ROBUST IMAGE SEGMENTATION USING GENETIC ALGORITHM WITH A FUZZY MEASURE

DAE N. CHUN* and HYUN S. YANG††

*Media Technology Section, Electronics and Telecommunication Research Institute (ETRI), 161 Kajjong-dong, Yusong-gu, Taejon, Korea 305-600, and, ††Department of Computer Science/Center for Artificial Intelligence Research, KAIST, 373-1 Kusong-dong, Yusong-gu, Taejon, Korea 305-701

(Received 23 August 1994; in revised form 28 September 1995; received for publication 26 October 1995)

Abstract—In this paper we present new region-based image segmentation methodology on gray-level images using a genetic algorithm with a fuzzy measure. We first propose a fuzzy validity function which measures a degree of separation and compactness between and within finely segmented regions, and an edge strength along boundaries of all regions. We apply the genetic algorithm to search a good or usable region segmentation, which maximizes the quality of regions generated by split- and-merge processing. The iterative algorithm provides a useful method for image segmentation without the need for critical parameters or threshold values, iterative visual interaction or a priori knowledge of an image. Copyright © 1996 Pattern Recognition Society. Published by Elsevier Science Ltd.

Genetic algorithm Split-and-merge image segmentation Validity measurement
Fuzzy objective function

1. INTRODUCTION

Image segmentation is a process of segmenting an image into a set of disjoint regions whose characteristics such as intensity, color, texture, etc. are similar. In the low-level image segmentation there exists two fundamental problems. The first is that most segmentation results are not always crisp or correct, because images possess grayness ambiguity and spatial ambiguity or both due to the multi-levels of brightness in an image. Also, features for image segmentation basically involve incomplete, ill-defined and vague factors arising from deficiencies of available information in the given situation. This problem is known as an uncertainty problem. The second is that image segmentation techniques using numerous control parameters are dependent on image characteristics and environment. Therefore, the techniques may not be applicable uniformly to several images because these parameters typically interact in a nonlinear fashion. To solve the above problems, there has been much research related to the uncertainty and the quality measurement in computer vision.

In this paper we apply the qualitative guideline for a good image segmentation established by Haralick and Shapiro.1) Based on the assumptions, we propose a measure based on the fuzzy set decomposition in order to provide an objective function which measures the degree of separation among segmented regions and the edge strength along region boundaries. In addition to this measure we also consider a new contrast measure of regions based on the concept of the fuzzy c-means (FCM) algorithm2) in the spatial domain.

For obtaining an optimal solution satisfying the given criteria, we use the genetic algorithm to search a usable region segmentation, which is maximized for the quality of regions generated by a split-and-merge process, instead of using some heuristic thresholds. The iterative algorithm provides a useful method for segmentation without critical parameters or threshold values. Also, these values are not regulated with human judgement during each iterative step. Although the simulated annealing technique3) has the potential for providing a good solution, we will describe our experiments using the genetic algorithm alone.

The paper is organized as follows. In the following section, we briefly review some validity criterion and objective functions related to the fuzzy segmentation. Section 3 proposes a fuzzy validity function in measuring the contrast and the compactness between and within regions. Section 4 presents an efficient search algorithm using a genetic algorithm and its implementation strategy. In Section 5 we describe the experimental results and the last section concludes and describes future research plans.

2. MEASUREMENT FOR IMAGE SEGMENTATION

In this section we briefly review various aspects of the optimization criteria involved in measuring the quality of image segmentation which have been found
to be useful. However, these measures sometimes do not appear to correlate with human judgement.

2.1. Nonspatial measurement

Nonspatial criterion is widely used to consider the variance of features and histograms, except for geometrical information in an image. The criterion has been mainly applied to measure the degree of uniformity or the homogeneity of regions. A nonspatial uniformity measure $U$ proposed by Levine and Nazif\(^{(44)}\) is given by:

$$U = 1 - \sum_j w_j \sigma_j^2 / N, \tag{1}$$

where $w_j$ is the weight associated with the contribution of region $j$ to the measure, $\sigma_j^2$ is the feature variance of pixels over region $j$ and $N$ is a normalization factor. The uniformity or homogeneity of the feature over the given region is inversely related to the variance of the feature evaluated at every pixel belonging to that region. The variance is also used as a spectral-similarity to merge regions.\(^{(55)}\) The spectral similarity $S(i,j)$ between two regions $i$ and $j$ is expressed in terms of the following measure:

$$S(i,j) = \frac{|m_i - m_j|}{\max(1, \sigma_i + \sigma_j)}, \tag{2}$$

where $m$ and $\sigma$ are the means and the standard deviations of the regions. However, the variance may lose important spatial information in providing a global view of the image data.

