Associative Classification using a Bio-Inspired Algorithm

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Abstract

This paper proposes an ambitious bio-inspired algorithm for associative classification (AC) based on Quantum-Inspired Artificial Immune system (QAIS) for building an efficient classifier by searching association rules to find the best subset of rules for all possible association rules. it integrates concepts of quantum computing (QC) and artificial immune system (AIS) as a bio natural inspired algorithm. It employees a mutation operator with a quantum-based rotation gate to control and maintain diversity, and guides the search process. The proposed QAIS is implemented and evaluated using benchmark datasets(Blake & Merz 1998) including Adult, Nursery, Iris and Breast-Cancer datasets. The obtained results are analysed and compared with experimental implementation results of AIS-AC algorithm (Do et al 2009). The experimental results showed that the proposed algorithm is preformed well with large search space and has higher accuracy, and maintained diversity.

Keywords: Associative classification, Q-gate operator, QC, AIS, Bio-inspired optimization algorithms.

1 Introduction

Associative classification (AC) has shown a great dominance over many classification techniques. Associative classification uses association rule mining for rules discovery process to identify data class labels. Associative classification also integrates the rule discovery and classification process to build the classifier that supports in decision making process. The main advantages of the associative classification approaches is to discover high quality association rules in a very large space of candidate rules and integrate these rules with the classification process efficiently.

Bio-inspired optimization algorithms (BIOAs) represent a set of computational intelligence paradigms in machine learning, computer science and some engineering disciplines, which model various natural phenomena like the concept of evolution and the behavioral pattern displayed by various species. BIOAs serve as an attractive alternative for solving complex problems which can't be solved by the usual techniques . These BIOAs include Genetic Algorithms (GAs), Particle Swarm Optimization (PSO), and Differential Evolution (DE), Artificial neural networks (ANN), Artificial Immune system (AIS), Fuzzy logic, Rough computing and quantum computing have been applied in various applications domain including decision support systems, data mining and knowledge discovery.

Artificial Immune Systems (AIS) have emerged during the last decade, Artificial immune systems can be defined as a computational system that is inspired by theoretical immunology, observed immune principles and mechanisms. The AIS uses the population-based search model of evolutionary computation algorithms that it is regarded as a suitable way for dealing with complex search space.

Quantum-Inspired Artificial Immune System (QAIS) is firstly introduced based on clonal selection algorithm and some concepts of quantum computing and proved that it is more effective than the immune operation. In the last decade, we could notice that there is a great interest in studying biologically inspired systems as artificial neural networks, evolutionary computation, DNA computation, and recently artificial immune systems (AIS). An immune system is biological system within an organism that protects it against disease by detecting and killing pathogens. It consists of a complex of cells, molecules and organs and It has the ability to distinguish antigen and antibody. It has three immunological principles the immune network theory, negative selection mechanism, and clonal selection principle. In this paper we focus in clonal selection principle and mutation operator using quantum theory.

Nowadays, Immune system applications spread in many fields as data mining, production,... etc since it has some features like learning, memory acquisition,pattern recognition,diversity generation,noise tolerance, detection and optimization. Associative classification uses association rules to predict data class label. The main issue with the associative classification approach is the high quality association rules discovery in a very large space of candidate rules and incorporating these rules in the classification process by an efficient way so applying QAIS for associative classification will useful because we will get the benefit of immune system features and quantum computing contribution.

So, the main aim of this paper is to develop a bio-inspired algorithm for associative classification for building an efficient classifier by searching association rules to find the best subset of rules for all possible association rules. The rest of this paper is organized as follows. Section 2 presents the related work of the QAIS and AC with evolutionary algorithms besides problems and issues. The proposed algorithm is pre-

sented in section 3. The experiments setup and results are presented in section 4, where the last section is devoted to conclusions and further researches.

