# **Segmentation based on Genetic Algorithm**

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### 1. Problem

Image segmentation is a challenging task in many fields. Image segmentation aims at partitioning an image into certain regions satisfying a homogeneity criterion that takes into account one or more pixel features, such as color, texture, intensity, and so on. It can be used as pre-process for pattern recognition, auxiliary tool for medical image analysis, modelling method for 3-D printing and so on. Therefore, a well-designed segmentation method is very important and practical to our life.

## 2. Goal

In this project, we plan to design a segmentation method based on the framework of segmentation proposed by *Amelio and Pizzuti*[1]. The method proposed by them has a strong power in image segmentation, with fewer parameters. However, by implementing their evaluation function, we found that the results of this method often fall in local optimization. So we intend to start our research aiming at finding the better solution based on the previous work.

### 3. Problem Definition

The image is defined as a graph G = (V, E, w), where V is the set of n nodes of graph G, E is the set of edges, and W: E->R is a function that assigns a value to graph edges. Each node corresponds to a pixel in the image, and a graph edge (i, j) connects two pixels i and j, provided that these two pixels satisfy some suitably defined property. The weight W(i, j) associated with an edge V(i, j) represents the likelihood that pixels V(i, j) associated with an edge V(i, j) represents the definition of weight between two pixels is defined as follow:

$$w(i, j) = \begin{cases} e^{-\max_{x \in line(i, j)} ||Edge(x)||_2^2/2a^2} & \text{if } ||X(i) - X(j)||_2 < r, & i \neq j \\ 0 & \text{otherwise} \end{cases}$$

where  $a = (max_{y \in I} || Edge(y) ||) \times \delta$ , Edge(x) is the image edge strength at position x, line(i, j) is a straight line between i and j.

The original evaluation function defined by [1] is as follow:

WNCut = 
$$\sum_{i=1}^{k} \frac{\text{cut}(A_i, V - A_i)}{\text{assoc}(A_i, V)} + \frac{\text{cut}(A_i, V - A_i)}{\text{assoc}(V - A_i, V)}$$

Where "cut()" and "assoc()" is defined as:

$$cut(A, B) = \sum_{i \in A, j \in B} w(i, j).$$
$$assoc(A, V) = \sum_{i \in A, t \in V} w(i, t)$$

# 4. How to play Evolutionary in Image Segmentation

# 4.1 Representation in GA

In the task, an individual of the population consists of n genes  $g_1, g_2, ..., g_n$  and each gene can assume value in the range $\{1,...,n\}$ . For example, if node i connects with node j, the  $g_i = j$  is set (As Fig. 2(a) shows).

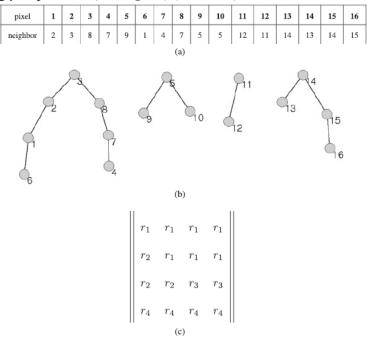


Figure 2:(a) Locus-based representation of individual  $J_1$ . (b) Corresponding segmentation of the graph G of Figure 1(d) in four segments composed by the pixels  $r_1 = \{1, 2, 3, 4, 6, 7, 8\}$ ,  $r_2 = \{5, 9, 10\}$ ,  $r_3 = \{11, 12\}$ , and  $r_4 = \{13, 14, 15, 16\}$ . (c) Image partitioning.

In the pixel connection, only pixels satisfying the h-Neighborhood are regarded as neighbors. This h-Neighborhood definition not only considers the spatial closeness, but also the pixel affinity. Within the distance radius r, only pixels with top-h highest weight are regarded as a pixel's neighbor. For example in Fig. 1(c) and Fig. 6, if we define the h = 2, for node 3, the top-2 highest weight are 1.0 and 0.9, so the node 2, 4, 7, 8 are kept as its neighbor and node 6 (w=0.7) is removed.

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1 \rightarrow \{(2; 1.0), (6; 0.7)\}
2 \rightarrow \{(1; 1.0), (3; 1.0), (7; 0.9)\}
3 \rightarrow \{(2; 1.0), (4; 1.0), (7; 0.9), (8; 0.9)\}
4 \rightarrow \{(3; 1.0), (7; 0.9), (8; 0.9)\}
5 \rightarrow \{(6; 0.5), (9; 1.0), (10; 1.0)\}
6 \rightarrow \{(1;0.7), (2;0.7), (3;0.7), (7;0.6)\}
7 \rightarrow \{(2; 0.9), (3; 0.9), (4; 0.9), (8; 1.0)\}
8 \rightarrow \{(3,0.9),(4,0.9),(7,1.0)\}
9 \rightarrow \{(5; 1.0), (6; 0.5), (10; 1.0)\}
10 \rightarrow \{(5; 1.0), (6; 0.5), (9; 1.0)\}
11 \rightarrow \{(7; 0.8), (8; 0.8), (12; 1.0)\}
12 \rightarrow \{(7; 0.8), (8; 0.8), (11; 1.0)\}
13 \rightarrow \{(9; 0.4), (10; 0.4), (14; 1.0)\}
14 \rightarrow \{(9; 0.4), (10; 0.4), (13; 1.0), (15; 1.0)\}
15 \rightarrow \{(10; 0.4), (14; 1.0), (16; 1.0)\}
16 \rightarrow \{(11; 0.3), (12; 0.3), (15; 1)\}
                              (a)
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Figure 6: Nearest neighbors  $nn_i^h$  for  $1 \le i \le 16$  and h = 2.

