An Adaptive Clonal Selection Algorithm for Edge Linking Problem

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Summary
Edges produced by existing edge detection algorithms often contain discontinuities. Edge linking as a post-processing step is very important for computer vision and pattern recognition. Nevertheless, subject to the lacking of information in the image, difficulties arise when it is tackled. The clonal selection algorithm (CSA), inspired by the basic features of adaptive immune response to antigenic stimulus, can exploit and explore the solution space parallelly and effectively. In this paper, by introducing receptor editing and making the proportions of receptor editing and hypermutation change adaptively, we propose an improved CSA for edge linking of images. The algorithm is tested on a set of artificial images devised with the aim of demonstrating the sort of features that may occur in real images. For all problems, the algorithm produced smooth contours while the details of the object shape are preserved.

Key words:
clonal selection algorithm, edge linking, constrained optimization problem, image processing

1. Introduction

The boundary lines are considered one of the most important features of an object in an image. Many computer vision systems rely on the uses of boundary line information to derive the object shape, to measure the object's parameters and to perform the object recognition task. However, low level edge detection operators do not usually guarantee the generation of contiguous boundaries of objects. In order to obtain a precise description and accurate analysis of an object, edge linking is necessary. An image is treated as a set of binary points on a two-dimensional plane which represent the edges and corners of an object. An edge linking algorithm has to infer from the points a description of the object or objects present in the image [1]. Main difficulties come from the lack of information and the variety of ways in which the points could be interpreted.

Semantic knowledge of the form of the object may assist the extraction process, but generally, this is not available. So the task is simply to extract the most sensible object purely from the data in the image. Thus, the extraction mechanism must be able to cope with various fundamental object primitives, and tolerate affine transformations of composite objects.

William and Shah [2] proposed a multiple scale edge linking algorithm, but the complexity of the algorithm is at the order of 3^n, where n is the number of the image pixels, which need a huge amount of time even for small size images. Farag and Delp [3] proposed a linear path metric function for a sequential search process. Though less amount of calculations is needed compared to the multiple scale algorithm, a prior information about the processed image has to be known. Another effort was made by Xie [4] which also aimed to achieve lower computation complexity. But the algorithm performs poorly and produces non-localized edge points when texture images were used. A dynamic programming method was proposed in [5]. However, it was restricted by the exhaustive searches of the admissible solutions and complicated parameter control [6].

Over the last few years, artificial immune system (AIS) has attracted more and more interest. Clonal selection algorithm (CSA) [7], which was designed based on the Clonal Selection principle of adaptive immunity, has been verified as having a great number of useful mechanisms from the viewpoint of programming, controlling, information processing and so on [8-11]. One important advantage of CSA is that its mathematical foundation is very simple and its computation complexity is low. This makes it an efficient tool in solving NP-hard problems. In our earlier research, it has been used to pattern recognition [12] and traveling salesman problem [13,14]. In a T cell dependent immune response, the repertoire of antigen-activated B cells is diversified basically by two mechanisms: hypermutation and receptor editing [15-18]. While hypermutation diversifies the repertoire in a global way, receptor editing offers the ability to escape from local optima on an affinity landscape. In order to exploit their characteristics to a large extent, we propose an adaptive CSA in which the ratios of hypermutation and receptor editing change adaptively during the process.

Within our survey, three main algorithms have been proposed in the literature involving the elastic net, active contours and Kohonen map. Burr proposed a modification of the elastic net algorithm in [23]. Furthermore, the original elastic net method has been demonstrated to be most competitive as reported in [1]. As a result, simulations of the elastic net are done to make a

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comparison. Besides, the improvement towards the original clonal selection algorithm CLONALG [7] is confirmed by simulations.

The remainder of this paper is organized as follows: in the next section, we provide a general description of the problem and the principle of clonal selection. In Section 3 the proposed algorithm is presented. Simulation results and comparisons with the original elastic net method are analyzed in Section 4. Finally, we give some remarks to conclude the paper in Section 5.

2. Problem Description and The Principle of Clonal Selection

2.1 Problem Description

Extracting features from images is a common computer vision problem. First, edge detectors yield pixels in an image lie on edges. The next step is to try to collect these pixels together into a set of edges. That is, the edge linking process has to infer from the pixels a description of the object or objects present in the image.