2 Problem Background and Related Works

Quantum-Inspired Immune system is introduced by Yangyang and Licheng ,they proposed a new immune clonal algorithm, called a quantum inspired immune clonal algorithm (QICA), based on the concept and principles of quantum computing, such as a quantum bit and superposition of states. QICA uses a quantum bit, the smallest unit of information (Li& Jiao 2005). A multiuser detection application is proposed using Quantum Immune system by Yangyang et al (Li et al 2006). Research in Quantum Immune and its applications has been increased in the last years, Qun et al proposed a quantum-inspired immune algorithm (QIA) for Hybrid flow shop problems (HFSP) to minimize Makespan which have been proved to be NP-hard in when the objective is to minimize the Makespan (NiU et al 2009). Soliman and Adly proposed an ambitious algorithm based on Quantum-Inspired Immune system (QAIS) for building an efficient classifier by searching association rules to find the best subset of rules for all possible association rules (Soliman & Adly 2012).

Researchers also apply the Quantum Immune algorithm in the Multi-objective optimization area, Gao et al,proposed a novel quantum-inspired artificial immune system (MOQAIS) is presented for solving the multi-objective 0-1 knapsack problem (MKP), their algorithm is composed of a quantum-inspired artificial immune algorithm (QAIS) and an artificial immune system based on binary encoding (BAIS) (Gao et al 2010).

Another quantum immune algorithm is introduced for finding Pareto-optimal solutions to multiobjective optimization problems based on quantum computing and immune system. Experimental results showed that the MOQAIS algorithm is able to find a much better spread of solutions and has better convergence near the true Pareto-optimal front compared to the vector immune algorithm (VIS) and the elitist non-dominated sorting genetic system (NSGA-II) (Gao & Wang 2011). Qiaoyu et al introduced a new kind of quantum immune clonal algorithm for continuous space optimization. They updated quantum bits using quantum rotation gate to accelerate convergence and mutation is performed by quantum non-gate to avoid hasty convergence (Qiaoyu et al 2010). Lian et al proposed an immune-inspired quantum genetic optimization algorithm (IQGOA) based on clonal selection algorithm. Their Experimental results have shown that it is superior to clonal selection algorithm and Genetic Algorithm (GA) on performance (Lian 2011). Wang et al present a load balancing strategy based on Quantum Immune Evolutionary algorithm to optimize loading distribution by quantum coding and quantum evolution operator. It ensures the diversity of population by using immune operator vaccinations and immune selection when quantum is into the local optimum (Su & Wang 2011). The first Associative Classification approach was introduced with the classification based on associations (CBAs) algorithm. He integrated the two mining techniques classification and association rule mining. The integration is done by focusing on a specific subset of association rules whose right-hand-side are restricted to the classification class attribute and they refer to this subset of rules as the class association rules (CARs)(Ma 1998). Based on U-Apriori algorithm and CBA algorithm, propose an associative classifier for uncertain data, uCBA (uncertain Classification Based on Associative), which can classify both certain and uncertain data. Their algorithm redefines the support, confidence, rule pruning process and classification strategy of CBA(Qin et al 2010). Mamta et al proposed a new model (associative classifier) based on weightage and utility for useful mining of substantial class association rules. This model uses the CBA-RG algorithm to produce a set of class association rules from a database and as well as exploits the downward closure property of the a priori algorithm(Punjabi et al 2011). A new associative classification method called CMAR, classification based on Multiple Association Rules. The method extends an efficient frequent pattern mining method, FP-growth, constructs a class distribution-associated FP-tree, and mines large database efficiently(Li et al 2001). Classification based on Predictive Association Rules, (CPAR), is developed by Yin and Han at 2003. CPAR depends on a greedy algorithm to generate rules directly from training data Instead of generating a large number of candidate selection rules(Han 2003). Some predictive rule mining techniques such as CPAR, PRM and FOIL with statistical and Laplace as rule evaluation measures for predicting Tuberculosis. CPAR and PRM were better than FOIL and also statistical measure results in less generation time compared to Laplace measure (Asha et al 2011). An efficient algorithm to solve a specific problem called (the SSR-CARM problem) in binomial time $O(k^2n^2)$ which avoids selecting all k significant rules in a one-by-one manner(Wang et al 2005).

