IMMUNE CLONAL ALGORITHM BASED FEATURE SELECTION FOR EPILEPTIC EEG SIGNAL CLASSIFICATION

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ABSTRACT

Detecting epileptic EEG signal automatically and accurately is significant in evaluating patients with epilepsy. In this study, the immune clonal algorithm (ICA) is employed to perform automatic feature selection, reducing the number of features the classifier deals with and improving the classification accuracy. In the experiment, EEG signal was decomposed into five sub-band components by a discrete wavelet transform. Features were extracted as input to train three classifiers (NB, SVM, KNN and LDA) to judge whether the EEG signal was epileptic or not. Then, ICA was introduced to select a feature subset to train the classifiers. Experimental results show that the classification accuracy based on selected features is significantly higher than that on original features. We also analyzed the relative importance of each feature.

1. INTRODUCTION

Epilepsy is a neurological disorder and the occurrence of an epileptic seizure has been unpredictable till now. The electroencephalogram (EEG) signal reflects the electrical activities of the neurons in the brain, which provides us an efficient tool to examine brain activity. Though EEG signals play an important role in evaluating epilepsy, such as determining epileptogenic zone for presurgical evaluations [1], checking the long term EEG recordings manually is often time-consuming and tedious. Thus, a number of machine learning and pattern recognition algorithms have been introduced to automatically analyze EEG signals [2].

How to detect and classify the epileptic EEG signal automatically and accurately with machine learning methods has been studied for several years. Many existing approaches for seizure detection and prediction pay attention mainly to two key aspects of EEG processing schemes: feature extraction and classifier design. Features are usually extracted by frequency analysis [3], wavelet analysis [4] or a nonlinear method [5]. Adeli and colleagues demonstrated that individual EEG frequency sub-bands can provide more information than the entire EEG [6]. Their method decomposes the raw EEG signal into five sub-bands corresponding to delta, theta, alpha, beta and gamma rhythms using a discrete wavelet transform, which provides both time and frequency views simultaneously. A wide range of classifiers which are prevalent in pattern recognition studies have been applied to EEG data, like artificial neural networks [7], artificial neuro-fuzzy inference system [8], learning vector quantization [9], support vector machine [10], K-nearest neighbor algorithm [11], linear discriminant analysis [12] and Extreme Learning Machine [13]. Obviously, the performance of any classifier depends on whether the extracted features can effectively depict the essential characteristics of raw EEG data.

Recently, many nature-inspired algorithms such as genetic algorithms [9][12] and genetic programming [11][14] have been used to select a more effective feature subset with respect to original features. In this paper, the immune clonal algorithm was employed to select the feature subset, aiming at improving EEG signal classification accuracy and reducing the dimensionality of the feature space.

This paper is organized as follows: Section 2 introduces clinical EEG data and the discrete wavelet transform, which is an effective non-stationary signal processing tool. After that, the features for each sub-band are extracted. Then, four frequently-used classifiers, termed naive bayes (NB), linear discriminant analysis (LDA), K-nearest neighbor algorithm (KNN) and support vector machine (SVM), are briefly described. Later, the immune clonal algorithm (ICA) and ICA-based feature selection, which are the key techniques within the proposed framework, are discussed in detail. In section 3, the proposed method is used to solve two classification problems: a two-group classification task (seizure-free and seizure) and a three-group classification task (normal, interictal and ictal). Both the mean dimensionality of selected feature space and the frequencies of each feature in multiple trials are examined for the two experiments.

