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Author(s)	Shojaeilangari, Seyedehsamaneh; Moradi, Mohammad Hassan
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A New Unsupervised Pre-processing Algorithm Based on Artificial Immune System for ERP Assessment in a P300-based GKT

¹S. Shojaeilangari and ²M.H. Moradi

¹Electrical and Electronic Engineering Department, Nanyang Technological University, Singapore, Singapore

²Biomedical Engineering Faculty, Amirkabir University of Technology, Tehran, Iran

Abstract: In recent years, an increasing number of researches have been focused on bio-inspired algorithms to solve the elaborate engineering problems. Artificial Immune System (AIS) is an artificial intelligence technique which has potential of solving problems in various fields. The immune system, due to self-regulating nature, has been an inspiration source of unsupervised learning methods for pattern recognition task. The purpose of this study is to apply the AIS to pre-process the lie-detection dataset to promote the recognition of guilty and innocent subjects. A new Unsupervised AIS (UAIS) was proposed in this study as a pre-processing method before classification. Then, we applied three different classifiers on pre-processed data for Event Related Potential (ERP) assessment in a P300-based Guilty Knowledge Test (GKT). Experiment results showed that UAIS is a successful pre-processing method which is able to improve the classification rate. In our experiments, we observed that the classification accuracies for three different classifiers: K-Nearest Neighbourhood (KNN), Support Vector Machine (SVM) and Linear Discriminant Analysis (LDA) were increased after applying UAIS pre-processing. Using of scattering criterion to assessment the features before and after pre-processing proved that our proposed method was able to perform data mapping from a primary feature space to a new area where the data separability was improved significantly.

Keywords: Artificial immune system, guilty knowledge test, lie-detection, pre-processing, unsupervised learning

INTRODUCTION

Application of biological metaphors to solve engineering problems has attracted the attention of many researches. Artificial neural networks and evolutionary computation are good typical examples that show the success of this idea. Biological immune system exhibits many information processing characteristics such as pattern matching, feature extraction, diversity, learning and memory. Artificial Immune System (AIS) inspired by the biological immune system is a new computational intelligence method which has found application in a vast range of areas such as machine learning (Suliman and Rahman, 2010), data mining (Chen *et al.*, 1996), pattern recognition (Kudo and Sklansky, 2000), control (Lie *et al.*, 2000), optimization (Tan *et al.*, 2008), classification (Bereta and Burczynski, 2006) and statistic (Coutinho, 1980).

One of the initial works that suggested a computational system inspired from natural immune system was performed by Farmer and Packard (1986). In this work, the authors proposed a model based on the

idiotypic network theory for pattern recognition which explained the immune memory mechanism. It was suggested that the biological immune system can be viewed as a learning system and used as an inspiration to build machine learning techniques. Based on these ideas, Cook and Hunt developed a technique for DNA sequence classification (Cook and Hunt, 1995). After that, a modified version of artificial immune based algorithm was proposed by Timmis to develop a general technique for data reduction and clustering (Timmis *et al.*, 1999).

Forrest proposed an algorithm inspired by a mechanism of immune system which trains the T-cells to recognize antigens and prevent them from attacking to the body's own cells (Forrest *et al.*, 1994). This algorithm was named Negative Selection (NS) that is based on self/non-self recognition as one of the interesting mechanism of the adaptive immune system (Xue-wen, 2003). Nowadays, the various versions of this algorithm are used for pattern recognition tasks.

In this report, our proposed method has been examined in the context of lie-detection dataset. Recording the brain potentials is one of the old non-

invasive techniques for studying the brain functions Abootalebi *et al.* (2004). This technique as a common used method measures event-related changes in the electroencephalogram (EEG) which are known as Event-Related Potentials (ERP). ERPs are affected by the recognition of important events and have been extensively studied in the P300 waves. The P300-based GKT is a guilty knowledge test which utilizes P300 amplitude as an index of actual recognition of concealed information. This test has been suggested as an alternative approach for conventional polygraphy. Therefore, the designed GKT was applied to several subjects and their respective brain signals were recorded. After removing the noise of signals and pre-processing stages; for analysis of signals, some suitable features were extracted and then our new hybrid method consisting of Unsupervised Artificial Immune System (UAIS) and classification was applied.

