

# A Novel Genetic Programming Based Morphological Image Analysis Algorithm

Jun Wang and Ying Tan\*

Key Laboratory of Machine Perception (Ministry of Education), Peking University  
 Department of Machine Intelligence, School of Electronics Engineering and Computer Science, Peking University, Beijing, 100871, P.R. China  
 wangjun@cis.pku.edu.cn, ytan@pku.edu.cn

## ABSTRACT

This paper gives an applicable genetic programming (GP) approach to solve the binary image analysis and gray scale image enhancement problems. By showing a section of binary image and the corresponding goal image, this algorithm automatically produces a mathematic morphological operation sequence to transform the target into the goal. While the operation sequence is applied to the whole image, the objective of image analysis is achieved. With well-defined chromosome structure and evolution strategy, the effectiveness of evolution is promoted and more complex morphological operations can be composed in a short sequence. In addition, this algorithm is also applied to infrared finger vein gray scale images to enhance the region of interest. Whose effect is examined by an application of identity authentication, and the accuracy of authentication is promoted.

### Categories and Subject Descriptors:

I.2.8[ARTIFICIAL INTELLIGENCE]: Problem Solving, Control Methods, and Search

### General Terms: Algorithms

**Keywords:** Genetic Programming, Mathematics Morphological, Image Analysis, Image Enhancement

## 1. PROPOSED GP ALGORITHM

By giving an original image and a learning target—goal image, this algorithm is designed to use a GP approach to automatically produce a sequence of mathematic morphological operations, which are applied to the original image to obtain result close to the goal. In this algorithm, a chromosome is an individual [1], which is composed by a sequence of genes, as illustrated in Fig. 1. This algorithm initiates 1024 chromosomes at the beginning which are all single genes, and evolves for 300 generations to output the best individual.

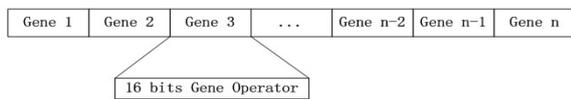


Figure 1: Chromosome definition

\*Corresponding author.

One single gene is a primitive unit of morphological operation accompanied with logical operations, and the structure of the gene is shown in Table 1. The number of genes in each chromosome may be different while each gene has a fixed length, and the max length is limited to 20 genes. Two processing sequences are kept in each chromosome, which are mutually affected by logical operations. The objective fitness function is the correlation coefficient between a processed image and the goal [4].

Table 1: The meaning of each bit in a gene

	Index	Meaning
Unused	1-2	null
Function Area	3	switch
	4	storage flag
	5	direct/difference flag
	6	logical operation flag
	7-8	logical operator
Terminal Area	9	erosion/dilation flag
	10-11	SEs size
	12	SE class
	13-16	SEs index

The direct/difference flag means to choose the morphological operation result directly or the arithmetic difference between it with the input as the current output. The storage flag means whether the result of this gene should be stored or not [2]. The logical operator flag represents which logical operation will be applied to the current gene. Four logical operations are defined in this algorithm, *AND*, *OR*, *NOT* and *XOR*. Some logical operations need two operands. One operand is the current morphological operation result, and the other one is the storage mentioned above. A new operation *switch* is brought forward. If the switch flag is true, the input of the current gene is substituted by the backup one. By the combination of switch and store, two operation processes are expressed in one chromosome.

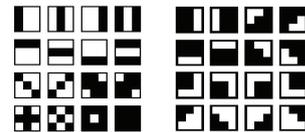


Figure 2: Patterns of 3×3, regular/irregular

Only basic morphological operations “erosion” and “dilation” are used in this algorithm, which depend on the pattern of structuring element (SE) [3]. Three sizes of SEs are defined

as  $3 \times 3$ ,  $5 \times 5$  and  $7 \times 7$  in this algorithm. Each size has two styles, regular—SEs are symmetrical and irregular—asymmetrical, and each style has 16 patterns.

A structural evolution strategy is brought forward: Structural mutation—a gene is divided into three parts, flow control, logical operation and morphological operation, which are mutated separately, and the mutation position is well-distributed; Structural crossover—the basic unit of crossover is a gene, and a crossover in the middle of a gene is not allowed, as shown in Fig. 3.

