IOSR Journal of Computer Engineering (IOSR-JCE)
e-ISSN: 2278-0661,p-ISSN: 2278-8727, Volume 16, Issue 6, Ver. I (Nov – Dec. 2014), PP 57-66
www.iosrjournals.org

A Fuzzy Inference Approach for Association Rule Mining

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Abstract: *The association rule mining is most popular and real time applicable approach for finding interesting relations between items. Many of the ARM (Association rule Mining) approaches are well investigated in the literature, but it generates large number of association rules. If the dataset size is larger, then huge rules may occur, often it is a critical situation where decision making is difficult or unattainable because knowledge is not directly present in frequent patterns. This paper presents an improved AIRM (Association Inference Rule Mining) algorithm where fuzzy logic based C-Means clustering concept has been adopted to discover inference knowledge from frequent patterns. For experimental study, we apply this approach on a clinical dataset of 1000 patients, contained symptoms having different diseases. Proposed approach follows three phase procedure in order to achieve inference knowledge, in the first phase preprocess the data, second phase apply the ARM and finally FIS has to be applied to discover inference knowledge by matching inference rules and put the data in the appropriate class on the basis of their matching degree. The new approach is efficient and outperforms as compared to a previous AIRM algorithm in order to match inference rules and knowledge discovery process.*

Keywords: *ARM, Inference Rule Mining, Fuzzy Symptoms, Fuzzy Inference, Forward Channing.*

I. Introduction

In the branch of data mining, association rule mining plays a vital role in the knowledge discovery process by generating striking patterns. It was first introduced by Agrawal et.al [2] for market basket analysis to find frequently purchased items by customers. It became much popular due to its high applicability in various areas such as medical, share market, DNA pattern recognition, web mining, etc. Formally association rule is defined as $P \rightarrow Q$ where P and Q are two distinct items in general, if a customer buys, product P also buy product Q at the same time formally Association rule represents the relationship among the items in the database. Apriori and FP-Growth are two most popular association rule mining algorithms in literature, Apriori algorithm introduced by Agarwal et.al [1] in 1994, it adopts the Apriori property and candidate generation process to generate association rules. FP-Growth is a tree based approach introduced by Han et.al [10] in 2000 it follows two step procedure, in first step it scan the database once and in second step it generates the Frequent Pattern tree, then it discover frequent patterns using pattern base. Traditional Association rule mining (ARM) approaches Apriori [1], FP-growth [10] generates a huge number of frequent patterns which are not able to produce direct knowledge or inference, It is a serious issue when we mine the clinical data where different combinations of symptoms may belongs to common disease because patient's symptoms may vary patient to patient but disease may be the same. Here traditional ARM approaches fail due to their crispy nature, for example, if a patient has a high fever, low blood pressure, severe headache and cold, then it may be prone to malaria. This information cannot be discovered just by applying traditional ARM approaches; here fuzzy logic can play an essential role to discover inference knowledge by using of additional concept of forward inference system. In our previous framework [5] by K. Chaturvedi et al. an identical inference mechanism framework has presented for association rule mining, which follows five step procedure to discover inference knowledge from frequent patterns, here the fact matching process reflects some kind of weakness due to their exact fact matching process. This process may drop many of interesting patterns (frequent symptoms). In this paper, we propose a modified approach of previous work to overcome this situation and efficient fact matching process, for this Fuzzy C-Means clustering [7, 4] approach has been adopted for fact matching which performs efficiently in both of the cases either in exact or partial matching.

Rest of the paper is organized as follows: section 2 outlines the theoretical background of inference mechanism including association rule mining and fuzzy C-means clustering, section 3 addresses the related work in the field of fuzzy inference and inference rule mining, a detailed methodology of the proposed AFIRM (Association Fuzzy Inference Rule Mining) is presented in section 4 with an illustrative example, section 5 presents a analytical study on proposed approach and finally section 6 presented a concluding remark.

II. Theoretical background

1.1 Association Rule Mining

Definition 1: Let P be a set of patients, which contains different patients P_1, P_2, P_3,……….P_n which may occur in different transactions, P= {P_1, P_2, P_3,……….P_n }.

