3—21 Genetic Hough Transform for Curves Detection

Yao Dong WANG *
Foundation Research Group
Media Drive Corporation

Noboru FUNAKUBO †
Tokyo Metropolitan
Institute of Technology

Abstract

Fast Hough algorithms that are based on polling are referred to as probabilistic Hough transform(PHT). The optimization model is the related method of detecting curves. In this paper, we propose a new curves detection approach called the genetic Hough transform(GHT), inspired by the efforts of using equivalence classes in genetic algorithm(GA). It combines advantage of the PHT and optimization model, and made use of genetic samplings to accelerate form of desired peaks. Our approach can simultaneously detect several curves in an image. It also has advantages of fast speed, small storage and high accuracy. Throughout the paper, experiments are conducted to verify the new algorithm.

1 Introduction

One of the key issues in image processing is to detect interesting objects from an image. Hough transform(HT) is a classical algorithm for detecting lines from a binary image. It has been suggested to accelerate the Hough transform by polling instead of voting, randomly selecting just a small part of the data set as input to the algorithm [1, 2, 3]. Fast Hough algorithms that are based on polling are referred to probabilistic Hough transform. The computational advantage of probabilistic Hough transform diminishes if the poll size becomes large. It is possible to reduce poll size while maintaining a low error rate by fast forming peak in poll. The dynamic generalized Hough transform(DGHT) [2] and randomized Hough transform (RHT) [3] are two representative methods in this family.

Another related technique referred to optimization model is based on minimal subset principle [4, 5]. A minimal subset of points is the smallest subset necessary to produce a unique instance of a curve. It was shown that detecting a curve was equivalent to finding the optimum value of a cost function with multiple local optima. The curves detection approach based on optimization model using a GA was heuristically proposed in reference [6]. It is shown that the genetic approach is an improvement over random search.

The main difference between optimization model and probabilistic Hough transform(PHT) is that optimization model does not use scores accumulation in the parameter space. The optimization model is a guess-and-test method but not a HT-like method. And, the optimization model performance for finding multiple curves in the global optimal sense is also an interesting question to be answered, since it has no accumulation array for globally managing the parameter space and accumulating evidences [3].

In order to simultaneously detect several curves using GA, we must solve the multimodal function optimization problem. Based on niching method, we have presented an extended GA with promoting each desirable subsolution convergence to simultaneously detected primitives [7]. It is based on equivalence classes principle, where the equivalence class may be regarded as the set of minimal subset defined a curve. In this paper, the basic ideas of the genetic sampling and classifying mapping are further developed into Hough transform.

2 The GHT Method

2.1 The Basic Idea

Assume now that we want to detect a specific curve $f(\overline{p}_i, \overline{a}) = 0$, $i = 1, 2, ..., R$. (where $\overline{p}$ is a datum point and $\overline{a}$ is the parameter vector containing R independent parameters) from a binary image. A description of the basic principles of the genetic Hough transform(GHT) method is given in the following.

Initial population is created by randomly selecting samples with R points. Each random sampling is mapped onto one point $\overline{a}$ in the parameter space, and the candidate $\overline{a}$ is put into initial population. The implementation of GHT is a series of genetic generations on the initial population. At

---

*Address: 3-195 Tsukuba, Kumagaya, Saitama 360-0037 Japan. E-mail: wangyd@mediadrive.co.jp

†Address: 6-6 Asahigaoka, Hino, Tokyo 191-0065 Japan. E-mail: funakubo@ecrsb.ec.tmit.ac.jp

each generations, the some samples are produced by genetic operations(crossover, mutation and neighborhood trial). The new samples is classified into classified population(CP) by classifying mapping. A search is finished after a sufficient number of generations. The samples in CP are taken as detected candidate curves by checking their scores.

Genetic sampling. Although one can selects randomly R points(minimal subset) directly from image data, a more efficient way is to combine some good minimal subsets to produce a better sample by genetic operations. Here, "better" means a sample which has higher fitness value.

