

A Hierarchical Distributed Genetic Algorithm for Image Segmentation

Hanchuan Peng ^{†‡}, Fuhui Long [†], Zheru Chi [†], and Wanchi Siu [†]

[†] Center for Multimedia Signal Processing, Department of Electronic and Information Engineering, The Hong Kong Polytechnic University, Hung Hom, Kowloon, Hong Kong. Email: {phc, fhlong, zheru}@eie.polyu.edu.hk

[‡] Department of Biomedical Engineering, Southeast University, Nanjing 210096, China. Email: phc@seu.edu.cn

Abstract - In this paper a new hierarchical distributed genetic algorithm is proposed for image segmentation. Firstly, a technique of histogram dichotomy is proposed to explore the statistical property of input image and produce a hierarchical quantization image. Then a Hierarchical distributed genetic algorithm (HDGA) is imposed on the quantized image to explore the spatial connectivity and produce final segmentation result. HDGA is a major improvement of the original Distributed Genetic Algorithm (DGA) and Multiscale Distributed Genetic Algorithm (MDGA) in four aspects: (1) HDGA does not require the *a priori* number of image regions, however it can effectively and adaptively controls the segmentation quality; (2) the chromosome structure is revised from the original label(multilabel)-condition-fitness format to a more compact (storage-efficient) label-fitness format; (3) the fitness function is revised to utilized the spatial connectivity, but not the original "reconstruction" error; (4) three revised genetic operations are presented to make the algorithm computation-efficient. Our experiments give proofs for the advantages of HDGA.

1 Introduction

Image segmentation is the process by which an image is segmented into a group of homogeneous regions. It is the front-end processing stage in image/video processing systems. Genetic algorithms have been applied to this problem according to a variety of principles (Bhandarkar and Zhang, 1999). Distributed genetic algorithm (DGA) (Andrey and Tarroux, 1994) was proposed for parallel image segmentation without *a priori* assumption of image, except the number of segmentation regions. The main idea of DGA is a simplified classifier system where the labeling function is implemented as a set of binary-coded production rules. Each image pixel in DGA has a three-segment chromosome: label-condition-fitness. The label of each pixel is iteratively modified using the genetic algorithm. Multiscale distributed genetic algorithm (MDGA) (Long, Zheng, and Zhang, 1998) was presented to segment images from coarse to fine. The chromosome structure is multilabel-condition-fitness, where multilabels are used to code the multilayer structures of regions. Unfortunately, both DGA and MDGA need the predefined image region number, which is usually not available before segmentation. At the mean time, DGA and MDGA often produce

unpredictable poor results because of the improper initialization. Therefore a more powerful genetic algorithm is required. In this paper we propose a Hierarchical Distributed Genetic Algorithm (HDGA) based on grayscale image histogram dichotomy. In section 2 the technique of hierarchical histogram dichotomy is proposed and proved. In section 3 the HDGA is proposed with newly designed chromosome, fitness function and genetic operations. In section 4 the experimental results are reported. Finally the discussion and conclusion are given.

2 Hierarchical Histogram Dichotomy

We regard the original grayscale image I as a union of non-overlapping homogeneous regions. Notice that image quantization has been recognized as globe image segmentation (Scheunders, 1996), and the initialization is critical to the performance of DGA. Hence we propose the HDGA as a two-stage image segmentation paradigm, which is composed of histogram dichotomy (for image quantization and genetic algorithm initialization) and an improved genetic algorithm (for image segmentation).

Instead of the usual Lloyd-Max quantization method, we produce the hierarchy of image regions with histogram dichotomy. The image histogram is repeatedly dichotomized into hierarchical continuous intervals until every interval has a pixel-by-pixel Mean square error (MSE) less than a given threshold T_σ . The histogram MSE on the gray level interval $[d, u]$ is defined as:

$$\sigma_{[d,u]}^2 = \frac{\sum_{k=d}^u P(k)(k - r_{[d,u]})^2}{\sum_{k=d}^u P(k)} \quad (1)$$

where d and u are lower and upper limits of the current histogram interval, the function $P(k)$ is the normalized grayscale histogram ($\sum_k P(k)=1$), r is the quantized gray level of the histogram interval, as defined in eqn(2):