2. METHODS AND MATERIALS

2.1. Clinical Data

We developed and evaluated our epileptic EEG classification methodology on the publicly available EEG database provided by the Department of Epileptology, Bonn University, Germany, which was described in [5]. The complete data set consists of five sets (denoted A-E) each containing 100 single-channel segments, each of which was 23.6s in length and sampled at 173.61Hz. Sets A and B consist of segments taken from surface EEG recordings that were

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carried out on five healthy volunteers using a standardized electrode placement scheme. Volunteers were relaxed in an awaken state with eyes open (A) and eyes closed (B), respectively. Sets C, D, and E originated from EEG archive of presurgical diagnosis. EEGs from five patients were selected, all of whom had achieved complete seizure control after resection of one of the hippocampal formations, which was therefore correctly diagnosed to be the epileptogenic zone. Segments in set D were recorded from within the epileptogenic zone, and those in set C were recorded from the hippocampal formation of the opposite hemisphere of the brain. While sets C and D contain only activity measured during seizure free intervals, set E only contains seizure activity. All EEG signals were recorded with the same 128-channel amplifier system, using an average common reference. Typical EEGs of the five sets are shown in Fig. 1.

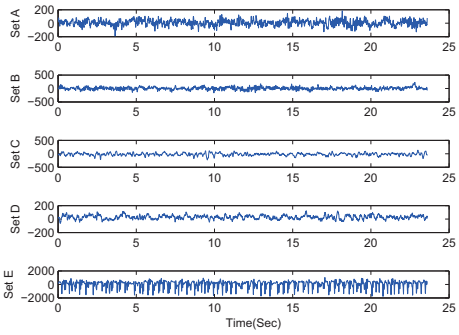


Fig. 1. Examples of five different EEG signal sets.

2.2. Discrete Wavelet Transform

EEG signals are non-stationary and are characterized as spatio-temporal dependent. Though a Fourier transform (FT) of an EEG signal can help us obtain its frequency content, the time information is lost. Taking this problem into consideration, a short time Fourier transform (STFT) is a series Fourier transform with a fixed time window cannot get a good balance between time and frequency resolutions. The wavelet transform (WT) emerged as an effective tool to deal with non-stationary signals because it can adapt the window size according to the frequency. At high frequencies, fine resolution is obtained and at low frequencies, long windows are used to encompass those frequency contents.

Generally, the raw EEG signals are decomposed into finer sub-band components by a multi-level discrete wavelet transform (DWT) using high-pass and low-pass filters [6]. After the first level decomposition, two signals which represent the detail (high frequency) and the approximation (low frequency) are obtained. The approximate signal can be further decomposed by a second-level decompostion, and this process can continue till the granularity can fulfill the demands.

Raw EEG signals are filtered to remove frequencies above 60 Hz before being put through a multi-level DWT. In this paper, Daubechies order-4 (DB4) wavelet is chosen as basis for analyzing the EEG data. After four levels of decomposition, the original EEG signal is decomposed into five frequency bands, δ (0-4 Hz), θ (4-8 Hz), α (8-15 Hz), β (15-30 Hz), and γ (30-60 Hz). Fig. 2 shows the wavelet decomposition results of EEG samples chosen from set A and E.

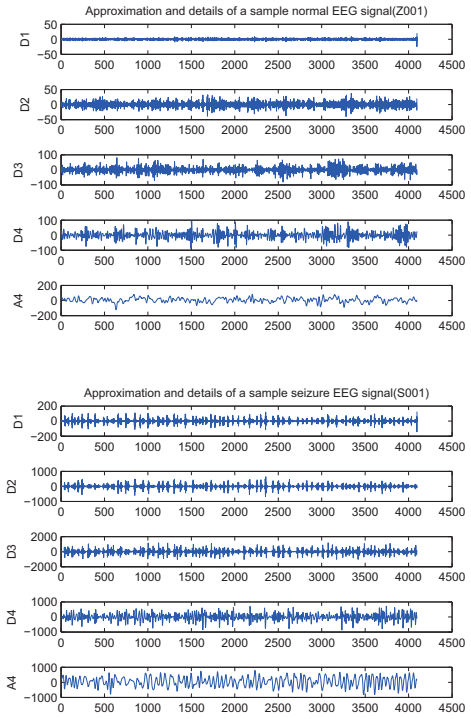


Fig. 2. Approximation and details of Normal and Epileptic EEG signals.