2.2. Spatial measurement

Spatial measures for segmentation consider the location of pixels and geometrical properties of the segmented regions, such as edge, connectivity, shape, etc. The structural uniformity measure proposed by Bhanu\(^{(6)}\) used an average gray level $\bar{f}(i,j)$ in a $3 \times 3$ window centered around the pixel $(i,j)$ such that:

$$U = \sum_{i,j} \left[ f(i,j) - \bar{f}(i,j) \right]^2. \tag{3}$$

It measures the consistency of a pixel with respect to its neighbors and reveals the homogeneity of the regions. Levine and Nazif\(^{(44)}\) checked the validity of existing lines or edges in an image segmentation to measure the connectivity of edges. The validity of the existing lines is determined by measuring the local gradient across lines and the adjacency of a region to the left and right of the line. The connectivity of lines is estimated by measuring the degree of discontinuity in the lines and the length of lines. Sahoo, Soltani and Wong\(^{(37)}\) proposed a shape measure of the object in an image, which is estimated by calculating the generalized gradient values at every pixel. Also, the fuzzy-c-means (FCM) algorithm is used to measure the amount of fuzziness of the spatial criteria,\(^{(32)}\) such as partition coefficient, classification entropy, proportion exponent, separation coefficient and separation indices. Xie and Beni\(^{(46)}\) defined compactness and separation to find the FCM with the smallest $S$ defined as:

$$S = \frac{\sum_{i=1}^{N} \sum_{j=1}^{n} \mu_{ij}^c \| V_i - X_j \|^2}{\min_{i,j} \| V_i - Y_j \|^2}, \tag{4}$$

where $X = \{ X_j, j = 1, 2, \ldots, n \}$ with $V_i$ ($i = 1, 2, \ldots, c$) is a fuzzy c-partition of the data set and $\mu_{ij}$ ($i = 1, 2, \ldots, c; j = 1, 2, \ldots, n$) is the fuzzy membership of data point $j$ belonging to class $i$. In the equation the smallest $S$ indicates a valid optimal partition. However, the $S$ function does not represent the geometrical properties of the image because it uses the distance between the centroid of the clusters. As a criterion for image enhancement and threshold selection, Pal and Rosenfeld\(^{(49)}\) defined a compactness measure by the area of the region and the perimeter of the region, i.e. the length of the arcs along the regions. Yan and Keller\(^{(10)}\) proposed the conditional fuzzy measures for image segmentation.

Texture has been shown to be a very important clue for region identification by the human. The textured regions should not be divided into the uniform sub-regions which correspond to the units of the textural pattern. The texture can be qualitatively evaluated by measuring one or more of the properties, such as coarseness, smoothness, granulation, randomness, co-occurrence and autocorrelation function, etc.\(^{(11-13)}\)

3. Fuzzy Validity Measurement

In general, the validity measurement for segmented images involves many questions because it is very difficult to formulate the problem in a mathematically tractable manner that provides useful results. In this section we focus on the fuzzy validity measure of the separation and compactness within segmented regions and an edginess measure of region boundaries. These measures will be applied to a fuzzy objective function and a criterion for mutation in a genetic algorithm.

3.1. Compact and separation measure

The compactness criterion measures the consistency of a pixel with respect to its neighbors and reveals the homogeneity or the uniformity of region. Two aspects can be considered; one is the similarity of the intensity in the region and the other is the smoothness or texture properties of the region. In this paper we do not consider the smoothness or texture properties. On the other hand, the separation measure can be computed on the basis of the average differences of features between adjacent regions. This measure is similar to the concept proposed by Beveridge\(^{(55)}\) as equation (2).

