
A Simple and Fast GA-SA Hybrid Image Segmentation Algorithm

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Abstract

Image segmentation is an important process of image analysis. Most of the published approaches for image segmentation need to set appropriate parameter values to cope with the uncertainty problem. However, the parameter values are usually problem dependent and hardly obtained. In this paper, a simple and fast GA-SA hybrid image segmentation algorithm (HISA) is proposed. In HISA, the well-known K-means algorithm is used to split an image into many small regions first. Then, the genetic algorithm is applied to search a good or usable region segmentation, which maximizes the quality of regions that generated by split-and-merge processing. The simulated annealing algorithm (SA) is combined with a genetic algorithm (GA) to reduce the length of chromosomes for improving the convergence speed. The proposed algorithm HISA can lead to better computational efficiency and higher segmentation accuracy. Experimental results using several natural images to demonstrate the feasibility and the efficiency of the proposed algorithm.

1 INTRODUCTION

Image segmentation is an important process of image analysis. It is a process of segmenting an image into a set of disjoint regions whose characteristics such as intensity, color, and so on, are similar [2]. Segmentation algorithms for monochrome images are generally based on one of two basic properties of gray-level values: discontinuity and similarity. In the first category, the approaches partition an image based on abrupt changes in gray level. The principal approaches in the second category are based on thresholding, region growing, and region splitting/merging [11].

Large amounts of segmentation algorithms have been developed [8, 9]. These can be categorized into three groups [10]: edge-based approaches [11-15], clustering-based approaches [12, 13], and region-based approaches

[11-13]. Region-based approaches include region growing, merging and splitting/merging approaches [10]. Splitting/merging process is to subdivide an image initially into a set of arbitrary disjointed regions, and then it merges and/or splits the regions in an attempt [11]. We investigate the image segmentation problem and propose a splitting/merging algorithm in this paper.

There exists two fundamental problems in the low-level image segmentation. One is that most of the segmentation results are not always crisp or correct, because the images process grayness ambiguity and the spatial ambiguity which is known as an uncertainty problem. The other is that image segmentation approaches use numerous control parameters depending on image characteristics and environment. Therefore, these approaches depending on control parameters may not be applicable to several images [2].

To cope with the first problem, most approaches use many parameters that are dependent on image property to segment the images correctly. However, setting appropriate parameters is also a difficult problem [19-21]. As a result, it is essential to solve these two fundamental segmentation problems.

There are more and more approaches using GAs to select appropriate parameters or region associations [1-6]. Although these approaches can obtain correct segmentation results, there still exists some key points to improve execution performance: (1) without complex preprocesses; (2) simple encoding and easy implementation; (3) feasible solutions; and (4) non-random merging.

Bhandarkar and Zhang used a stochastic annealing algorithm to replace the selection mechanism of GA to segment images [1]. Chun and Yang proposed a split/merge approach, which segmented an image into small regions using a fuzzy-c-means (FCM) algorithm first, and adapted GA computations to merge these regions [2]. Bhanu et al. adapted the fourteen parameters of the Phenix algorithms using GAs in single objective and multi-objective approaches [3][4]. Haseyama et al. proposed a new approach which adapted the Markov random field (MRF) model [5][6]. However, the computation time of all the above approaches is very long.

In light of the above problems, a simple and fast image segmentation algorithm (HISA) is proposed. The K-means algorithm is used to split image first, and then merge regions using a simple encoding genetic algorithm. An appropriate fitness function is designed for HISA. Finally, the simulated annealing algorithm is applied to reduce the length of chromosome of GA to improve the convergence speed. HISA can lead to better computational efficiency and higher segmentation accuracy. The merits of HISA are as follows:

- (1) Without setting thresholds;
- (2) Without complex preprocesses;
- (3) Simple encoding and easy implementation;
- (4) Non-random merging; and
- (5) Reduce the chromosome by using SA and short computation time.

The segmentation approaches using GAs and image evaluation functions are presented in Section 2. The proposed GA-SA hybrid image segmentation algorithm (HISA) is presented in Section 3. The comparisons of experiments are given in Section 4. Finally, the conclusions drawn from this study and advantages of our approach are summarized in Section 5.

2 RELATED WORK

In the image segmentation problem, there are more and more approaches using genetic algorithms to select appropriate parameters or region associations [1-6]. The related references are presented in subsection 2.1 and the image evaluation functions are shown in subsection 2.2.