$$r_{[d,u]} = \frac{\sum_{k=d}^u P(k)k}{\sum_{k=d}^u P(k)} \quad (2)$$

When the MSE of a histogram interval is larger than T_σ , this interval will be split into two subintervals, whose sum of MSE is minimized. That is, the interval division point $c_{[d,u]}$ is chosen as:

$$c_{[d,u]} = \arg \min \{ \sigma_{[d,c]}^2 + \sigma_{[c+1,u]}^2 \} \quad (3)$$

By the above method, a hierarchical tree of histogram intervals can be obtained. Each histogram interval corresponds to one or more image regions, which have the internal approximate homogeneity in sense of minimal

MSE. It can be observed that the sum of interval MSEs in a higher level is always smaller than that in the lower level. This method is in accordance with the optimal image quantization (Scheunders, 1996), however, the hierarchy of histogram offers flexibility to control the quantization quality, without *a priori* knowledge of image region number.

Generally there are strong quantization noises, especially in the slow varying areas of gray levels. In addition, the spatial connectivity information in images is not considered in image quantization. Hence we integrate this histogram dichotomy technique into the following HDGA paradigm.

3 Hierarchical Distributed Genetic Algorithm

In HDGA, a pixel (m,n) in the image has a chromosome $l_{m,n}$ and each chromosome consists of two parts: label $b_{m,n}$ and fitness $f_{m,n}$. The genetic population consists of all pixel chromosomes, therefore the population has the same size as the image pixel number (this is the meaning of the word "distributed"). The chromosome label is defined as the pixel quantization level, and the chromosome fitness is defined as:

$$f_{m,n} = \left| b_{m,n} - \frac{1}{H_{m,n} - 1} \sum_{p,q \in \Omega_{m,n}, p \neq m, q \neq n} b_{p,q} \right|$$

$$(1 \leq m \leq M, 1 \leq n \leq N)$$

(4)

where $\Omega_{m,n}$ is a neighbor area of the pixel (m,n) , M and N are image width and height, separately. For each pixel chromosome, its label is initialized as the pixel gray level from histogram dichotomy quantization.

Notice that the chromosome in HDGA is much simpler than that of DGA and MDGA, while it can make full use of the quantization result of histogram dichotomy. What's more, the new fitness function defined in eqn.(4) can better utilize the spatial relationship in image than the fitness function in DGA and MDGA, where only the error between the original image pixel and the current chromosome condition is considered.

Three genetic operations of HDGA are designed:

- (a) Selection: select the $l_{p,q}$ with the largest fitness $f_{p,q}$ in $\Omega_{m,n}$ to replace $l_{m,n}$.
- (b) Crossover: randomly cross over $l_{m,n}$ and $l_{p,q}$, which has the largest fitness $f_{p,q}$ in $\Omega_{m,n}$, and transform the result to be one of these two parents according to its discrimination to these parents.
- (c) Mutation: randomly select one $l_{p,q}$ in $\Omega_{m,n}$ to replace the current chromosome $l_{m,n}$. A small mutation rate r_m is defined.

Because of the simplified chromosome, HDGA differs much to DGA: although the genetic selection operation in HDGA is similar to the LTS operation in DGA, the genetic

crossover and mutation operations in HDGA are different from those in the original DGA.

The whole process of HDGA, just like other genetic algorithms, is organized based on the above three genetic operations. For the ending condition, the total number of chromosomes that do not change labels in the current generation is counted and the unchanged rate r_u is calculated. If r_u is larger than a preset threshold T_u in two continuous generations, then HDGA stops. Otherwise a new generation begins.

4 Experiments

The computer simulation is made on a database of 1000 images. These images belong to 5 categories: People-children, People-male, Picture-frames, Business goods, Vegetables & fruits. Each category has 200 true-color (24-bit) 320×240 images. In our experiments each image is converted to be 256 gray level (8-bit) image. A typical image example is shown in Fig.1.

Parameters of HDGA are $T_\sigma=76.8$, $T_u=0.9$, $\Omega_{m,n}=3 \times 3$ neighborhood of pixel (m,n) , $r_m=0.001$. For comparison, the region number in DGA is chosen to be the final total number of histogram intervals from HDGA histogram dichotomy. Other DGA parameters are chosen to the same as those of HDGA, or carefully adjusted to the best according to Andrey and Tarroux (1994).