Classifying mapping. In order to realize the classifying mapping, we have to solve the set of R equations $f(\overline{p}_i, \overline{a}) = 0$, $i = 1, 2, ..., R$. The solution $\overline{a}$ is classified to an equivalence class by calculating similarity of individuals in classified population. If there exists an equivalence class $\overline{cp} \in$ CP, $\overline{cp} = [para(cp), fitness(cp), score(cp)]$ with its parameter being regarded as equivalent as $\overline{a}$ subject to a given similarity, then we let $score(cp) = score(cp)+1$, and if fitness value of this $\overline{a}$ is higher than $fitness(cp)$, then the new sampling $\overline{cp} = [para(cp), fitness(cp)]$ will adopted as representation of this class and we also replace the $para(cp)$ and $fitness(cp)$ of $\overline{cp}$ with this new sampling; while if none exists, we insert a new element $\overline{cp} = [para(cp), fitness(cp), 1]$ into the classified population.

The core idea of GHT is the combined use of genetic sampling in the image space and score accumulation in the parameter space, and classifying mapping as the bridge between the two spaces. In GHT method, the optimal curve with higher fitness value is produced, and a similar new instance is reproduced with itself by genetic operations. It is the characteristic method which has GA's ability to find the global optimum sampling and it also keeps score accumulation with accumulating evidences in the parameter space.

2.2 Genetic Sampling and Classifying Mapping

Niched GAs have received much attention because of their ability to find multiple good, diverse solutions. The two representative niching methods of sharing and deterministic crowding were modelled for GA's "hard" problem with many local optima [8].

The genetic sampling is produced by genetic operator, and the classifying mapping is realized by equivalence classes in GA. In literatures [6, 7], it has been shown that the genetic operations for samples did indeed combine them to often produce better results.

In order to use niching method, it is necessary to classify individuals of population into several equivalence classes by similarity of species. The some curves are called similar curves, if the parameter values of those curves do not exceed a certain value.

Assume that $\overline{i}(i_1, i_2, ..., i_R), \overline{j}(j_1, j_2, ..., j_R)$ are the parameter vectors of two individuals respectively, and the distance d_{ij} between individual $\overline{i}$ and individual $\overline{j}$ is similarity between these two individuals:

$$d_{ij} = \sum_{k=1}^{R} w_k |i_k - j_k| \tag{1}$$

where R is the size of minimal subset, w_k is the weight of each parameter of individual which is inversely proportional to the value of allowable range of each parameter, and $\sum_{k=1}^{R} w_k = 1$.

We can classify $\overline{i}$ and $\overline{j}$ into an equivalence class, if d_{ij} is smaller than the threshold value σ_{share} determined according to application.

Our approach is implemented by a series of loop steps which are selecting samples, classifying samples to equivalence classes, evaluating samples etc. Therefore, number of elements in equivalence classes will gradually increase along with processing.

Since the equivalence class is able to represent parameter detected curve and the number of elements in equivalence classes can represent the voting numbers in parameter space, it is clear that the number of elements in equivalence classes is correspond to the score accumulation in HT.

In the GHT method, the new mechanism, namely genetic sampling and classifying mapping, replaces the roles of random sampling and converging mapping in RHT. Therefore, it is an RHT-like method, and it also has other favorable properties. First, genetic sampling can speed up the computation than random sampling by use of genetic operations. Second, the samples with high score in equivalence class can reproduce a better samples as genetic seed. Third, classifying mapping can divide samples into equivalence classes(i.e., clusters) by similarity among samples. We will make use of these properties to form desirable peaks rapidly, and realize high speed Hough transform.

2.3 The Implementation of GHT

The components of our method are individual population, classified population(it can be regarded as accumulation population), and there are interactions between them. The classified population stores the representative individual with highest fitness value and the score in each equivalence class.

Classifying mapping. In process of finding the curves using GA, the equivalence classes and their score are formed through partitioning individuals of population into different equivalence classes according to similarity among individuals.
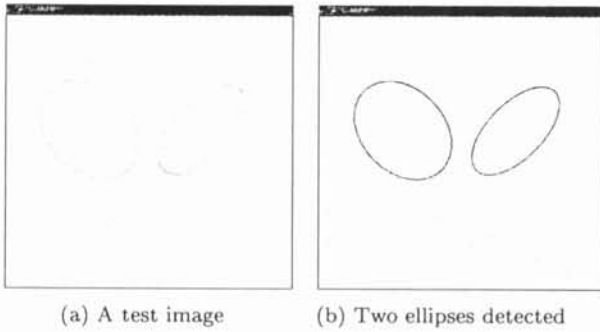
(a) A test image   (b) Two ellipses detected

Figure 1: A test image and detected result.

