**Improved Clonal Selection Algorithm for Knapsack Problem**

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**Abstract**

Clonal selection theory is one of the important theories in immunological area. Applying clonal selection to optimization problems can also be found in many papers. In this paper, the classical Clonal Selection Algorithm (CSA) is extended by introducing the receptor editing mechanism which provides a chance for autoreactive cells to survive during affinity maturation process. To demonstrate the effectiveness and applicability of the novel CSA (NCSA), experiments are carried out on the knapsack problem. Simulation results show that the NCSA has a better performance when compared to the traditional CSA and other algorithms.

**Keywords**: Clonal Selection Algorithm, Receptor Editing, Affinity Maturation, Knapsack Problem

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**1. Introduction**

Biology-inspired algorithms, using the biology system as a source of inspiration for solving computation problems, have emerged and gained much attention over the last few decades. Such as Genetic Algorithm (GA) [12][19], Evolutionary Algorithm (EA) [2][18], and Ant Colony Optimization (ACO) [6], [1],[22]. These algorithms are robust, global in operation, and may be applied generally without recourse to domain-specific heuristics. The natural immune system is also one such system that has tremendous potential in many engineering applications.

Clonal selection theory is one of the most important theories in immunological area [5]. Different algorithms based on the clonal selection theory have also been studied in recent years. Clonal selection algorithm (CSA) is one of the famous immune algorithms.

The CSA [5], based on the clonal selection principle proposed by Burnet [3], has received a rapid increasing interest and has been verified as having a great number of useful mechanisms from the viewpoint of immune programming [13], controlling [21], optimization [4] and so on.

In Burnet’s model, random mutation is allowed to enhance affinity. Furthermore, receptor diversity is generated during lymphocyte development by random combinatorial joining of antigen receptor gene fragments. Unfortunately, these random rearrangements of receptor gene fragments frequently produce nonfunctional receptors because of out-of-frame, or autoreactive.

Although CSA is very attractive from the viewpoint of a novel biology-inspired algorithm, this algorithm suffers from several problems, such as premature convergence and difficulties in reaching high-quality solutions in reasonable time [20].

To overcome the low efficiency problem of the random hypermutation, a novel clonal selection algorithm [7] has been proposed by considering the Receptor Editing (RE) mechanisms. We have also proposed several receptor editing-based CSAs (RECSA) for combinatorial optimization problems [8], [9].

In those receptor editing-based algorithms mentioned above, low affinity cells has to be deleted. However clonal deletion, previously regarded as the major mechanism of immune cell tolerance, has been shown by recent studies to operate secondarily and only when receptor editing is unable to provide a non-autoreactive specificity [14].

The organization of the remaining content is as follows: Section 2 reviews the clonal selection theory and receptor editing mechanism. Section 3 describes the novel receptor editing-based clonal selection algorithm. In Section 4, knapsack problem is discussed to demonstrate the effectiveness of the hypermutation and receptor editing mutation process and the applicability of NCSA. Finally, concluding remarks follow in Section 5.
2. Immune Clonal Selection Theory

The clonal selection theory, proposed by Burnet in 1959 [3], is developed to explain the essential features which contain sufficient diversity, discrimination of self and nonself and long-lasting immunologic memory.

When an immune system is exposed to an antigen, some B cells can recognize the antigen with different certain affinities which reflect the degree of match and become active. Activated B cells will be stimulated to proliferate and eventually mature into terminal antibody secreting cells, called plasma cells. Proliferation of the B cells is a mitotic process whereby the cells divide themselves, creating a set of clones identical to the parent cell. The proliferation rate is directly proportional to the affinity level, i.e. the higher affinity levels of B lymphocytes, the more of them will be readily selected for cloning and cloned in larger numbers.

According to the clonal selection theory, random point mutation is performed during the maturation process. However, frequently, a large proportion of the cloned population becomes dysfunctional or develops into harmful anti-self cells after the mutation. Moreover, the authors [14] interpret that clonal deletion, previously regarded as the major mechanism of central B cell tolerance, has been shown to operate secondarily and only when receptor editing is unable to provide a non-autoreactive specificity.