2.3. Feature Extraction

After the discrete wavelet transform, the raw EEG signal is decomposed into sub-band components including several details (D) and one approximation (A). Each sub-band signal represents the original signal in different frequency bands. Because computing the nonlinear features mentioned in [14] and [13] is so time-consuming, we prefer to use some simple statistical features which are capable of revealing the important time-frequency characteristics of EEG signals. They are described as follows: (S, l represents the sub-band signal and the wavelet decomposition level respectively; N is the number of coefficients for details or approximate at each decomposition level).

1. Mean of the absolute values of each sub-band signal

$$F_i = \frac{1}{N}\sum_{j=1}^{N}|S_{ij}| \tag{1}$$

2. Average energy of each sub-band signal

$$F_i = \frac{1}{N}\sum_{j=1}^{N}|S_{ij}|^2 \tag{2}$$

3. Standard deviation of each sub-band signal

$$F_i = \sqrt{\frac{1}{N-1}\sum_{j=1}^{N}S_{ij}^2} \tag{3}$$

4. Fluctuation coefficient of each sub-band signal

$$F_i = \frac{1}{N-1}\sum_{j=1}^{N-1}|S_{i,j+1} - S_{ij}| \tag{4}$$

5. Skewness of each sub-band signal

$$F_i = \frac{1}{N}\sum_{j=1}^{N}(\frac{S_{ij}-\mu_i}{\sigma_i})^2 \tag{5}$$

where $i = 1, 2, \ldots, l$.

Each raw EEG signal is decomposed into four details and one approximation using Daubechies order-4 (DB4) wavelet with level 4. Then, five features mentioned above are extracted from each sub-band signals. As a result, a feature vector (F) with 25 elements is generated. The definition of each element is shown in Table 1.

Table 1. Definition of each element in feature vector.

Feature \ Frequency	δ	θ	α	β	γ
Mean	F_1	F_6	F_{11}	F_{16}	F_{21}
Energy	F_2	F_7	F_{12}	F_{17}	F_{22}
Standard deviation	F_3	F_8	F_{13}	F_{18}	F_{23}
Fluctuation coefficient	F_4	F_9	F_{14}	F_{19}	F_{20}
Skewness	F_5	F_{10}	F_{15}	F_{20}	F_{25}

The scale of features may be different, so the normalization process is necessary to standardize all features to the same level before training the classifiers.

2.4. Classifiers

In this study, four popular classifiers: naive bayes, linear discriminant analysis, K-nearest neighbor algorithm and support vector machine [15], are employed to evaluate the classification accuracy of the two above-mentioned classification problems.

2.5. ICA Based Feature Selection

Immune clonal algorithm (ICA) is one of the most popular nature-inspired algorithms. Its main point is to simulate the mechanism of how immune system of a vertebrate resists outside invasion. The excellent performance of immune clonal algorithm makes it useful in solving complex optimization problems [16]. The immune system's ability to adapt its B-cells to new types of antigens is powered by processes known as clonal selection and affinity maturation by hyper-mutation [17].

In the artificial immune system, antigens represent the problem to be solved and constraints, while antibodies represent candidate solutions. In general, an antibody population $A = \{a_1, a_2, \ldots, a_n\}, a_i \in \Omega, i = 1, 2, \ldots, n$ is an *n*-dimensional group of antibodies *a* (where Ω is the feasible region and the positive integer *n* is the size of antibody population *A*). According to the clonal selection theory [18], a general iterative flow of an artificial immune system can be described by the following steps: proportional cloning, recombination, hyper-mutation, fitness assignment and population evolution (roulette selection is used in this paper). The appendix gives the detailed steps of the immune clonal algorithm and below is the ICA-based feature selection method.

Feature selection and dimensionality reduction are important steps in pattern classification. Current research applies the immune clonal algorithm to automatically select an effective feature subset and improve the classification performance.

