QR-DCA: A New Rough Data Pre-processing Approach for the Dendritic Cell Algorithm

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Abstract. In this paper, we propose a new approach of data pre-processing based on rough set theory for the Dendritic Cell Algorithm (DCA). Our hybrid immune inspired model, denoted QR-DCA, is based on the functioning of dendritic cells within the framework of rough set theory and more precisely, on the QuickReduct algorithm. As the DCA data pre-processing phase is divided into two sub-steps, feature selection and signal categorization, our QR-DCA model selects the right features for the DCA classification task and categorizes each one of them to its specific signal category. This is achieved while preserving the same DCA main characteristic which is its lightweight in terms of running time. Results show that our new approach generates good classification results. We will also compare our QR-DCA to other rough DCA models to show that our new approach outperforms them in terms of classification accuracy while keeping the worthy characteristics expressed by the DCA.

Keywords: Artificial immune systems, Dendritic cells, Rough sets, QuickReduct.

1 Introduction

Artificial Immune Systems (AIS) are a class of computationally intelligent systems inspired by the principles of the natural immune system. As AIS is being developed significantly, novel algorithms termed "2nd Generation AISs" have been created. One such 2nd Generation AIS is the Dendritic Cell Algorithm (DCA) [1] which is derived from behavioral models of natural dendritic cells (DCs). As a binary classifier, the DCA performance is mainly based on its data pre-processing phase which is divided into two main phases which are feature selection and signal categorization. More precisely and for data pre-processing, DCA uses the Principal Component Analysis (PCA) to automatically select features and to categorize them to their specific signal types; as danger signals (DS), as safe signals (SS) or as pathogen-associated molecular patterns (PAMP) [2]. DCA combines these signals with location markers in the form of antigen to perform antigen classification. For signal selection, PCA transforms a finite number of possibly correlated vectors into a smaller number of uncorrelated vectors, termed "principal components" which reveal the internal structure of the given data with the focus on data variance [2]. Nevertheless, using PCA as a dimensionality reduction technique presents some shortcomings as it is not necessarily true

M. Tomassini et al. (Eds.): ICANNGA 2013, LNCS 7824, pp. 140–150, 2013.

that the first selected principal components that capture most of the variance are the adequate features to retain [3]. Consequently, choosing these components for the DCA may influence its classification task by producing unreliable results. For feature categorization, DCA uses the PCA ranking of attributes which is based on variability and maps this obtained order to the ranking of the signal categories of the DCA which is in the order: Safe, PAMP and Danger; implying the significance of each signal category to the signal transformation of the DCA [2]. However, this categorization reasoning which is based on attributes' ranking and where the variability of attributes is equivalent to importance could not be considered as a coherent and consistent categorization procedure. Hence, in [4], a first work, named RC-DCA, was developed to solve these issues. RC-DCA is based on Rough Set Theory (RST) to perform data pre-processing. It is based on the reduct and the core RST fundamental concepts to select the most important features and to categorize them to their specific signal types. In [4], it was shown that applying RST, instead of PCA, is more appropriate for the DCA data pre-processing phase leading to a better binary classifier. However, to select the right set of features, RC-DCA generates all possible subsets and retrieves those with a maximum rough set dependency degree. Obviously, this is an expensive solution to the problem and is only practical for very simple data sets. Most of the time only one reduct is required as, typically, only one subset of features is used to reduce a data set, so all the calculations involved in discovering the rest are pointless. In addition, this time consuming task led to neglect the main DCA characteristic which is its lightweight in terms of running time [5]. Thus, in this paper, we propose a novel bio-inspired hybrid model of the DCA based on a new signal selection and categorization technique. Our new model, named QR-DCA, is based on the behavior of natural dendritic cells and grounded on the framework of rough set theory for data pre-processing where it adopts the QuickReduct algorithm. The main contributions of this paper are to introduce the concept of RST, specifically the QuickReduct algorithm, in the DCA data pre-processing phase and to show how our proposed new model, QR-DCA, can find a trade-off between generating good classification results and preserving the lightweight of the algorithm. We, also, aim to compare the results obtained from QR-DCA to other rough DCA models proposed in literature.

