Multi Objective Evolutionary Algorithms for Association Rule Mining: Advances and Challenges

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Abstract

Association rule mining is an important research area in data mining field. The challenge, posed by many methods, is the amount of time consumed for generating frequent items sets. To overcome this, evolutionary algorithms have been used widely. Moreover, apart from support and confidence, there are many other metrics available to measure the quality of association rules. That is the reason why multi-objective approach plays a crucial role. Therefore, two methodologies namely, multi-objective and evolutionary algorithms as a combination proved to be a preferred choice. Though numerous works have been proposed for mining association rules, use of multi-objective evolutionary algorithms are still in its infancy stage. This paper explores the challenges and advances that have been made in this regard in terms of nature of algorithm, encoding mechanism, objective functions and operators.

Keywords: Association Rule Mining, Categorical, Quantitative and Fuzzy Association Rules, MOEAs,

1. Introduction

The problem of association rule mining (ARM) was presented in 1993 and 1994 [2, 1]. The origin of Association Rules linked to well-known *market basket analysis*, where the purchase behavior of customers is analyzed. The goal is to discover regularities among products purchased in a supermarket. The rules were formed from transactional data (e.g., point-of-sale data), and the information codified by the rules (e.g., if buy(pen) and buy(paper) then buy(book) (in short, pen $\wedge$ paper $\Rightarrow$ book)), can later be utilized in order to take decisions involving promotions, product placement, etc. The idea is to discover *if-then* rules to infer interesting relations between variables in large databases. Nowadays, their use has found the way into many different fields, including electronic commerce, web usage mining, bioinformatics, intrusion detection, health care environment etc.

Many classical algorithms, so far, have been developed such as APRIORI, ECLAT or FP-GROWTH.[6] which are computationally expensive. These algorithms work in two phases. First, frequent item-sets are detected by using a measure called *support count* and a user-defined parameter called *minimum support*. Second phase generates the rules using another user-defined parameter called *minimum confidence*. Evolutionary algorithms proved beneficial as they directly generate association rules skipping the frequent item set generation. Traditionally, support and confidence are maximized to have quality rules. But there are many other metrics available to measure the goodness of association rules [7]. Therefore, the problem of ARM can be posed as a multi objective optimization problem where the goal is to find association rules while optimizing several such goodness criteria simultaneously [5].

The rest of the paper is organized as follows: Section 2 briefs about the background and preliminaries. Section 3 surveys the research progresses that have been made for ARM involving evolutionary algorithms. Section 4 list out the challenges and difficulties and Section 5 concludes the paper.

2. Background and Preliminaries

2.1 Types of Association Rules: Broadly, there are two types of association rules.

- Categorical Association Rule
- Quantitative Association Rule.

Fuzzy association rule is a variation of Quantitative Association Rule.

2. 2 Multi objective Evolutionary Algorithms

Last two decades witnessed an increased interest in the use of GAs for multi objective optimization. Some of the most traditional multi-objective evolutionary methods are VEGA (Vector Evaluated Genetic Algorithm; Shaffer, 1985), MOGA (Multiple Objective Genetic Algorithm; Fonseca & Fleming, 1993), NPGA (Niched Pareto Genetic Algorithm; Horn & Nafpliotis, 1993), and NSGA (Non-dominated Sorting Genetic Algorithms; Srinivas & Deb, 1994). The newly developed evolutionary methods, that incorporate elitist strategy, are SPEA (Strength Pareto Evolutionary Algorithm; Zitzler & Thiele, 1999), PAES (Pareto Archieved Evolution Strategy; Knowles & Cornes, 1999), PESA (Pareto Enveloped-based Selection Algorithm; Knowles et al., 2000), SPEA2 (Strength Pareto Evolutionary Algorithm; Zitzler et al., 2001) and NSGAII (Non-dominated Sorting Genetic Algorithm II; Deb et al., 2002). The researches for ARM use some of the standard algorithms, some variants and some non-standard (i.e. not same as above mentioned algorithms) MOEAs as well.