Decision trees are proposed to summarize associative classification rules. The proposed classification model benefit from the advantages of associative classification and decision trees (Chen & Hung 2009). They proposed a novel associative classification model, which first mines multi-class classification information from need-rating data, then constructs a rating classifier, and finally predicts customers' ratings for products (Jiang et al 2010). A new associative classification algorithm based on weighted voting (ACWV). It takes into account both the quality and number of rules instead of relying on only several high-quality rules (Zhu et al 2010). An associative classifier algorithm using demand-driven, so that the corresponding algorithm achieves high classification performance even in the case of limited labelling efforts (Veloso & Meira 2011). With an effective approach to building compact and accurate associative classification – Gain-based Association Rule Classification (Chen, Liu, Yu, Wei, & Zhang, 2006) in forms of association rules, they explores a way of fuzzy extension to GARC in dealing with the problem caused by crisp partitions for continuous attribute domains in data (Chen et al 2011). A fuzzy associative classification model based on variant apriori and multi-objective evolutionary algorithm NSGA-II (MOEA-FACM) is proposed. MOEA-FACM adopts fuzzy confirmation measure based on probabilistic dependence to assess fuzzy associative rule in order to generate good quality rule set. Then a small number of fuzzy associative rules are selected from the prescreened candidate rule set using NSGA-II (Weigang & Xiuli 2011).

Also, Mangalampalli proposed a fuzzy associative classification algorithm for object class detection in images using interest points which relies only on the positive class for training (Mangalampalli et al 2010). Dixit studied and optimized an artificial immune system based classification system. They evaluated the

performance of the AIS based classification system by computing accuracy at different clonal factors and varying number of generations. They used three standard datasets to compute the accuracy .They found that the system gives highest accuracy with clonal factor 0.4 (DIXIT & CHANDEL 2011). The clonal selection algorithm for Associative Classification (AC) is investigated and proposed a new approach known as AIS-AC for mining association rules effectively for classification with treating the rule mining process as an optimization problem of finding an optimal set of association rules according to some predefined constraints. AIS-AC approach is efficient in dealing with the complexity problem on the large search space of rules and It avoided searching greedily for all possible association rules, so it could find an effective set of associative rules for classification (Do et al 2005, 2009).

Association Classification Rules Mining problem is treated as a multi-objective problem rather than a single objective one. They developed a binary multi-objective particle swarm optimization model to optimize the measures like coverage and confidence rules for rule discovery then a small number of rules are targeted from the extracted rules to design an accurate and compact classifier which can maximize the accuracy of the rule sets and minimize their complexity simultaneously (Das et al 2011). Shahzad presented a hybrid classification algorithm called ACO-AC, combining the idea of association rules mining and supervised classification using Ant Colony Optimization (ACO). ACO is used to mine only effective subset of class association rules instead of searching for all possible rules in large search space. The mining process stops when the discovered rules achieves a minimum coverage threshold (Shahzad 2010).

3 Proposed algorithm

In our proposed algorithm we deal with the associative algorithm process as an optimization problem to find the optimal (best) classification association rules (CARs) that will build the classifier. Rules discovery process differs from the rule discovery in the basic association rule mining algorithm. We search classification association rules using quantum-inspired Immune system. We considered each CAR as an immune cell and each generation is a set of class association rules.

Rule Selection process implicitly consists of two parts rule discovery (generation) and rule evaluation (selection). Rule discovery come from the testing dataset starting from initial population then memory population increases through generations. We search for rules with the highest confidence values and confidence measure as the affinity in immune system so we select rules with high affinity and the selected rules should satisfy the support constraint to filter specific rules from the population before the selection process. We terminate this process when generation count equals the number of generations and classification process applied after getting the CARs from memory pool. We build the classifier and apply it on benchmark datasets then evaluate its accuracy.

3.1 Algorithm Steps

The main steps of the proposed algorithm are described in Algorihtm1. Where the detailed description of these steps are introduced in the following subsections.

3.2 Selection process

In this process , rules with the support less than minSupport threshold are eliminated; where *selectionNumber of* rules with the highest confidence are selected. The selection criteria is based on the best fitness.