2 The Dendritic Cell Algorithm

1)Introducing Dendritic Cells: DCs are antigen presenting cells that possess the ability to capture and process antigens [6]. DCs differentiate into three main states upon the receipt of signals: PAMPs, danger, safe. The first DC maturation state is the immature state (iDCs). The differentiation of iDCs depends on the combination of the signals received leading either to a full maturation state or to a partial maturation state. Under the reception of safe signals, iDCs migrate to the semi-mature state (smDCs) causing antigens tolerance. iDCs migrate to the mature state (mDCs) if they are more exposed to danger signals and PAMPs than safe signals. mDCs present the collected antigens in a dangerous context.

2)Abstract View of the Dendritic Cell Algorithm: The initial step of the DCA is data pre-processing where feature selection and signal categorization are achieved. More precisely, DCA selects the most important features, from the initial input database, and assigns each selected attribute to its specific signal category (SS, DS or PAMP). To do so, DCA applies the PCA [7].

For signal selection, PCA selects the first "principal components" which reveal the internal structure of the given data with the focus on data variance. PCA reduces data dimension, by accumulating the vectors that can be linearly represented by each other [2]. Once features are selected, PCA is applied to assign each attribute to its specific signal type. In fact, PCA performs a ranking procedure by using a sum of the absolute values of the weights used for signal transformation by the DCA. Once ranking is performed, the attributes are mapped into the DCA input signal categories, by correlating the PCA ranking with the ranking of signal categories - which implies the significance of each signal type to the signal transformation of the DCA - which is in the order: Safe, PAMP, and Danger [2]. DCA adheres these signals and antigen to fix the context of each object (DC) which is the step of Signal Processing. The algorithm processes its input signals in order to get three output signals: costimulation signal (Csm), semi-mature signal ($Semi$) and mature signal (Mat). A migration threshold is incorporated into the DCA in order to determine the lifespan of a DC. As soon as the Csm exceeds the migration threshold; the DC ceases to sample signals and antigens. The migration state of a DC to the semi-mature state or to the mature state is determined by the comparison between cumulative $Semi$ and cumulative Mat. If the cumulative $Semi$ is greater than the cumulative Mat, then the DC goes to the semi-mature context, which implies that the antigen data was collected under normal conditions. Otherwise, the DC goes to the mature context, signifying a potentially anomalous data item. This step is known to be the Context Assessment phase. The nature of the response is determined by measuring the number of DCs that are fully mature and is represented by the Mature Context Antigen Value (MCAV). $MCAV$ is applied in the DCA final step which is the Classification step and used to assess the degree of anomaly of a given antigen. The closer the $MCAV$ is to 1, the greater the probability that the antigen is anomalous. Those antigens whose $MCAV$ are greater than the anomalous threshold are classified as anomalous while the others are classified as normal. More DCA details and its pseudocode can be found in [1].

3 Rough Set Theory

In RST [8], an *information table* is defined as a tuple $I = (U, A)$ where U is non-empty set of primitive objects and A is non-empty set of attributes. A may be partitioned into C and D, called *condition* and *decision* attributes, respectively. With any $P \subset A$ there is an associated equivalence relation $IND(P)$ defined as: $IND(P) = \{(x, y) \in U^2 : \forall a \in P, a(x) = a(y)\}$, where $a(x)$ denotes the value of feature a of object x. The family of all equivalence classes of $IND(P)$