Definition 2: Let S sets of symptoms contains different symptoms S_1, S_2, S_3…....S_m: S= {S_1, S_2, S_3…....S_m} where $S \subseteq P$ in transactional data base DB.

Definition 3: An association rule represented in the form of an implication of $S_1 \rightarrow S_2$ where $S_1, S_2 \subset S$, $S_1 \cap S_2 = \phi$, S_1 is called the antecedent and S_2 is called consequent. Support (S) of an association rule is defined as the percentage of records that contain the total number of records in the database.

$$Support, S(S_1 \rightarrow S_2) = Supp(S_1 \cup S_2)$$

1.2 Inference Rule Mining

The inference engine is a software tool that deduces new knowledge or fact by using domain fact knowledge to discover inference knowledge. Basically, it is the logic unit in the expert system. It uses general rules of inference to reason from the knowledge base and draw conclusion which are not explicitly stated but can be inferred from the knowledge base.

Let S be the set of symptoms contains different symptoms S_1, S_2, S_3, S_4, S_5…., S_n and DIS is the set of disease D_1, D_2, D_3, D_4. Suppose that we have following rules:

R_1: IF S = (S_1, S_3, S_5) Then DIS=D_1
R_2: IF S = (S_2, S_4, S_5) Then DIS=D_2
R_3: IF S = (S_1, S_2, S_5) Then DIS=D_3
R_4: IF S = (S_3, S_5) Then DIS=D_4

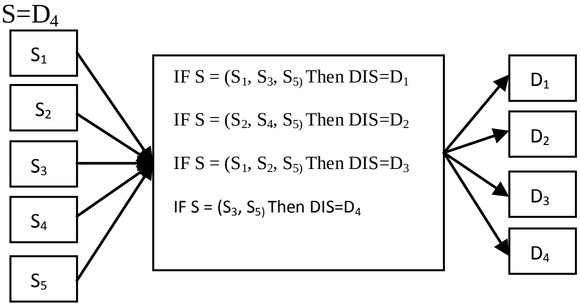

Figure-1, Disease Inference System

1.3 Fuzzy C-Means clustering

Fuzzy C-means (FCM) clustering algorithm first introduced by Dunn [7] and then improved by Bezdek [4] Fuzzy C-means is a clustering algorithm, but it is some kind different to the other traditional clustering algorithm because of its fuzzy nature and also have the capacity of handling delicate data. It is a strong approach from the data analysis perspective because it provides the way of organizing data into multiple predefined clusters or groups, based on their similarity among the classes from which it belongs to. But the additional extensibility of this approach is a common itemset that may refer to multiple clusters based on their degree of membership or similarity. Similarity refers to the mathematical calculation of similarity in the general distance calculation between objects using some well-defined distance measures.

In Fuzzy C-Mean clustering algorithm, Object function "O", calculated in the each iteration.

$$O_m = \sum_{p=1}^{N} \sum_{q=1}^{C} U_{pq}^{m} \left\| X_p - C_q \right\|^2$$

m – Any real number greater than 1.
N – Number of data points.
C – Number of clusters required.
Xp – pth data point.
Cq – center vector for cluster q.
||Xp-Cq|| - similarity of data point of Xp to the center vector Cq of cluster q.
Degree of membership for pth data point in cluster q can be calculated as follows.

$$U_{pq} = \frac{1}{\sum_{k=1}^{C} \left(\frac{\left\| X_p - C_q \right\|}{\left\| X_p - C_r \right\|} \right)^{\frac{2}{m-1}}}$$

Where cluster center C_q can calculate as follows:

$$C_q = \frac{\sum_{p=1}^{N} U_{pq}^{m} - X_p}{\sum_{r=1}^{C} U_{pq}^{m}}$$

The process will stop when

$$MAX_{ij}\left\{ \left| U_{pq}^{r+1} \right| - U_{pq}^{r} \right\} < \varepsilon$$

Where, ε is the termination decisive factor between 0 and 1.