Algorithm 1 QAIS for Associative Classification

1: Initialize a random population of rulesP_0 of size n, set the *memoryset* $M = \Phi$ and $gCount = 0$
2: **while** $(gCount < NoOfGenerations)$ **do**
3: **for** each rule R in p **do**
4: **if** $Support(R) < minSupport$ **then**
5: Remove Rule R from P
6: **end if**
7: **end for**
8: Sort rules in P according to affinity value in descending order.
9: Select the first *selectionNo* affinity rules and insert them into P instead other rules.
10: Clone P by cloning best *nClones* rules.
11: Mutate P by algorithm 2.
12: Prune rules inside P.
13: **for** each rule R in p **do**
14: **if** conf(R) > minConfidence **then**
15: Insert R into M
16: **end if**
17: **end for**
18: Reselect randomly new population (Pnew) from M and make P=Pnew
19: Increment $gCount$ by one.
20: **end while**

3.3 Cloning Process

The cloning process is performed by using the clonal rate of a rule is directly related to the affinity value (confidence) of the. We denote clonal rate of a rule as CR.

Clonal rate of a rule is directly proportional to the affinity of the rule so the clones directly depend on affinity value so we pick proportion of the population *nClones* to be clonned.*nClones*is calculated as folllows:

Given *selectionNo* is the best affinity selected rules and the dataset size N then calculate clonal factor(cf) the proportion of *selectionNo* in the dataset.

$$cf = \frac{selectionNo}{N} \tag{1}$$

and nClones get by the following equation:

$$nClones = cf * selectionNo. \tag{2}$$

Finally we make clones of the best nClones rules.

3.4 Mutation process

In this process, each cell is mutated using quantum-based rotation Q-gate operator, a high probability is given for each low affinity cell to be mutated more than high affinity cell and then a new offspring is produced.

3.4.1 Mutation Operator

As mentioned above, the used mutation operator is a quantum-based rotation Q-gate. By selecting a subset $C_s \subseteq C$ where C is the population rules and

assume there exists a parent cell

$$\begin{bmatrix} \alpha_1 & , & \alpha_2 & , & \alpha_3 & , & \dots & , & \alpha_n \\ \beta_1 & , & \beta_2 & , & \beta_3 & , & \dots & , & \beta_n \end{bmatrix} \quad (3)$$

where:

$$|\alpha_{i^2}|^2 + |\beta_{i^2}|^2 = 1,\ i = 1, 2, ..., n. \quad (4)$$

The item j is selected randomly from cell i such that

$$\begin{bmatrix} \alpha_j^{'} \\ \beta_j^{'} \end{bmatrix} = \begin{bmatrix} \cos(\theta) & -\sin(\theta) \\ \cos(\theta) & \sin(\theta) \end{bmatrix} \begin{bmatrix} \alpha_j \\ \beta_j \end{bmatrix} \quad (5)$$

where:

$$\theta_j = \theta_{j-1} + p_j * \delta \quad (6)$$

$$\delta = \begin{cases} U(0, \theta_j) & , p_j = -1 \\ U(\theta_j, \frac{\Pi}{2}) & , p_j = +1 \end{cases} \quad (7)$$

θ_j is the rotated angle

The rotated angle is calculated as follows:

$$\theta_j = \arctan(\frac{\beta_j}{\alpha_j}). \quad (8)$$

then recalculate support and confidence of mutated solutions. The main steps of the quantum-based rotation Q-gate mutation are described in algorithm 2.

3.5 Pruning Process

In this process, covered rules by the memory set rules are pruned to insure that those covered rules will not be exist in the coming generations and reduce complexity by eliminating redundancy.

3.5.1 Pruning Criteria:

Rule R^* : $itemset^* \Rightarrow c$ is covered by rule R : $itemset \Longrightarrow c$ if the following condition is satisfied:

1. $itemset \subset itemset^*$and
2. Confidence value of R is Greater than or equal R^*.

3.6 Reselection process

We reselect from memory set randomly to form the new population .The memory set contains the best uncovered rules with highest affinity value so the next generation will converge to the optimal solutions.