Let any region $r_j$ ($j = 1, 2, \ldots, n_j$) be adjacent to the region $r_k$, where $n_j$ is the number of adjacent regions of $r_j$. The $s_{ij}$ denotes a separation which is the distance between average gray-levels of two region $m_i$ and $m_j$, i.e. $s_{ij} = |m_i - m_j|^2$ and $c_{ij}$ denotes a compactness which is the sum of variances of two adjacent regions, i.e. $c_{ij} = \sigma_i^2 + \sigma_j^2$. Then, the compact and separation
measure $G_i$ of a region $i$ defines as follows:

$$G_i = \frac{1}{n_i} \sum_{j=1}^{n_i} \left( \frac{S_{ij}}{c_{ij}} \right).$$  \hspace{1cm} (5)

Given a segmented image, the total compact and separation measure of the image is computed as:

$$G = \frac{1}{n} \sum_{i=1}^{n} W_i(p_i) G_i,$$  \hspace{1cm} (6)

where $n$ is the total number of regions in an image. The weight function $W_i$ considered for minimizing the error of statistics information due to the size of the region $i (p_i)$ is defined as:

$$W_i(p_i) = \begin{cases} \frac{2(p_i^2)}{\beta^2} & \text{if } p_i \leq \frac{2}{\beta} \\ \frac{1}{\beta} - \frac{2(p_i - \beta)^2}{\beta^2} & \text{if } \frac{2}{\beta} \leq p_i < \beta \\ 1 & \text{if } p_i \geq \beta \end{cases},$$  \hspace{1cm} (7)

where $\beta$ is the minimum size of the region and $\beta$ is the size of the region which maximized the weight. As a result, it need not consider the weight effect related to the size of the region when the size $p_i$ is more than $\beta$.

### 3.2. Local contrast measure

The contrast is more sensitive near the boundary of a region than the average intensity of a region. Therefore, we now consider a validity measure of lines existing along the boundary between two adjacent regions. The intensity distance along the boundary pixels among adjacent regions is given as:

$$d_{ij} = \frac{1}{n_{ij}} \sum_{k=1}^{n_{ij}} \| x_{jk} - x_{jk} \|_2,$$  \hspace{1cm} (8)

where $x_{jk} (j = 1, 2, \ldots, n_i, k = 1, 2, \ldots, n_j)$ is $k$th boundary pixel of the region $r_j$ with adjacent region $r_i$, and $n_{ij}$ is the number of common boundary pixels of region $r_i$ with adjacent region $r_j$. An example of how such boundaries of adjacent regions is defined is shown in Fig. 1.

By applying the above distance, a degree of membership between the region $r_i$ and its adjacent regions $r_j$ ($j = 1, 2, \ldots, n_i$) can be defined as:

$$\mu_{ij} = \frac{d_{ij}^2 m-1}{\sum_{k=1}^{n_i} d_{ik}^2 (m-1)},$$  \hspace{1cm} (9)

where $m$ is the exponent weight and the summation term is to calculate the total boundary distance of region $r_i$ with all adjacent regions. The following properties must be true to be a fuzzy $c$-means algorithm, i.e. $\sum_{j=1}^{n_i} \mu_{ij} = 1$, $0 \leq \sum_{j=1}^{n_i} \mu_{ij} \leq n$, $\mu_{ij} \in [0, 1]$. Conceptually, $\mu_{ij}$ indicates a relative possibility to select any region to split or merge. Using equation (9), a contrast measurement function of each region $r_i$ is defined as:

$$C_i = \begin{cases} \min \left( \frac{\min(\mu_{ij})}{\max(\mu_{ij})} - \min(\mu_{ij}) \right) & \text{if } \min_{j} \neq \max_{j} \\ 1 & \text{if } \min_{j} = \max_{j} \end{cases}$$  \hspace{1cm} (10)

Assuming that a region is entirely surrounded by another region, then $C_i = 0.5$. The higher the contrast $C_i$ that is, the closer to 1, the more the ambiguity in making a decision selecting a region for splitting or merging. The contrast measure will be applied to select a region for merging or splitting among adjacent regions by a mutation operator in genetic algorithm.