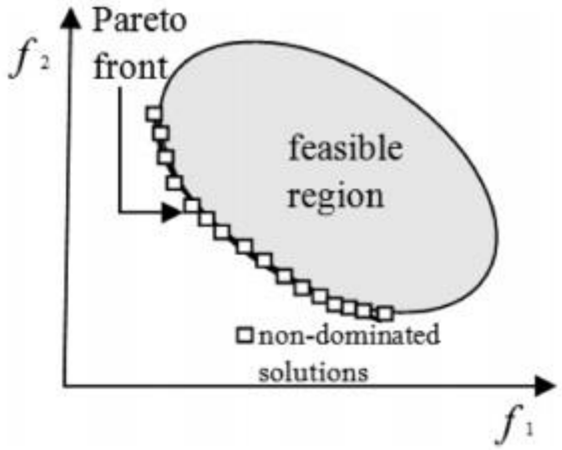

Fig 1. Pareto Front

2.3 Terminologies for Evolutionary Algorithms

The Evolutionary algorithms are characterized by Encoding mechanism, objective functions, evolutionary operators.

- There are mainly two chromosome representation techniques. In the first approach (Pittsburgh approach), a set of possible association rules are encoded in each chromosome. The second method is Michigan approach, in which each chromosome represents exactly one rule. This approach is suitable for Association Rule Mining.
- There are three different approaches that can be found to tackle the objectives in fitness function in multi-objective problems [6]. First, the original multi-objective problem can be transformed into a single-objective problem by using a weighted function. It involves the use of a GA whose fitness function is the weighted average of different objectives. Second, the lexicographical approach, in which the objectives are ranked in order of priority. Third, the Pareto approach, which consists of as many non-dominated solutions as possible and returning the set of Pareto front to the user.
  Most of the studies using multi-objective GAs for ARM have been performed using the Pareto approach. Such a front is given in Fig 1 for two objectives f_1 and f_2.
- Generally, both standard and varied *selection*, *crossover* and *mutation* operators used for Association Rule Mining.

3. MoEAs for Association Rule Mining

A comparison, of the proposed methods in the literature, is mentioned in Table 1, in terms of underlying MOO tool, encoding mechanism, objective functions, and evolutionary operators. The innovations, implementation details for each category of association rules are discussed in subsections below.

3.1. *Categorical Association Rule Mining*

The proposed works, related to categorical association rule mining, are discussed below.

- Ghosh et el. [8] proposed association rule mining as a multi objective problem rather than single objective one. The authors adopted

Michigan approach to represent the chromosomes (i.e. rules). Each chromosome has length 2n, where ‘n’ is the number of items. Each gene, in the chromosome, represents an attribute. If the gene is 00, the attribute is in the antecedent part. . If the gene is 11, the attribute is in the consequent part. The attribute does not exists in the rule, if the gene is 01or 10. This method uses a Pareto based genetic algorithm to solve the multi-objective rule mining problem using three measures—comprehensibility, interestingness and the predictive accuracy(i.e. Confidence). This algorithm works on a sample of the original database, and used the random sampling method.

- In a similar approach as in [8], the work [9] uses binary encoding for the chromosomes with a little change. The presence of an attribute in the antecedent and consequent part are represented by bits 10 and 01, whereas other bit combinations represent the absence of the attribute from the rule. It uses Pareto based co-evolutionary algorithm in order to overcome the weakness of lexicographic order method. Two new measures, statistical correlation and comprehensibility, along with confidence as objection functions are proposed. The co-evolutionary operators, used, are Pareto neighborhood crossover operator, combination crossover and annexing operator. The outcome in terms of running time is compared with that of a classical method *F-growth* and found to be lesser.

- In [10], a non-standard MOEA is used for the ARM problem. Best solutions, encountered over generations, are filled into a secondary population called the “Pareto Archive”. In the production process, elitism is applied in order to allow solutions from the “Pareto archive” to participate to the reproduction. The classical roulette selection based on the Pareto ranking is used. The proposed crossover operator has two versions depending upon the fact that the parents may share (or not) a common attribute: Crossover by value exchange and Crossover by insertion. Four mutation operators were used as mentioned in Table 1. This algorithm proposes to consider the ARM problem as a multi-objective combinatorial optimization problem in order to be able to find non frequent but interesting rules.

- The work [11] uses NSGA II. Six different measures (support, confidence, interest, comprehensibility, cosine and attribute frequency) have been considered as objectives. Three of these measures have been taken at a time and optimized simultaneously. Because NSGA II known to perform well when the number of objective functions is at most three. Eventually, it demonstrates that this method obtains some rules which cannot be obtained by the traditional mining methods.