One approach for the extraction process is to assume the existence of a single object only, and then to link the edge points in a meaningful way - to form a contour which should represent the object in the image. Such edge linking reduces the problem to that of enumerating the image points, and then ordering them into a sequence which describes a path corresponding to a computer model of the contour [1] .

2.2 The Principle of Clonal Selection

Clonal Selection principle is a form of natural selection [19] and it explains the essential features which contain sufficient diversity, discrimination of self and non-self and long-lasting immunologic memory. This theory interprets the response of lymphocytes in the face of an antigenic stimulus and is illustrated in Fig.1.

When an animal is exposed to an antigen, some subpopulation of its bone marrow derived cells (B lymphocytes) can recognize the antigen with a certain affinity (degree of match). Then the B lymphocytes will be stimulated to proliferate and eventually mature into terminal (non-dividing) antibody secreting cells, called plasma cells. Proliferation of the B lymphocytes is a mitotic process whereby the cells divide themselves, creating a set of clones identical to parent cells. The proliferation rate is proportional to the affinity level. B lymphocytes which have higher affinity levels have larger opportunities to be selected for cloning.

In the proliferating process, new cells are generated by exactly copy the parent cells. The diversity of the

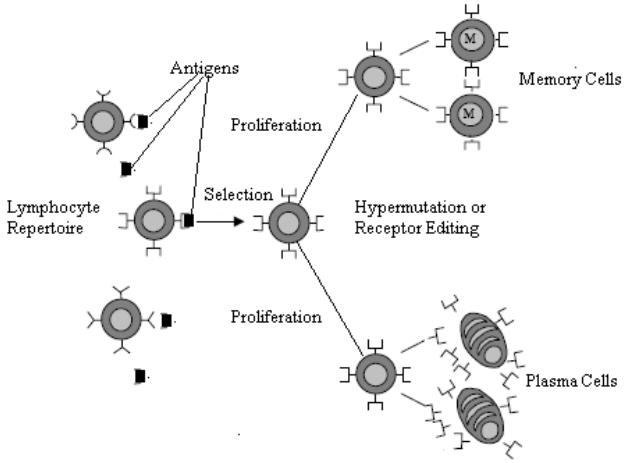

Fig. 1 The clonal selection principle.

immune system is maintained mainly by two mechanisms: somatic hypermutation and receptor editing. According to somatic hypermutation, the clonal cells are mutated at a rate which is inversely proportional to their affinity levels. This is considered to give "better" cells more chances to survive. This process is also known as affinity maturation. The immune system is capable of evolving antibodies to successfully recognize and bind with known and unknown antigens through affinity maturation, though kinds of immune repertoires are limited. On the other hand, cells with low affinity receptors may be further mutated and are programmed for cell death by the immune system through a process called apoptosis. Receptor editing is indicated to play an important role in shaping the lymphocyte repertoire [20,21]. Antigen molecule is composed of two chains, both resulting from the somatic rearrangement of various genetic segments. One of the two chains is the heavy chain which consists of three kinds of segments: variable (V), diversity (D) and junction (J) segments. In each individual pro-B cell, a rearrangement is achieved through gene sequences deletion and results in a unique VDJ combination. The other one is the light chain, whose locus lack D segments, only V and J segments be assembled. Rearrangements on this chain happen through gene sequences inversion and deletion.

In addition to somatic hypermutation and receptor editing, about 5-8% of the least stimulated lymphocytes is replaced per generation by newcomer cells from the bone marrow and join the pool of available antigen recognizing cells to maintain the diversity of the population.

3. Adaptive Clonal Selection Algorithm

The clonal selection algorithm (CSA) based on the clonal selection principle can be briefly interpreted as follows.

From an immunological standpoint, the CSA is developed in which various immune system aspects are taken into account such as maintenance of the memory cells, selection and cloning of the most stimulated cells, death of non-simulated cells, reselection of the clones with higher affinity and generation of diversity. From a computational perspective, the clonal selection idea leads to algorithms that iteratively improve candidate solutions to a given problem through a process of cloning, mutation and selection.

In this section, we present and analyze our proposed clonal selection algorithm. Fig.2 shows the flow of the proposed algorithm.

Generally, the proposed model can be described as follows:

Step 1. Create an initial pool of *m* antibodies (*m* initial solutions Ab_1, Ab_2, … , Ab_m) and initialize the parameters.