### 3.3. Edginess measure

In the previous subsection we only considered the local property which is the intensity distance along boundary pixels between adjacent regions. In this section we define the degree of edginess over all region boundaries in the whole image. This edginess provides a quantitative measure of the edge ambiguity in an image.

At each pixel in an image, one can measure the gradient of intensity at each pixel in position $(i, j)$, denoted by $I_{ij}$. The magnitude of each gradient $|VG|$ introduced by Prewitt is computed as:

$$|VG(i, j)| = \left[ \left( \frac{\partial G(i, j)}{\partial x} \right)^2 + \left( \frac{\partial G(i, j)}{\partial y} \right)^2 \right]^{1/2},$$  \hspace{1cm} (11)

where

$$\left( \frac{\partial G(i, j)}{\partial x} \right)_{ij} = \frac{1}{4} \left[ (I_{i+1,j-1} \delta_{i,j} + I_{i+1,j+1} + I_{i-1,j+1} + I_{i-1,j-1}) \right] \hspace{1cm} \text{(12)}$$

and

$$\left( \frac{\partial G(i, j)}{\partial y} \right)_{ij} = \frac{1}{4} \left[ (I_{i-1,j-1} \delta_{i,j} + I_{i+1,j-1} + I_{i+1,j+1} + I_{i-1,j+1}) \right].$$  \hspace{1cm} (13)

The relative degree of edginess $E$ can then be expressed as:

$$E = \sum_{(i,j)} \mu_{ij} |VG(i, j)| \leq 1, |VG| \leq |VG|,$$  \hspace{1cm} (14)

where $|VG|$ indicates the magnitude of new region maps when the regions are repeatedly split and merge.
and $|VG|$ is the magnitude of the initial finely segmented region map. For considering the ambiguity of the magnitude, the membership function $\mu_{ij}$ is applied by Zadeh's standard S-function.\(^{15}\)

3.4. Fuzzy fitness function

We need to define a function which measures the overall quality of the segmented image generated during the split-and-merge process. Using equations (6) and (14) we define the measure as the product of the compact and separation $G$ and the magnitude of the gradient $E$, i.e.

$$F = GE.$$  \hspace{1cm}(15)$$

The measure uses as a fitness function in the genetic algorithm is referred to in the next Section. In our various experiments, although we have investigated several measures referred in Section 2 except the measure function, we have not been satisfied that they are empirically effective on a wide range of test images.

4. IMAGE SEGMENTATION USING A GENETIC ALGORITHM

4.1. Overview of genetic algorithm

The genetic algorithm\(^{16}\) proposed by John Holland has been recently exploited in pattern recognition problems involving optimization processes that provide a suitable solution in handling uncertainty in pattern analysis.\(^{17}\) The genetic algorithm (GA) is an adaptive procedure that searches for good solutions by using a collection of search points known as a population in order to maximize some desirable criterion. Also, the GA, as a stochastic random search technique, is known to use the accumulating information to prune the search space; while a purely random search ignores information about the environment.

The GA is an iterative procedure with a parallel test-and-go technique, which maintains a finite set of representations for solving a given problem. During each iteration step, known as generation, each individual is evaluated and recombined with others on the basis of its overall quality or fitness. Each individual is represented as a chromosome encoded as a string of genes which may take one of several values or alleles.

Some recent attempts in applying the genetic algorithms for machine vision problems such as image segmentation,\(^{18}\) primitive extraction,\(^{19}\) scene recognition\(^{20}\) and image interpretation\(^{21}\) are reported in the literature. Bhanu, Lee and Ming\(^{18}\) proposed a learning technique for the image segmentation using the GA. The algorithm allows the segmentation process to adapt to image characteristics affected by the variable environmental conditions such as time of day, time of year, clouds, rain, etc. Also in handling uncertainty in pattern analysis, Pal\(^{22}\) reported a necessity of a fuzzy fitness function.