2.1 SEGMENTATION USING GENETIC ALGORITHMS

Genetic algorithm is an adaptive procedure that searches for good solutions by using a collection of search points known as population in order to maximize some desirable criteria. There are many approaches using GAs in solving image segmenting problem. Some famous segmentation algorithms are discussed as follows.

S. M. Bhandarkar and H. Zhang combined the stochastic annealing approaches with GA to segment images [1]. In Bhandarkar's approach, the preprocessing phase is very complex, which includes image dissimilarity enhancement, thresholding, connected component labeling, edge tracing, RAG generation, and initial cost evaluation. They used two dimensional chromosome encoding approach and the merge direction is based on random search mechanism.

D. N. Chun and H. S. Yang used a fuzzy-c-means (FCM) algorithm to split an image into various small regions first, and merge them by using GA [2]. This approach may create infeasible solutions in the evolution process, thus the repairing procedure may cost a lot of time. Moreover, it is well-known that the computation time of FCM is very long.

B. Bhanu et al. adapted the fourteen parameters of the Phnenix algorithms using GAs in single and multi objective approaches [3][4]. These approaches require multiple frames of the same target and the structures of chromosomes are very complex, which include image characteristics (image statistics and external variables), segmentation parameters, and the quality or fitness of the parameter set. Because there are more than 10^{40} conceivable parameter combinations, the computation time will be long. M. Haseyama et al. proposed a new approach which adapted the Markov random field (MRF) model [5][6]. Haseyama's approaches need a source image only, but the representation of chromosomes is much more complex. The chromosome consists of the pixel coordinates, a threshold of average contrast for the simple region growing, a set of parameters for observed digital image, the simple region growing direction, and many parameters of MRF model.

However, the computation time of all the above approaches is very long. The comparisons of the above-mentioned segmentation algorithms and HISA are shown in Table 1. The fourth comparisons of [3]-[6] in Table 1 are ignored because they are not split/merge approaches.

Table 1: Comparisons of various segmentation algorithms.

	[1]	[2]	[3]	[4]	[5]	[6]	HISA
Without complex preprocesses		✓	✓	✓	✓	✓	✓
Simple encoding		✓					✓
Feasible solutions	✓		✓	✓	✓	✓	✓
Non-random merging			—	—	—	—	✓
Short computation time							✓

2.2 IMAGE EVALUATION

The evaluation function is the critical part in measuring the quality of image segmentation. Generally speaking, there are two kinds of measurement functions: the nonspatial measurement and the spatial measurement. The nonspatial criterion is widely used to consider the variance of features and histograms, except for the geometrical information in an image. The spatial measures for segmentation consider the location of pixels and the geometric properties. It measures the consistency of a pixel with respect to its neighbors and reveals the homogeneity of the regions [2].

Let N be the number of segmented regions, r_i is one of the segmented regions ($i = 1$ to N). The properties of r_i are as follows:

- (1) m_i is the average gray-level value of r_i ;
- (2) σ_i^2 is the variance of pixels gray-level values of r_i ;
- (3) P_i is the amounts of pixels of r_i ; and
- (4) n_i is the number of adjacent regions of r_i .

There are three main image evaluation functions according to the above properties, described as follows:

- (1) Average gray-level values of regions

The average gray-level value is the most significant characteristic for computing the dissimilarity between

adjacent regions. Eqn. (2.1) is the general formulation [2][17][22]:

$$MAX \quad S_{ij} = |m_i - m_j|^2 \quad i, j \text{ adjacent} \quad (2.1)$$

(2) Variance of gray-level values of regions

Variance of gray-level value is used for computing similarity in a region. Eqn. (2.2) is the general formulation [1][2][22]:

$$MIN \quad \sum_{i=1}^N s_i^2. \quad (2.2)$$

(3) Size of regions

In the split/merge techniques, it is general tendency to merge regions. Eqn. (2.3) is the general formulation [22]:

$$MAX \quad \frac{(P_i * P_j)}{(P_i + P_j)} \quad i, j \text{ adjacent} \quad (2.3)$$

Our HISA computes the dissimilarity of every region using Eqn. (2.1) first. Region r_j is the most similar region of r_i if s_{ij} is the smallest value of s_{ik} ($k = 1$ to n_i). Because the purpose of image segmentation is to segment an image into various regions whose characteristics are similar, the best merge direction of r_i is to merge into r_j .