III. Related work

Study of the inference rule has a wide area of the range, in [8] Ronald Fagin et al. Presents a brief overview of inference rules, they also gave a brief discussion on the applicability of inference in various areas like inference in propositional logic, non-standard propositional logic, propositional modal logic and inference in first order logic, etc. Additionally, in [19] Sowapna Singh presents an interactive comparative study on various inference engines on the basis of different measurement criteria. Rechard Chow et al. [6] Proposed an approach for inference detection for finding association rules of sensitive nature. They used the additional concept of accepting all of the rules of sensitive nature with high support. The mechanism proposed to detect sensitive contents or in practice it identifies the secure documents that needed to get reviewed before release. A fuzzy cognitive map based approach proposed in [14] for web mining amplification by Kun Chang Lee et al. It follows three step procedure to achieve objectives, the first step is association rule mining, second step apply the transformation to transforming casual knowledge and finally third step apply the inference amplification to achieve desired results. GenBR algorithm [9] proposed by Guichong Li et al. An approach for prune redundant rules and to discover useful and understandable rules as inference called basic association rules. Loannis Hatzilygeroudis proposed a neural network based inference mechanism [11] for integrated rule based learning, they also presented the construction process of neural and explored their generalization capabilities. In [13] Jian-Bo Yang et al. Presented Belief rule based inference methodology using the evidential reasoning. They also proposed a neural methodology for modeling hybrid rule base using a belief structure. An inference mechanism framework for association rule mining proposed in [5] by K. Chaturvedi et al. This paper presents a theoretical and numerical study on association rule based inference mechanism for discovering knowledge from a medical dataset where patient dataset has been used to discover highly effected disease in a particular time slice. It also presents an algorithm AIRM to achieve the appropriate objective; this paper is an extension of AIRM to optimize the algorithm proposed in [5]. A fuzzy association based classification presented in [3] for high dimensional problems with genetic rule selection. It follows three step procedure to achieve the required objective, first is a fuzzy association rule extraction for classification, in second step candidate rule preprocessing has to be conducted and finally in third step it performs the rule selection and lateral tuning. Similarly [15, 17, 20] presents fuzzy association rule mining approaches to mine very large datasets, analyzing association rules and time series prediction respectively. Jeoung Nae et al. [12] presented a fuzzy inference system using hierarchical fair competition based parallel genetic algorithm, it deals with multimodal of high dimensionality, they also use the concept of Fuzzy C-means algorithm to classify the data in clusters. Data mining is more popular in the field of medical science due to its high applicability and analysis ability in medical and clinical data mining, [18] proposed a road map for mining of clinical data by exploring the steps involve in clinical data mining, they also explore the way of creating a clinical data warehouse including the data preprocessing and data mining processes, paper [16, 21] also proposed practical and applied fuzzy logic based approaches for medical diagnosis.

IV. Proposed Work

In this paper, we propose a novel approach for disease prediction through fuzzy symptoms using association rule mining. It follows four phase procedure to achieve required inference from trainee dataset and the phases are as follows:

1.4 Data Pre-processing:

Dataset preprocessing is the very first phase of AFIRM (Association Fuzzy Inference Rule Miner), it is a two step process, first step generates the index table of symptoms to assign a unique value to each symptom and second step is the mapping step, where mapping has to apply between index table and original dataset to map the symptoms by respective index values. As an outcome, it generates a new mapped dataset as table-3, for smooth and efficient processing.

1.5 Association Rule mining:

As further processing, in order to mine the dataset and to discover frequent patterns or frequently occurring symptoms, association rule mining has to be performed on preprocessed data. Under this process ARM algorithm [10] reads the mapped dataset and generate frequent patterns as per predefined minimum threshold value and store in frequent pattern base as table-4.

1.6 Fuzzy Inference Rule Mining:

The huge number of generating frequent patterns may be insufficient to draw conclusions; over here, there will be a need for an additional inference mechanism to discover inference knowledge. Conceptually inference is a rule matching procedure to find a fact or a meaningful conclusion. In this phase, we adopted the fuzzy C-means clustering approach to match frequent symptoms with factual knowledge which resides in fact database (domain knowledge) as shown in figure 2 and 3.

