

Bio-Inspired Generalized Global Shape Approach for Writer Identification

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Abstract—Writer identification is one of the areas in pattern recognition that attract many researchers to work in, particularly in forensic and biometric application, where the writing style can be used as biometric features for authenticating an identity. The challenging task in writer identification is the extraction of unique features, in which the individualistic of such handwriting styles can be adopted into bio-inspired generalized global shape for writer identification. In this paper, the feasibility of generalized global shape concept of complimentary binding in Artificial Immune System (AIS) for writer identification is explored. An experiment based on the proposed framework has been conducted to proof the validity and feasibility of the proposed approach for off-line writer identification.

Keywords—Writer identification, generalized global shape, individualistic, pattern recognition.

I. INTRODUCTION

IN the development of digital age, paper documents are still exchanged. In some situation, writer identification is needed to identify the original writer of handwritten document. Usually, writer identification performed on legal papers by a way of signature. However, it is also needed to identify handwritten documents without signature such as in threaten letter, authorship determination of old or historical manuscript etc. Handwriting has long been considered individualistic and writer individuality rests on the hypothesis that each individual has consistent handwriting [1]. Therefore, it ignited the researchers to explore this field in order identify the writer of handwriting. However, it still poses a challenge because human capability is superior when compared to computerized system in observing and recognizing the style of handwriting.

Meanwhile, Artificial Immune Systems (AIS) is one of the recent biologically inspired approaches that emerge from computer science field. AIS computational technique has led to the development of useful computational tools to solve complex problems such as in pattern recognition, fault detection, classifications, computer security, and optimization [2], [3], [4], [5]. This paper is intended to explore the feasibility of Negative Selection Algorithm and

Generalized concept in AIS for off-line handwritten writer identification domain.

This paper is organized into several sections. Writer identification is briefly described in Section 2, followed by AIS in pattern recognition in Section 3. Section 4 describes a proposed framework of bio-inspired writer identification and experiment conducted. And finally, conclusion is drawn in Section 5.

II. WRITER IDENTIFICATION

Writer identification is one of the areas that attract many researchers to work in. It is utilized in forensic and biometric application where an author of a questioned document can be identified based on handwriting. The identification of author for questioned handwritten document has a great importance on the criminal justice system and widely explored in forensic handwriting analysis [6], [7], [8], [9], [10]. The relation of character, shape and the styles of writing are different from one person to another. Features of handwriting are different according to these varieties of handwriting styles. However, handwriting is a skill that is personal to individual characteristics [11], [12] and it is individualistic [6], [9], [13], [14], [15]. It is a challenge to find the best solution in order to identify the writer accurately.

Most of the researchers in pattern recognition tried to solve writer identification problem based on the image processing and pattern recognition technique [1], [16], [17], [18], [19]. There is a close relationship between the tasks of writer identification and general handwriting recognition [16]. It involved typical pattern recognition framework, which are feature extraction and classification task [17], [18], [19]. In pattern recognition community, it is a well known that feature extraction and classification task are essential to achieve a good performance in recognizing patterns.

The main issue in writer identification is how to acquire features that reflect the author for these varieties of handwriting [9], [16], [17], [20], [21], [24], either for one writer or many writers. These features are required to classify in order to identify which group or classes that they are closed to. The shape or style of writing from one person to another is different. Even for one person, the styles are different in times. However, as mention before everyone has their own style of writing and it is individualistic. Each person's handwriting is seen as having a specific texture [15]. It must be a unique feature that can be generalized for each person in handwriting.

Previous works have been done in order to acquire the features from the handwriting such as, local graphemes

Manuscript received Ogos 31, 2006. This work is supported by STGL-012-2006, SAGA GRANT (Scientific Advancement Fund Allocation), Academy of Science, Malaysia.

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features [20]; text line geometrical quantity [16]; dynamic features [24]; character formulated [8]; texture analysis [21], [17]; text line based features [23], [14]; but none of them focus on generalized global shape features from handwriting.

III. AIS IN PATTERN RECOGNITION

AIS draw inspiration from vertebrate immune system, the same as artificial neural network from nervous system. (de Castro and Timmis, 2002b) defined AIS as an adaptive systems, inspired by theoretical immunology and observed immune functions, principles and models, which are applied to problem solving. The natural immune system is an adaptive learning system that employs many parallel and complementary mechanisms for defense against foreign pathogens. It is a distributed system, capable of learning to identify previously unseen invaders and remembering what it has learnt. Numerous immune algorithms now exist, based on processes identified within human immune systems.

In the work of pattern recognition, immune recognition is based on the complementary bind region between the receptor and a portion of the antigen called epitope. It is important to note that the recognition in the immune system is based on shape complementary [2]. This recognition concept in Immune System (IS) is performed by using 3 mechanisms which are (i) Negative Selection (T-cells that recognize self-antigens are excluded from the population of T-cells during the maturation process); (ii) Clonal Selection (if B-cell encounters a non-self antigen with a sufficient affinity, it will proliferates and differentiates into memory cells) and (iii) Immune Network (if B-cell recognizes a self-antigen, it might result in suppression). However, this paper will only focus on NSA. NSA in AIS has been applied to detect computer viruses [7]; tool breakage detection and time-series anomaly detection [9]; network intrusion detection [10], [11]; color image classification [12], creative design classification [13], cancer classification [22].

