An Evolutionary Dynamic Clustering Based Colour Image Segmentation

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Abstract

We have presented a novel Dynamic Colour Image Segmentation (DCIS) System for colour image. In this paper, we have proposed an efficient colour image segmentation algorithm based on evolutionary approach i.e. dynamic GA based clustering (GADCIS). The proposed technique automatically determines the optimum number of clusters for colour images. The optimal number of clusters is obtained by using cluster validity criterion with the help of Gaussian distribution. The advantage of this method is that no a priori knowledge is required to segment the color image. The proposed algorithm is evaluated on well known natural images and its performance is compared to other clustering techniques. Experimental results show the performance of the proposed algorithm producing comparable segmentation results.

Keywords: Segmentation, Clustering, Genetic Algorithm, Clustering Metric, Validity Index.

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1. INTRODUCTION

Image segmentation, i.e., the partitioning of an image into relevant regions, is a fundamental problem in image analysis. Accurate segmentation of objects of interest is often required before further analysis can be performed. Despite years of active research, fully automatic segmentation of arbitrary images is still seen as an unsolved problem.

Colour image segmentation emerges as a new area of research. Colour image segmentation can solve many contemporary problems in medical imaging, mining and mineral imaging, bioinformatics, and material sciences. Naturally, color image segmentation demands well defined borders of different objects in an image. So, there is a fundamental demand of accuracy. The segmented regions or components should not be further away from the true object than one or a few pixels. So, there is a need for an improved image segmentation technique that can segment different components precisely. Image data have some particular characteristics that differentiate them from other form of data. Image data may have corrupted values due to the usual limitations or artifacts of imaging devices. Noisy data, data sparsity, and high dimensionality of data create difficulties in image pixel clustering. As a result, image pixel clustering becomes a harder problem than other form of data. Although there are some existing algorithms for unsupervised color image segmentation, none of them has been found to be robust in determining an accurate number of components or segments. Image segmentation is a very important field in image analysis, object recognition, image coding and medical imaging. Segmentation is very challenging because of the multiplicity of objects in an image and the large variation between them. Image segmentation is the process of division of the image into regions with similar attributes.

The method for the segmentation of digital images can be broadly classified in: (a) edge and line oriented segmentation, (b) region growing methods, (c) clustering, and (d) region splitting methods. Edge and line oriented segmentation work on either individually analyzing each data band or considering the whole vector space. After edge extraction, a processing should be applied to create objects and segments that represent the elements present in the scene. Region growing and splitting method deals commonly with feature extraction and thresholding. In many object based image segmentation applications, the number of cluster is known a priori, but our proposed scheme is automatically determined the optimal number of clustering. The proposed technique should be able to provide good optimal results whereas the K-means algorithm which may get stuck at values which are not optimal [16]. Some of the several unsupervised clustering algorithms developed include K-means [13, 14], fuzzy K-means, ISODATA [11], self-organizing feature map (SOM) [15], particle swarm optimization (PSO) [10], learning vector quantizers (LVQ) [12], Dynamic GA based Clustering [17] etc.

Colour images are more complex than gray scale images as instead of a single intensity value for a pixel, each pixel is usually denoted by three component values such as Red, Green and Blue. Clustering based methods are ideal to use for gray scale images can be easily extended to cope with higher dimensity, although, the increased dimensionality also leads to more computationally expensive process. Various segmentation techniques have been developed for image segmentation include Unsupervised Colour Textured Image Segmentation Using Cluster Ensembles and MRF Model [18], Determination of Number of Clusters in k-means Clustering and application in Colour Image Segmentation [20], Unsupervised Colour Image Segmentation based on Gaussian Mixture Model [21] etc.

This paper presents automatic image segmentation of colour images using GA-based clustering. One natural view of segmentation is that we are attempting to determine which components of a data set naturally “belong together”. Clustering is a process whereby a data set is replaced by clusters, which are collections of data points that “belong together”. Thus, it is natural to think of image segmentation as image clustering i.e. the representation of an image in terms of clusters of pixels that “belong together”. The specific criterion to be used depends on the application. Pixels may belong together because of the same colour or similarity measure.