Step 2. Compute energies of all antibodies as the sum of distances between each two adjacent points in one antibody. (Affinity (A (.)) is defined as the reciprocal of the energy.) Then the *m* antibodies are resorted in a descending order of their affinities.

Step 3. Select *n* (*n*<*m*) best individuals based on their affinities from the *m* original antibodies. These antibodies are referred to as elites.

Step 4. The *n* best antibodies are placed in *n* elite pools ($pool_1$, $pool_2$, ... , $pool_n$) in ascending order.

Step 5. Adjust the ratios of receptor editing and hypermutation and for the current generation according to:

$$ratioRE = ratioRE - ratioRE * \quad (1)$$

$$ratioHM = 1 - rati \quad (2)$$

where is the current generation and is the maximum number of generation. $rati$ is initialized to ma which is a user-defined parameter.

Step 6. Clone the antibody in each elite pool with a rate proportional to its affinity, i.e., the higher an antibody's affinity is, the more clones it will have. The amount of clones generated for these antibodies is given by Eq.1:

$$p_i = round(\frac{n-i}{n} \quad (1)$$

where *i* is the ordinal number of the elite pools, *Q* is a multiplying factor which determines the scope of the clone and *round(.)* is the operator that rounds its argument towards the closest integer.

After this step, we obtain antibodies as $Ab_{1,1}, Ab_{1,2}, \dots, Ab_{1,p_1}; \dots; Ab_{n,1}, Ab_{n,2}, \dots, Ab.$

Step 7. Subject the clones in each elite pool through either hypermutation or receptor editing process. Each antibody is subjected to hypermutation or receptor editing randomly according to the ratios generated in Step 5.

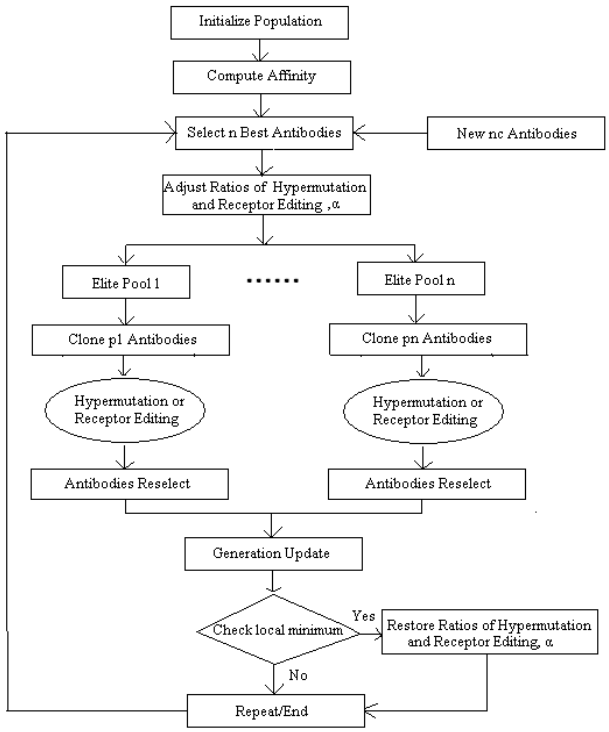

Fig. 2 Flow Diagram of CSA

Step 8. Determine the fittest individual B_i $(A(B_i) = \max\left(A\left(Ab_{i,1}, \dots, Ab_{i,p_i}\right)\right), i = 1,2,.$ in each elite pool from its mutated clones.

Step 9. Update the parent antibodies in each elite pool with the fittest of the clones and the probability $P(Ab_i -$ is according to:

$$p = \begin{cases} 1 & A(Ab_i) < A \\ 0 & A(Ab_1) \geq A \\ \exp\left(\frac{A(B_i) - A(Ab_i)}{\alpha}\right) & other \end{cases} \quad (2)$$

where is a positive parameter which is defined to control the probability with which the parent antibody is replaced by its best offspring if its affinity is not improved. is increased each generation until it reaches a predefined up-value to provide a lower replacement probability.

This is done to maintain the diversity of the population. But this is not used to AB_1 which is the best individual among the parents. So the best information of the original population is passed to the next generation. Obviously, when a parent's affinity is improved by its offspring, it should be replaced.

Step 10. Replace the worst *nc* antibodies with new random generated ones every *k* generations to introduce diversity and prevent the search from being trapped in local optima.