A. Negative Selection Algorithm

Negative Selection Algorithm was proposed by Forrest in [25] for various anomaly detection problems. It was inspired by Negative Selection property in human immune system that uses the property of self/non-self discrimination to detect foreign antigens. It presents an alternative paradigm to perform pattern recognition by storing information about the complement set (non-self cell) of the pattern to be recognized. It is also provides tolerance for self cells and deal with the immune system's ability to detect unknown antigens while not reacting to the self cells. In the biological system, this is achieved in part by T-cells which have receptors on their surface that can detect foreign antigens.

Negative Selection Algorithm works on similar principles, generating detectors randomly and eliminating the ones that detect self, so that the remaining non-self cells can detect any non-self. It has two main stages which are censoring and monitoring. The first stage of NSA is to control the generation of detectors in random and the other one is to monitor the changes by using the detectors generated in earlier stage. The matching of detector set with new antigens based on certain matching rule. Non-self is detected if there is a match between the antigen and any of

the detectors. The NSA by [25] and summarized by [27] is as follows:

- 1) Define self as a collection of strings S of finite length L that needs to be monitored.
- 2) Generate a set of detectors R each of which fails to match any self string in S .
- 3) Monitor S for changes by continually matching the detectors in R against S . If any detector matches, then a change is known to have occurred, because the detectors are designed not to match any of the original strings in S .

According to Xiao in [26], the original NSA is not suitable for pattern recognition task. The NSA is originally used to solve change detection problems with only two states defined, either normal or abnormal. In pattern recognition task, negative selection must be extended to multi-state, equivalent to number of classified groups. Xiao in [26] modified the original NSA to be used for pattern recognition in engineering creative design.

B. Generalization in AIS

Generalized shape concept is important in immune system where an antibody can recognize an antigen based on the shape. Antigens and antibodies are considered to be points in an abstract shape space, where coordinates of points in the space represent generalized physico-chemical properties associated with various physical properties related to binding, such as geometric shape [27]. The affinity between an antibody and an antigen involve binding process where it must be bind complementary with each other. However, it must not be completely bind between these two elements, to recognize the antigen or virus. Antibody can detect the virus via regions of complementary with a set of features that called generalized shape of a molecule [28]. Fig. 1 below illustrates the generalized shape concept of complementary binding in AIS. This generalization capability can recognize not only the specific pattern, but also any structurally related pattern. This capability is attained by a process called cross-reactivity and can be modeled using the affinity threshold [29].

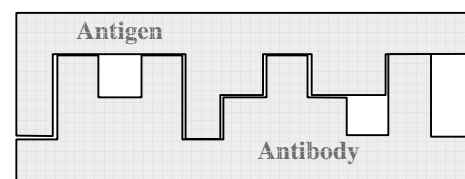


Fig. 1 Generalized shape concept of complementary binding in AIS

Generalization can be seen as the capability of a input data set respond appropriately to another set of data. A given attribute of string data can match not only with the exact or complete complementary, but also to an acceptable complementary process within the given threshold. The volume resulting from the cross-reactivity threshold is called recognition region. If the value of affinity binding for recognition region is larger than or equal to the pre-define cross-reactivity threshold, then it is assumed that a recognition event is occurred between the molecules in the

system. In computational system, each antibody and antigen is assumed to be implicitly described by a vector of numbers i.e. a coordinate vector, which represent the geometric shape characteristics relevant to shape complementary in binding [27].

IV. PROPOSED BIO-INSPIRED FRAMEWORK AND EXPERIMENT

A simple experiment was conducted base on the proposed framework in Fig. 2. This experiment is to proof the feasibility of bio-inspired generalized approach in writer identification. It has three main tasks, which are Granular Data Collector, Bio-inspired Training Environment and Bio-inspired Classifier.