- Ali Hadian et el. [12] proposed the binary chromosome encoding as in[8]. The four measures Support, Confidence, Comprehensibility, and Interestingness are used as objectives. Cluster-Based Multi-Objective Genetic Algorithm (CBMOGA) is used which optimizes the support counting phase by clustering the database. Clusters are based on the number of items in each transaction. The benefit of CBMOGA is that it prevents some unnecessary comparisons as compared to MOGA. Though CBMOGA outperforms the MOGA, the speedup highly depends on the distribution of transactions in the cluster tables.

- The disadvantage of binary encoding scheme is that it leads to large chromosome length. To overcome this, an integer encoding scheme is being used in ARMMGA [13]. For example, if A_i represents the ith item, then the chromosome {3 | 2 5 4 1 3} represents the rule $A_2A_5A_4 \Rightarrow A_1A_3$. However, this representation gives rise to a variable length chromosome length, thereby in need of a specialized crossover operator. The classical measures support and confidence are optimized simultaneously. It proposes a method without taking the minimum support and confidence into account. The promising point in this algorithm is that the value of the fitness function only specifies the order of chromosomes in population and has not any other effect on genetic algorithm operator; therefore, the algorithm is convergence with any usually arbitrarily fitness function.

Table1. Comparison of Association Rule Mining Methods using MOEAs (in Chronological Order)

Algorithm	**Underlying Tool**	**Type**	**Encoding**	**Objective Functions**	**Evolutionary Operators**
Ghosh and Nath[8], 2004	MOGA	Categorical	Binary(Michigan)	Confidence, Comprehensibility, Interestingness	Multi point cross over, Bit-flip mutation
Kaya and Alhajj[22], 2003 Kaya and Alhajj[23], 2004	SPEA Variant	Fuzzy	Real-valued (membership functions)	Number of large item sets, Time taken to find all large item sets	Multi-point cross over, Standard real-value mutation
Mehmet Kaya[24], 2005	Non-standard (Pareto based GA)	Fuzzy	. Real-valued (membership functions)	Strongness, Interestingness, Comprehensibility	Four point Crossover, Mutation not mentioned
Hu and Yang-Li[9], 2007	Pareto-based co evolutionary	Categorical	Binary(Michigan)	Statistical correlation, Comprehensibility	Pareto-neighbourhood cross over, Combination, annexing
Khabzaui et el.[10], 2008	Non-standard	Categorical	Not mentioned	Support, Confidence, J-measure, Interest, Surprise	Value exchange crossover, Insertion crossover, value/attribute mutation, insertion/deletion mutation
Altas et el.[14], 2008(MODENAR)	MODE	Numeric	Mixed(integer+real)(Michigan)	Support, Confidence, Comprehensibility, Amplitude of interval	DE/rand/1
Alhajj and Kaya [25], 2008	SPEA Variant	Fuzzy	Real-valued (membership functions)	Number of large item sets, Time taken to find all large item sets	Multi-point cross over, standard real-value mutation
Chen et el.[26], 2008	MOGA	Fuzzy	Real-valued (membership functions)	Number of large 1-item sets, suitability of membership functions	Max-min arithmetic crossover, one point mutation
Anand et el.[11], 2009	NSGA-II	Categorical	Binary(Michigan)	Combination(3 at a time) of support, Confidence, Interest, Comprehensibility, Cosine, Attribute frequency	Crossover not mentioned, bit flip mutation.

Table 1(Continued)

Algorithm	**Underlying Tool**	**Type**	**Encoding**	**Objective Functions**	**Evolutionary Operators**
Ali Hadian et el.[12], 2010 (CBMOGA)	MOGA variant	Categorical	Binary(Michigan)	Support, Confidence, Comprehensibility, Interestingness	No specific mention of Crossover and Mutation
Qodmanan et el[13], 2011	Non-standard	Categorical	Integer(Michigan)	Support, Confidence	Order I crossover, random replacement mutation
Martin et el.[16], 2011(NSGA-II-QAR)	NSGA-II	Numeric	Real-valued(Michigan)	Lift, comprehensibility, performance(Support x Confidence)	Multipoint crossover, standard real-value mutation
Mathews et el.[27], 2011	NSGA-II	Fuzzy	Mixed(integer+real)(Michigan)	Temporal support, temporal confidence, fuzzy support, membership function width	Modified uniform crossover, random change mutation
K.Y.Fung et el.[17], 2012	NSGA-II	Categorical and numeric	Both Michigan and Pittsburgh	Accuracy, Comprehensibility, Definability.	Two point Crossover and bitwise Mutation, Arithmetic Crossover and polynomial Mutation
B. Minaei-Bidgoli et el[18], 2013(MOGAR)	Non-standard	Numeric	Michigan	Confidence, Interestingness, Comprehensibility,	K-point Crossover, Bit flip Mutation
D.Martin et el[19], 2014(QAR-CIP-NSGA-II)	NSGA-II variant	Numeric	Michigan	Interestingness, Comprehensibility, Performance	Standard Crossover and Mutation.
M.M.Ballesteros et el[20], 2014(GarNet)	NSGA-II	Numeric	Michigan	Support, accuracy and Confidence	Interval based crossover, probabilistic mutation.
Mehrdad Almasi et el[21], 2015(Rare-PEARs)	Non-Standard	Numeric	Michigan(integer+real)	Support, Confidence, Lift, Centrality Factor, Length of Rule and Coverage	One-point crossover, standard real-value mutation.