In this paper, both the population size and the proportional cloning factor N_c are set to 100. The probabilities for recombination and hyper-mutation are 0.9 and 0.1 respectively. Each antibody consists of 25 genes, each of which is set to binary, namely 0 or 1 and each gene represents the corresponding feature described in Table 1. A value of 0 implies that the corresponding feature is excluded from the feature set, while 1 indicates the feature is included. The initial population is generated randomly. The fitness functions for the 2-group classification ($f1$) and the 3-group classification ($f2$) are

$$f_1 = (e_1 + e_2)/2 \tag{6}$$

and

$$f_2 = (e_1 + e_2 + e_3)/3, \tag{7}$$

where e_1, e_2 in Eqn.(6) are the misclassification rates of the classifier in the seizure-free (set A, C) and seizure (set E) groups respectively. Similarly, e_1, e_2 and e_3 in Eqn.(7) are the misclassification rates of the classifier in the normal group (set A, B), interictal group (set C, D) and ictal group (set E) respectively. The training samples are used to train the classifiers for classification. The misclassification rates are obtained by calculating the error counts of the classification. The iterative aim is to minimize the fitness function and the algorithm terminates when maximum generation is reached.

The whole flow of feature selection using the immune clonal algorithm is depicted in Fig. 3.

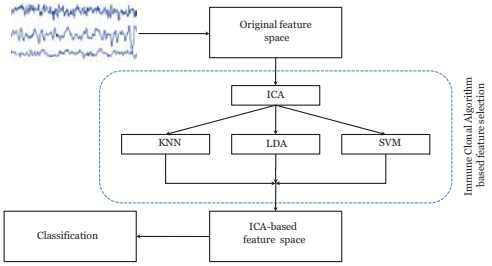


Fig. 3. Diagram of the ICA based feature selection.

3. EXPERIMENTAL RESULTS

In the present study, two classification problems are considered; the EEG signals are divided into two (seizure-free and seizure) groups or three groups (normal, interictal and ictal). Accordingly, different clinical datasets are used for the different tasks. For the former task, three datasets (A, C and E) are examined and they should be classified into the seizure-free (set A, C) and seizure (set E) groups. For

the latter task, all five datasets (A, B, C, D and E) are used; they should be classified into the normal group (set A, B), interictal group (set C, D) and ictal group (set E).

Each EEG segment containing 4096 points for each class (normal, interictal and ictal) was divided into four equal epoches; thus, each segment will form 400 samples. In the recently published literature, nearly all the training and testing samples are randomly selected [11][12][13]. Because the EEG signal are timing dependent and the pathological state can only be predicted by obtained EEG signal, the former 200 samples per class are chosen for training and the latter 200 samples for testing in this paper.

3.1. Classification with all Features

To classify EEG signals into two groups (seizure-free and seizure) and three groups (normal, interictal and ictal), all features are used to train NB, LDA, KNN and SVM with linear and RBF kernel functions and k is set to 3 in KNN. For SVM classifier, the kernel-related optimal parameters are tuned by 5-fold cross-validation for classification. This process are repeated twenty times and the mean and standard deviation of classification accuracies of different classifiers are summarized in Table 2 and Table 3.

Table 2. Classification accuracy with all features.

	Seizure-free	Seizure	Avg
NB	95.25	86.50	**92.33**
LDA	95.00	96.50	**95.50**
KNN	95.25	95.50	**95.33**
SVML	96.00	94.50	**95.50**
SVMRBF	97.75	98.00	**97.83**

Table 3. Classification accuracy with all features.

	Normal	Interictal	Ictal	Avg
NB	78.00	88.00	53.50	**77.10**
LDA	94.75	93.00	96.00	**94.30**
KNN	96.25	93.00	95.50	**94.80**
SVML	96.75	93.25	93.00	**94.60**
SVMRBF	98.75	96.75	96.50	**97.50**

In table 3, the accuracy obtained by naive bayes classifier is relatively low. The possible reason is that the conditional independence assumption is not tenable in 3-group classification problem. Patients in interictal period is really with epilepsy; however, in this study we classify the interictal and ictal patients into different classes.