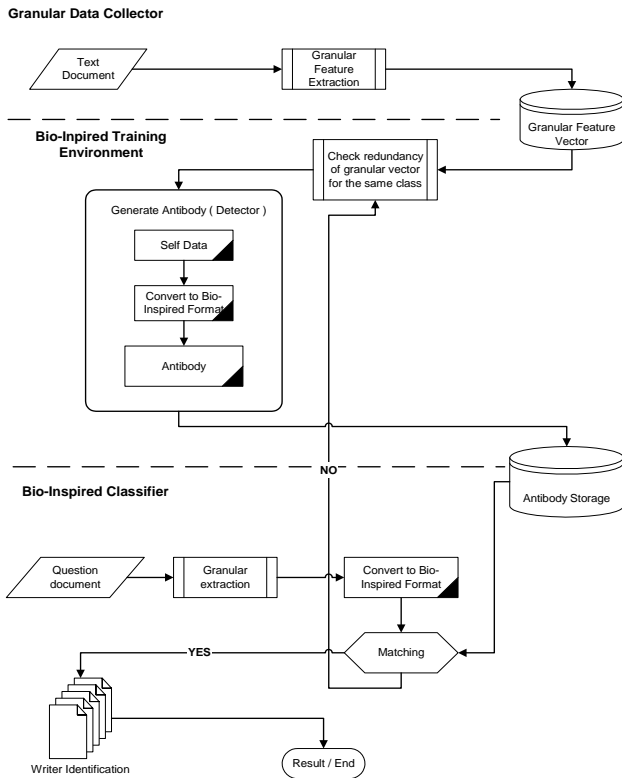


Fig. 2 Proposed Framework of Bio-inspired Writer Identification

A. Granular Data Collector Phase

In the task Granular Data Collector, global moments function specifically on Geometric Moment Function has been used to extract the handwriting image. A set of moments computed from digital image generally represents global characteristics of the image shape, and provides a lot of information about different types of geometrical features of the image [30]. The invariants feature vectors are converted using the mathematical formulation of $f: \mathcal{R} \rightarrow \sum^m$ into symbolic representation.

Image of words need to be transformed into suitable format in order to be manipulated and processed. Feature extraction is performed on those images using moment functions to generate respective invariant values. Table I

TABLE I
DATA REPRESENTATION OF 'SINCE' USING GMI

Feature Vector	
1	-1.780028
2	-9.653448
3	-14.781119
4	-15.007411
5	-30.545805
6	0.000000
7	-1.780028

B. Bio-Inspired Training Phase

In Bio-inspired Training phase, sets of self data are obtained from first task. These data sets are transformed and represented into Bio-Inspired Format by performing the modified NSA to generate antibody data set. The modified NSA used in this work is shown as below:

- Define self as N sets of strings S is used for pattern matching (how many classes according to how many writer is observed).
- Generate N sets of detectors in complimentary and each should fail to match with self set define in [i].
- Present the input pattern to monitor process - if any match occurs at the i^{th} set of detectors, the input pattern belongs to the corresponding groups. The process is repeated until the last writer in handwriting database.

The identified antibodies are generated and stored for matching procedure with antigen in the classification task.

C. Classification Phase

In classification phase, the concept of generalized global shape will be applied where the shape of handwritten word is recognized with the complementary binding of self cell and antibody. The questioned document is extracted, and the features are transformed into binary format as antigens. This will be defined and act as antigens (or as self data for the examined word image). A binary matching rule is defined in terms of individual bit matching of detectors and antigens represented as binary string [31].

In the process, r-Contiguous matching technique is used. The binary matching of r-contiguous is defined as: Given

$$\text{Antigen } x = x_1x_2x_3\dots x_n$$

and

$$\text{Detector } d = d_1d_2d_3\dots d_n,$$

where,

$$d \text{ matches } x \equiv \exists i \leq n - r + 1$$

such that

$$x_j = d_j \text{ for } j = i, \dots, i + r - 1$$

The two strings are match if there is a sequence of six bits where all the bits are identical. For negative selection using XOR operator, matching is achieved with complements, i.e., 0 matches with 1. These antigens are compared to antibody from the antibody database. If there is no matched, then the antigen will go through the generate antibody process to produce a new data (memory). The new data are saved to the database. Otherwise, it will be listed as potential writer which will later be sorted by percentage. The highest percentage is claimed as the potential owner of the questioned document.

In this initial experiment, 10 writers with 20 words of each person (all 200 words) from AIM database has been used in training data set. All the extracted features from these writers are saved in granular feature vector database. For data testing, the different set of 5 words image from writer no 10 is extracted to be used as features from question document. Result from the experiment is shown in Table II. The accuracy of word 1 to word 4 for the 10th writer is the highest in accuracy for all writers, accept for word 5. However, the differences of accuracy between writer no 9 and writer no 10 is only 5%. In overall, it shows that the writing from question document can identify the 10th writer as the owner of the writing. Thus, it is proven the feasibility of deploying the bio-inspired generalized global shape approach in writer identification.

TABLE II
RESULT FROM THE EXPERIMENT

Writer	Words Image Accuracy in %				
	word 1	word2	word3	word4	word5
W1	65	71	58	51	63
W2	72	67	67	45	51
W3	68	70	73	59	58
W4	70	70	59	48	56
W5	66	67	68	54	48
W6	65	70	69	58	57
W7	67	67	60	51	55
W8	65	70	60	47	54
W9	77	72	66	62	69
W10	98	98	78	65	64
Target Writer	W10	W10	W10	W10	W10
Result Writer	W10	W10	W10	W10	W9

V. CONCLUSION AND FUTURE WORK

We have presented a bio-inspired of generalized shape with complimentary binding concept in AIS for identifying the potential writer of handwriting. GMI is utilized as the feature extraction technique to extract global shape features of handwritten word. An initial experiment has been conducted to explore and proof the feasibility of proposed approach. In future work, we will use other feature extraction techniques and a bigger set of data to perform the experiment for comparison.

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