3.2. *Quantitative Association Rule (QAR) Mining*

The works related to QAR are briefed below.

- The chromosomes encode the lower and upper bounds of the intervals of the attributes participating in a rule. In [14], where the MODENAR algorithm uses such a chromosome encoding where each attribute has three components. The first component indicates whether the attribute is present or absent in the rule, and if present, in which part (antecedent or consequent) in the rule it is. The second and third components indicate the lower and upper bounds of the ranges of the attribute. The first component can have integer values 0, 1, or 2, which indicate the presence of the attribute in the antecedent of the rule, the presence of the attribute in the consequent of the rule, and the absence of the attribute from the rule, respectively. The second and third components can take real values from the corresponding attribute ranges. It is to be noted that as MODENAR uses differential evolution as an optimizer and works on real-valued chromosomes, the authors used a round-off operator to handle the integer part of the chromosome. Support, confidence value and the comprehensibility of the rule are maximization objectives while the amplitude of the intervals, which conforms the itemset and rule, is minimization objective. MODENAR used the standard version of the crossover and mutation operators adopted by the version of differential evolution called DE/rand/1. Additionally, a rounding operator is used to round off the first part of the attribute that requires an integer (0, 1, 2) for computing the objective function values. ARs are directly mined without generating frequent item sets.

- The work NSGA-II-QAR [16] uses the same encoding scheme as in [14]. The only difference is that in this case, the first part of the chromosome, instead of using the values 0, 1, 2, adopts the values 0, 1, and − 1, respectively, to denote the same meaning. In both cases, the algorithms used a Michigan encoding strategy. The three objectives interestingness, comprehensibility and performance are maximized. As evolutionary operator multipoint crossover is utilized and the two parts of the chromosome undergo two different mutations. It uses an extension of the well-known MOEA NSGA-II. This method follows a database-independent approach which does not rely upon the minimum support and the minimum confidence thresholds. An experimental comparison between NSGAII-QAR and MODENAR is provided in [16].

- In [17], a two-stage rule-mining approach is proposed to generate rules with a simple chromosome design in the first stage of rule mining. In the second stage of rule mining, entire rule sets are refined to determine solutions considering rule interaction. For a rule-mining problem, the proposed multi-objective GA approach could simultaneously consider the accuracy, comprehensibility, and definability of approximate rules. The promising feature is that it uses both categorical and quantitative attributes and targets to define the design profile of a product. The proposed multi-objective GA approach could simultaneously consider the accuracy, comprehensibility, and definability of approximate rules as objectives.

- The work [18] uses the three measures; confidence, interestingness, and comprehensibility have been used as different objectives for our multi objective optimization which is amplified with genetic algorithms approach. The method uses *rough* values which are defined with upper and lower intervals to represent a range or set of values. Michigan approach is used for representing rules in chromosomes. Eventually, the best rules are obtained through Pareto optimality. It uses K-point crossover and bit flip mutation.

- QAR-CIP-NSGA-II [19] maximizes the comprehensibility, interestingness and performance of the objectives in order to mine a set of quantitative association rules with a good trade-off between interpretability and accuracy. This model extends NSGA II to perform an evolutionary learning of the intervals of the attributes and a condition selection for each rule. It uses Michigan type encoding fro chromosomes and as similar as[16]. It uses standard crossover and mutation. Moreover, this proposal introduces an external population (EP) and a restarting process to the evolutionary model in order to store all the non-dominated rules found and improve the diversity of the rule set obtained. The results attained over nine real world datasets have shown how the EP and restarting process improves the percentage of patterns covered by the rules of the total patterns in the dataset and allows obtaining a greater number of rules than the classical approach.