Observation of convergence. The equivalence classes are formed in genetic generation one after another by classifying mapping. Here, the number of elements in equivalence class can be regarded as voting score in parameter space. An equivalence class is desirable(that is, convergent) if its score is larger than the following threshold function $b_{threshold}(t)$.

$$b_{threshold}(t) = K \cdot t \qquad (2)$$

where K is a scale constant and t is the number of generations.

Promotion of convergence. The number of elements in equivalence class may also be increased by genetic operator and neighborhood operator [7]. One of reasons is that combination of neighborhood points is often belonged to this equivalence class itself. Thus, the score of equivalence class will be improved along with the enlargement of elements in the equivalence class.

Maintenance of multiple peaks. To solve multimodal function optimization problem is equal to maintain b desirable equivalence classes in population [9]. We maintain multiple subpopulations with combination of sharing function and limiting replaced objects.

3 Experiments

Figure 1 shows a test image and detected result, which contains two ellipses; two ellipses have 158 and 163 pixels respectively and there are also 200 random outlier(noise) points. The voting histogram in Figure 2(a) is for the projected estimate of the x center coordinate of the ellipses by RHT. The two maximum peaks denote the two ellipses detected. The histogram shows that distribution of voting is wide. This is because the vote is only performed using random sampling.

In order to compare both results, we try to detect the same ellipses by using GHT. For finding multiple objects at the same time, sharing function was used to prevent that exploration falls into local optima. The histogram in Figure 2(b) was obtained after 200
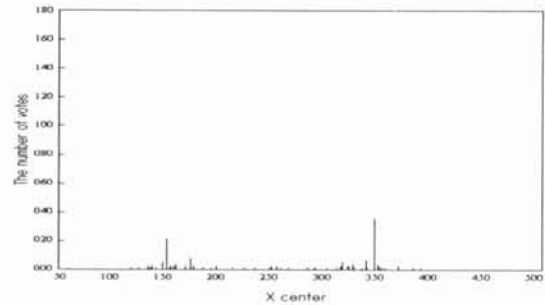
(a) Histogram for x center by RHT
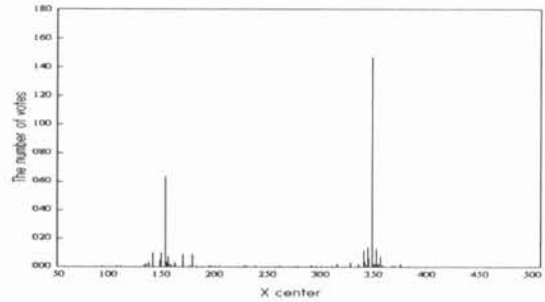
(b) Histogram for x center by GHT

Figure 2: Ellipses detection by RHT and GHT.

generations. One can observe that the two peaks in Figure 2(b) are much sharper and higher than those in Figure 2(a). It is shown that GHT can promote the sharpness of peaks using genetic sampling.

Figure 3(a) shows an image including objects: three ellipses. They have 333, 362 and 377 pixels respectively, and outlier points have 4133 pixels except the three ellipses. We try to detect the ellipses using GHT from this image. Figure 3(b) shows the extracted ellipses drawn as dark line superimposed on the edge chain image.

For the three ellipses detected above ($EC\ 1 \sim EC\ 3$), the variations of their numbers of votes are shown graphically in Figure 4. It is shown there that the observation and confirmation of convergence can be achieved through the desirable threshold function($b_{threshold}(t) = 0.17t$) drawn as a dot line. Here, the equivalence classes will be divided into the convergent sets($EC\ 1 \sim EC\ 3$) and not convergent ones by this threshold line. The number of elements(votes) in convergent equivalence class is considerably increased because its neighborhood points are often belonged to themselves, whereas on another case they are not belonged to themselves.

In the GHT of this experiment, since the characteristic of connected edge is used, we compare it with RHT under the same condition. Using the RHT method was slower than the GHT for forming peak in parameter space. This result is demonstrated graphically in Figure 5, where each graph plots the score of the higher three instances in the