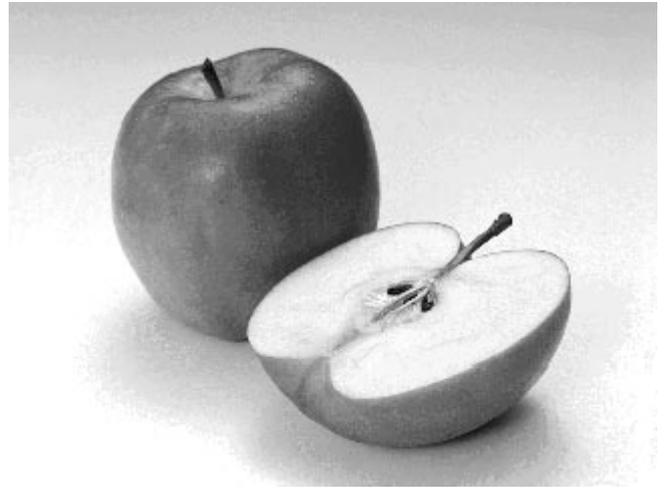


Fig.1 An example image for segmentation

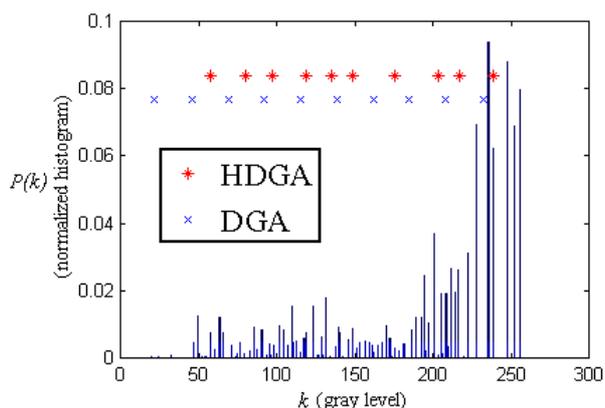


Fig.2 The quantization intervals of HDGA and DGA

For the input image in Fig.1, the quantization intervals of both HDGA and DGA are shown on the normalized histogram in Fig.2. Because DGA employs a uniform quantization (the equally distributed \times row in Fig.2), it can not make full use of the statistical information, and in most cases, it will result in wrong segmentation. On the contrary, HDGA slices the histogram into hierarchical intervals, each of which has homogeneity in the sense of minimal MSE (the unequally distributed $*$ row in Fig.2).