Recently, research of GA has focused on three operators such as reproduction, crossover and mutation. Reproduction is a process in which individual strings are copied according to their objective function as some measure of goodness we want to maximize. The crossover invovles exchanging elements from mating of two parent chromosomes to create one or more child chromosomes. The crossover is implemented by randomly choosing a point in the string called the crossover point and exchanging the segments. There are various crossover mechanisms that have been developed to be efficiently applied to applications, for instance, edge recombination,\(^{23}\) cycle crossover,\(^{24}\) order crossover,\(^{25}\) position based crossover,\(^{25}\) partially mapped crossover (PMX)\(^{26}\) and so on. The mutation process creates new individuals by modifying one or more bit strings. The operator increases the variability of the population and prevents premature convergence to a poor local minimum. One of the interesting aspects in designing a genetic algorithm is to invent operators that construct the new potential solutions.

In this paper we apply the GA to search a good and usable region segmentation which maximizes the segmentation quality of the regions generated during the split-and-merge process. To do so, we have to design the crossover and the mutation mechanism for splitting and merging of the regions, as well as an encoding scheme of the chromosome for representing the regions. However, the basic procedure of GA is based on the Simple Genetic Algorithm (SGA).\(^{16}\) We describe the detailed mechanism in next sections.

4.2. Encoding scheme of chromosome

Now we define a set of individuals in a population generated during $t$ generation cycles, $P(t) = \{I_k| k = 1, 2, \ldots, m\}$, where $m$ is the number of

![Fig. 2. An example of chromosome structure about segmented regions. (a) An original regions map; (b) new region map with two merged regions $(r_1, r_2)$ and $(r_3, r_4)$; (c) the chromosome structure of Fig. 2a; (d) the chromosome structure of Fig. 2b.](image-url)
individuals or the population size. The size affects both the ultimate performance and the efficiency of GA. Each individual is generated by some encoded form known as a chromosome.

Given \( n \) segmented regions in an image, the chromosome of the individual presents a group of segmented regions, i.e., \( I_i = \{ r_j = 1, 2, \ldots, n \} \) and each \( r_j \) is sequentially the fixed \( i \)th position of the structure. The value of the \( i \)th position which is termed a gene denotes \( I_i[j] \) and these genes have integer values assigned as the region identity.

For example, Fig. 2(a) shows an original region map of an image with 14 sample regions and Fig. 2(b) shows a new region map after two regions \( r_1 \) and \( r_2 \) merged into \( r_{14} \) and \( r_{14} \), respectively. Figures 2(c) and (d) illustrate the chromosome structures of Figs 2(a) and (b), respectively.

4.3. Two-point crossover recombination operator

The crossover is often more important in the early stages of a GA, while mutation is important for later fine-tuning. In this Section, we propose a new modified crossover mechanism based on partially mapped crossover (PMX)\(^{126}\) so that it can be efficiently implemented for the image segmentation since the PMX crossover mechanism is fundamentally defined to solve the Traveling Salesman Problem (TSP). That is to say, the value cannot be merged or split with one another because each gene value indicates a city node in the PMX mechanism. However, the modified crossover ignores the conditions.

The new crossover is first begun by selecting two chromosomes of parents \( (P_1 \) and \( P_2 \) satisfying \( F(P_1) < F(P_2) \) in a population. The selection is randomly determined by the Roulette Wheel\(^{127}\) slot whose size is proportional to the fitness value. Also, the crossover of \( P_1 \) and \( P_2 \) is determined by a probability of the crossover rate \( P_{\text{crossover}} \). As a result, \( P_{\text{crossover}} \) chromosomes undergo crossover. Two crossover points \( (c_1 \) and \( c_2 \)) are selected at random. Then the elements between two crossover points in the \( P_2 \) directly inherit the child and the remaining elements are inherited from the other \( P_1 \).