3.2. Classification with Selected Features

The immune clonal algorithm is then used for selecting the optimal feature subset to maximize the classification accuracies. Each of the accuracies is the mean of twenty independent trials with timing-dependent training and testing data, which means that both the training and testing data are fixed. The accuracies of different classifiers are summarized in Table 4 for two-class experiment and Table 5 for three-group experiment. From these two tables, it is clear that the mean accuracies obtained with the selected feature subset are obviously higher than the accuracies obtained with all features. Overall, SVM with an RBF kernel outperforms the remaining classifiers for both tasks. The results confirm the value of the immune clonal algorithm as a feature selector for seizure detection based on EEG signals.

Table 4. Classification accuracy with features selected by immune clonal algorithm.

	Seizure-free	Seizure	Avg
NB	95.26(0.01)	92.63(0.02)	**94.38(0.01)**
LDA	95.61(0.22)	98.40(0.48)	**96.54(0.14)**
KNN	97.19(0.33)	96.68(0.59)	**97.00(0.26)**
SVML	96.63(0.21)	97.18(0.52)	**96.81(0.59)**
SVMRBF	98.39(0.22)	99.43(0.44)	**98.73(0.12)**

Table 5. Classification accuracy with features selected by immune clonal algorithm.

	Normal	Interictal	Ictal	Avg
NB	78.84(2.47)	89.00(1.95)	70.75(4.17)	**81.29(0.89)**
LDA	96.54(0.58)	93.05(0.34)	95.83(0.94)	**95.00(0.12)**
KNN	97.58(0.73)	94.60(0.73)	95.75(1.08)	**96.02(0.18)**
SVML	98.40(0.21)	94.96(0.09)	94.10(0.35)	**96.17(0.05)**
SVMRBF	99.78(0.16)	98.68(0.34)	98.00(0.69)	**98.98(0.13)**

For showing the efficiency of ICA based feature selection algorithm, we compare it with the popular particle swarm optimization (PSO) based feature selection. Table 6 and Table 7 give the results for two classification problems. The classification accuracies based on ICA and PSO selected features are obviously better than accuracies based on original features. Generally, the proposed algorithm slightly outperforms the PSO based feature selection algorithm in classification accuracies.

Table 6. Classification accuracy with features selected by particle swarm optimization.

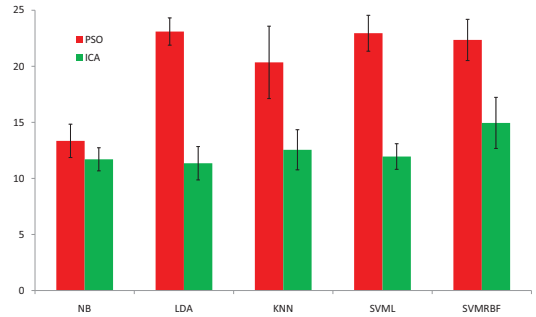
	Seizure-free	Seizure	Avg
NB	95.25(0.02)	90.45(0.05)	**93.65(0.01)**
LDA	95.53(0.20)	97.28(0.53)	**96.11(0.16)**
KNN	95.81(0.64)	96.43(1.07)	**95.97(0.36)**
SVML	96.08(0.32)	95.88(0.60)	**95.98(0.14)**
SVMRBF	98.17(0.32)	98.92(0.69)	**98.42(0.23)**

Table 7. Classification accuracy with features selected by particle swarm optimization.