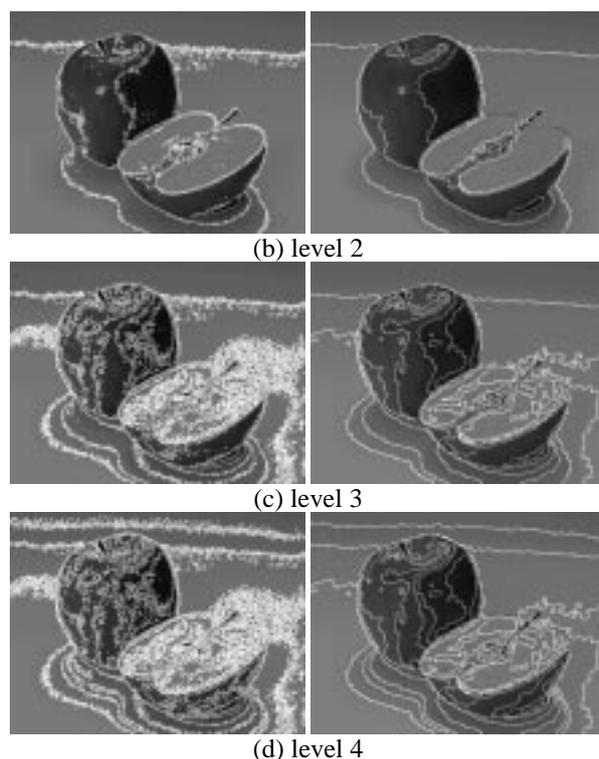


Fig.4 The segmentation of different layer

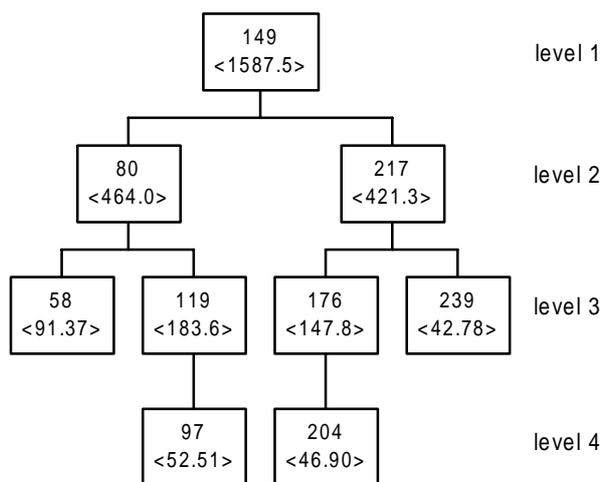
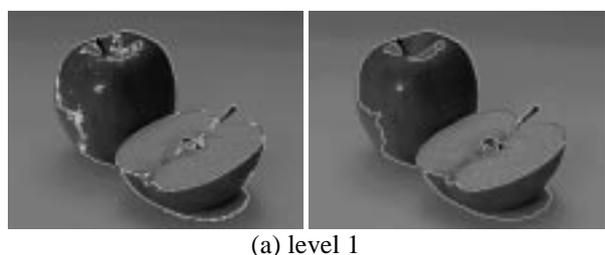


Fig.3 The hierarchy of histogram dichotomy



(a) level 1

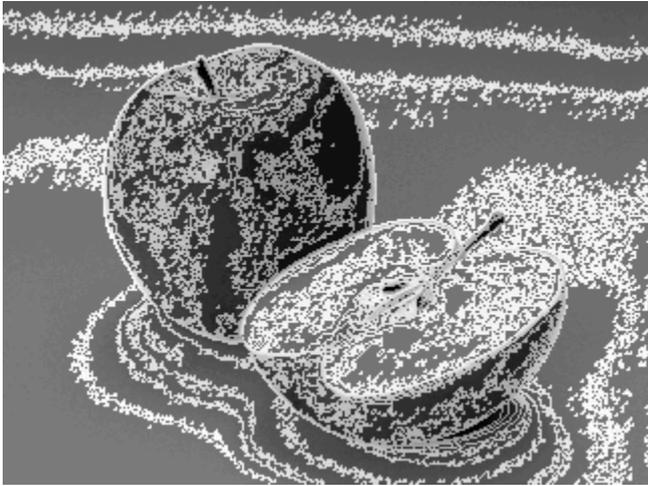
The histogram interval hierarchy tree produced by histogram dichotomy is shown in Fig.3. From top to bottom, the hierarchy tree has four levels. For each tree node, the first row is the interval division point and the second bracketed row is the sum of MSEs of left and right intervals divided by the division point. Note that the gray level range is $[0, 255]$.

In Fig.3, the intervals of each level are obtained from the inorder traversal. For example, for level 3, the histogram intervals are seen as $\{[0,58], [59,80], [81,119], [120,149], [149,176], [177,217], [218,239], [240,255]\}$.

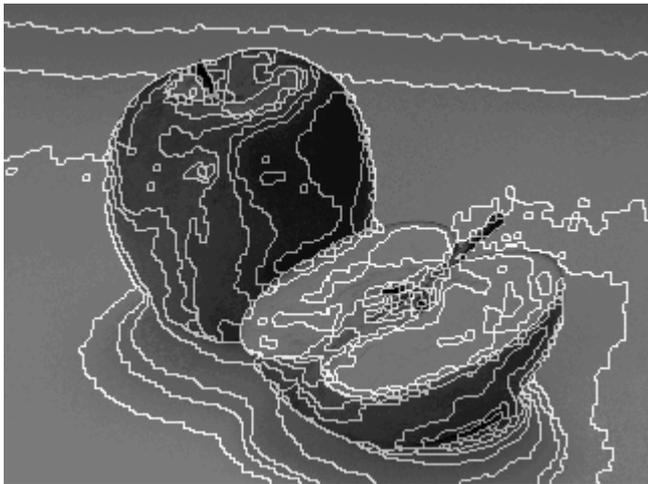
For each level in Fig.3, the image segmentation results are shown in Fig.4. The left column images in Fig.4 are the edges of quantization results of histogram dichotomy. The right column images are the edge of segmentation after HDGA. For the sake of visualization, all image region edges are overlapped on the original input image. We see that with the increase of histogram dichotomy level, HDGA can segment the image in more details.