However, we should solve one problem for efficiently implementing the operator. For example, if a region \( r_j \) is merged to an adjacent region \( r_i \), i.e., \( I_i[j] = i \) and \( I_i[i] = j \), then any other region \( r_j \) which is already merged to \( r_i \), i.e., \( I_i[i] = j \), is again changed as \( I_i[i] = i \). Therefore, all regions merged into region \( r_i \) are included in only one value. The detailed algorithm of the two-point crossover mechanism is given below:

Procedure Two-point crossover mechanism

begin
Randomly select two chromosomes \( P_1 \) and \( P_2 \) by Roulette Wheel.
if \( F(P_1) < F(P_2) \) by \( P_{\text{crossover}} \) \{ Select two crossover points \( c_1 \) and \( c_2 \) \( (c_1 < c_2) \) at random.
for \( (j = c_1, c_1 + 1, \ldots, c_2) \) \{ if \( (P_2[j] < c_1 \) or \( P_2[j] > c_2) \) \{ for \( (i = 1, \ldots, c_1 - 1, c_2 + 1, \ldots, n) \) if \( P_2[i] == P_2[j], P_2[i] = j \) \}
\}
else \( Child[j] = P_2[j] \)
\}
for \( (j = 1, \ldots, n) \) \{ if \( (c_1 \leq P_1[j] \leq c_2) \) \( Child[j] = P_1[j] \)
else \{ \}
\}
Endprocedure

An example of the crossover procedure is given in Fig. 3. The regions in the 5-, 6-, 7-, 8-, 9- and 10th positions are inherited from \( P_2 \) and the remaining regions are inherited from \( P_1 \). The \( r_{10} \) of 11th position in \( P_1 \) are modified as \( r_5 \) by \( P_2 \). Figure 4 shows the physical region representations of these chromosomes shown in Fig. 3.

4.4. Dynamic mutation operator

Mutation is a secondary search operator which increases the variability of the population. The mutation operator creates new individuals by changing one or more of the gene values in the chromosome with a probability equal to the mutation rate \( P_{\text{mutation}} \). Consequently, approximately \( P_{\text{mutation}} \) mutations occur per generation. For efficiently applying the operator to the image segmentation problem, we modify the traditional mutation operator which randomly selects any gene in a chromosome and its allele.

The operator entails the two decision phases as described below: The first is to randomly select a gene, that is, any region in the whole image, to be mutated in

![Diagram](image-url)
Fig. 4. The physical region representations of chromosomes shown in Figs 3 and 5. (a) The regions of the Fig. 3(a) chromosome \( P_1 \); (b) the regions of the Fig. 3(b) chromosome \( P_2 \); (c) the regions of the Fig. 3(c) chromosome \( \text{child} \); (d) the regions of the Fig. 5(b) chromosome (mutated child).

The chromosome is represented by the roulette wheel slot sized in proportion to the local contrast measure \( C_i \) described to equation (10), although the criterion in a traditional genetic algorithm is purely random. In the second phase the region selected by the first phase is randomly determined to be merged with any region \( r_j \) \((j = 1, 2, \ldots, n)\) around its adjacent regions or to split from already merged regions. In the case of merging the merging region \( r_j \) has to satisfy the following condition: \( \max_i (1/\mu_{ij}) \). The detailed algorithm for this mutation process is given below.

Procedure Dynamic mutation mechanism
begin
Calculate the local contrast \( C_i \) of each gene in the chromosome \( \mathcal{I}_i \).
Select any mutating gene \( i \) according to a roulette wheel sized in proportion to \( C_i \).
The gene \( i \) is randomly determined to merge or to split.
if (merging)
Merged after selecting one adjacent region \( r_j \) with \( \max_i (1/\mu_{ij}) \)
else if (splitting)
If the region is already merged by other regions, then split from the regions, otherwise skip.
end
End procedure

Fig. 5. New child chromosome generated by mutation operation. (a) The chromosome structure to be mutated [Fig. 3(c)]; (b) new chromosome generated by the mutation operation [the region \( r_5 \) is merged with \( r_j (m_j) \) and \( r_i \) is split from the region which is already merged with \( r_i, r_{13} \) and \( r_{14} (m_{14}) \)].

changed by the mutation rate \( p_m \) due to the above first phase [Fig. 5(a)]. Also, they are determined to be merged with any \( r_j \) and to be split from \( r_{14} \) due to the second phase, respectively [Fig. 5(b)].