Recent investigations [10], [17], [15] indicate that receptor editing has played a major role in shaping the lymphocyte repertoire. Both B and T lymphocytes that carry antigen receptors are able to change specificity through subsequent receptor gene rearrangement.

One of the key features of immune system is the ability to respond to an enormous number of different antigens. To account for this diversity, an equally enormous number of immune cell receptors are necessary. This is achieved by the unique structure of the antibody molecule, which is composed of two chains, heavy chain and light chain, each resulting from the rearrangement of various gene segments [16].

![Clonal selection process with receptor editing](image)
then joined to the assembled DJ, forming a unique VDJ combination. Secondary rearrangement also plays an important function in the process governing B lymphocyte tolerance. It occurs in the light chain, whose locus lack D regions, only V and J segments be assembled. Following an initial VJ rearrangement, upstream V segments can be further rearranged to downstream J segment, deleting or displacing the previously rearrange VJ segment. Furthermore, numerous V regions are in reverse orientation on the chromosome, these V are rearranged by inversion rather than by deletion of the intervening sequences, and hence preserve the V segments encoded in it. This retains a high number of V for more rearrangement.

Figure 1 illustrates the clonal selection process including receptor editing mechanisms.

3. Receptor Editing Based CSA

In this section, according to what mentioned above, we characterize the novel CSA (NCSA) by interpreting its general approaches involving initialization, affinity evaluation, clonal operator, affinity maturation (hypermutation and receptor editing), and clonal selection. These above procedures are iterated until a pre-specified termination criterion is satisfied. Figure 2 shows the overall structure of NCSA.

![Figure 2. Overall structure of NCSA](image)

The whole produce of the proposed algorithm can be represented as follows:

- **Step 1** Create an initial pool of \( m \) antibodies (candidate solutions \( C_1, C_2, ..., C_m \)). Compute the affinity of all antibodies \( A(C_1), A(C_2), ..., A(C_m) \) and then sort them in a descending order, where \( A(.) \) is the function to compute the affinity.

- **Step 2** Select the \( n \) (\( n \leq m \)) best (fittest) cells based on their affinities from the \( m \) original cells. These cells will be referred to as the elites.

- **Step 3** Place each of the \( n \) selected elites in \( n \) separate and distinct pools \( EP_1, EP_2, ..., EP_n \). They will be referred to as the elite pools.

- **Step 4** Clone the elites in each elite pool with a rate proportional to its fitness, i.e., the fitter the antibody, the more clones it will have. The amount of clone generated for these antibodies is given by
Eq.(1):
\[ p_i = \text{round}\left( \frac{n - i}{n} \times M \right) \]  

where \( i \) is the ordinal number of the elite pools, \( M \) is a multiplying factor which determines the scope of the clone and \( \text{round}(.) \) is the operator that rounds its argument towards the closest integer. After this step, we can obtain \( \Sigma p_i \) antibodies just as \((EP_{1,1}, EP_{1,2}, ... , EP_{1,p_1}, ... , EP_{n,1}, EP_{n,2}, ... , EP_{n,p_n})\).

**Step 5** Subject the clones in each pool through affinity maturation processes. As mentioned in Section I, clonal deletion has been shown by recent studies to operate secondarily and only when receptor editing is unable to provide a non-autoreactive specificity [14]. Namely, receptor editing allows the immune system to rescue immune cells when hypermutation is failure.

**Step 6** Determine the fittest individual \( B_i (A(B_i) = \arg\max_i(A(EP_{1,1}, ..., EP_{i,p_i})), i = 1, 2, ..., n) \) in each elite pool from amongst its mutated clones.

**Step 7** Update the parent antibodies in each elite pool with the fittest individual of the clones.

### 4. Experimental Results

In this section, the knapsack problem is discussed to demonstrate the applicability of NCSA. To solve this combinatorial optimization problem, NCSA is tested using the parameters setting as given in Table I.