Step 11. Record number of generations during which the affinity hasn't been improved. If the number is larger

Table 1 Values and descriptions of parameters

Parameter	Description	Value
V_{max}	Maximum number of Generations	2000
Nc	The best Nc antibodies are permitted to have offspring	100
Nb	Number of antibodies	150
Nn	Nn antibodies are replaced by new generated ones during one exchange	10
No	The best antibody have No offspring	50
$exchange$	Antibodies are replaced per $exchange$ generations	50
RE_{max}	The maximum proportion of receptor editing	0.8

than the predefined integer, restore $ratioRE$ and α to their initial values.

Step 12. Determine if the maximum number of generation has been reached. If it has, terminate and return the best antibody; otherwise, go back to Step 4.

Table 1 gives values of the parameters used in the program and their descriptions.

Hypermutation and receptor editing play complementary roles in the process of affinity maturation. Hypermutations allow the immune system to explore the local area by making small alterations [18]. And by allowing an antibody to take large leaps through the landscape, receptor editing offers the ability to escape from local minima. In our program, the ratios of hypermutation and receptor editing ($Ratio$ and $Rati$) are adjusted adaptively to exploit their characteristics well. $Rati$ is initialized to a reasonable value and decreased every generation. in Expression (2) is increased to decrease the probability with which the parent antibody is replaced by its best offspring if its affinity is not improved. This is designed to protect parent antibodies while their affinities have been improved for several generations. The minimal value for Rat is set to *0* and the maximal value of is also predefined. Meanwhile, number of generations during which affinity hasn't been improved is recorded. If it exceeds a predefined number, the algorithm is considered to have trapped in a local minimum and $Rati$ and are restored to their initial values. Once the affinity changes (better or worse), the algorithm has escaped from the local minimum.

4. Simulation Results and Evaluations

To interpret which is the correct order to link the edge points is a tough task. It can only be a qualitative measure. But there are still some results which are clearly either 'wrong' or 'bad'. The test images are designed with efforts to ensure that they mostly had an obviously correct interpretation [1]. Qualitative evaluation considers how well the resulting contour describes the object assumed to be present in the image.

In our simulation and almost all of the techniques for edge linking, points are linked with straight lines. This is adequate for long boundary segments, but small curved boundaries may be missed [22]. However, because it has the advantage of high computational efficiency and any curves can be represented in linear segments, it is widely used.