is denoted by $U/IND(P)$. The equivalence classes of the P-indiscernibility relation are denoted $[x]_P$. Let $X \subseteq U$, the P-lower approximation of a set can now be defined as: $\underline{P}(X) = \{x|[x]_P \subseteq X\}$. The P-lower approximation is the set of objects U that are surely in X. Let P and Q be equivalence relations over U, then the positive region can be defined as: $POS_P(Q) = \bigcup_{X \in U/Q} \underline{P}(X)$. The positive region contains all objects of U that can be classified to classes of U/Q using the knowledge in attributes P. An important issue in data analysis is discovering dependencies between attributes. Intuitively, a set of attributes Q depends totally on a set of attributes P, denoted $P \Rightarrow Q$, if all attribute values from Q can be uniquely determined by values of attributes from P. In particular, if there exists a functional dependency between values of Q and P, then Q depends totally on P. Dependency can be defined in the following way: For P, $Q \subset A$, Q depends on P in a degree k $(0 \leq k \leq 1)$, denoted $P \Rightarrow_k Q$, if $k = \gamma_P(Q) = |POS_P(Q)|/|U|$; If k = 1 Q depends totally on P, if $k < 1$ Q depends partially (in a degree k) on P, and if k = 0 Q does not depend on P. RST performs the reduction of attributes by comparing equivalence relations generated by sets of attributes. Attributes are removed so that the reduced set provides the same quality of classification as the original. A *reduct* is defined as a subset R of the conditional attribute set C such that $\gamma_R(D) = \gamma_C(D)$. Note that a given data set may have many attribute reduct sets. The intersection of all the sets in R is called the *core*, reflecting those attributes that cannot be eliminated without introducing more contradictions to the data set. In RST, a *reduct* with minimum cardinality is searched for; in other words an attempt is made to locate a single element of the minimal reduct set. A basic way of achieving this is to calculate the dependencies of all possible subsets of C. Any subset X with $\gamma_X(D) = 1$ is a reduct; the smallest subset with this property is a minimal reduct. However, for large data sets this method is impractical and an alternative strategy is required. One possible way to avoid these extra calculations, is to apply the QuickReduct Algorithm [9] that attempts to calculate a minimal reduct without exhaustively generating all possible subsets. It starts off with an empty set and adds in turn those attributes that result in the greatest increase in $\gamma_P(Q)$, until this produces its maximum possible value for the data set (usually 1). An illustrative example of the QuickReduct Algorithm application as well as its pseudocode can be found in [9].

4 QR-DCA: The Solution Approach

In this Section, we present our QR-DCA model based on RST, and specifically on the QuickReduct algorithm, for the automatic DCA data pre-processing phase including feature selection and signal categorization.

4.1 The QR-DCA Signal Selection Process

For antigen classification, our learning problem has to select high discriminating features from the original input database which corresponds to the antigen

information data set. We may formalize this problem as an information table, where universe $U = \{x_1, x_2, \ldots, x_N\}$ is a set of antigen identifiers, the conditional attribute set $C = \{c_1, c_2, \ldots, c_A\}$ contains each feature of the information table to select and the decision attribute D of our learning problem corresponds to the class label of each sample.

For feature selection, QR-DCA computes, first of all, the dependency of the entire database $\gamma_C(D)$. To do so, QR-DCA has to calculate the positive region for the whole attribute set C: $POS_C(D)$ (as presented in Section 3). Once the consistency of the database is measured, QR-DCA starts off with an empty set and moves to calculate the dependency of each attribute c a part: $\gamma_c(D)$. The attribute c having the greatest value of dependency is added to the empty set. Once the first attribute c is selected, QR-DCA adds, in turn, one attribute to the selected first attribute and computes the dependency of each obtained attributes' couple $\gamma_{\{c,c_i\}}(D)$. The algorithm chooses the couple having the greatest dependency degree. The process of adding each time one attribute to the subset of the selected features continues until the dependency of the obtained subset equals the consistency of the entire database already calculated: $\gamma_C(D)$.

The generated subset of the selected features, constituting the reduct, shows the way of reducing the dimensionality of the original data set by eliminating those conditional attributes that do not appear in the set. Those discarded attributes are removed in each QR-DCA computation level since they do not add anything new to the target concept nor help the QR-DCA to perform well its classification task. However, the reduct features represent the most informative features that preserve nearly the same classification power of the original data set. Using the reduct concept, our method can guarantee that attributes of extracted feature patterns will be the most relevant for its classification task.