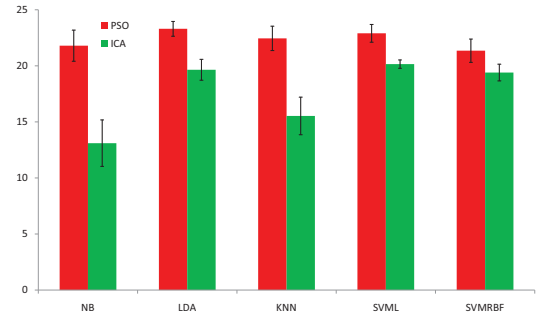
	Normal	Interictal	Ictal	Avg
NB	75.10(3.54)	88.23(1.99)	72.404.15)	**79.82(1.23)**
LDA	95.38(0.50)	93.01(0.25)	95.49(0.92)	**94.48(0.10)**
KNN	96.54(0.70)	93.98(0.57)	95.75(0.82)	**95.32(0.17)**
SVML	98.18(0.47)	95.03(0.23)	94.23(0.41)	**96.12(0.08)**
SVMRBF	99.11(0.33)	97.96(0.20)	97.45(0.22)	**98.32(0.13)**

For each classifier, the feature selection using ICA and PSO are run for twenty independent trials. After twenty trials, mean dimensionality of selected feature space is checked in the results of twenty trials; this is shown in Fig. 4.

From Fig. 4, the dimensionality of the selected feature subspace based on ICA is obviously lower than that based on PSO. The former is around twelve for the two-group classification task while it is slightly more (about 15) for SVM with RBF kernel, which is far less than the dimensionality of the original feature space (25). For the three-group classification task, the mean dimensionality of the selected feature subspace is located in 15-19. It makes sense

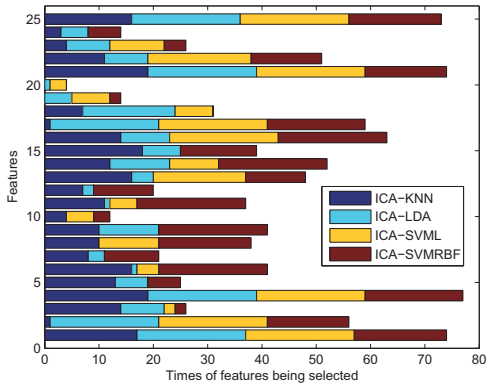


(a) features selected by different algorithms for 2-group classification.

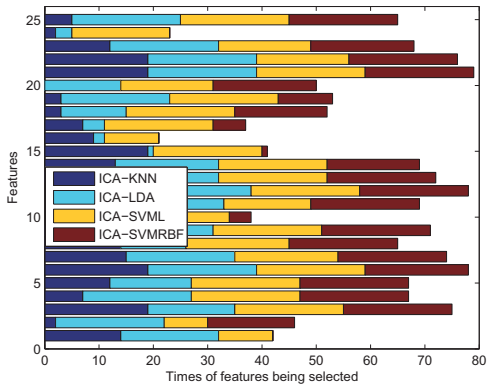


(b) features selected by different algorithms for 2-group classification.

Fig. 4. The dimensionality of selected feature space.



(a) Statistical results of features selected by ICA for 2-group classification.



(b) Statistical results of features selected by ICA for 3-group classification.

Fig. 5. Statistical results of features selected by ICA.

that more features are needed to detect the differences among three classes than for two classes. The latter is around twenty for the two-group classification task and twenty-two for the three-group classification task. This means the PSO based feature selection algorithm is less efficient than ICA based feature selection algorithms in this study.

3.3. Features Selected by Immune Clonal Algorithm

The frequencies of each feature's being selected can be found more clearly from Fig. 5. Features located in δ and γ band signals are encouraged by two-group classification task while EEG components in all the frequency bands except the θ are beneficial to three-group classification. The application of wavelet decomposition to EEG data prior to feature calculation enables the extraction from sub-band components. Analyzing features selected by the immune clonal algorithm reveals the probable relative importance of individual features from specific sub-band to the accuracy of the classifier. It will be more efficient and accurate to automatically detect seizure based on the features selected by the immune clonal algorithm instead of using all features. This study in the field of information science may lead toward decoding the mental status corresponding to some specific frequency bands in physiology.