There are many classification systems which have been used for EEG signals classification problems for different tasks such as clinical diagnosis. There have been several studies focusing on ERP assessment in a P300-based GKT. These studies from independent laboratories applied different methods to achieve high classification performance. Farwell and Donchin obtained 87.5% classification accuracy using bootstrapped correlation difference (BCD) method (Farwell and Smith, 1991). Rosenfeld used Bootstrapped Amplitude Difference (BAD) and BCD methods and had reached to a detection rate of 80-95% (Rosenfeld *et al.*, 2004). Abootalebi obtained 86% classification accuracy using linear discriminant analysis (LDA) classifier with optimum features selected by genetic algorithm (Abootalebi *et al.*, 2009).

Our research is a continue of previous studies including P300 GKT and classification of wavelet features based on LDA and Genetic Algorithm (GA) reported by Abootalebi Abootalebi *et al.* (2009). Indeed, the previous works were more focused on data collection and feature extraction; however, we attempted to improve the pattern recognition part using AIS in our research. We investigated the pattern detection capability of AIS for boosting of the previous results. In this study, a new hybrid method was proposed to be used for ERP assessment in a P300-based GKT problem. This method involves two stages: pre-processing via an unsupervised artificial immune system and classification by several classifiers. The first stage of our proposed approach conducted a data pre-processing to map the data to an improved feature space for assisting the classification performance in the second stage. To prove this claim, we used the scattering criterion before and after pre-processing the data.

Background: Similar to other artificial intelligence techniques such as Artificial Neural Networks or Genetic Algorithms, AIS has been emerged to solve different domain problems with high performance. This section

introduces the natural and artificial immune system for better understanding of our proposed algorithm.

Natural immune system: Immune system is the most complex functional system that protects the body from disease. Any substance (as a toxin or enzyme) that stimulates an immune response in the body is called antigen (Ag). Defence mechanism of the body is regulated by interaction of innate and adaptive immune responses. When an Ag stimulates human immune system, at first, the innate immune system generates a response that is not specific but it is able to repel the attack in many cases. If the innate immune system does not succeed to repel the intrusion, the adaptive immune system will be activated. Adaptive immune system consists of two types of lymphocytes known as T- and B-cells (Igawa and Ohashi, 2005). They are rather similar, but differ by their functional roles.

Adaptive response is much more important from computational point of view because of its specific metaphors. The main characteristic of adaptive immune system is that it can learn via interaction with its environment. When an antigen is detected in the body for the first time, a primary immune response is activated to recognize and eliminate the antigen. After elimination the Ag, several immune cells that could detect the Ag are kept as memory cells. In next exposure to the similar Ag, the memory cells generate a faster and more effective response which is named secondary response of immune system. Therefore the adaptive immune system is able to remember past encounters with Ags to generate specific and effective responses in future.

The principle of clonal selection explains how the adaptive system recognizes and eliminates specific Ags by means of B-cells (Castro and Timmis, 2002). When B-cell's receptors which are named antibodies (Ab) recognize an Ag, it is selected to expand and produce Abs in high amounts. The Abs bind to the Ag and finally lead to eliminate it. The number of B-cell progenies (clones) is proportional to the affinity of the selected B-cell and the Ag. Therefore, the cells with highest affinity proliferate more. During reproduction, the B-cell clones suffer a mutation process to produce B-cells with more affinity with the presented Ag. The mutation rate, opposite of clonal rate is inversely proportional to the affinity. Indeed, the B-cells who have more affinity with the Ag mutate with the smaller mutation rate and vice-versa. Additionally, the best B-cells whose Abs present high affinity with the Ag are selected as memory cells. Memory B-cells are kept for future responses to the same or similar antigenic patterns. Figure 1 illustrates the clonal selection principles as a biological inspired model which is performed pre-processing task in our proposed