3 GA-SA HYBRID IMAGE SEGMENTATION ALGORITHM

The simple and fast image segmentation algorithm HISA is designed. The K-means algorithm is used to split an image first and, then, using the simple HISA to merge these regions. SA is applied to reduce the length of chromosome for improving the convergence speed. The flowchart of HISA is shown in Fig. 1.

3.1 SPLIT METHOD

The well-known K-means algorithm [24] is used to separates the pixels in the image into various small regions based on both their intensity and the relative location of regions. Because the properties of the K-means algorithm are simple and fast, several K-means algorithm based image segmentation algorithms have been proposed [16][18].

Because the gray-level variations of pixels are larger than the coordinate values, pixels in the same split region may not continuous (Fig. 2a). The small regions (1 or 2 pixels) are filtered out and merged to adjacent regions to cope with this problem (Fig. 2b). This approach improves the quality of splitting regions without setting thresholds.

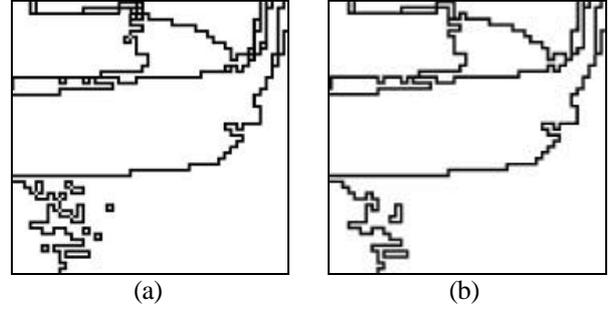


Fig. 2. An example of filter procedure. (a) Segmented image includes small regions. (b) Result after a filter procedure.

3.2 DESIGN OF THE GENETIC ALGORITHM

After the split procedure, GA is used to search an optimal combination of regions. The procedure of GA is as follows:

(1) Chromosome encoding

The binary representation is used. Assume the amounts of split regions are N , an example of chromosome structure about segmented regions is shown in Fig. 3(a). A split image with merge directions of regions is shown in Fig. 3(b). The merge result of the value '0011010' is shown in Fig. 3(c). Value 1 of gene represents the region reserved, and value 0 represents the region merged to the most similar region computed using Eqn. (2.1). This encoding method can guarantee that the merging process can obtain the feasible solutions always.

(2) Fitness function

Many evaluation equations are surveyed and an appropriate fitness function for HISA is designed. To cope with the split/merge problem, the dissimilarity of adjacent regions and the pixels of segmented regions are considered. The fitness function is formulated as Eqn. (3.1).

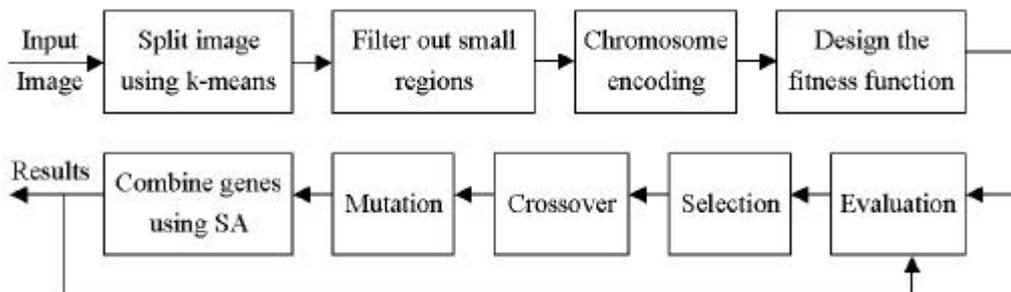


Fig. 1. Flowchart of HISA.

$$\text{MAX } F = \frac{1}{N} \sum_{i,j} (|m_i - m_j|^2 * \frac{P_i * P_j}{P_i + P_j}) \quad i, j \text{ adjacent} \quad (3.1)$$

(3) Selection

A rank-based selection is used, which selects the best n individuals to replace the worst n individuals.

(4) Crossover

Two chromosomes selected from the populations are called *Parent1* and *Parent2*. Single-point crossover is applied in HISA.