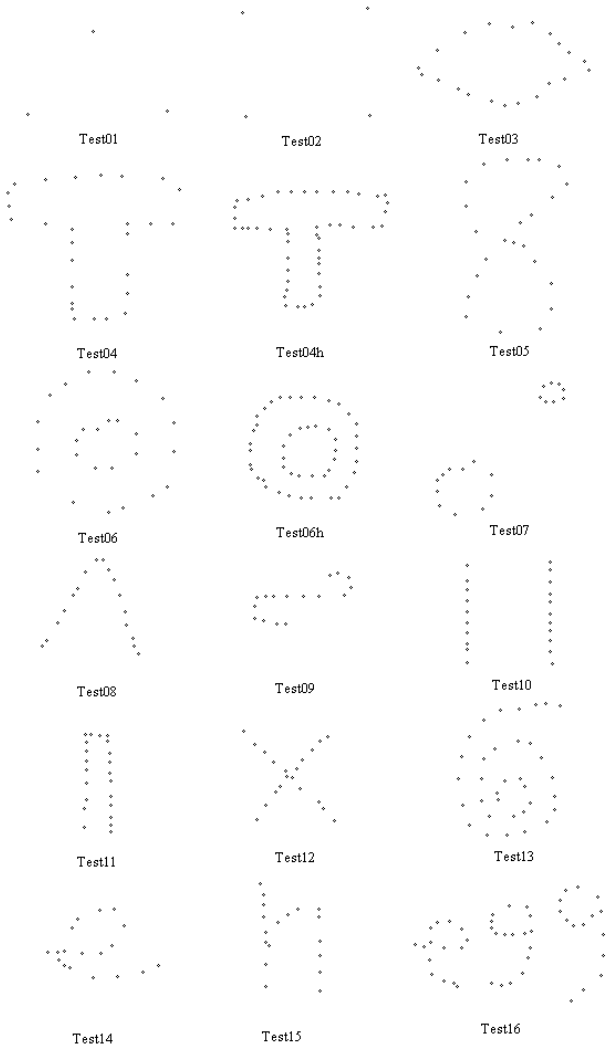

Fig. 3 Test bed images

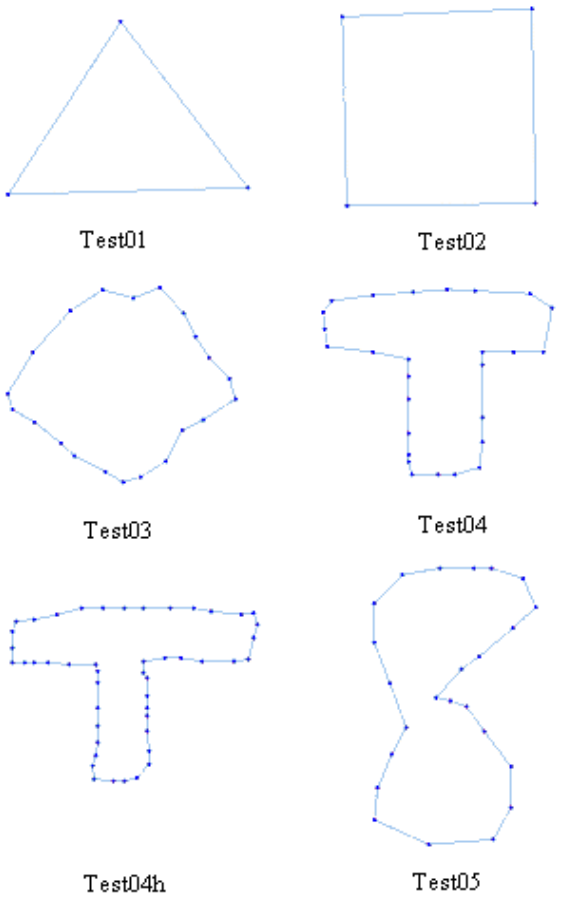

Fig. 4 Result contours for several test images

In order to assess the efficiency of our problem, simulation results are compared with several traditional algorithms. The original elastic net method has been demonstrated to be most competitive as reported in [1]. As a result, it is chosen as a comparer. The elastic net [24] is a kind of artificial neural networks which is used for optimization problems. The essence of the method is: using an iterative procedure, a circular closed path is gradually elongated non-uniformly until it eventually passes sufficiently near to all the cities to define a tour. Besides, simulations of original clonal selection algorithm CLONALG [7] are also done to test the efficiency of the new operator.

Each image is drawn by hand and is drawn deliberately sloppily to simulate the noisy edge contours expected in real applications. For $Test04$ and $Test06$, there are two images $Test04h$ and $Test06h$ with more edge points in order to examine the technique's sensitivity to edge-point density. The three algorithms operate on the same test bed images and all of the simulations are done on the same computer.

According to [18], point mutations allow the immune system to explore the local area by making small