Fuzzy inference engine discover and classify this knowledge in three classes or clusters on the basis of their matching degree. Theoretically, this step matches and discovers disease related to frequent symptoms.

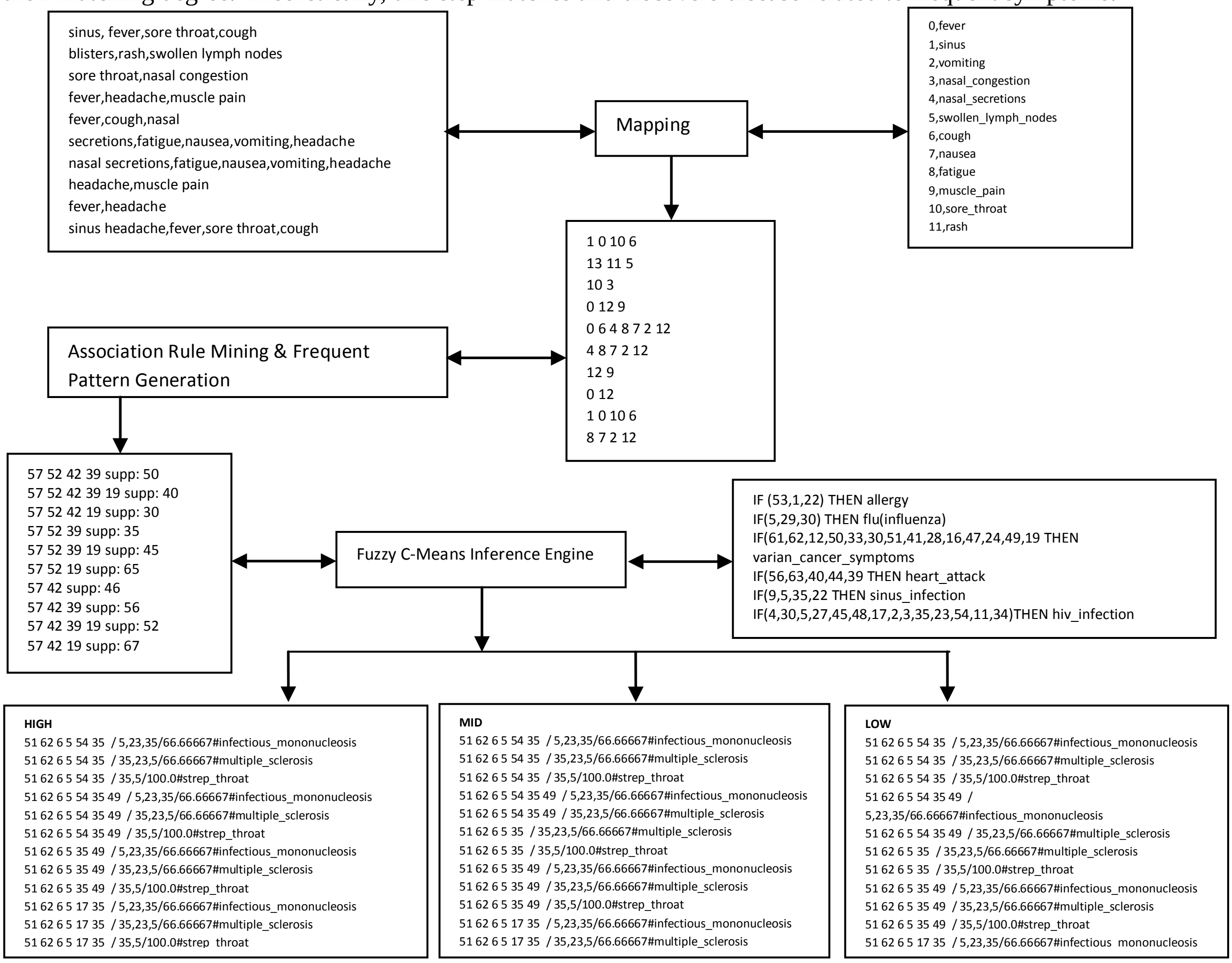

Figure -2, AFIRM activity diagram

1.7 Result Analysis & Knowledge Representation:

Above experiment generates three classes of resulting inference knowledge HIGH, MID and LOW on the basis of their degree of membership. Here cluster high contains facts with high matching degree, facts which do not fully matches with rules will be put in cluster mid and facts which has low matching degree will belong to cluster low. Result analysis is performed by pattern evaluation as shown in figure 4, 5 & 6 to obtain abstract knowledge.