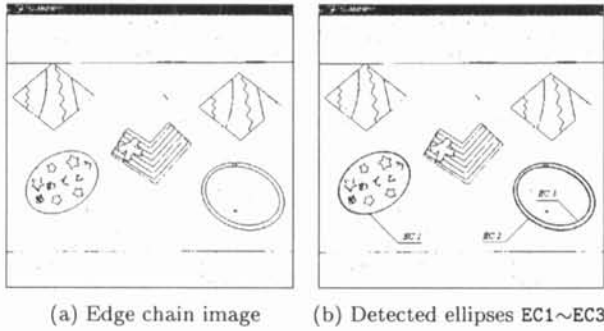(a) Edge chain image   (b) Detected ellipses EC1∼EC3
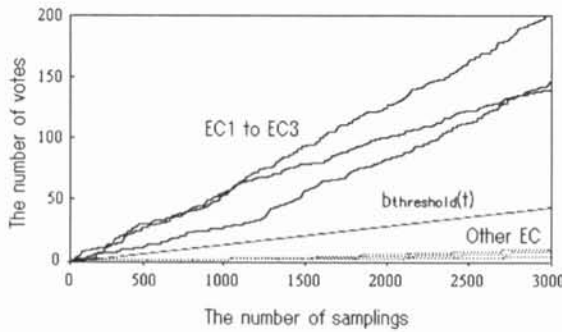
Figure 3: Three ellipses detection by GHT.

Figure 4: Variations of number of votes by GHT.

accumulation population versus the number of samplings in parameter space for both GHT and RHT.

4 Conclusion

In this paper, we proposed a new approach that improved detection speed by using genetic algorithm in Hough transform. The GHT is actually a combination of HT and GA, and it combines the probabilistic Hough transform and optimization model using simple GA. Furthermore, the GHT shares the advantages of the two algorithms. It has been shown that the present approach offers a significant improvement for the previously proposed implementation of the HT. In GHT method, the optimal curve with higher fitness value is produced, and similar new instance is reproduced with itself by genetic operations. It is characteristic method which has GA's ability to find the global optimum samplings and also keeps score accumulation with accumulating evidence in the parameter space. It has advantages of fast speed, small storage and high accuracy. The experiments have shown that the GHT can really improve the detection speed over RHT. In addition, from the comparison with optimization model using simple GA, it has shown that using equivalence genes GA method was an improvement over only using simple GA in recent literature [7].
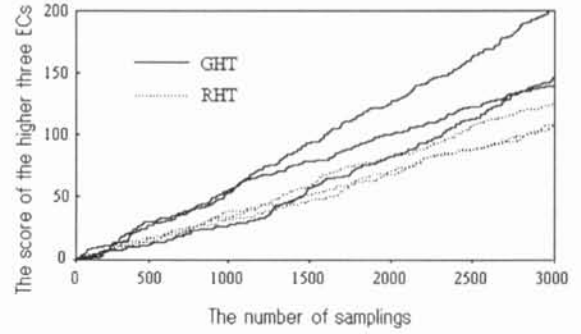

Figure 5: Comparison between GHT and RHT.

References

[1] N. Kiryati, Y. Eldar and A. M. Brucksrein, *Probabilistic Hough transform*, Pattern Recognition, vol. 24, no. 4, pp.303–316, 1991.

[2] V. F. Leavers, *The dynamic generalized Hough transform: Its relationship to the probabilistic Hough transforms and an application to the concurrent detection of circles and ellipses*, CVGIP: Image Understanding, vol. 56, pp. 381–398 (1992).

[3] L. Xu and E. Oja, *Randomized Hough transform(RHT): basic mechanisms, algorithms, and computational complexities*, CVGIP: Image Understanding, vol. 57, pp. 131–154 (1993).

[4] G. Roth and M. D. Levine, *Extracting geometric primitives*, CVGIP: Image Understanding, vol. 58, pp. 1–22, 1993.

[5] Y. C. Cheng and S. C. Lee, *A new method for quadratic curve detection using K-RANSAC with acceleration techniques*, Pattern Recognition, vol. 28, no. 5, pp.663–682, 1995.

[6] G. Roth and M. D. Levine, *Geometric primitives extracting using genetic algorithm*, IEEE Trans. Pattern Anal. and Mach. Intell., vol. 16, pp. 901–905, 1994.

[7] Y. D. Wang and N. Funakubo, *Detection of road sign boards using genetic algorithm*, to appear in Proceedings of the International Conference on Quality Control by Artificial Vision, 1998.

[8] S. W. Mahfoud, *Simple analytical models of genetic algorithms for multimodal function optimization*, Proceedings of the Fifth International Conference on Genetic Algorithms, p. 643, 1993.

[9] S. W. Mahfoud, *Population size and genetic drift in fitness sharing*, Foundations of genetic algorithms(3), pp. 185–233, Morgan Kaufmann, 1995.