4.2 The QR-DCA Signal Categorization Process

The second step of our QR-DCA model data pre-processing phase is feature categorization. More precisely, our method has to assign for each selected attribute, produced by the previous step and which is included in the generated reduct, its definite and specific signal category. The general guidelines for signal categorization are as follows:

- **Safe signals :** Their presence certainly indicates that no anomalies are present.
- **PAMPs :** Their presence usually means that there is an anomalous situation.
- **Danger signals :** Their presence may or may not show an anomalous situation, however the probability of an anomaly is higher than under normal circumstances.

From the previous definitions, both PAMP and SS are positive indicators of an anomalous and normal signal while the DS is measuring situations where the risk of anomalousness is high, but there is no signature of a specific cause. In other words, PAMP and SS have a certain final context (either an anomalous or a normal behavior) while the DS cannot specify exactly the final context to assign to the collected antigen. This is because the information returned by the

DS is not certain as the collected antigen may or may not indicate an anomalous situation. This problem can be formulated as follows:

Both PAMP and SS are more informative than DS which means that both of these signals can be seen as indispensable attributes. To represent this level of importance, our method uses the first obtained couple of features through the reduct generation. On the other hand, DS is less informative than PAMP and SS. Therefore, our method applies the rest of the reduct attributes, discarding the two first selected attributes that are chosen to represent the SS and PAMP signals, to represent the DS. More precisely, our method processes as follows:

As QR-DCA has already calculated the dependency of each attribute c a part, $\gamma_c(D)$, QR-DCA selects the attribute c having the greatest dependency degree to form the SS as it is considered the most informative feature added to the reduct. With no additional computations and since QR-DCA has already computed the dependency of each attributes' couple $\gamma_{\{c,c_i\}}(D)$ when adding, in turn, one attribute c_i to the selected first attribute c that represents the SS, QR-DCA chooses the couple having the greatest dependency degree. More precisely, QR-DCA selects that second attribute c_i to form the PAMP signal. And finally, the rest of the reduct attributes are combined and affected to represent the DS as it is less than certain to be anomalous.

Once the selected features are assigned to their suitable signal types, our method calculates the values of each signal category using the same process as the standard DCA [1]. The output is thus a new information table which reflects the signal database. In fact, the universe U of the induced signal data set is $U = \{x_1^{'}, x_2^{'}, \ldots, x_N^{'}\}$ a set of antigen identifiers and the conditional attribute set $C = \{SS, PAMP, DS\}$ contains the three signal types: SS, PAMPs and DS. Once data pre-processing is achieved, QR-DCA processes its next steps which are the Signal Processing, the Context Assessment and the Classification step as the DCA does and as described in Section 2.

5 Experimental Setup

To test the validity of our QR-DCA hybrid model, our experiments are performed on two-class databases from [10] described in Table 1. We try to show that our QR-DCA can find a trade-off between generating good classification results and having a lightweight in terms of running time. Thus, we will compare the QR-DCA performance to our first work, RC-DCA, published in [4] which is also based on RST for the DCA data pre-processing phase. The common idea between QR-DCA and RC-DCA is to assign for each selected feature a specific signal category: either as SS, DS or PAMP. Nevertheless, RC-DCA generates all the possible reducts, which is a time consuming task, to select the reduct having the minimal set of features among the other generated reducts. In addition, RC-DCA differs from our new rough DCA model in the categorization step which focuses on proposing different solutions in case where this method produces one reduct or a family of reducts. More details about RC-DCA can be found in [4]. The QR-DCA performance is also compared to another rough DCA work,

named RST-DCA [11]. The main difference between RST-DCA and both QR-DCA and RC-DCA is that RST-DCA assigns only one attribute to form both SS and PAMP as they are seen as the most important signals. As for the DS categorization, RST-DCA combines the rest of the reduct features and assigns the resulting value to the DS. Like RC-DCA, RST-DCA generates all the possible reducts and proposes solutions to handle both cases (generating one reduct or a family of reducts) for data pre-processing. More details about RST-DCA can be found in [11].