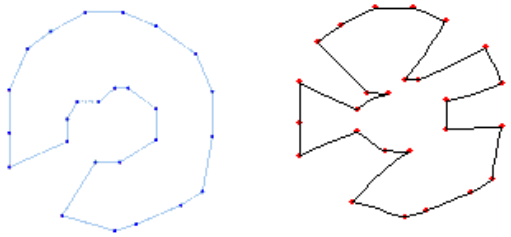

Fig. 5 Result contours for Test06 generated by our algorithm and Elastic Net

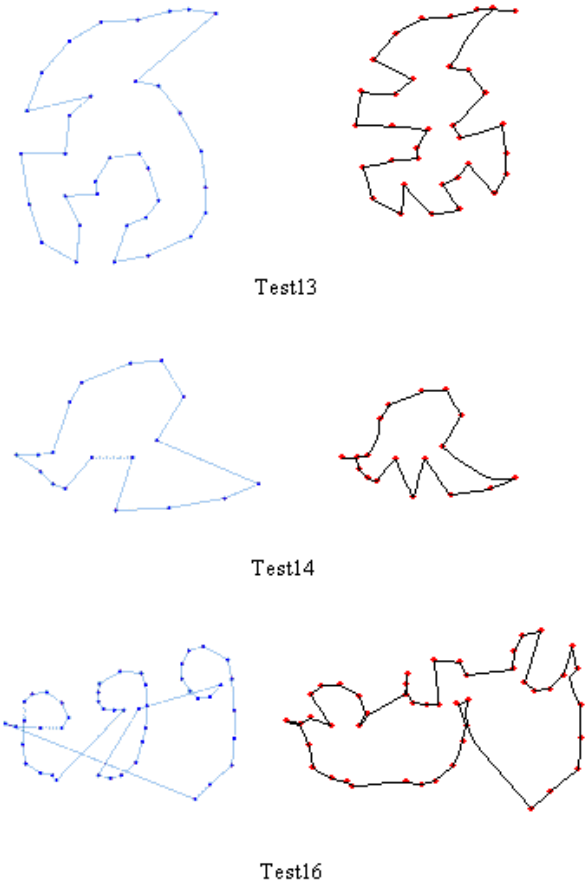

Fig. 6 Result contours for *Test13*, *Test14* and *Test16*

alterations in the shape of the antibody-binding site and receptor editing offers the ability to escape from local optima on an affinity landscape by allowing an antibody take large leaps through the landscape. So we initialize a large receptor editing ratio and decrease it each generation to get high affinity antibodies.

For images from $Test01$ to $Test05$, all of the three algorithms found the best solution. Fig. 4 gives the result images. $Test01$ and $Test02$ are very low density

images and are designed to assess how the techniques cope in the absence of strong image forces.

Among all of the test images, *Test06*, *Test06h*,

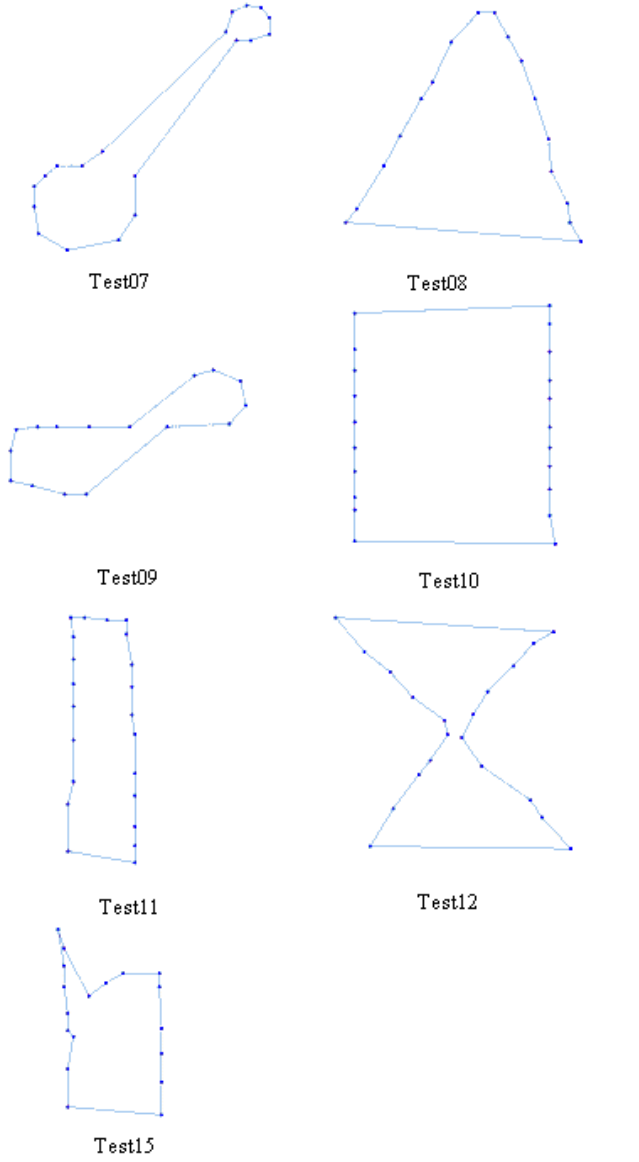

Fig. 7 Result contours for other images

Test07 and *Test11* have more than one feature: they obviously have two separate parts. As pointed out in [1], *Test06* has two interpretations: two concentric circles or a star. The proposed algorithm and CLONALG generated two concentric circles and elastic net generates a star shape as shown in Fig. 5. This is also the case for *Testo6h*

For complex images, the proposed algorithm exhibited its efficiency. It generated more precise contours than elastic net and CLONALG. The results are displayed in Fig.6.