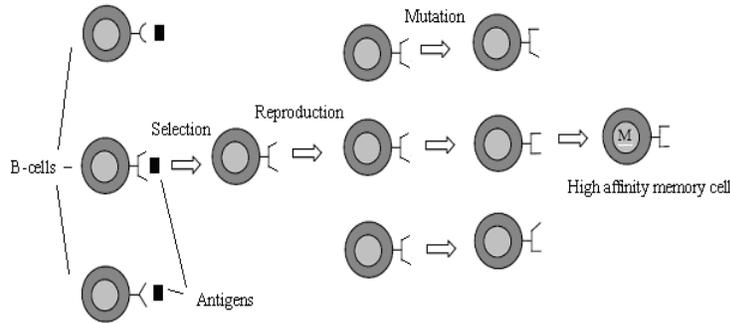


Fig. 1: Clonal selection principle

method. As it is shown in Fig. 1, the clonal selection model includes 3 stages. The first step is selection of a B-cell which matches with the Ag stronger than other B-cells. The second step is reproduction; selected B-cell proliferates and reproduces itself with the same form of receptors. The third step is mutation; the reproduced B-cells undergo to a mutation process to generate mutated B-cells with antigenic receptors presenting higher affinities with the selective Ag. Finally, the best muted B-cell which is nominated M in Fig. 1 is selected as a memory cell.

Artificial immune system: AIS was proposed in 1990s as a new computational research area (Omkar et al., 2008). AISs are defined as the abstract computational systems developed using theories and ideas which are extracted from natural immune system. AISs aim at solving complex engineering problems such as pattern recognition. Like Artificial Neural Network, Genetic Algorithm and other Evolutionary Algorithms, AIS is capable of learning new information, saving this information at its memory, recalling the learned information and then performing the pattern recognition task.

AIS algorithms are resulted of modelling the processes that naturally occur in human body. While a general computational model inspired by natural immune system is a subject of researches, two fundamental concepts “antibody and antigen” are important to be modelled properly. As we mentioned in section “Natural immune system”, antibodies can detect antigens by matching them and the variation of antibodies is less than antigens, therefore the matching between them is not perfect. The major purpose of AIS is to produce and keep small number of antibodies which are able to recognise a big number of antigens in a best way, even though those have never been seen.

One of the most important problems of studies in AIS field is representation type for modelling of immune cells. Among different representation methods have been proposed, we used the most commonly one named shape-

space representation. This model quantitatively describes the interactions between antibodies and antigens (Ozsen et al. 2007). The major idea behind shape-space is that the degree of matching between antibodies and antigens determines the strength of their binding which depends on their shape (Timmis et al., 2008).

Used data source: The applied method for generation of lie-detection dataset was as follows (Abootalebi et al., 2009).

Subject and data acquisition: The EEG signals were recorded from Sixty-three subjects (60 male, 3 female) in the modified GKT experiment. After recording and amplifying the signals having information of brain electrical activities, they were digitized at a rate of 256 samples per second and then filtered in [0.3-30] Hz range to prepare for analysing stage.

Stimulation and recording procedure: In the examination, after guidance of a subject about the protocol, a box containing a jewel was given to him/her and asked to perform protocol without presentation of examiners. At this moment, the subject could choose one of two possible roles; guilty or innocent. When subject played the guilty role, he/she was expected to open the box, examine the jewel precisely and memorize the details of it. While in the second case, subject acts in the innocent role and had nothing to do with the box and thus had no information about the object.

After that, examiner returned to the room and started to perform protocol. Subject sat in front of a monitor and recording was started with attachment of electrodes. During the recording, pictures of five different jewels (each one with 30 iterations) contained one target, one probe and three irrelevant, were showed successively and randomly on the monitor. The probe was the object in the box and target has been previously presented to the subject before the start of the examination.

The subject is given one push button in each hand, right hand click as "YES" and left one click as "NO".