(5) Mutation

Each bit of the binary-coded genes is varied according to the mutation probability.

(6) Termination conditions

Terminate the program if no improvement for 20 generations.

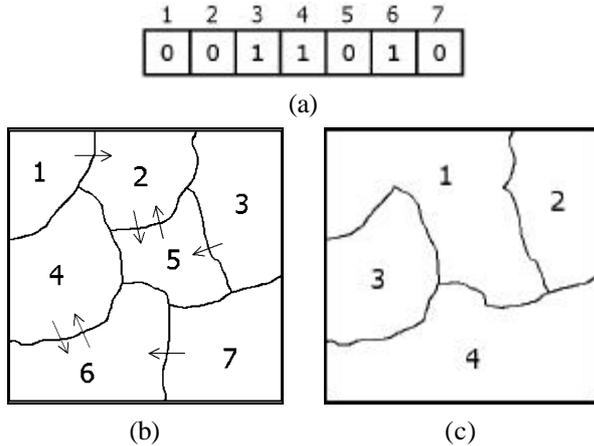


Fig. 3. An example for encoding the chromosome. (a) A binary chromosome with the value '0011010'; (b) A split image with merge directions of regions; (c) Merged result of (b).

3.3 GENES COMBINATION METHOD

We apply SA to reduce the length of chromosome. A single iteration of a SA algorithm consists of three phases: (1) perturb; (2) evaluate; and (3) decide. In the perturb phase, the current solution x_i to a multivariate objective function $E(x)$ is systematically perturbed to yield another candidate solution x_j . In the evaluate phase, $E(x_j)$ is computed. In the decide phase, x_j is accepted and replaces probabilistically using a stochastic decision function. The new candidate solution x_j is accepted with probability p .

In HISA, the temperatures of every gene are given and the bit values are checked every generation. If the bit value in the best chromosome is 0, decrease its temperature. While the genes' temperatures are under the setting termination temperature, ignore these genes and reduce the length of the chromosome.

After the reducing procedure, original regions may be merged into larger regions. It's necessary to compute new

information for new regions, such as m_p , P_i , and amounts of regions.

4 EXPERIMENTAL RESULTS

In this section, three experiments with several natural images are used to demonstrate the feasibility and the efficiency of our proposed algorithm HISA. All the test image sizes are 256x256 pixels, and the general values of GA's parameters are as follows: (1) population size is 20; (2) selection rate is 0.2; (3) crossover rate is 0.9; and (4) mutation rate is 0.05. The parameters of SA are as follows: (1) initial temperature is 1.0; (2) perturbation function is $T = T * 0.8$; and (3) the terminate temperature is 0.1. The proposed image segmentation algorithm was implemented using programming language C on an Intel Celeron-333 MHz computer.

In the first experiment, seven natural images are used for test. The outdoor and indoor images with simple background are shown in Fig. 4 and Fig. 5. The contours of objects are segmented clearly. The indoor images with complex scene are shown in Fig. 6 and Fig. 7. In the indoor-A image, the contours of basketball, desk lamp, and package are segmented. In the indoor-B image, the contours of desk lamp, monitor, and chair are segmented. The Lena image is segmented and shown in Fig. 8. The plume and fair of Lena are merged because their intensities are similar, but the eyes are also merged because the areas of eyes are too small. The contour of animal Husk is segmented clearly and shown in Fig. 9. A complex animal image Baboon is also tested. The segmented results is shown in Fig. 10. It is very difficult to segment this image finely because the variance of the image intensity is very large. But the fuscous part in the center of image is still segmented clearly by HISA. The test results are shown in Table 2.

In the second experiment, an example is designed for illustrating the importance of the SA. We omit the SA procedure and segment the same images again. The test results using the same parameter and encoding methods are shown in Table. 3. In the absence of the SA mechanism, the computation time is very long and the number of generations needed for convergence is fairly large. Considering the convergence speed and the quality, the comparisons of HISA with/without the SA procedure are shown in Fig. 11 and Fig. 12.

In the last experiment, the comparison of different segmentation techniques is presented. The reported data and the segmented images are referred from references because it is very difficult to implement these approaches. The segmented images using method [1] are shown in Fig. 13. The Bhandarkar's approach used 507.42 minutes (63 iterations) to segment an image. The computation speed of this method is very slow. The segmented images using method [2] are shown in Fig. 14. The computation time is never described in this paper, but this approach requires much computer storage and computation time in a single processor [2].