4 Experimental Results and Discussion

Data preprocessing is the initial step for any data mining algorithm. Data preprocessing is performed to convert the data in a specific format which can be easily dealed by the algorithm. The proposed algorithm is implemented and evaluated using benchmark datasets Adult, Nursery, Iris and Breast-Cancer from the UCI Machine Learning Repository (Blake & Merz 1998). Each record regards as an immune cell and each item has a predetermind possible values stored in itemsets population. The obtained results

Algorithm 2 Mutation process

1: **for** each cell $i \in C_s$ **do**
2: Given itemset S_j of possible values:

$$S_j = \{item_1, item_2, ...item_L\} \quad (9)$$

where: $L = size(S_j)$
3: **while** L > 1 **do**
4: $r = U(0, 1)$
5: **if** $r < (\alpha_j^{'})^2$ **then**
6: $S_j \leftarrow S_j\{1 : \lfloor L/2 \rfloor\}$
7: **else**
8: $S_j \leftarrow S_j\{\lfloor L/2 \rfloor + 1 : L\}$
9: **end if**
10: $L = size(S_j)$
11: **end while**
12: $selected_j = S_j\{1\}$
13: **end for**

DataSets	Avg Affinity of all Generations
Iris	0.988
B-Cancer	0.853
Nursery	0.926
Adult	0.768

Table 1: Average Affinity values of analysed Datasets

are compared with experiment implementation result of AIS-AC algorithm (Do et al 2009).

In mutation process, a point (item,value) are picked to be mutated. We get the "item" which is equal to the itemset population name and get a possible value from its itemsets population. The search criterion is the high value of affinity which is regarded as the algorithm compass. AIS is essentially based on the mutation operator so it can achieve a diverse number of local optima. All experiments are performed within 70 % minimum confidence (minConfidence) and minimum support values (minSupport) are %10,%5,%2.5,%0.6.

4.1 Affinity Analysis

The performance of the proposed algorithm is evaluated using affinity analysis for all datasets. The affinity vales are recorded, averaged and visualized of each generation for all datasets including Adult, Iris, Nursery and Breast-Cancer. The obtained averaged affinity values for each dataset overall generations are reported in table 1.

Where the obtained average affinity values of each generation at various support value are visualized as shown in Figures 1 & 2 for all datasets. As shown in figure 1 the average affinity growth rate is increased through generations.

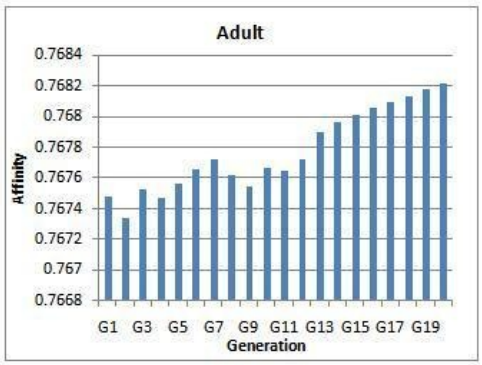
For Adult dataset with minConfidence and minSupport values, figure 1(a) showed that the affinity value is between 0.6 and 0.98 and it increses through generations with its growth rate which different for various support values.

For Iris dataset, as shown in figure 1(b) the affinity value is improved through runs with different support values and the average affinity value is between 0.9 and 0.99. The algorithm in Iris dataset explores the search space faster than any other dataset since the small size of data so it is clear that the lowest value of average affinity is 0.9.

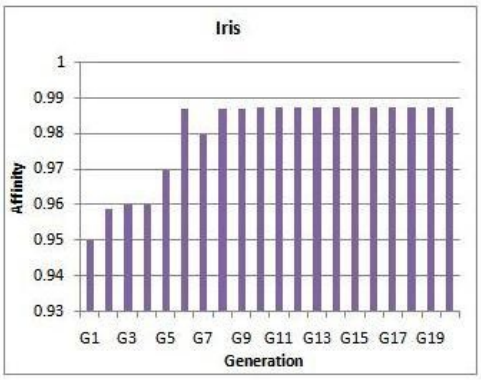
For Nursery dataset the affinity analysis is performed within minConfidence value %50 and minSupport values. We run the model with confidence equals

% 70 but we found that the model overfit the data, so we run with minConf = 0.5. As shown in figure 2(c) the affinity value is improved through runs and achieve good evolution and average affinity is between 0.91 and 0.98 so we have a small interval and small growth rate, but when the support value decreased the growth rate is increased since the lower support value will get small confidence value so the growth will be clear.