The result contours for the other images are shown in Fig.7. Because our algorithm is designed to produce closed contours, all of the result contours are closed, even

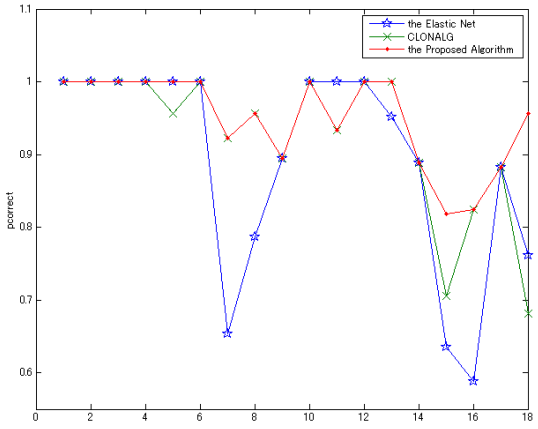

Fig. 8 Accuracy Rates of the three algorithms

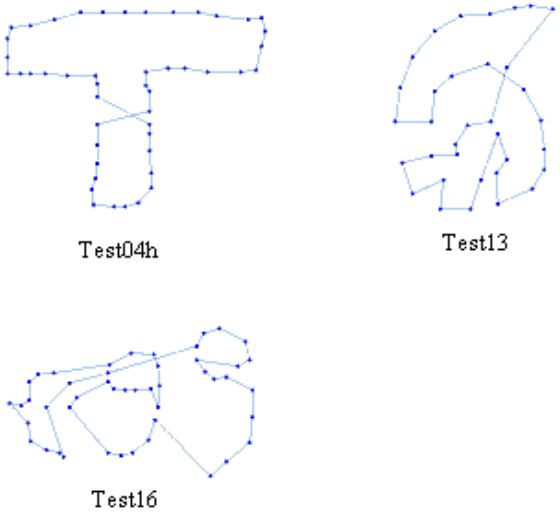

Fig. 9 Contours generated by CLONALG

for *Test07* , *Test10* , *Test11* and *Test15* which are obviously open. But because there are at most two redundant edges, the result images are still very close to the original ones.

Because all of the test bed images used in our simulation have obvious correct interpretations, we defined a parameter *pcorrect* as the proportion of correct edges occupied in all of the edges to measure the algorithm's efficiency.

$$pcorrect = \frac{number\ of\ correct\ edges}{number\ of\ edges} \times 100\% \quad (3)$$

Image	Size	Open/Closed	Description	Elastic Net	CLONALG	The Proposed Algorithm
Test01	3	Closed	Simple triangle	100.0%	100.0%	100.0%
Test02	4	Closed	Simple square	100.0%	100.0%	100.0%
Test03	21	Closed	Closed polygon	100.0%	100.0%	100.0%
Test04	27	Closed	*T* shape	100.0%	100.0%	100.0%
Test04h	47	Closed	Higher density *T* shape	100.0%	95.7%	100.0%
Test05	24	Closed	Figure of eight	100.0%	100.0%	100.0%
Test06	26	Closed	Two concentrate circles	65.4%	92.3%	92.3%
Test06h	47	Closed	Higher density circles	78.7%	95.7%	95.7%
Test07	19	Closed	Two disjoint circles	89.5%	89.5%	89.5%
Test08	17	Open	Inverted *V* shape	100.0%	100.0%	100.0%
Test09	16	Open	Curved open contour	100.0%	93.3%	93.3%
Test10	21	Open	Two parallel lines	100.0%	100.0%	100.0%
Test11	22	Open	Close parallel lines	95.2%	100.0%	100.0%
Test12	20	Open	Two crossing lines	88.9%	88.9%	88.9%
Test13	34	Open	Spiral	63.6%	70.6%	81.8%
Test14	18	Open	Handwritten letter *e*	58.8%	82.4%	82.4%
Test15	18	Open	Handwritten letter *h*	88.2%	88.2%	88.2%
Test16	47	Open	Handwritten word *egg*	76.1%	68.1%	95.7%

Table 1 Test bed images and accuracy rates of Elastic Net and the Proposed Algorithm

Fig.8 shows the accuracy rates of the elastic net, CLONALG and the proposed algorithm while Table 2 gives the description of the test bed images. From Fig.8 and Table 2, we can see the adaptive CSA obviously outperformed the elastic net in most conditions, especially for complex images. However, difference between CLONALG and the proposed algorithm is not so obvious: only three accuracy rates ($Test04h$, $Test13$ and $Test16$) are different. The result contours are displayed in Fig. 9. But the corresponding images are relatively bigger and more complex. These results also contribute to the conclusion that the proposed adaptive CSA is more efficient on difficult problems. This is accordant with the theory proposed in [18]: the importance of receptor editing is dependent on the size of the primary B-cell repertoire (the size of antibody) and large repertoire helps the immune response avoid being trapped in local optima. As a result, the proposed algorithm is considered to be more useful on realistic problems.