- The work GarNet[20] is a multi-objective evolutionary algorithm for mining quantitative association rules that has been developed to discover gene association networks. It is based on NSGA II. The representation of an individual consists of two data structures. The upper structure includes the intervals bounds of all the attributes of the dataset. The bottom structure indicates the membership of an attribute to the rule represented by an individual. The type of each attribute can have three values: 0 when the attribute does not belong to the rule and 1 or 2 if it belongs to the antecedent or the consequent of the rule, respectively. If an attribute is wanted to be retrieved for a specific rule, it can be done by modifying the value equal to 0 of the type by a value equal to 1 or 2 depending on the antecedent or consequent. Support, accuracy and Confidence are used as three objectives to be optimized simultaneously.

- In this paper [21], the proposed algorithm (Rare-PEARs) gives a chance to each rule with different length and appearance (antecedent and consequent parts of rules) to be created. Therefore, various interesting, rare or interesting and rare rules can be found. Some of these rules might be uninteresting (those that contain frequent item sets). However, it has been tried to avoid them by Rare-PEARs. To accomplish this goal, the method decomposes the process of association rule mining into N-1 sub-problems (N is the number of attributes, and each sub-problem is handled by an independent sub-process during Rare-PEARs execution). Each sub-process starts individually with a different initial population. It then explores the search space of its corresponding sub-problem to find rules with semi-optimal intervals for each of the attributes. This process is done by a new definition of Non-Dominated concept. Support, Confidence, Lift, Centrality Factor, Length of Rule and Coverage are used as objectives to be optimized.

3.3. *Fuzzy Association Rules*

One of the major problems of mining numeric association rules is that these algorithms deal with sharp boundaries between consecutive intervals. Thus, they cannot represent smooth changes from one interval to another, which can be easily handled by fuzzy association rules [5]. The OEA-based fuzzy ARM techniques have been developed in the past decade.

- Various MOEAs have been applied in different works on fuzzy ARM. Kaya *et al.* [22], [23], [25] used a variant of SPEA for fuzzy rule mining. In [26], a multi objective GA (MOGA) is used for this purpose. NSGA-II has been utilized in [27]. But, there is no mention of any comparison among different MOEAs for fuzzy rule mining in any of the work..

- There are two categories of chromosome representations for fuzzy ARM [5].
    1. In the first approach, a chromosome encodes a set of fuzzy clusters that correspond to each attribute. The goal is to find a suitable set of fuzzy clusters that partition the range of values in each attribute domain. This representation is employed in a series of works done by Kaya *et al.* in [22], [23], [25]. In these works, each chromosome represents the base values of a variable number of membership functions representing the fuzzy sets for each quantitative attribute. Fuzzy sets are represented by standard triangular membership functions. Chromosomes use real values. Here, a chromosome does not represent association rules. It represents a suitable fuzzy clustering of the attribute domains. The evolved fuzzy membership functions are then used as the linguistic values of the corresponding attributes [5]. Fuzzy association rules are mined using standard algorithms based on minimum support and minimum confidence criteria. The work [26] uses a similar encoding approach.
    2. In second approach, each chromosome directly represents association rule. This is a kind of Michigan approach. In [27], such an encoding mechanism is applied to mine temporal fuzzy association rules. A mixed representation, of chromosomes combining integer and real values, is used. The chromosome encodes the lower and upper bounds of the temporal interval in the rules as integers. The indices of the items participating in the rule are also

encoded as integers. Eventually, the real valued parameters of the triangular membership functions corresponding to each item are encoded in the chromosome. Thus, this representation induces variable-length chromosomes needing special evolutionary operators.