For data pre-processing and for all the mentioned rough DCA works including QR-DCA, each data item is mapped as an antigen, with the value of the antigen equal to the data ID of the item. In all experiments, a population of 100 cells is used and 10 DCs sample the antigen vector each cycle. To perform anomaly detection, a threshold which is automatically generated from the data is applied to the MCAVs. The MCAV threshold is derived from the proportion of anomalous data instances of the whole data set. Items below the threshold are classified as class 1 and above as class 2. The resulting classified antigens are compared to the labels given in the original data sets. For each experiment, the results presented are based on mean MCAV values generated across 10 runs.

We evaluate the performance of the rough DCA methods in terms of number of extracted features, running time, and accuracy which is defined as: $Accuracy = (TP + TN)/(TP + TN + FN + FP)$; where TP, FP, TN, and FN refer respectively to: true positive, false positive, true negative and false negative. We will also compare the classification performance of our QR-DCA method to well known classifiers which are the Support Vector Machine (SVM), Artificial Neural Network (ANN) and the Decision Tree (DT).

Table 1. Description of Databases

Database	Ref	♯ Instances	♯ Attributes
Spambase	SP	4601	58
SPECTF Heart	SPECTF	267	45
Cylinder Bands	CylB	540	40
Chess	Ch	3196	37
Ionosphere	IONO	351	35
Congressional Voting Records	CVT	435	17
Tic-Tac-Toe Endgame	TicTac	958	10

6 Results and Analysis

Let us remind that the first step of the standard DCA classification algorithm is data pre-processing which is based on the use of PCA. In [11] and [4] and by the development of both RST-DCA and RC-DCA, we have proved that applying PCA for both feature selection and signal categorization is not convenient for the DCA as both phases are not consistent. We have also shown that applying rough set theory with DCA is a good alternative leading to a better classification

performance. However, these two rough DCA models suffer from some limitations; principally the time taken by the algorithms to process which contradicts the main characteristic of the standard DCA: its lightweight in terms of running time. Thus, in this paper, we have developed a new rough DCA hybrid model, QR-DCA, where we show that this proposed solution can find the trade-off between generating good classification results and processing in less time than both RC-DCA and RST-DCA. This is confirmed by the results presented in Table 2. From these results, we will also show that assigning for each selected feature a specific signal category, a process performed by both QR-DCA and RC-DCA, lead to a better performance than assigning the same attribute to both SS and PAMP, a process performed by RST-DCA.

Table 2. Comparison Results of the Rough DCA Approaches

Database	Accuracy (%)			♯ Attributes			Time (s)		
	DCA			DCA			DCA		
	QR	RC	RST	QR	RC	RST	QR	RC	RST
SP	98.87	98.45	94.5	11	8	8	1976.05	3184.83	2923.41
SPECTF	93.26	88.38	82.4	12	4	4	5.49	1423.02	1361.77
CylB	97.46	97.46	96.67	7	7	7	12.68	1441.93	1398.12
Ch	98.84	98.84	98.02	11	11	11	571.05	1779.83	1697.01
IONO	96.58	97.15	96.29	22	19	19	15.88	668.32	591.13
CVT	97.93	98.85	96.55	11	8	8	7.03	17.83	10.54
TicTac	96.65	95.3	93.52	8	6	6	49.89	62.66	58.80

From Table 2, we can notice that RST-DCA and RC-DCA models have the same number of selected features. This is explained by the fact that both models are based on the same feature selection phase. They generate all the possible reducts and choose the one having the smaller number of features. However, our QR-DCA new version has either the same number of features as both RST-DCA and RC-DCA or more features. This is explained by the fact that QR-DCA, by applying the QuickReduct algorithm, follows the features' path that generates the highest dependency degree. Consequently, the taken path may either lead to a final reduct including the smallest number of features or to a path including more selected features; but still this obtained reduct includes the most important features to retain. For instance, applying QR-DCA to the IONO database, the number of selected attributes is 22. However, when applying RST-DCA or RC-DCA, the number of selected features is 19. Applying the three rough DCA models to the Ch database, the number of the selected features is the same: 11. We have also to mention that obtaining the same number of features does not mean that this reduct includes the same attributes; the attributes may differ.