As to $Test04$ and $Test04h$, both of the elastic net and the proposed algorithm have the accuracy rate 100%. But CLONALG produces only 95.7% accuracy rate for$Test04h$. The accuracy rate of the elastic net for $Test06h$ is 13.3% higher than that for $Test06$ while the difference for the adaptive CSA and CLONALG is only3.4%. This testifies that the proposed algorithm is less sensitive to edge-point density than the other two algorithms

Though the elastic net produced a perfect contour for $Test09$ while the other two algorithms didn't, its performance on the other images is worse than the proposed algorithm by a large extent. Though all of them produced 100% accuracy rates for several images, the elastic net and CLONALG have minimum accuracy rates 58.8% and 68.1% respectively. And the proposed algorithm performed more steadily and generated high accuracy rates for all of the test bed images with a minimal value 81.8%. So the proposed algorithm can deal with images with different features.

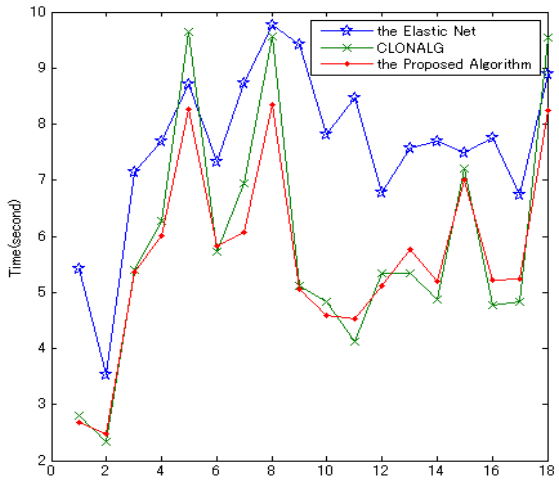

Fig. 10 Processing time of the three algorithms

We also considered the processing time of each algorithm as played in Fig.10. From this figure, we can see that the elastic net takes the longest time while the new operators doesn't increase processing time largely and the proposed algorithm takes the shortest average time among the three techniques.

5. Conclusions

In this paper, an adaptive clonal selection algorithm has been proposed. Hypermutation and receptor editing have been shown to have complementary effects during affinity mutation [18]. In order to exploit their characteristics to a large extent, we have proposed an adaptive clonal selection algorithm by adjusting the ratios of receptor editing and hypermutation adaptively each generation. The performance of the proposed algorithm has been evaluated by 18 hand-written images and the result contours have been compared with those generated by the elastic net and CLONALG. The proposed algorithm has been shown to be less sensitive to edge-point density and applicable for more kinds of images. It also outperformed the other two techniques on complex images. The simulation results indicated that the proposed algorithm used receptor editing and hypermutation effectively and generated meaningful contours within a short time.

In order to simplify the description of the algorithm's mechanism, CSA has introduced only a little part of information processing principles. There are still some other mechanisms such as immune memory, obliviscence, chaotic and adaptive properties which are not considered or only mentioned a little. Bringing these principles into CSA is believed to be necessary to develop and perfect artificial immune system. In the future we will put efforts on the improvement of the algorithm.

Different edge detection algorithms always generate edges with different qualities. Good edge detection algorithms obviously can easy the task of edge linking. Recently, an improvement process of edge images is proposed. In [25], ant colony optimization is adopted to improve traditional edge detection. It is indicated to have improved edge images detected by traditional approaches efficiently. Adopting this improvement process before edge linking is another direction of our research.

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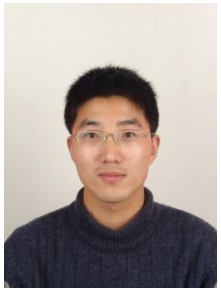

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