Finally, for Breast-Cancer dataset, figure 2(d) showed that the affinity value is improved through runs with different support values and the average affinity value is between 0.82 and 0.91. The affinity analysis showed the ability of the proposed algorithm to obtain higher affinity values and increased through generations for all datasets.



(a)



(b)

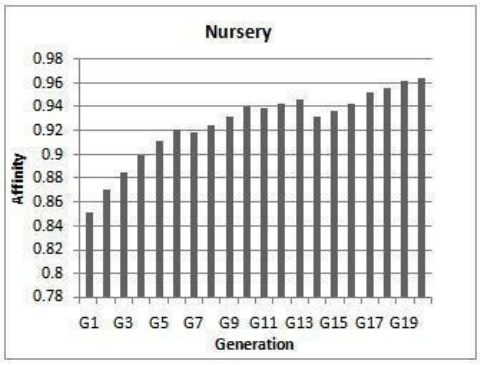
Figure 1: Affinity values for Adult & Iris datasets

4.2 Accuracy Analysis

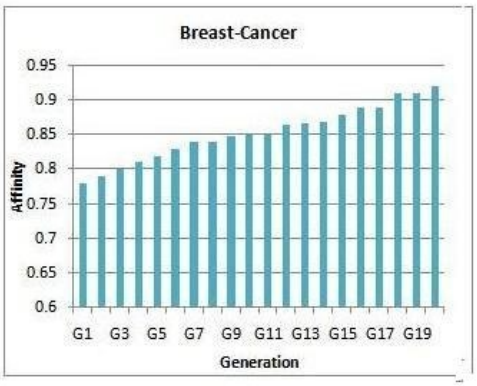
Suppose the accuracy when a rule $R : itemset \Longrightarrow c$ is used to predict the class label of a transaction T is the probability of which c is the class label of the transaction that contains the itemset $iset$ (Do et al 2009). Accuracy can be calculated by:

$$accuracy(R) = p(c \mid itemset)$$

Now, the probability of which c is the class label of T that contains the itemset $iset$ should be calculated. Each transaction T which contains $iset$ can be regarded as a "trial". If a trial belongs to c, then the outcome is "success," otherwise the outcome is "false". The accuracy of proposed algorithm is calculated using the probability of success on a random trial(Do et al 2009).



(c)



(d)

Figure 2: Affinity values for Nursary & Breast Cancer datasets

Support		0.1	0.05	0.025	0.006	0.003
Iris	AIS-AC	0.92	0.92	0.91	0.91	0.92
	QAIS	0.92	0.92	0.92	0.91	0.92
B-Cancer	AIS-AC	0.68	0.67	0.64	0.66	0.68
	QAIS	0.71	0.64	0.67	0.69	0.70
Nursery	AIS-AC	0.89	0.91	0.92	0.97	0.98
	QAIS	0.91	0.8	0.54	0.53	0.53
Adult	AIS-AC	0.74	0.77	0.77	0.7	0.72
	QAIS	0.77	0.79	0.73	0.7	0.71

Table 2: Accuracy values of analysed Datasets

The accuracy of the proposed algorithm is calculated and compared with AIS-AC (Do et al 2009) for all datasets as reported in table 2 with different minimum support values, and visualized as shown in figures 3 and 4. As reported 2 and showed in figures 3 and 4 the accuracy of QAIS is decreasing when the support value is decreasing that mean larger number of rules.