Table 2: Results obtained from the HISA.

Image	Time of split procedure (sec.)	Time of filter procedure (sec.)	Time of merge procedure (sec.)	Total used time (sec.)	Split regions	Merge regions	Generations	Fitness value
Airplane	88.7	3.9	19.9	112.5	144	3	181	7312516.9
Clock	105.0	17.8	83.3	206.1	581	6	94	7708348.0
Indoor-A	105.3	20.2	164.3	289.8	739	9	162	2967265.9
Indoor-B	104.5	25.0	334.5	464.0	1112	17	152	771983.4
Lena	105.7	14.2	82.4	202.3	534	5	133	5080131.5
Husk	104.7	18.1	145.7	268.5	661	10	114	4651404.9
Baboon	105.0	85.4	2462.0	2652.4	2993	8	234	1192713.5

Table 3: Results without the SA mechanism.

Image	Time of split procedure (sec.)	Time of filter procedure (sec.)	Time of merge procedure (sec.)	Total used time (sec.)	Split regions	Merge regions	Generations	Fitness value
Airplane	88.7	3.9	75.2	167.8	144	38	300	45539.6
Clock	105.0	17.8	547.9	670.7	581	181	300	6851.4
Indoor-A	105.3	20.2	889.5	1015.0	739	240	300	3368.3
Indoor-B	104.5	25.0	1873.6	2003.1	1112	275	300	1519.3
Lena	105.7	14.2	474.6	594.5	534	170	300	4727.5
Husk	104.7	18.1	740.9	863.7	661	217	300	6715.7
Baboon	105.0	85.4	18299.6	18490.0	2993	1281	300	46.8

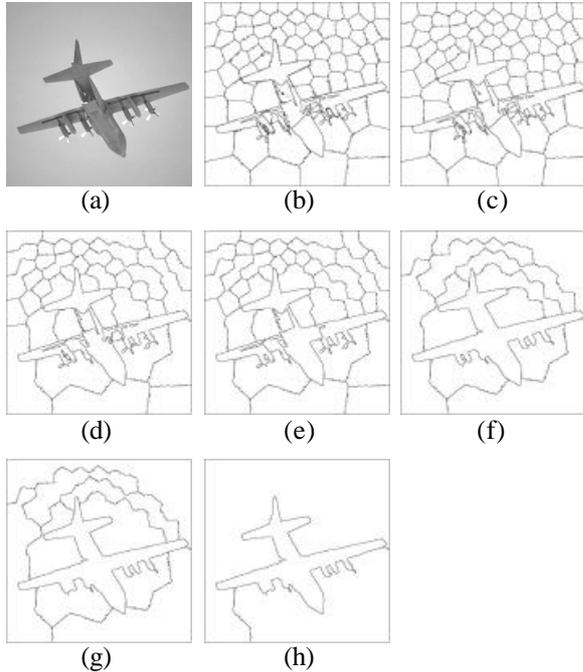


Fig. 4. Airplane image. (a) Original image; (b) 80 regions after K-means procedure; (c) 144 regions after filter procedure; (d)-(h) generation/regions are 1/70, 10/54, 50/14, 150/11, and 181/3.

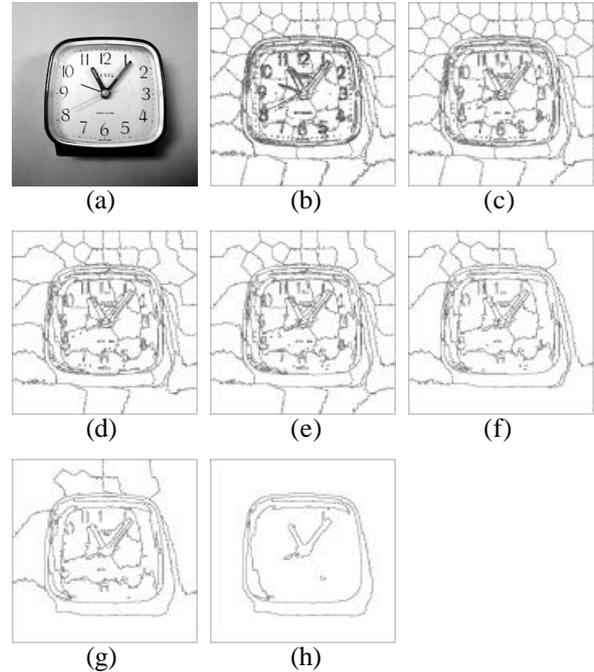


Fig. 5. Clock image. (a) Original image; (b) 80 regions after K-means procedure; (c) 581 regions after filter procedure; (d)-(h) generation/regions are 1/308, 10/256, 50/82, 60/35, and 94/6.