Table 1: Number and name of all extracted features

Number of feature	Type of feature	Name of feature
1	Morphologic	LAT
2		AMP
3		LAR
4		AAMP
5		ALAR
6		PAR
7		NAR
8		ANAR
9		TAR
10		ATAR
11		TAAR
12		AASS
13		PP
14		TPP
15		PPS
16		ZC
17		ZCD
18		SSA
19	Frequency	f_mode
20		f_median
21		f_mean
22	Wavelet	D (0-125)
23		D (125-250)
24		D (250-375)
25		D (375-500)
26		D (500-625)
27		D (625-750)
28		D (750-875)
29		D (875-1000)
30		T (0-125)
31		T (125-250)
32		T (250-375)
33		T (375-500)
34		T (500-625)
35		T (625-750)
36		T (750-875)
37		T (875-1000)
38	Wavelet energy	A (0-62)
39		A (63-125)
40		A (125-187)
41		A (188-250)
42		A (250-312)
43		A (313-375)
44		A (375-437)
45		A (438-500)
46		A (500-562)
47		A (563-625)
48		A (625-687)
49		A (688-750)
50		A (750-812)
51		A (813-875)
52		A (875-937)
53		A (938-1000)
54	Wavelet entropy	Ewt (0-125)
55		Ewt (125-250)
56		Ewt (250-375)
57		Ewt (375-500)
58		Ewt (500-625)
59		Ewt (625-750)
60	Wavelet entropy	Ewt (750-875)
61		Ewt (875-1000)
62		Swt (0-125)
63		Swt (125-250)
64		Swt (250-375)
65		Swt (375-500)
66		Swt (500-625)
67		Swt (625-750)
68		Swt (750-875)
69	Swt (875-1000)	

Then, subject was asked to reply "YES" to the items saw them previously and "NO" for unknowns. All subjects (guilties and innocents) answered "YES" for targets and "NO" for probes and irrelevant. Thus, innocents and guilties, both replied honestly to targets and irrelevant,

but the innocents replied honestly and guilty answered falsely for probes.

In designed protocol, each subject participated two times in experiment which the boxes and all jewels were different and subjects could choose a guilty role in one experiment and innocent role in another. Therefore, for 63 subjects, totally 126 tests were performed, which 33 subjects chose the innocent role and 30 subjects chose guilty role in the first experiment. Signals recorded from these two experiments were analysed independently. At the end of experiments, due to misconducting of protocol with subjects or examiner and inappropriate quality of recorded signals, A few test results were removed. Finally, 59 recorded of guilty cases and 51 recorded from innocent were used for future stages.

Data analysis: In this study, we have used classification based method for analysing of the recorded signals. This is done by extraction of several suitable and common used features from the raw data.

Four different feature sets were proposed: morphologic features (18 features), frequency features (3 features), wavelet features (32 features) and wavelet energy and wavelet entropy features (16 features). Therefore, totally 69 features have been extracted. The number and name of extracted features are given in Table 1. For more detailed information refer to (Abootalebi *et al.*, 2009)

METHODOLOGY

Our proposed method involves two stages: pre-processing stage with unsupervised artificial immune system and classification stage. The use of AIS in the first stage maps the data to a new feature space and then its performance was evaluated through applying three different classifiers: Support Vector Machine (SVM) (Cortes and vapnik, 1995; Comak and Arslan, 2008), K-nearest neighbourhood (KNN) (Sahan *et al.*, 2007) and Linear Discriminant Analysis (LDA) (Bostanov, 2004; Abootalebi *et al.*, 2009).

This study was conducted in 2008-2009 at Amirkabir University of Technology, Iran. The dataset was collected by Abootalebi at the same university (Abootalebi *et al.*, 2009).

Unsupervised artificial immune system: The natural immune system has strong clustering capability that this property has been used in AIS literatures for solving the engineering problems. In our proposed algorithm which was inspired from this property, the presented input samples are named Ags while forming memory and output units called Abs. In this algorithm, for each Ag presented to memory antibodies, the best mature Ab of memory population saved as an output unit which is the best

representation of the input sample. Therefore, the output matrix of this stage has the same size as matrix of the input data.