In Fig.5 the comparing image segmentation results of HDGA (the level 4 in Fig.3 and Fig.4) and DGA are shown. Fig.5(a) and (c) are the edges of the initial quantization images of HDGA and DGA, respectively. Fig.5(b) and (d) are the final segmentation image region edges. We see that HDGA better segments the image than DGA. This seems to be a natural outcome of the better initialization based on histogram dichotomy. In addition, the role of genetic algorithm can be seen by comparing Fig.5(a) and (b), as well as Fig.5(c) and (d): the spatial relationship of image is

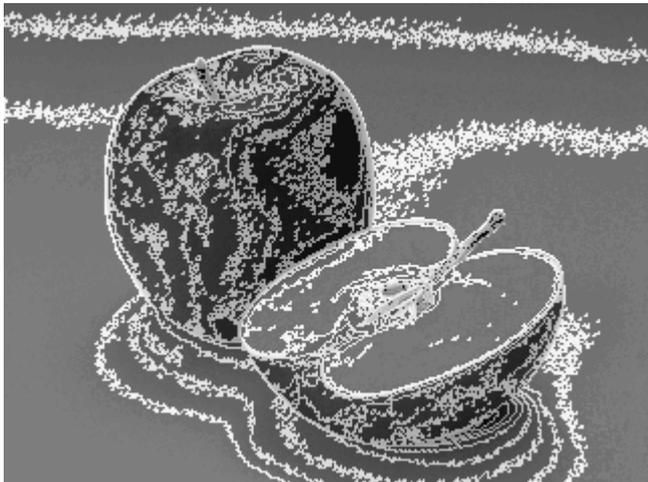
well utilized to remove small regions (quantization noises) and produce clear segmentation edges.



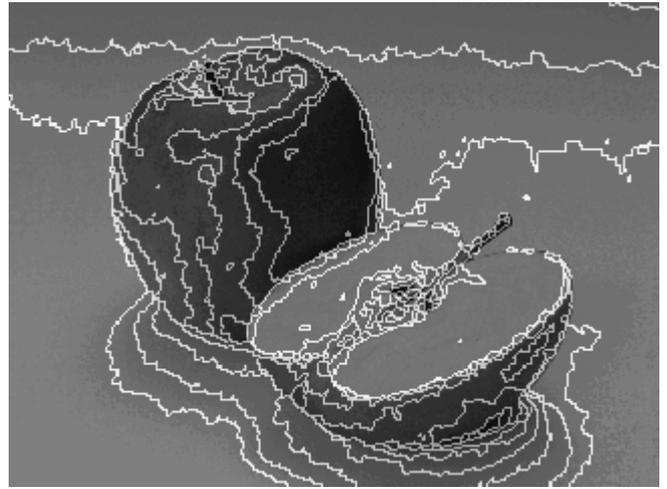
(a) initial quantization image edges of HDGA



(b) final segmentation image edges of HDGA



(c) initial quantization image edges of DGA



(d) final segmentation image edges of DGA

Fig.5 Segmentation results of HDGA and DGA

Table 1: The homogeneity of image regions

Category	Average S_{σ} [HDGA]	Average S_{σ} [DGA]	$\frac{S_{\sigma}$ [HDGA]}{ S_{σ} [DGA]}
People-children	319.6175	401.8327	79.54%
People-male	310.6658	411.1724	75.56%
Picture-frames	284.7555	402.6727	70.72%
Business goods	280.6534	369.0727	76.04%
Vegetables & fruits	310.6988	404.2918	76.85%

For quantitative comparison of the segmentation quality, we can examine the homogeneity of final image regions after segmentation. Sum of MSE over all image segmentation regions, *i.e.* $S_{\sigma}=\sum\sigma^2$, is calculated as the index. Table 1 gives the average results for HDGA and DGA on the five categories of images, and the ratio of S_{σ} [HDGA] to S_{σ} [DGA]. Clearly, the image regions produced by HDGA has better internal coherence than those produce by DGA. Typically S_{σ} [HDGA] is 20~30% less than S_{σ} [DGA], as shown in the third column of Table 1.