Natural colour images are particularly noisy due to the environment they were produced. Therefore, it is hard to develop a robust and faithful unsupervised technique for automatic determination of number of objects in a colour image. Although there are a few existing approaches for unsupervised colour image segmentation, none of them has been found robust in all situation. Initially we tried SNOB [8], a Minimum Message Length (MML) based unsupervised data clustering approach to address this problem [19].

Genetic Algorithm based clustering technique has been used to cluster datasets [1-5]. In this paper we present an efficient image segmentation algorithm using automatic GA based clustering algorithm. The result of this algorithm produced a better result to compare with other techniques.

The rest of the paper is organized in the following manner: Section II introduces Genetic Algorithms. Section III gives an overview of the GA based clustering approach. Proposed algorithm is discussed in section IV. Section V summarizes the experimental results.

2. GENETIC ALGORITHM

Genetic Algorithm (GA) is a population-based stochastic search procedure to find exact or approximate solutions to optimization and search problems. Modeled on the mechanisms of evolution and natural genetics, genetic algorithms provide an alternative to traditional optimization techniques by using directed random searches to locate optimal solutions in multimodal landscapes [6,7]. Each chromosome in the population is a potential solution to the problem. Genetic Algorithm creates a sequence of populations for each successive generation by using a selection mechanism and uses operators such as crossover and mutation as principal search mechanisms - the aim of the algorithm being to optimize a given objective or fitness function.

An encoding mechanism maps each potential solution to a chromosome. An objective function or fitness function is used to evaluate the ability of each chromosome to provide a satisfactory solution to the problem. The selection procedure, modeled on nature's survival-of-the-fittest mechanism, ensure that the fitter chromosomes have a greater number of offspring in the subsequent generations.

For crossover, two chromosomes are randomly chosen from the population. Assuming the length of the chromosome to be l, this process randomly chooses a point between 1 and l-1 and swaps the content of the two chromosomes beyond the crossover point to obtain the offspring. A crossover between a pair of chromosomes is affected only if they satisfy the crossover probability.

Mutation is the second operator, after crossover, which is used for randomizing the search. Mutation involves altering the content of the chromosomes at a randomly selected position in the chromosome, after determining if the chromosome satisfies the mutation probability. In order to terminate the execution of GA we specify a stopping criterion. Specifying the number of iterations of the generational cycle is one common technique of achieving this end.

3. GENETIC ALGORITHM BASED CLUSTERING

The searching capability of GAs can be used for the purpose of appropriately clustering a set of n unlabeled points in N-dimension into K clusters [1]. In our proposed scheme, the same idea can be applied on image data. We consider a colour image of size mxn and every pixel has Red, Green and Blue components. The basic steps of the GA-clustering algorithm for clustering image data are as follows:

3.1 Encoding

Each chromosome represents a solution which is a sequence of K cluster centers. For an N-dimensional space, each cluster center is mapped to N consecutive genes in the chromosome. For image datasets each gene is an integer representing an intensity value of the three components Red, Green and Blue.

3.2 Population initialization

Each of the P chromosomes is initialized to K randomly chosen points from the dataset. Here P is the population size.

3.3 Fitness computation

The fitness computation is accomplished in two steps.
First, the pixel dataset is clustered according to the centers encoded in the chromosome under consideration, such that each intensity value $x_i(r,g,b)$ of colour image combined with three component red, green and blue (24 bit), i = 1, 2, ..., mxn is assigned to cluster with center $z_j(r,g,b)$, j = 1, 2, ..., K,

$$\text{if } \| x_i(r,g,b) - z_j(r,g,b) \| < \| x_i(r,g,b) - z_p(r,g,b) \|,\ p = 1,2,\ldots,K, \text{ and } p \neq j. \quad (1)$$