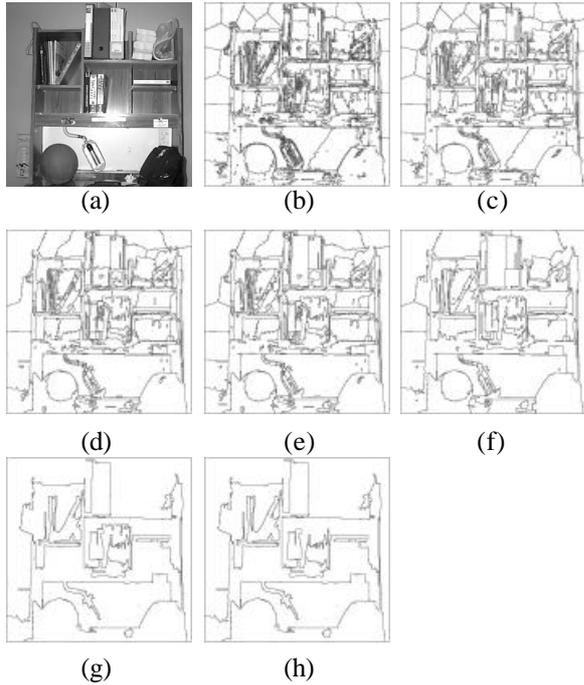


Fig. 6. Indoor-A image. (a) Original image; (b) 80 regions after K-means procedure; (c) 739 regions after filter procedure; (d)-(h) generation/regions are 1/392, 10/336, 50/119, 100/10, and 162/9.

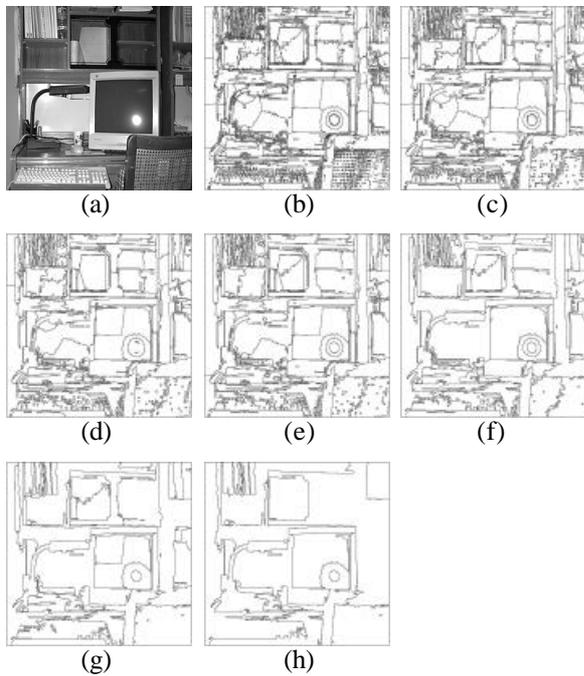


Fig. 7. Indoor-B image. (a) Original image; (b) 80 regions after K-means procedure; (c) 1112 regions after filter procedure; (d)-(h) generation/regions are 1/586, 10/508, 50/183, 100/59, and 152/17.