4. CONCLUSION

The present work develops an approach using four different classifiers (NB, SVM, KNN and LDA) with features extracting from wavelet decomposition based sub-bands EEG signals for automatic epileptic seizure detection. The immune clonal algorithm, a popular nature-inspired algorithm, is employed for feature subset selection. The results demonstrate the effectiveness of using simple sub-band EEG statistical features. The performance of all three classifiers with features selected by the immune clonal algorithm is improved significantly. The relative importance of the extracted features can be evaluated by the frequencies of features being selected in independent trials. More importantly, the proposed method can be used as a subsidiary method for automatically detecting epileptic seizure in clinical practice.

5. APPENDIX IMMUNE CLONAL ALGORITHM

The main steps of immune clonal algorithm which is used to select feature subset can be described as follows.

1. Proportional Cloning. In immunology, cloning means asexual propagation so that a group of identical cells can be descended from a single common ancestor, for example a bacterial colony whose members arise from a single original cell as the result of mitosis. In this study, the proportional cloning operator T^C on the antibody population

$A = \{a_1, a_2, \ldots, a_{|A|}\}$ is defined as

$$\begin{aligned} A_1(k) &= T^C(a_1, a_2, \ldots, a_{|A|}) \\ &= T^C(a_1) + T^C(a_2) + \ldots + T^C(a_{|A|}) \\ &= (a_1^1, a_1^2, \ldots, a_1^{q_1}) + \ldots + (a_{|A|}^1, a_{|A|}^2, \ldots, a_{|A|}^{q_{|A|}}) \end{aligned}$$

where *k* is the *k*-generation and $q_i, i = 1, 2, \ldots, a_{|A|}$ is a adaptive parameter determined by the fitness value of each antibody to control the clonal size of each original ancestor. It means that the antibody with a greater fitness value will clone a larger number of offspring. So the values of q_i can be properly calculated as

$$q_i = \lceil N_C \times f(a_i) / \sum_{j=1}^{|A|} f(a_j) \rceil \tag{8}$$

where N_C is an expectant value of the size of the clone population [16]. Alternatively, q_i can be set as a constant.

2. Recombination. If $C = \{c_1, c_2, \ldots, c_{|C|}\}$ is the population after applying the proportional cloning operator $A = (a_1, a_2, \ldots, a_{|A|})$, then the recombination operator T^R on the clone population *C* is defined as

$$\begin{aligned} A_2(k) &= T^R(c_1, c_2, \ldots, c_{|C|}) \\ &= T^R(c_1) + T^R(c_2) + \ldots + T^R(c_{|C|}) \\ &= \text{crossover}(c_1, A) + \ldots + \text{crossover}(c_{|C|}, A) \end{aligned}$$

where $\text{mutate}(c_i, A), i = 1, 2, \ldots, |C|$ denotes the offspring generated by crossover operator on clone c_i and an antibody randomly selected from *A*.

3. Hyper-mutation. If $R = \{r_1, \ldots, r_{|R|}\}$ is the resulting population after recombination, then the hyper-mutation operator T^M on the clone population R is defined as

$$\begin{aligned} A_3(k) &= T^M(r_1, r_2, \ldots, r_{|R|}) \\ &= T^M(r_1) + T^M(r_2) + \ldots + T^M(r_{|R|}) \\ &= \text{mutate}(r_1) + \ldots + \text{mutate}(r_{|R|}) \end{aligned}$$

where $\text{mutate}(r_i), i = 1, 2, \ldots, |R|$ denotes changing each element of the variable vector r_i by a general mutation operator with probability P_m, so each individual in the clone population R at each time step will undergo about $m \times P_m$ mutations, where *m* is the dimension of the variable vector.

4. Fitness Assignment and Population Evolution. The fitness evaluation is the most important step in population evolution and it is the fitness value that determines the evolutionary direction of the clone population. Generally speaking, the fitness function will be constructed according to the goal of real optimization problem. After the fitness value of each antibody in clone population is computed, a proper method will be employed to generate a population as the initial population in the next iteration. In this way, the population evolves from generation to generation, and the optimal solution of the target problem will be approximated.

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