Notation used in the algorithm is as follow:

- N : The number of Ag_s in dataset
- L : The number of features of input data
- M : The number of produced memory Ab_s
- Ag : Input sample (length: L)
- Ab : Feature vector
- Mem : Memory Ab population (size:(M, L))
- $clone_Ab$: Cloned Ab population
- $mutate_Ab$: Mutated Ab population
- $cand_Ab$: Candidate Ab in Ab_mutate population
- out_Ab : Output Ab population (size:(N, L))
- eps_Mem : Threshold value which is used to add candidate Ab_s to memory population
- $Radii_Ab$: Threshold value which is used to add candidate Ab_s to output population

Algorithm: At the first step, all of the data must be normalized to ensure that the Euclidean distance between each two samples is in the interval of (0-1). Then, the initial values of parameters and vectors are determined. In beginning; the memory cell population is randomly chosen from the input data (Ozsen and Gunes, 2009).

- (1) For each Ag_i ; ($i:1, \dots, N$)
 - (1.1) Calculate the Euclidean distances between Ag_i and the memory Ab_s
 - (1.2) If the minimum distance calculated is less than a threshold value named as $dist_{Ab-Ag}$, then save the nearest Ab to Ag_i in out_Ab matrix and go to step1.
 - (1.3) Generate a memory Ab for Ag_i ; steps (1.3.1)-(1.3.3) are iterated until termination condition is met.
 - (1.3.1) Select n nearest Ab_s to Ag_i and clone them ($clone_Ab$).
 - (1.3.2) Mutate each Ab $clone_Ab$ ($mutate_Ab$).
 - (1.3.3) Calculated the distances between all Ab_s in the $mutate_Ab$ population and Ag_i then keep the nearest Ab as a candidate memory Ab for Ag_i ($cand_Ab$) and stop iterative process if the distance between $cand_Ab$ and Ag_i is less than $Radii_Ab$.
 - (1.4) Save the $cand_Ab$ in out_Ab .
 - (1.5) If the minimum the distance between Ab_s of Mem population and $cand_Ab$ is less than threshold value named as eps_Mem , concatenate $cand_Ab$ as a new memory Ab .

The proposed algorithm was inspired of previous works in AIS field, but it was different from them in some aspects. The first point is that the proposed algorithm in this study had unsupervised learning, because there is no utilization of data labels. Another innovation of this algorithm is that it was applied for data mapping, not other purposes such as data reduction in previous works

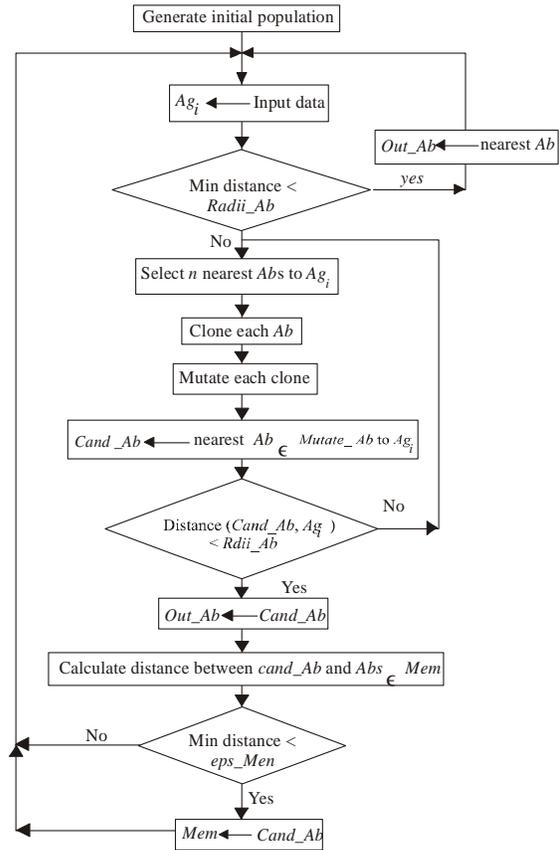


Fig. 2: Flowchart of the UAIS algorithm

(Sahan et al., 2007; Polat and Günes, 2008); therefore, the output of the proposed algorithm had the same dimension as the input data. Indeed, in spite of previous works, the output of this algorithm was different from memory population.