The algorithm Association Fuzzy Inference Rule Mining (AFIRM) presented as the extension of AIRM [5], by adopting the concept of fuzzy C-means clustering to match the facts, because accurate fact matching may drop many interesting facts. To overcome this problem AFIRM algorithm proposed in this paper which outperform as comparable to AIRM algorithm [5] from outcome perspective.

Figure-3 shows a schematic representation of fuzzy C-means clustering based inference mechanism for association rule mining to discover inference knowledge.

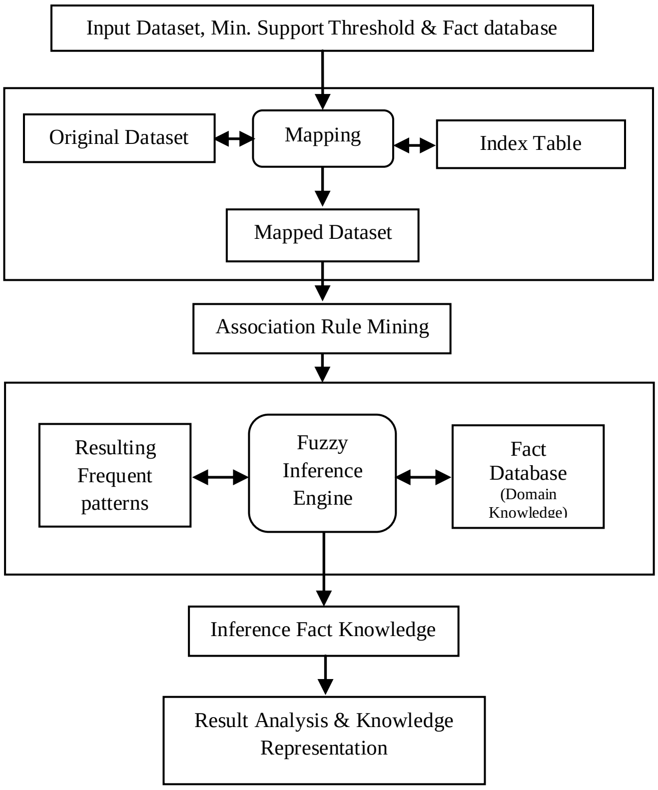

Figure -3 Fuzzy inference systems.

Algorithm: Association Fuzzy Inference Rule Miner (abbreviated as AFIRM)
Abbreviation used:

Abbreviation	Meaning
DS	Dataset
FP	Frequent patterns
ARM	Association rule mining
Infr	Inference
Min_sup	Minimum support
FIS	Fuzzy inference system
FCM	Fuzzy C-Means

1. Begin:
2. Load (Dataset), Min_Sup_Threshold, Fact_DS
   //Data Preprocessing
3. Index=Gen_Index(Dataset)
4. Mapped_DS=Mapping(Dataset, Index)
   //Association Rule Mining
5. FP=ARM(Dataset,Min_Sup_Threshold)
   // FP-Growth By Han et.al [4]
6. For Each FP [i]
7. For Each Fact_DS[j]
   //Fuzzy Inference Rule Mining
8. Infr_Fact[i] = FCM(FP[i], Fact_DS[j])
   //Fuzzy C-Means Clustering algorithm [4, 7]
9. Endfor
10. Endfor
11. Result_Analysis(Infr_Fact)
12. End

Procedure: FCM(FP, Fact_DS)

1. Begin
2. Initialize matrix U for degree of membership U=[uij]

3. At each step calculate centers vector C (k) & U (k).
4. Calculate the d-dimension center of the cluster.
5. Update U(k), U(k+1)
6. Repeat step 2 till MAX_{ij}< termination decisive factor
7. End.