5. Experimental Results

In this section we present experimental results using the genetic algorithm with a fuzzy measure. The fundamental idea of the image segmentation is based on the split-and-merge segmentation method. To demonstrate the capability of the proposed segmentation algorithm, three images are first constructed in the experiments. Figure 6(a) shows the original test image of size 128 \( \times \) 128 pixels with four clear regions. Figure 6(b) shows a noisy image which is corrupted and additive zero-mean independent, identically distributed Gaussian noise with a standard deviation 20. Figures 6(c) and (d) show a blurred image with spot noise from the Fig. 6(a) image and an image blurred by a 5 \( \times \) 5 matrix from the Fig. 6(b) image, respectively.

For finely segmenting these images, we used the fuzzy-c-means (FCM) algorithm proposed by Bezdek. Also, assuming that these images were sufficiently fragmented with eight gray levels converged in 10 iterations. These segmentation results shown in Fig. 7 represent boundaries of regions which are segmented into 49, 310, 89 and 101 regions, respectively. These regions include at least more than 5 pixels to reduce the computation time. Therefore, the minimum size of these regions has an effect on the parameters of the weight function described in equation (7). The values of the parameters \( x \) and \( \beta \) are fixed at 5 and 20 for all test images.

The issue of concern for the experiments was the selection of the appropriate control parameters for the GA. The scope of major parameters of GA characterized by the following three parameters.

- Population size \( (m) \): In general, the population size affects both the ultimate performance and the efficiency of GA. A small population discourages premature convergence to suboptimal solutions. On the
Fig. 6. Test images. (a) Original test image of the size of 128 × 128 pixels with four clear regions; (b) noisy image corrupted with Gaussian noise (deviation = 20.0, mean = 0.0); (c) spot noisy image blurred by 5 × 5 matrix from the Fig. 6(a) image; (d) blurred image by 5 × 5 matrix from the Fig. (b) image.

Fig. 7. Finely segmented regions of those images in Fig. 6.
Fig. 8. The segmentation process of the original image in Fig. 6(a) during the progression of generations ($P_{\text{crossover}} = 0.2, P_{\text{mutation}} = 0.1$).
Fig. 9. The segmentation process of the noisy image in Fig. 6(b) ($P_{\text{cross-er}} = 0.2$, $P_{\text{mutation}} = 0.1$).
Fig. 10. The segmentation process of the spot noisy image in Fig. 6(c) ($P_{\text{cross}} = 0.2, P_{\text{mutation}} = 0.1$).
Fig. 11. The segmentation process of the blurred noisy image in Fig. 6(d) ($P_{\text{crossover}} = 0.2; P_{\text{mutation}} = 0.1$).
other hand, a large population requires more evaluations per generation, possibly resulting in a slow rate of convergence. In the current experiments, the population size is fixed to 60.

- Crossover rate ($P_{\text{crossover}}$): The crossover rate controls the frequency with which the crossover operator is applied. The higher the rate, the more quickly new structures are generated into the population. If the crossover rate is too low, the search may stagnate due to the lower exploration rate. The current experiments allowed the crossover rate to vary between 0.1 and 0.3, however, the variety of the rate scarcely affects the convergence and the segmentation results. Thus, the crossover rate is fixed to 0.2.

- Mutation rate ($P_{\text{mutation}}$): In this application the mutation rate is used as an important parameter, which increases the variability of the population, even though the experiments allowed various values, ranging from 0.04 to 0.1, for the mutation rate. The mutation rate was experimentally fixed to 0.1, since the mutation rate was an appropriate value to prevent premature convergence to suboptimal solutions and to provide the best segmentation results.

The segmentation results in Figs 8–11 show the process of segmentation of four images shown in Fig. 6. The regions are repeatedly and randomly split and merged with their adjacent regions per generation and so good segmentations reproduce and bad segmentations disappear. Each result is one of the best fitness $F$ described in equation (15) within the population of a given generation.

Figure 12 plots the varieties of fitness as the mutation rate $P_{\text{mutation}}$ when the crossover rate $P_{\text{crossover}}$ is fixed 0.2 about the image shown in Fig. 6(a). As shown in Fig. 6(a), the probability seems to play an important role in controlling the speed of segmentation.