The mutation mechanisms are different in literatures of AIS and we use the most commonly mechanism named hypermutation in our algorithm. It is performed proportional to distance between two cells as Eq. (1) (Sahan et al., 2007):

$$Ab'_{j,l} = Ab_{j,l} \pm Dist_{j,i}(Ab_{j,i}) \quad (1)$$

Here, $Ab'_{j,l}$ is the mutated value and $Ab_{j,l}$ is the old value of l^{th} attribute of j^{th} Ab .

$Dist_{j,i}(Ab_{j,i})$ stands for the distance between Ag_i and Ab_j . The flowchart of the algorithm is shown in Fig. 2.

Performance evaluation: In this study, to assess the classification performance, Leave-One-Out (LOO)

validation was used. For 110 subjects (59 guilty cases and 51 innocent), we performed 110 experiments. For each experiment, we used total single records (for example 20-30 single records of each subject) of 109 subjects for training and remaining samples for testing. On the other hand, for a given subject, the probe sweeps of other subjects (both guilty and innocents) with their real labels were used for training phase of a selected classifier. Then, the classification algorithm was tested on the probe sweeps of the given subject. The number of sweeps recognized as guilty subject were counted and saved in parameter *Ng*. *Ng* as an analogous output for each subject is a criterion for guilty probability of that person. At the end, we selected a threshold to make a final decision on the guilty or innocent of the given subject. Therefore, if *Ng* was greater than the threshold, a guilty subject was recognized.

It should be noted that the LOO method is completely matched with lie-detection structure. In fact, if brain lie-detection experiment is tested for a new subject, the used classifier should be trained with data of 110 subjects who have definite labels and then apply to data obtained from new subject (111th subject), therefore it is predictable that the detection accuracy of this subject is completely close to the result of LOO method.

Generally, the LOO method for evaluation of classifiers is very time consuming in training phase, because the process should be repeated *n* times (*n* is the number of subjects).

EXPERIMENTAL RESULTS

To evaluate our proposed approach, we used lie detection dataset consist of 2552 samples, 69 features and two classes.

The details of parameters setting for UAIS algorithm in our experiment, is shown in Table 2. These parameters are selected by trial and error. Two important parameters which considerably affect on classification results are *Radii_Ab* and *eps_Mem*. The value of parameter *Radii_Ab* determines recognition radii of memory *Abs* and should be selected in the interval of (0-1). The parameter *eps_Mem* is a threshold that determines the number of memory *Abs* and just like *Radii_Ab* should be tuned in the interval of (0-1). If it was set too large, the number of memory *Abs* produced in the training phase would be very small. Therefore the recognition of new pattern and consequently, the classification accuracy would be unsatisfied. If it was fitted very small, the number of *Abs* saved as memory would be excessively large while this requires longer classification running time. This may not be a considerable problem for some applications such as lie-detection, while the processing time is a critical issue as well as classification accuracy in many fields like

Table 2: Used parameters in UAIS algorithm

Value	Used parameters
0.001	<i>eps_Mem</i>
0.1	<i>Radii_Ab</i>
10	<i>Clonal rate</i>
0.5	<i>Mutation rate</i>

Table 3: The effect of UAIS pre-processing on classification accuracy of SVM, KNN and LDA classifiers

Accuracy (%)				
(without pre-processing)				
-----			Accuracy (%)	
Min	Max	Mean	(with pre-processing)	Classifier
81.36	93.64	86.49	68.32	SVM
86.33	96.61	92.58	61.41	KNN(K = 1)
81.00	94.11	86.75	66.31	LDA

medical diagnosis. *Clonal rate* is an integer value that determines the number of clones that each *Ab* is allowed to produce. *Mutation rate* indicates the probability that any feature of an *Ab* can be mutated.

The disadvantage of this method is that the result of pre-processing is not reproducible. The reason of this phenomenon is obviously related to random mutation of *Abs*. To make sure that the result is in confidence range, we repeated the whole process (pre-processing and classification) 10 times separately and then the average classification accuracy as a final result was reported. It is notable that in each experiment, the training phase of UAIS pre-processing algorithm was implemented independently from the previous experiment results.