For experimental study a training data set is shown in table-1, where symptoms are given, having 20 patients.

TABLE -1: Patient Dataset

Patent #	Symptoms
1	sinus_headache,fever,sore_throat,cough
2	blisters,rash,swollen_lymph_nodes
3	sore_throat,nasal_congestion
4	fever,headache,muscle_pain
5	fever,cough,nasal_secretions,fatigue,nausea,vomiting,headache
6	nasal_secretions,fatigue,nausea,vomiting,headache
7	headache,muscle_pain
8	fever,headache
9	sinus_headache,fever,sore_throat,cough
10	fatigue,nausea,vomiting,headache
11	sinus_headache,fever,cough
12	blisters,rash,swollen_lymph_nodes
13	fever,headache,muscle_pain
14	fever,sore_throat,cough
15	cough,nasal_secretions
16	fatigue,nausea,vomiting,headache
17	fever,sore_throat,cough
18	fatigue,nausea,vomiting,headache
19	fever,sore_throat,cough
20	blisters,rash,swollen_lymph_nodes

In second step an index number has to be assigned to each and every item for smooth processing of data. For this purpose an index table has to be made as shown in table-2 where each symptom assigned by a unique index number.

TABLE -2: Index table

Index ID	Symptoms
0	fever
1	sinus_headache
2	vomiting
3	nasal_congestion
4	nasal_secretions
5	swollen_lymph_nodes
6	cough
7	nausea
8	fatigue
9	muscle_pain
10	sore_throat
11	rash
12	headache
13	blisters

The third step is mapping step where mapping has been performed between original data set and index table, as shown in table-3, shows a mapped dataset where each symptom mapped with their respective index value.

TABLE -3: Mapped Dataset

Patent #	Mapped Symptoms
1	1,0,10,6
2	13,11,5

3	10,3
4	0,12,9
5	0,6,4,8,7,2,12
6	4,8,7,2,12
7	12,9
8	0,12
9	1,0,10,6
10	8,7,2,12
11	1,0,6
12	13,11,5
13	0,12,9
14	0,10,6
15	6,4
16	8,7,2,12
17	0,10,6
18	8,7,2,12
19	0,10,6
20	13,11,5

Fourth phase of this approach says to perform the ARM algorithm on the mapped dataset to find frequent pattern or frequent symptoms with minimum support 20%, as shown in table-4.

TABLE -4: Frequent patterns with support counts

Frequent Patterns	Support Count
8	5
8,12	5
8,7	5
8,7,12	5
8,7,2	5
8,7,2,12	5
8,2	5
8,2,12	5
7	5
7,12	5
7,2	5
7,2,12	5
2	5
2,12	5
10	6
10,6	5
10,6,0	5
10,0	5
6	8
6,0	7
12	9
12,0	4
0	10

Frequent Patterns	Support Count
fatigue	5
fatigue,headache	5
fatigue,nausea	5
fatigue,nausea,headache	5
fatigue,nausea,vomiting	5
fatigue,nausea,vomiting,headache	5
fatigue,vomiting	5
fatigue,vomiting,headache	5
nausea	5
nausea,headache	5
nausea,vomiting	5
nausea,vomiting,headache	5
vomiting	5
vomiting,headache	5
sore_throat	6
sore_throat,cough	5
sore_throat,cough,fever	5
sore_throat,fever	5
cough	7
cough,fever	7
headache	9
headache,fever	4
fever	10

Third phase generates a huge number of frequent patterns which makes the knowledge discovery process too tedious. Here decision making is difficult or sometimes impossible because knowledge is not directly present in the frequent pattern base (containing huge number of frequent patterns) as table-4 can't give knowledge directly in a practical sense. To resolve this problem and to mine knowledge from frequent patterns, a fact table (table-5) has to be used to find inference knowledge. For this purpose fuzzy C-means clustering algorithm matches the frequent symptoms(table-4) with fact knowledge(table-5) by forward chaining inference system and move toward for further processing.