#### 4.2 Crossover and Mutation

Provided there are two parent-individuals  $J_1$  and  $J_2$  as follow:

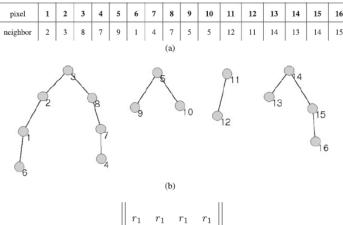




Figure 2: (a) Locus-based representation of individual  $J_1$ . (b) Corresponding segmentation of the graph G of Figure 1(d) in four segments composed by the pixels  $r_1 = \{1, 2, 3, 4, 6, 7, 8\}$ ,  $r_2 = \{5, 9, 10\}$ ,  $r_3 = \{11, 12\}$ , and  $r_4 = \{13, 14, 15, 16\}$ . (c) Image partitioning.

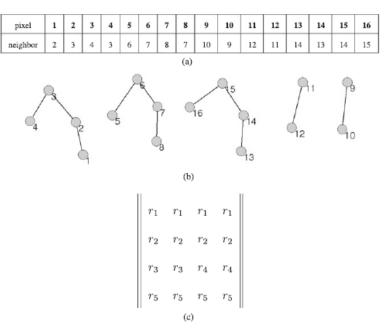


Figure 3: (a) Locus-based representation of another individual  $J_2$ . (b) Corresponding segmentation of the graph G of Figure 1(d) in five segments composed of the pixels  $r_1 = \{1, 2, 3, 4\}$ ,  $r_2 = \{5, 6, 7, 8\}$ ,  $r_3 = \{9, 10\}$ ,  $r_4 = \{11, 12\}$ , and  $r_5 = \{13, 14, 15, 16\}$ . (c) Image partitioning.

The crossover is implemented by an exquisite definition of mask that is generated randomly (As Fig. 4(a)). If mask[i] is 0, the  $g_i$  is selected from J1; otherwise,  $g_i$  is selected from J2. As Fig. 4 show, after crossover between J1 and J2, the segmentation of image is composed of the pixels  $\{1, 2, 3, 4, 5, 6, 7, 8\}$ ,  $\{9, 10\}$ ,  $\{11, 12\}$  and  $\{13, 14, 15, 16\}$ .

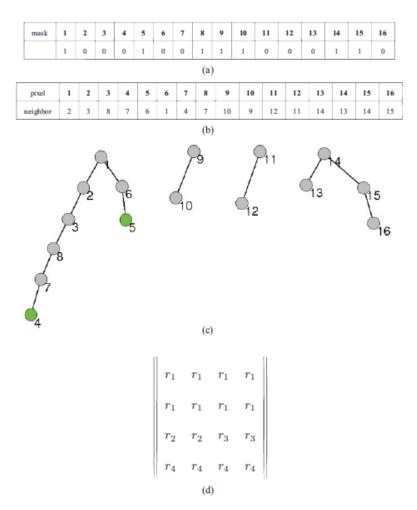


Figure 4: Crossover between the two individuals  $J_1$  and  $J_2$  of Figures 2–3. (a) Random mask generated. (b) Offspring generated from  $J_1$  and  $J_2$ . (c) Corresponding segmentation of the graph G of Figure 1(d) in four segments composed of the pixels  $r_1 = \{1, 2, 3, 4, 5, 6, 7, 8\}$ ,  $r_2 = \{9, 10\}$ ,  $r_3 = \{11, 12\}$ , and  $r_4 = \{13, 14, 15, 16\}$ . (d) Image partitioning.

The mutation operator, analogous to the initialization process, randomly assigns to a neighbor node *i*. For example in the Fig. 5, the node 9 is chosen at random and its neighbor 5 is substituted by the other neighbor 6. As Fig. 5 show, after mutation from J1, a new segmentation in three components constituted by {1, 2, 3, 4, 5, 6, 7, 8, 9, 10}, {11, 12} and {13, 14, 15, 16}.

	allele	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
	gene	2	3	8	7	9	1	4	7	6	5	12	11	14	13	14	15
(a) 12 13 14 19														15	6		
(b)																	
							$r_1$	. 1	"1	$r_1$	$r_1$						
							$r_1$		"1	$r_1$	$r_1$						
							$r_1$	. 1	"1	$r_2$	$r_2$						
							$r_3$		"3	$r_3$	$r_3$						

Figure 5: (a) Mutation on individual  $J_1$  of Figure 2 where 9 is the randomly chosen node. Its neighbor 5 is substituted with 6. (b) The new generated individual corresponds to the segmentation of graph G of Figure 1(d) in three segments composed of  $r_1 = \{1, 2, 3, 4, 5, 6, 7, 8, 9, 10\}$ ,  $r_2 = \{11, 12\}$ , and  $r_3 = \{13, 14, 15, 16\}$ . (c) Image partitioning.

(c)

#### 4.3 What we will do in this task?

Firstly, we will implement the framework of method [1] as a baseline and validate our assumption of its drawbacks.

Secondly, we will try to improve this method based on the re-definition of evaluation functions, find a better way to segment the objects.

Thirdly, we will conduct experiments to validate the effectiveness of our method by comparison.

# 5. Reference

[1] Amelio, Alessia, and Clara Pizzuti. "An evolutionary approach for image segmentation." *Evolutionary computation* 22.4 (2014): 525-557.