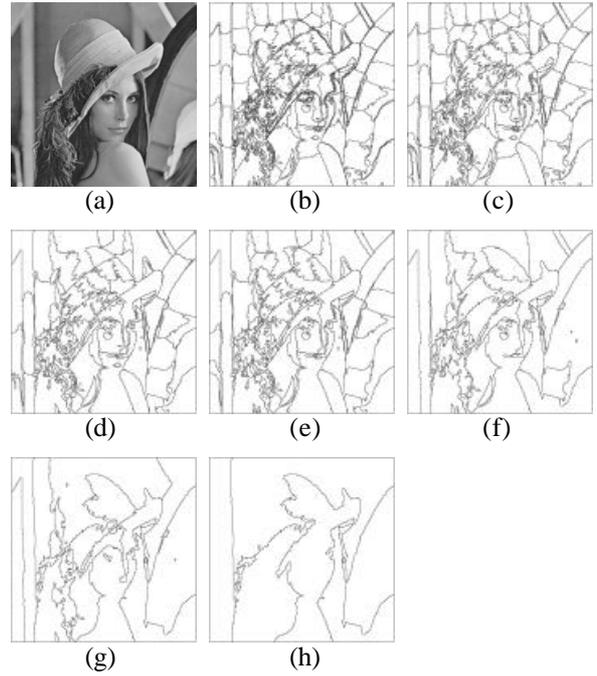


Fig. 8. Lena image. (a) Original image; (b) 80 regions after K-means procedure; (c) 534 regions after filter procedure; (d)-(h) generation/regions are 1/276, 10/249, 50/81, 100/26, and 133/5.

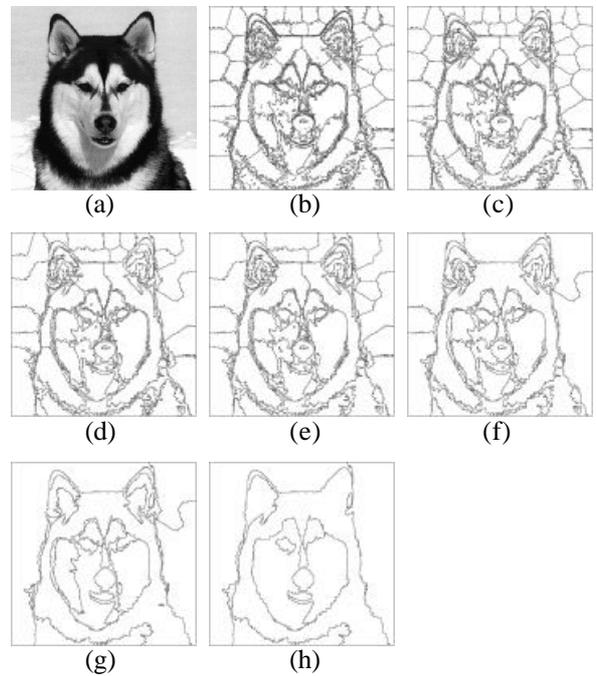


Fig. 9. Husk image. (a) Original image; (b) 80 regions after K-means procedure; (c) 661 regions after filter procedure; (d)-(h) generation/regions are 1/326, 10/291, 50/116, 100/32, and 114/10.

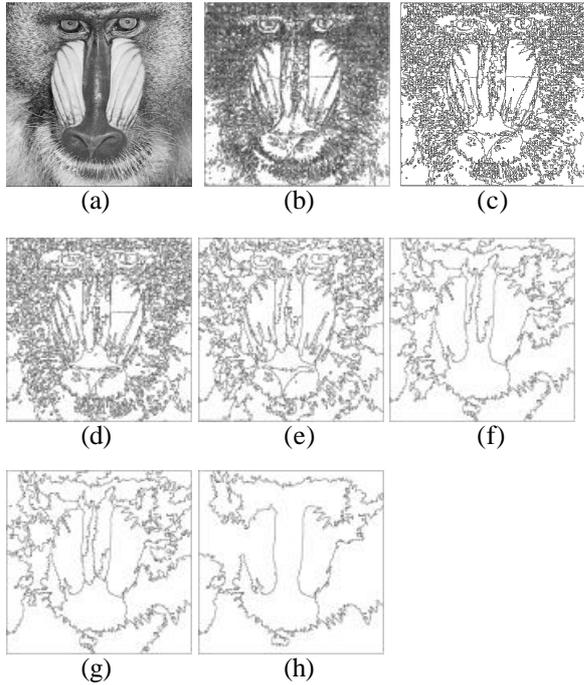


Fig. 10. Baboon image. (a) Original image; (b) 80 regions after K-means procedure; (c) 2993 regions after filter procedure; (d)-(h) generation/regions are 1/1596, 50/345, 150/33, 200/31, and 234/8.