The role of genetic algorithm in both HDGA and DGA is quantitatively examined using the parameter r_r , which is the reduction rate of image region edge pixel number. Because it is hard to count the accurate region number in an image, the edge pixel number is used alternately. Note that the genetic algorithms will not erase the large regions, however will filter small regions. Hence with the decrease of image regions, the total edge pixel number will substantially reduce. This phenomenon can be recognized in Table 2. So we see that genetic algorithms in both HDGA and DGA play important roles in improving the direct quantization segmentation results, -- and the mere image quantization can not lead to significantly good

segmentation (e.g. the left column in Fig.4, and Fig.5(a) and (c)).

Table 2: The rates of region edge pixel reduction

Category	r_r [HDGA]	r_r [DGA]
People-children	42~55%	40~51%
People-male	35~47%	48~55%
Picture-frames	38~50%	44~50%
Business goods	44~52%	50~56%
Vegetables & fruits	28~42%	35~62%

In Fig.6 the convergence speeds of HDGA and DGA are compared for the image in Fig.1. Obviously HDGA has a much faster convergence than DGA: usually HDGA just needs 5 generation to attain the prior set accuracy $T_u=0.9$, while DGA often needs tens of generations. Two main causes are the better initialization and improvement of genetic algorithm (i.e. refined genetic operations and fitness function). In addition, even in one generation, HDGA needs much less computation than DGA because the simplification of chromosome structure and refinement of genetic operations. In our experiments, it is also found that typically the histogram dichotomy costs about 0.5 second while the genetic algorithms often cost hundreds of seconds. Thus the histogram dichotomy is computationally efficient for HDGA.

5 Discussion and Conclusion

HDGA can take full advantages of the statistical information and spatial information of an image in segmentation, through histogram dichotomy and the improved genetic algorithm. Experimental results show that HDGA outperforms DGA in image quantization and genetic algorithm initialization, computation efficiency and convergence speed, and segmentation region homogeneity.

One apparent drawback of HDGA is due to the histogram dichotomy. In the cases there are odd number of gaussian distributed intervals on the histogram, the histogram dichotomy may lead to error. However, this

problem is not impossible to be overcome because an adaptive histogram multi-splitting technique can be proposed to estimate the optimal histogram subintervals in a given interval.

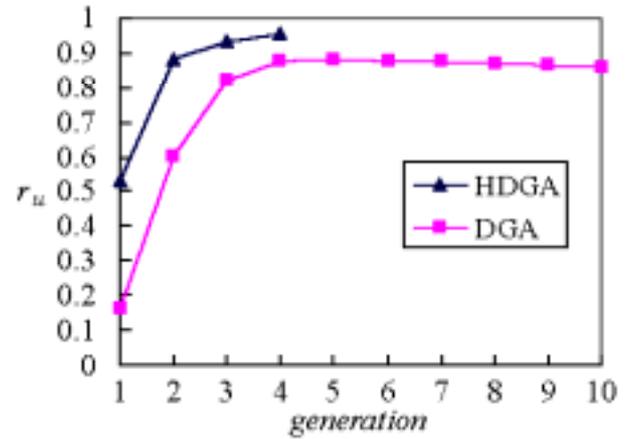


Fig.6 The convergence of HDGA and DGA

References

- 1 Bhandarkar, S.M., and Zhang, H., (1999): "Image segmentation using evolutionary computation," IEEE Trans. on Evolutionary Computation, **3**, (1), pp.1-21
- 2 Andrey, P., and Tarroux, P., (1994): "Unsupervised image segmentation using a distributed genetic algorithm," Pattern Recognition, **27**, (5), pp.659-673
- 3 Long, F., Zheng, N., and Zhang, X., (1998): "A new image segmentation method based on genetic algorithm of multilayer perceptron," Control Theory and Applications, **15**, (2), pp.232-236
- 4 Scheunders, P., (1996): "A genetic Lloyd-Max image quantization algorithm," Pattern Recognition Letters, **17**, pp.547-556