The next step involves adjusting the values of the cluster centers encoded in the chromosome, replacing them by the mean points of the respective clusters. The new center $Z_i(r,g,b)$ for the cluster C_i is gives by

$$Z_i(r, g, b) = \frac{1}{n_i} \sum_{x_j \in C_i} X_j(r, g, b), \ i=1,2,\ldots..,K. \quad (2)$$

Subsequently, the clustering metric M is computed as the sum of Euclidean distances of each point from their respective cluster centers given by

$$M = \sum_{i=1}^{K} M_i. \tag{3}$$

$$M_i = \sum_{x_j \in C_i} \| x_j(r,g,b) - z_i(r,g,b) \| \tag{4}$$

The fitness function is defined as

$$f = 1/M. \tag{5}$$

A low value of intra-cluster spread is a characteristic of efficient clustering. Hence our objective is to minimize the clustering metric M i.e. maximize f.

3.4 Selection

This paper employs the Roulette Wheel selection - a proportional selection mechanism in which the number of copies of a chromosome, that go into the mating pool for subsequent operations, is proportional to its fitness.

3.5 Crossover

In this paper we use single-point crossover with a fixed crossover probability of μ_c. The procedure followed is the same as that described in section 2.

3.6 Mutation

Each chromosome undergoes mutation with a fixed probability μ_m. A number δ in the range [0, 1] is generated with uniform distribution. If the value at a gene position is v, after mutation it becomes

$$\begin{aligned} &v \pm \delta * v, && v \neq 0 \\ &v \pm \delta, && v = 0. \end{aligned} \tag{6}$$

3.7 Termination criterion

We execute the processes of fitness computation, selection, crossover, and mutation for a predetermined number of iterations. In every generational cycle, the fittest chromosome till the last generation is preserved - elitism. Thus on termination, this chromosome gives us the best solution encountered during the search.

4. PROPOSED METHOD

We proposed a new segmentation algorithm that can produce a new result according to the values of the clustering. We consider a colour image f of size mxn. The proposed algorithm is:

1. Repeat steps 2 to 8 for K=2 to $K=K_{max}$.
2. Initialize the P chromosomes of the population.
3. Compute the fitness function f_i for i=1,…,P, using equation (5).
4. Preserve the best (fittest) chromosome seen till that generation.
5. Apply Roulette Wheel selection on the population.
6. Apply crossover and mutation on the selected population according to sections 3.5 and 3.6 respectively.
7. Repeat steps 3 to 6 till termination condition is reached.
8. Compute the clustering Validity Index for the fittest chromosome for the particular value of K, using equation (7), in order to determine the validity of the clustering on the given dataset.
9. Cluster the dataset using the most appropriate number of clusters determined by comparing the Validity Indices of the proposed clusters for K=2 to $K=K_{max}$.

4.1 Validity Index

The cluster validity measure used in the paper is the one proposed by Turi [8]. It aims at minimizing the validity index given by the function,

$$V = y \times \frac{intra}{inter} \tag{7}$$

The term intra is the average of all the distances between each pixel x(r,g,b) and its cluster centroid z_i(r,g,b) which is defined as

$$intra = \frac{1}{\mathrm{N}} \sum_{i=1}^{K} \sum_{x \in C_i} \| x(r,g,b) - z_i(r,g,b) \|^2 \tag{8}$$

Where ||x(r,g,b) – z_i(r,g,b)|| means the Euclidean distance, which is calculated as

$$\sqrt{(x_{red} - z_{ired})^2 + (x_{green} - z_{igreen})^2 + (x_{blue} - z_{iblue})^2},$$

where N is the total number of pixels, C_i is the cluster number, z_i is the centroids of cluster C_i, K is the total number of clusters. Intra cluster dependency is the sum of square of Euclidean distance of every element from the centroids of the cluster to which it belongs.