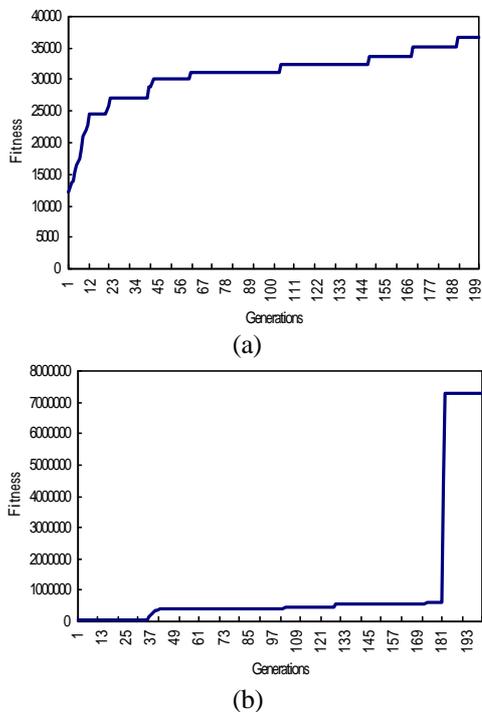


Fig. 11. Fitness values of the best chromosome for Fig. 4(a). (a) Without SA procedure, the best value is 36627 and used 52.2 seconds; (b) using HISA, the best value is 7312516 and used 19.9 seconds.

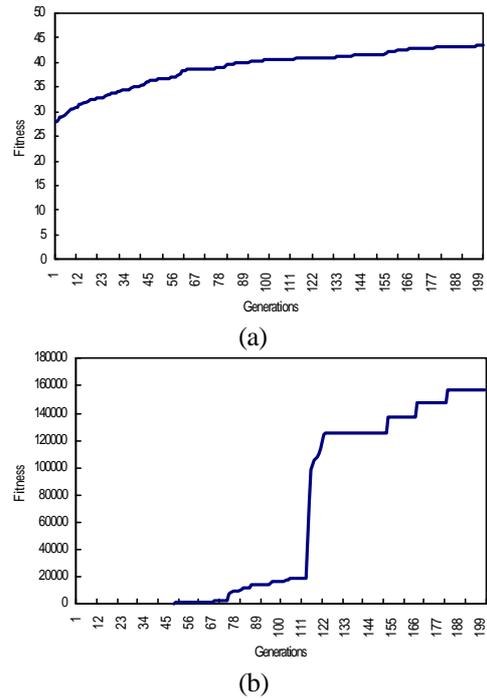


Fig. 12. Fitness values of the best chromosome for Fig. 10(a). (a) Without SA procedure, the best value is 43.5 and used 12618 seconds; (b) using HISA, the best value is 157238 and used 2457.2 seconds.

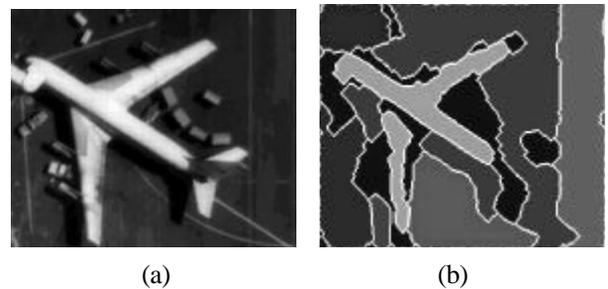


Fig. 13. Boeing image. (a) Original image; (b) segmented result using method [1].



Fig. 14. Lena image. (a) Original image of 128x128 pixels; (b) segmented result using method [2].

5 CONCLUSIONS

In this paper, a simple and fast GA-SA hybrid image segmentation algorithm (HISA) is presented. The simulated annealing is applied to reduce the length of chromosomes of GA for improving the convergence speed. The algorithm HISA can lead to better computational efficiency and higher segmentation accuracy. The computation time of the proposed HISA is much less than other GA-based image segmentation algorithms. The merits of the proposed algorithm are as follows: (1) without setting thresholds; (2) without complex preprocesses; (3) simple encoding and easy implementation; (4) non-random merging; and (5) reduce the chromosome by using SA to increase the computation speed.

At least, although the proposed region dissimilarity function was proven quite suitable for near piecewise constant images, the use of more complex functions may give better results on the expense of computational complexity during the merging process.

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