Based on these selected attributes, the accuracies of the algorithms are calculated. From Table 2, we can notice that the difference between the classification accuracies generated by both QR-DCA and RC-DCA is not significant. Thus,

we can say that QR-DCA has nearly the same classification performance as RC-DCA. For instance, when applying the algorithms to the SP data set, the classification accuracy of QR-DCA is set to 98.87% and when applying RC-DCA to the same database, the accuracy is set to 98.45%. In some databases, the QR-DCA classification accuracy is a bit less than the one generated by RC-DCA and sometimes a bit higher. We also remark, that in all databases, QR-DCA and RC-DCA outperform the classification accuracy generated by RST-DCA. For instance, the classification accuracy of RST-DCA when applied to the SP database is set to 94.5% which is less than 98.87% and 98.45% generated respectively by QR-DCA and RC-DCA. This is explained by the fact that RST-DCA differs from QR-DCA and RC-DCA in the signal categorization phase. Both QR-DCA and RC-DCA assign different features to different signal categories (DS, SS, PAMP). However, RST-DCA uses the same attribute to assign it for both SS and PAMP. As for the DS categorization, RST-DCA combines the rest of the reduct features to assign it for the DS. From these results, we can conclude that it is crucial to assign for each signal category a specific and different feature.

Another advantage of our QR-DCA is that it takes less time to process than RC-DCA and RST-DCA. This is confirmed by the results appearing in Table 2. For example, when applying the algorithms to the CylB database, the amount of time taken by QR-DCA to process is 12.68(s) which is less than the times taken by RC-DCA and RST-DCA which are 1441.93(s) and 1398.12(s), respectively. The QR-DCA lightweight in terms of running time is explained by the advantage of using the QuickReduct algorithm as it attempts to calculate a reduct without exhaustively generating all possible subsets. In contrast, both RST-DCA and RC-DCA generate all possible subsets and retrieve those with a maximum rough set dependency degree. Obviously, this is an expensive solution to the problem. Most of the time only one reduct is required as, typically, only one subset of features is used to reduce a data set, so all the calculations involved in discovering the rest are pointless.

We have also compared the performance of our QR-DCA to other classifiers including SVM, ANN and DT. The comparison made is in terms of the average of accuracies on the databases presented in Table 1. The parameters of SVM, ANN and DT are set to the most adequate parameters to these algorithms using the Weka software. Figure 1 shows that our QR-DCA has nearly the same classification performance as RC-DCA. It also shows that QR-DCA outperforms RST-DCA, SVM, ANN and DT.

To summarize, QR-DCA is a good classification technique proposed as an alternative to our RC-DCA first work. QR-DCA has the advantage of generating good classification results while preserving a lightweight in terms of running time. We have also shown that it is crucial that DCA assigns different attributes for each signal type. QR-DCA performs much better than the mentioned classifiers in terms of classification accuracy.

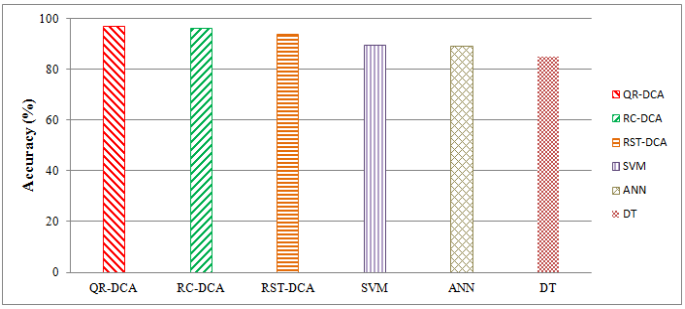

Fig. 1. Comparison of Classifiers' Average Accuracies on the 7 Binary Data sets

7 Conclusion and Further Work

In this paper, we have introduced a new hybrid DCA bio-inspired model based on RST. Our model aims to select the convenient set of features and to perform their signal categorization using the QuickReduct algorithm. Results show that our method is capable of finding a trade-off between generating good classification results and keeping the algorithm lightweight in terms of running time. As future work we aim to apply the fuzzy RST for the DCA data pre-processing phase.

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