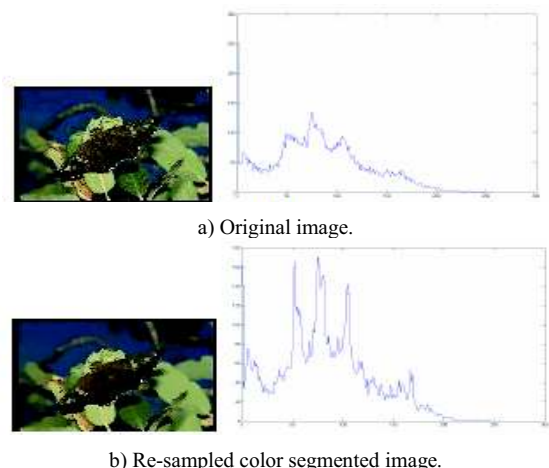


Figure 5. Color histograms.

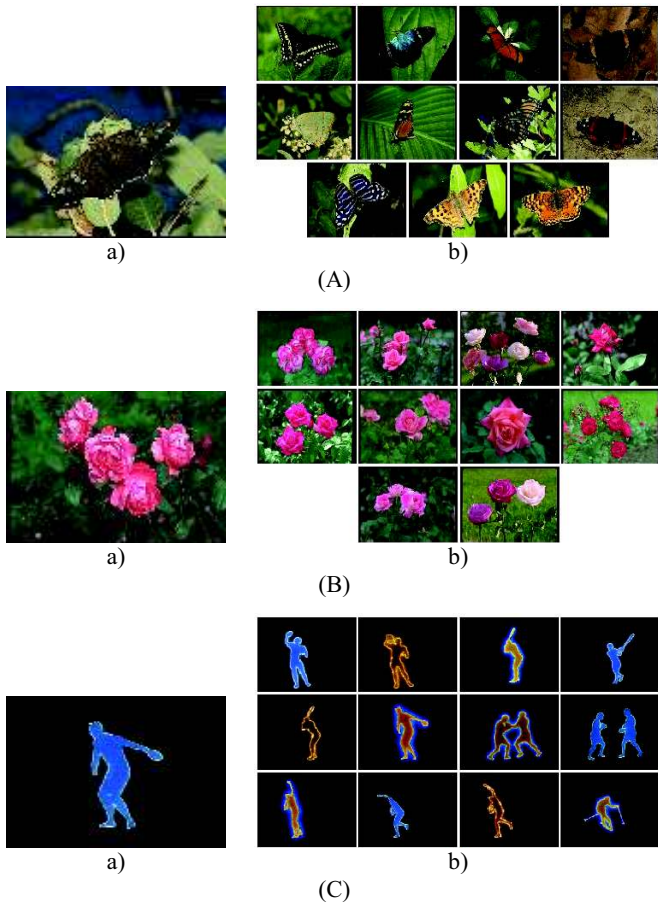


Figure 6 A, B, C: (a) Query image (b) retrieved images.

In the GA, $N_p=10$ random chromosomes of length n are generated. Each chromosome has $n=10$ genes which are the indices of the database images. The maximum value taken by the database image index is 160 (i.e., database have 160 images). The features are extracted for the generated chromosomes and also for the given query image. Then the chromosomes are subjected to crossover, mutation and selection techniques to obtain the optimal chromosome. We have selected crossover points $c_1=3$ and $c_2=8$ with a crossover rate $C_R=0.5$ and for mutation $N_M=5$. After completing the crossover and mutation operations, based on the conditions mentioned in the section 4.3 the optimal chromosomes were selected. These optimal chromosomes are indices of images relevant to the given query image Q . This process is repeated until it reaches the maximum iteration $I_{max}=100$. Figure 6 depicts some of the query images and relevant retrieved images.

$$precision = \frac{\text{Number of retrieved images relevant to the query image}}{\text{Total number of images retrieved}} \quad (12)$$

$$recall = \frac{\text{Number of retrieved images relevant to the query image}}{\text{Total number of relevant images in the database}} \quad (13)$$

The precision equation 12 and recall equation 13 that are computed for a given query image in Figure 6.A(a) are tabulated in Table 1 and the associated precision-recall graph is shown in Figure 7. The

retrieved images and the precision-recall graph show that the proposed GA based CBIR system claims effectiveness in retrieving images that are 70% similar to the given query image.

Table 1. Precision and Recall measurements computed for the proposed CBIR system.

S.No	Precision	Recall
1	0.8	0.16
2	0.75	0.3
3	0.72	0.36
4	0.7	0.42
5	0.68	0.48
6	0.62	0.5
7	0.53	0.7
8	0.38	0.76
9	0.29	0.8

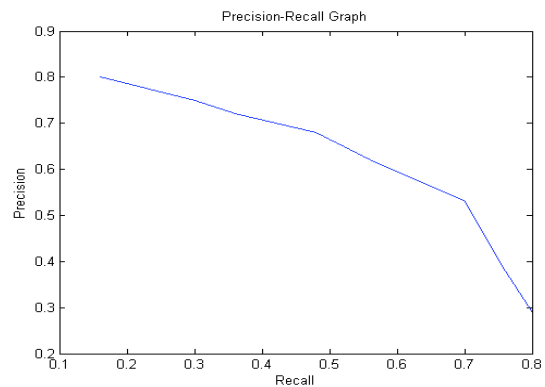


Figure 7. Precision-Recall plot for the Proposed CBIR system.

6. Conclusions

In this paper, we have proposed an efficient CBIR system based on GA for retrieving relevant images from image database, when a query image is given. First, the system extracted the features like texture, color, contourlet and shape from the image. Then, with the aid of GA-based similarity measure, images that are similar to the query image have been retrieved effectively. The proposed CBIR technique has been evaluated by querying different images. The implementation results have shown that the proposed technique effectively retrieves the relevant images from the database. This could be visualized from the precision-recall determined from the retrieval results. The proposed CBIR based on GA have the benefit of the shape feature in addition to other features, and the similarity measure using GA. The extracted images are 70 % similar to the given query image.

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Baddeti Syam received his BE degree in electronics and communications engineering from Andhra University, Visakhapatnam, India, in 1997, and M. Tech in electronics from the Cochin University of Science and Technology, India, in 1999. He is working towards his PhD at Andhra University, India. He is with Mandava Institute of Engineering and Technology, India, as an associate professor and HOD. He has 11 years of experience in teaching undergraduate students and post graduate students. His research interests are in the areas of radar signal processing, digital image processing and content based image retrieval. He is a life member of ISTE.



Yarravarapu Rao received his PhD in electrical communication engineering from Indian Institute of Science, Bangalore in 1998. At present, he is an assistant principal and senior associate professor in Instrument Technology Department, AU College of Engineering, Andhra University, India. He was with Eritrean Institute of Technology, Asmara, Eritrea for one year on academic assignment. He is completed two major research projects and published 30 research papers in the international journals and presented few of them in the international conferences. He will be visiting researcher, microelectronics division, EEE Department, Nanyang Technological University, in 2010. He had received "emerald literati network 2008 outstanding paper award (UK), best paper award and best student paper award in ICSCI - International conference in 2007, vignan pratibha award-2006 from Andhra University and selected as science researcher for Asia-Pacific region in 2005 by UNESCO and Australian expert group in Industry Studies at the University of Western Sydney and received young scientist award from Department of Science and Technology, Government of India in 2002. His present research focuses on carbon nanotube electronics, VLSI and thick film technology. He is a life member of ISTE and member of IMAPS, India.