For example, when the support value equals 0.1, for Iris dataset figure 3(a), the accuracy of QAIS is 0.93 and AIS-AC is 0.91 then if we jump to the support value of 0.025, the accuracy will be 0.91 and 0.9 respectively. For Breast-Cancer figure 3(b) dataset the accuracy will be 0.7 and 0.67 respectively with support value equals 0.01 then if we jump to the support value of 0.025 the accuracy value will be 0.67 and 0.63.

For Nursery dataset, as shown in figure 4(c) when the support value equals 0.1, the accuracy of QAIS is 0.96 and AIS-AC is 0.91 then when we jump to the support value of 0.006, the accuracy will be 0.92 and 0.53 respectively. In Adult dataset as shown in figure 4(d) the accuracy values of QAIS are better than AIS-AC when the support values equal 0.01 and

0.1, and the accuracy of both algorithms are equal when support value equal 0.006.

The analysis of obtained accuracy results showed that the accuracy of QAIS is better than AIS-AC over all data sets, and it is decreasing for both algorithms when support value is decreasing but QAIS is decreasing with lower rate.

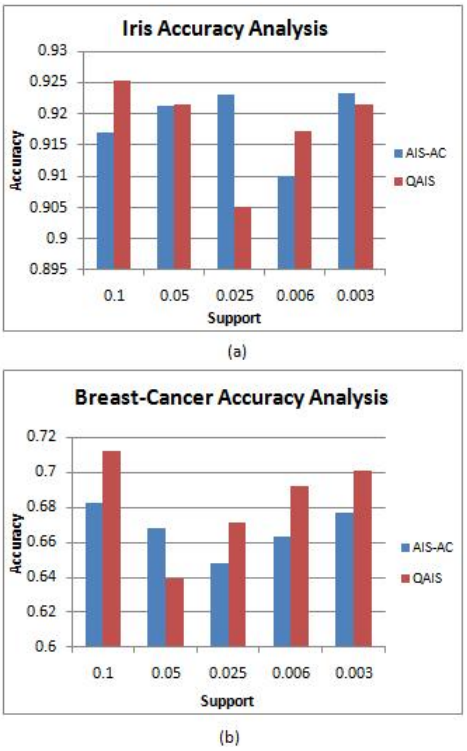


Figure 3: Accuracy values for Iris & Breast Cancer datasets

5 Conclusion

In this paper, a bio-inspired algorithm for associative classification is proposed. It is based on the clonal selection theory and quantum theory. The proposed algorithm generates association rules efficiently for classification process in a large search space. The Q-gate mutation operator is employed to control diversity of immune cells in the search space and guide the search process. The proposed algorithm able to deal with complex search space of association rules. The algorithm is implemented and evaluated for benchmark dataset. The obtained results are compared with results of AIS-AC and showed that the proposed algorithm is performed well and has significant accuracy and average affinity values. It evaluates discovered rules after each generation and eliminates bad rules from memory set.

For further research, quantum-inspired immune system can be enhanced by applying quantum cloning operator in addition to mutation operator, as well as more experiments.

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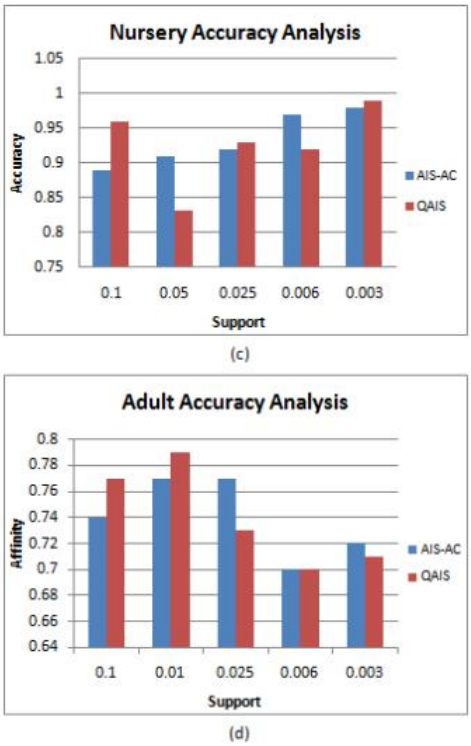

Figure 4: Accuracy values for Nursary & Adult datasets

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