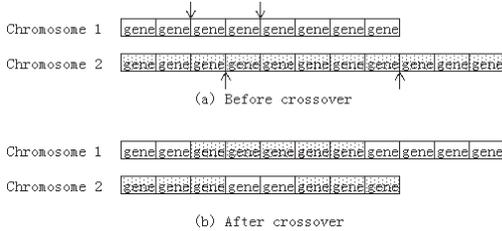


Figure 3: Crossover

## 2. EXPERIMENT ON BINARY IMAGES

As in [2], we also use an artificial data set composed by four features: squares, circles, rings and stars, and use this algorithm to obtain valid objects. This algorithm was trained on a small area of source image, and four operation sequences were produced to extract the four features separately. The heavy computation load of Quintana’s algorithm needed a cluster with 23 nodes in his experiments [2], while our algorithm finished the work on a PC workstation in a few minutes. Executing these sequences on the whole image, the average fitness values of obtained features were compared with Quintana’s in Table 2. This algorithm was also applied to an OCR music sheet, which had been used by Yoda in [4] to extract the four features: heads, hooks, staff lines and stems. In the training progress of heads detection, Yoda got the final fitness value of 0.963, and our algorithm got a more accurate value of 0.966.

Table 2: Performance comparison

Feature	Our algorithm	Quintana’s algorithm
Circles	<b>0.9822</b>	0.868
Rings	0.8583	<b>0.906</b>
Squares	<b>0.9900</b>	0.870
Stars	<b>0.9590</b>	0.922

## 3. EXPERIMENT ON GRAY SCALE IMAGES

This algorithm was applied to the enhancement of gray scale image on a dataset which had more than 2000 low quality finger vein images. Four images were chosen from the data set randomly as learning samples, and the corresponding feature images were calibrated manually as learning goals. This algorithm run with the learning sets and produced four operation sequences. A uniform threshold and a thinning method were adopted to get the skeleton feature results of the gray scale image. Results are shown in Fig. 4: (a) four learning samples; (b) corresponding goals; (c) learning results with a threshold and thinning; (d) threshold and

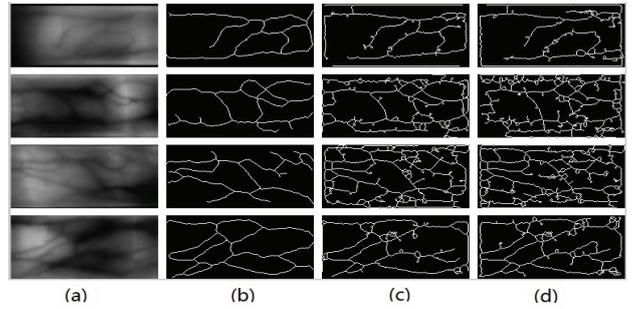


Figure 4: Learning pairs.

thinning results of (a). The images of the dataset were processed with combination of different numbers and orders of obtained operation sequences. The effect of the enhancement was measured by testing the false acceptance rate (FAR) of the identity authentication, as shown in Fig. 5. Group 1 is the FAR result of the contrastive method, and the others are results of combinations of operation sequences. The Group 2 shows the best performance, which reduces the FAR by about 8%.

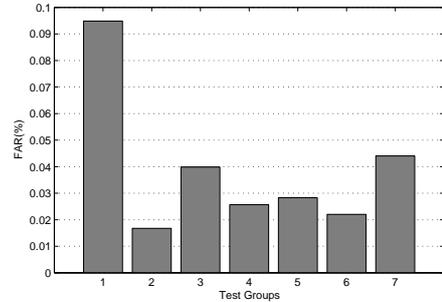


Figure 5: FAR test results.

## 4. ACKNOWLEDGMENTS

This work is supported by National Natural Science Foundation of China (NSFC), under grant number 60875080 and 60673020, and partially financially supported by the Research Fund for the Doctoral Program of Higher Education (RFDP) in China. This work is also in part supported by the National High Technology Research and Development Program of China (863 Program), with grant number 2007AA01Z453.

## 5. REFERENCES

- [1] J. R. Koza. *Genetic programming: on the programming of computers by means of natural selection*. MIT Press, Cambridge, MA, USA, 1992.
- [2] M. I. Quintana, R. Poli, and E. Claridge. Morphological algorithm design for binary images using genetic programming. *Genetic Programming and Evolvable Machines*, 7(1):81–102, 2006.
- [3] P. Soille. *Morphological Image Analysis: Principles and Applications*. Springer-Verlag New York, Inc., Secaucus, NJ, USA, 2003.
- [4] I. Yoda, K. Yamamoto, and H. Yamada. Automatic acquisition of hierarchical mathematical morphology procedures by genetic algorithms. *Image Vision Comput.*, 17(10):749–760, 1999.