Figure 13 represents the fitness values of all individuals in the population as each generation about the segmentation results shown in Fig. 6(d). Whenever each generation increases, the population is slowly evolved in proportion to individuals having high fitness values.

Figures 14(a) and (b) show the face part in the Lena image and an outdoor scene. Figures 15 and 16 display the segmentation results with the best fitness in the population during each iteration about these images, respectively.

In particular, we are interested in the segmented results in the texture area and unclear boundaries among regions over these images, since the fitness only deals with the measure of separation and compactness within segmented regions and of the edginess of region boundaries, as defined. In addition, the fitness based on statistics such as mean and variance is very sensitive to the size of the regions and the length of the boundary between adjacent regions. Due to these reasons, the fitness of the Lena image is continuously fluctuating, as
Fig. 13. The 3-D graph representation of the fitnesses of all individuals in the population as each generated about the Fig. 6(c) image.

Fig. 14. (a) The subimage of the face part in the Lena image; (b) an outdoor scene.
Fig. 15. The segmentation results of Fig. 14(a) image during the progression of generations ($P_{crossover} = 0.2$, $P_{mutation} = 0.1$).
Fig. 16. The segmentation results of Fig. 14(b) image during the progression of generations ($P_{\text{cross}} = 0.2$, $P_{\text{mutation}} = 0.1$).
6. CONCLUSIONS

In this paper, we have presented a robust split-and-merge image segmentation methodology using a genetic algorithm based on a random search and a parallel test-and-go technique. The algorithm provides a useful method for image segmentation without the need for critical parameters or threshold values.

Since the merits of the genetic algorithm are based on the randomness and the hill-climbing technique of the mutation operator, the segmentation is at least prevented from convergence to a local minimum and biased or unexpected results due to specified parameters. Furthermore, it can provide a partially optimum solution to maximize the given fitness per generation.

However, in the case of the complicated image such as the Lena image which includes unclear boundaries among regions and texture characteristics, the fitness $F$ is continuously fluctuating because it cannot find an optimal solution. Of course, the fitness measure is not guaranteed to be optimal as a universal measure of segmentation quality. Stopping rules such as the appropriate number of regions in an image through a prior knowledge may be required for the improvement of this problem. The algorithm is relatively simple to implement, but requires much computer storage and computation time in a single processor environment. Further work needs to be carried out in analysing the relationship of genetic parameters and implementing the parallelism for real-time application.

REFERENCES


About the Author—HYUN S. YANG was born in 1953. He received the B.S.E.E. degree from the Department of Electronics Engineering, Seoul National University, Korea, in 1976, and the M.S.E.E. and Ph.D. degrees from the School of Electronical Engineering, Purdue University, West Lafayette, U.S.A., in 1983 and 1986, respectively. From August 1986 to July 1988, he worked as an assistant professor in the Department of Electrical and Computer Engineering, University of Iowa, Iowa City. While attending Purdue University, he worked at the Robot Vision Laboratory as a research assistant from May 1983 to August 1985 and a research associate from September 1985 to August 1986. He was engaged in such research as 3-D shape representation and recognition, knowledge-based vision systems and intelligent robot manipulation with visual feedback. While he was with University of Iowa, he developed Robot Vision and Machine Intelligence Laboratory in the Department of Electrical and Computer Engineering. He is currently working with the Department of Computer Science, Korea Advanced Institute of Science and Technology (KAIST) as an associate professor and a director of Computer Vision and Intelligent Robotics Lab in the Center for Artificial Intelligence Research at KAIST. His current research interests include 3-D (three-dimensional) object representation and recognition, CAD-based 3-D robot vision, knowledge-based vision, neural network-based vision and mobile robots. He is currently a governing board member of the International Association for Pattern Recognition.

About the Author—DAE N. CHUN was born in 1962. He received the B.S. degree from the Department of Statistics, Kyungpook National University, in 1984 and the M.S. degree from the Department of Computer Science, KAIST, in Korea, in 1986. Since February 1986 he has been a Senior Engineer at Electronics and Telecommunication Research Institute. He is currently a Ph.D. student in KAIST. His research interests include pattern recognition, computer vision and computer graphics.