SVM as one of the well-known techniques for classification can use different kernel function such as sigmoid, polynomial and radial basis function (RBF). In this study, RBF kernel function which is an effective option for classifying multi-dimensional data was applied. In SVM classifier with RBF kernel, two parameters *C* and γ must be selected appropriately. KNN as the second selection of different classifiers has a parameter *K* should be set by the user. We defined it in the range of 1-15 from odd numbers (because of binary classification problem) while the best mean result corresponding to $k = 1$ was reported. LDA was our last selected classifier without any parameter setting.

It can be observed from Table 3 that UAIS algorithm significantly improved the classification accuracy. The detection rates are 86.49%, 92.58% and 86.75%, respectively for SVM, KNN and LDA, respectively. The increase of 18.17%, 31.17% and 20.44%, respectively in classification accuracy of three mentioned classifiers after pre-processing stage, are good evidence for effectiveness of the proposed approach. In order to compare the results before and after pre-processing, the related chart is shown in Fig. 3.

The result shows that our proposed algorithm can describe the data from a primary feature space to a new

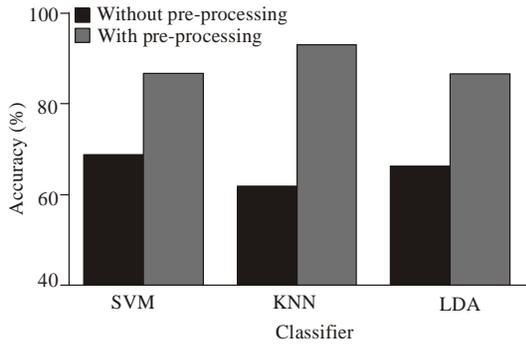


Fig. 3: Performance of different classifiers with and without applying UAIS pre-processing

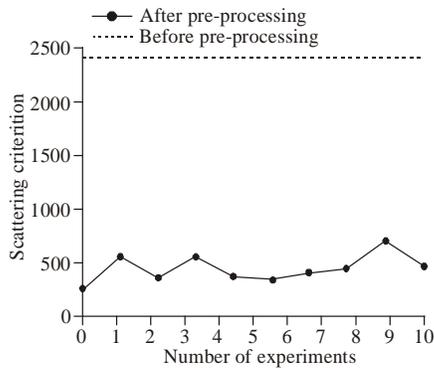


Fig. 4: Davies-boulding scattering values of lie-detection dataset before and 10 times after UAIS pre-processing

Table 4: Davies-boulding scattering value of lie-detection dataset before pre-processing and comparison with mean, maximum and minimum values after 10 times pre-processing

After pre-processing			Before pre-processing
Min	Max	Mean	
250.00	689.65	439.13	2403.80

feature space where the data separability of different classes has been improved. To prove this claimed, we used the scattering criterion of classes before and after pre-processing the data. Different standards defined to describe the within-class and between-class scattering to study of class distribution in feature space. In this report, we used Davies-Bouldin standard for this task (Davies and Bouldin, 1979). The results of scattering criterion before and after 10 times data pre-processing with AIS method presented in Fig. 4 and briefly in Table 4. The results show the ability of proposed algorithm to improve data separability.

CONCLUSION AND FUTURE WORK

In this report, we have proposed a new successful unsupervised pre-processing algorithm based on the

paradigm of artificial immune systems. This algorithm was capable of performing data mapping to a new feature space where data is more likely to be separable than primary feature space.

Then we classified the pre-processed data by three best known classifiers SVM, KNN and LDA. Experiments were conducted on the lie-detection dataset for ERP assessment in a P300-based GKT. The results strongly suggest that our pre-processing approach can assist the classification rate of recorded EEG signals.

UAIS algorithm as an effective method for pre-processing task has several parameters that affect on classification results. Optimizing the parameters in this algorithm by using of genetic algorithm or other optimizer methods is one of our purposes in future work. We also hope that our proposed method will be applied on further datasets.

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