<table>
<thead>
<tr>
<th>Number of initial populations</th>
<th>( m )</th>
<th>150</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of selected populations</td>
<td>( n )</td>
<td>100</td>
</tr>
<tr>
<td>Clone multiplying factor</td>
<td>( M )</td>
<td>50</td>
</tr>
<tr>
<td>Termination condition</td>
<td>( G_{\text{max}} )</td>
<td></td>
</tr>
</tbody>
</table>

*: the maximum number of generation \( G_{\text{max}} \) is different for each experiment

Knapsack problem is a well-known combinatorial optimization problem. It can be described as selecting a subset of items from among various items so that it is most profitable, given that the knapsack has limited capacity. The 0-1 knapsack problem is described as follows: given a set of \( m \) items and a knapsack, select a subset of the items to maximize the profit function \( f(X) \):

\[ f(X) = \sum_{i=1}^{m} p_i x_i \]  

subjects to the condition

\[ \sum_{i=1}^{m} w_i x_i \leq C \]  

where, \( X = (x_1, x_2, ..., x_m) \), \( x_i \) is 0 or 1, \( p_i \) is the profit of item \( i \), \( w_i \) is the weight of item \( i \), and \( C \) is the capacity of the knapsack. If \( x_i = 1 \), the \( i \)th item is selected for the knapsack.

In this paper, strongly correlated sets of data are considered as:

\[ w_i = \text{uniformly random}[1, v] \]  

\[ p_i = w_i + r \]  

where \( v = 10 \) and \( r = 5 \).
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Restrictive knapsack capacity is [11]:

\[ C = 2v \]  \hspace{1cm} (6)  

It should be noticed that the initial solutions of knapsack problem are all set to 0, that is \[ X_i = (x_{i1}, x_{i2}, ..., x_{im}) = (0, 0, ..., 0). \]

**Table 2.** Experimental results of knapsack problem with the restrictive knapsack capacity $C=20$ for 100, 250, and 500 items

<table>
<thead>
<tr>
<th></th>
<th>CSA</th>
<th>RECSA</th>
<th>NCSA</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>100</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>best</td>
<td>50.0</td>
<td>50.0</td>
<td>90.0</td>
</tr>
<tr>
<td>mean</td>
<td>47.0</td>
<td>46.5</td>
<td>79.5</td>
</tr>
<tr>
<td>worst</td>
<td>40.0</td>
<td>40.0</td>
<td>70.0</td>
</tr>
<tr>
<td>$\delta$</td>
<td>5.7</td>
<td>4.9</td>
<td>3.9</td>
</tr>
<tr>
<td><strong>250</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>best</td>
<td>50.0</td>
<td>60.0</td>
<td>100.0</td>
</tr>
<tr>
<td>mean</td>
<td>49.5</td>
<td>50.0</td>
<td>91.5</td>
</tr>
<tr>
<td>worst</td>
<td>40.0</td>
<td>40.0</td>
<td>90.0</td>
</tr>
<tr>
<td>$\delta$</td>
<td>2.2</td>
<td>3.2</td>
<td>3.7</td>
</tr>
<tr>
<td><strong>500</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>best</td>
<td>50.0</td>
<td>70.0</td>
<td>100.0</td>
</tr>
<tr>
<td>mean</td>
<td>50.0</td>
<td>51.0</td>
<td>99.0</td>
</tr>
<tr>
<td>worst</td>
<td>50.0</td>
<td>50.0</td>
<td>90.0</td>
</tr>
<tr>
<td>$\delta$</td>
<td>0.0</td>
<td>4.4</td>
<td>3.1</td>
</tr>
</tbody>
</table>

Table II shows the experimental results of the knapsack problem with 100, 250, and 500 items. The maximum number of generations and the number of runs are selected to be 500 and 20 respectively. $\delta$ represents the standard deviation. As the table shows, NCSA yields much better solutions compared with CSA and RECSA.
Figure 3 shows the comparisons of CSA, RECSA, and NCSA on the knapsack problem. The vertical axis shows the profit value of knapsack and the horizontal axis represents the number of generations. From the simulation results, it can be seen clearly that NCSA performs significantly better than CSA and RECSA in terms of convergence speed and the amount of profit.

5. Conclusions

By introducing the receptor editing mechanism, an improved clonal selection algorithm is proposed for knapsack problem. The experimental results showed that the NCSA performed better than CSA and RECSA for the restrictive knapsack problem in terms of convergence speed and the amount of profit. Our future work is to investigate the adaptive NCSA and explore other applications, such as FSS (Flow Shop Scheduling), FAP (Frequency Assignment Problem) and so on.

6. Acknowledgements

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7. References