- In the works [22], [23], [25], two criterias are optimized, that is, number of large itemsets and time spent to obtain the large itemsets. So, there are two objectives to evolve a possible fuzzy clustering of the numeric attributes. First is maximizing the number of large itemsets while the other is minimizing the time required to obtain all large itemsets given the clustering. After optimizing the clustering, membership functions are used as linguistic values for the fuzzy association rules extracted based on minimum support and minimum confidence criteria. In [26], where a similar encoding strategy is adopted as in [22], two objective functions are optimized simultaneously. The first objective function is stability of the encoded membership functions, which has two components, that is, overlap factor and coverage factor [5]. The stability is optimized to avoid generation of too redundant and too separated fuzzy sets for an item. The second objective is to maximize the total number of large 1-itemsets for given minimum support values. Although this paper is a consequence of the works of Kaya et al. with modifications in the objective functions and evolutionary operators, no comparison has been made between the works to check which is better over the other approach. In [27], Michigan form of chromosomes the authors used for temporal fuzzy association rule mining. So, the objective functions are related to the optimization of the encoded rules. It used four objective functions, namely temporal support, temporal confidence, fuzzy support, and membership function widths. The first three objective functions are obvious; the last objective function is used to prevent a membership function from covering the whole range of attribute values. Without this objective function, the solutions could evolve to cover the complete range of attribute values, since this gives higher support values as it includes more number of items [5].

- References [22], [23], have used standard multipoint crossover operations. In [25], arithmetic crossover is used. Also, they employed standard real-value mutation. In [26], the authors used max-min arithmetical crossover and one-point mutation. This crossover operator generates four offspring at a time out of which the two best offspring are chosen. The mutation operator is used to slightly change the center of the fuzzy set being mutated. Whenever mutation takes place at the center of a fuzzy membership function, it may disrupt the order of the resulting fuzzy membership functions. Hence, after the mutation, these fuzzy membership functions need rearrangement according to their center values. In [27], for a Michigan type of encoding, a modified uniform crossover operator is adopted. For mutating the genes representing the lower and upper bounds of the time interval, the values are generated within the endpoint range (*epr*) where the midpoint is the value of the current gene (*g*), such that the mutated value is a member of the set $\{-epr/2, \ldots, g, \ldots, epr/2\}$. This is done to reduce the effect of random sampling of the dataset [5].
- This paper [24] first introduces optimized fuzzy association rule mining in terms of three important criteria; strongness, interestingness and comprehensibility. Then, it proposes multi-objective Genetic Algorithm (GA) based approaches for discovering these optimized rules. Optimization technique according to given criterion may be one of two different forms; The first tries to determine the appropriate fuzzy sets of quantitative attributes in a pre-specified rule, which is also called as certain rule. The second deals with finding both uncertain rules and their appropriate fuzzy sets.

4. Points to Ponder

There are many challenges that have impacts on the overall performance of the proposed algorithms or methods. Those points that are found in literature listed out in this section.

- The use of minimum support and confidence thresholds has to be avoided as there is highly chance of missing out quality rules.
- Two major problems were encountered while obtaining rules using MOEAs. One is invalid rules and another is non-existent rules [11]. These two problems are reason for reduced performance of elitist MOEAs like NSGA-II to obtain more number of good rules. The search space tends to get stuck at local Pareto optimal solutions found so far or converge to very few Global Pareto optimal solutions if found[11].
- To improve the efficiency of an algorithm [8], which uses *sampling* of the database, some refinement is required because the sample may not truly reflect the actual database. Random sampling, regression based sampling or cluster based sampling could be a choice. A perfect sample will improve the correctness of the rules generated by the algorithm.
- Whenever a typical integer encoding scheme gives rise to variable length chromosomes [13], a specialized crossover operator is required.
- Finding the optimal interval of each rule's attribute is a challenge in QARs.
- Rapid convergence damages the efficiency of MOEAs. Some researches [19] solve this problem by restarting. They restart whenever it is found that the difference between two consecutive populations is less than "α" percent. To chose "α", sufficient exploration is needed. If this value is high, current generations may not have the chance to produce elite chromosomes.
- Most of popular methods for association rule mining cannot be applied to the numerical data without data discretization. There have been efforts to resolve the problem of dealing with numeric data in [18].
- In fuzzy association rules mining, it is not an easy task to know apriori the most appropriate number of fuzzy sets and their membership functions in order to cover the domains of quantitative attributes. Moreover, it is not realistic that experts can always provide the most appropriate fuzzy sets [25].

5. Conclusion

This paper surveys the evolutionary algorithms used for association rule mining and briefed about the technicalities, innovations and goals of the works. Although ARM algorithms, based on MOEAs, have gained popularity in recent years, their use in real-life applications is still limited. It would be useful if future works will be directed to the use of rule mining for gene expressions, financial databases, text mining, and bioinformatics.

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