On the other hand, inter is the inter cluster dependency which gives the idea about the extent to which each clusters are related. The higher this value the better clustering is obtained. It is represented as

$$inter = \min(\| z_i(r,g,b) - z_j(r,g,b) \|^2), \quad where \tag{9}$$
$$i = 1,2,\ldots K-1, \; j = i+1,\ldots, K$$

and Z_i and Z_j are the centroids. Intra cluster dependency is the minimum of the square of Euclidean distances of each centroids from the other.

Lastly, y is given as

$$y = c \times N(2,1) + 1 \tag{10}$$

Where c is a constant (selected value is 25), N(2,1) is a Gaussian distribution function with mean 2 and standard deviation 1, where the variable is the cluster number and is given as

$$N(\mu,\sigma) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{\frac{(k-\mu)^2}{2\sigma^2}} \tag{11}$$

Where K is the cluster number and μ=2 and σ=1 as per Turi's thesis on clustering. This is done to negate the occurrence of lower number of clusters 2 or 3.

This validity measure serves the dual purpose of

- minimizing the intra-cluster spread, and
- maximizing the inter-cluster distance.

Moreover it overcomes the tendency to select a smaller number of clusters (2 or 3) as optimal, which is an inherent limitation of other validity measures such as the Davies-Bouldin index or Dunne's index.

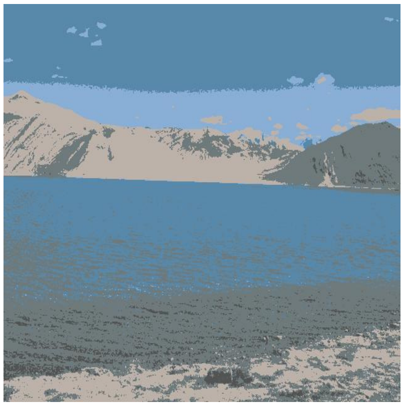
5. EXPERIMENTAL RESULTS

The proposed algorithm has been applied to well known natural colour images such as Lena, mandrill and peppers etc. All the results have been reported in Table 1. Column 2 of Table 1 represent the optimal range for the number of clusters for the images of Lena, mandrill and peppers etc have also been copied from [8] which is based on visual analysis by a group of ten expert people. These results have been compared to those of SOM and DCPSO [9] and to that of snob [8]. The results tabulated here for each image is the mean of 10 simulations. Figure1 are shown the some segmented output images using our proposed clustering method. The result of TABLE 1 is shows better than SOM and snob and always find a solution within the optimal range. The performance of the proposed algorithm with DCPSO produced comparable segmentation results [9].

The assumptions used for the implementation of the proposed algorithm are given as follows. The value of the parameter, c, for the validity index referred to from [8], is set to 25. The size of the population, P, is taken as 30, crossover rate, μ_c, as 0.9 and mutation rate, μ_m, as 0.01 [6]. The algorithm uses number of iterations as the terminating condition and it is set to 20. The value of K_{max} is empirically set for the individual images.

Table 1: Experiment of some natural images

Image	Optimal Range	Proposed Method	DCPSO using V	SOM	Snob
Lena	5 to 10	5	6.85	20	31
Peppers	6 to 10	6.7	6.25	20	42
Mandrill	5 to 10	6.5	6	20	39
Jet	5 to 7	6	5.3	14	22
Duck	-	7.2	-	-	-
Baboon	-	5.9	-	-	-
F16	-	6.6	-	-	-
Parrot	-	7.1	-	-	-



Original image

Segmented image by proposed method

FIGURE 1: Experimental results of some natural images

6. CONSLUSIONS

This paper presented a GA based dynamic colour image segmentation algorithm based on clustering technique which determines the optimal clustering of an image dataset, with minimum user intervention. This implies that the user does not need to predict the optimal number of clusters, required to partition the dataset, in advance. Comparison of the experimental results with that of other unsupervised clustering methods, show that the technique gives satisfactory results when applied on well known natural images. Moreover results of its use on images from other fields (MRI, Satellite Images) demonstrate its wide applicability. Hence, we can conclude that the proposed GA based dynamic clustering approach using a cluster validity measure [8], can be used as an efficient unsupervised image segmentation mechanism.

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