TABLE -5: Fact Database

Symptoms	Disease (Fact Knowledge)
runny nose,watery eye,cough	Allergy
fever,chills,fatigue	flu(influenza)

sinus headache,fever,sore throat,cough	sinus infection
abdominal pain,loss of appetite,fever	Appendicitis
blisters,rash,swollen lymph nodes	Herpes
sore throat,nasal congestion	common cold
fever,headache,muscle pain	Dengue
increased urine output,thirst,hunger,fatigue	Diabetes
fever,cough,nasal secretions,fatigue ,nausea,vomiting,headache	swine flu
sore throat,fever	strep throat

The task of fact matching is not simple because, as our example, some or all symptoms of a frequent pattern may be responsible for the same disease (all or partial symptoms may belong to common disease), i.e. if a patient has 60% of symptoms of malaria then he/she may prone by malaria infection with high probability. Similarly, if a patient has 30% of symptoms of viral infection, then he/she may prone by viral infection with low probability. Apart from that, our analysis says that if we adopt the exact matching procedure, it may drop many of interesting patterns. That may be responsible for incorrect prediction. The concept of Fuzzy logic is adopted here to match fact and to discover inference knowledge. Discovered knowledge can be classified in three class's minimum possibilities, medium possibility and high possibility as shown in the table -6.

TABLE -6: Disease with degree of membership and classes

Degree of Membership	Fact/ Disease	Cluster
75	sinus_infection	High
50	common_cold	Mid
50	strep_throat	Mid
50	sinus_infection	Mid
33.33	flu(influenza)	Low
25	sinus_infection	Low
14.28	swine_flu	Low
33.33	allergy	Low
25	diabetes	Low
33.33	appendicitis	Low
-	-	-
-	-	-

By the analysis of data presented in table-6, whole knowledge can be further classified in three resulting classes as shown in table-7, 8 and 9.

TABLE -7: Percentage of disease infection with High possibility

Disease	Percentage (%)
sinus_infection	100.00

TABLE -8: Percentage of disease infection with medium possibility

Disease	Percentage (%)
strep_throat	37.50
common_cold	37.50
sinus_infection	25.00

TABLE -9: Percentage of disease infection with minimum possibility

Disease	Percentage (%)
swine_flu	27.27
flu(influenza)	18.18
diabetes	11.36
appendicitis	9.09
sinus_infection	15.91
allergy	18.18

V. Result And Analysis

In this section result analysis has been carried out to analyze the possibilities of disease infection, the experimental study performing in section-3 generates three classes to represent the high, low and medium possibility of diseases infection, figure 4 & 5 depicts the result analysis of table 8 & 9 respectively over the training data. The analysis draws following inferences.

A. The possibility of sinus infection is very high (table -7).
B. There is a 37 % chance of getting affected by strep throat and common cold infection and 25% chance of getting affected by sinus infection under the medium level possibility.
C. There are 27%, 18%, 11%, 9%, 15% and 18% chance of getting affected by swine flu, flu (influenza), diabetes, appendicitis, sinus infection and allergy respectively under the low possibility.

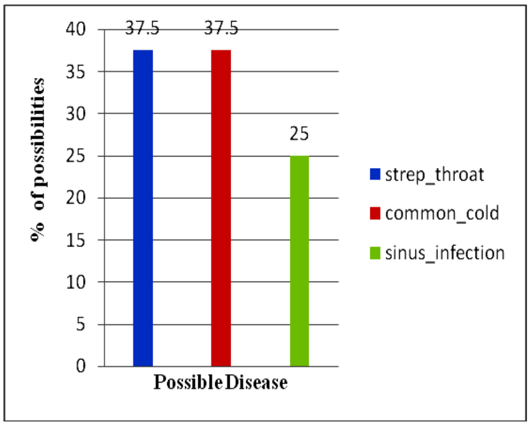

Figure -4, Diseases infection with medium possibility

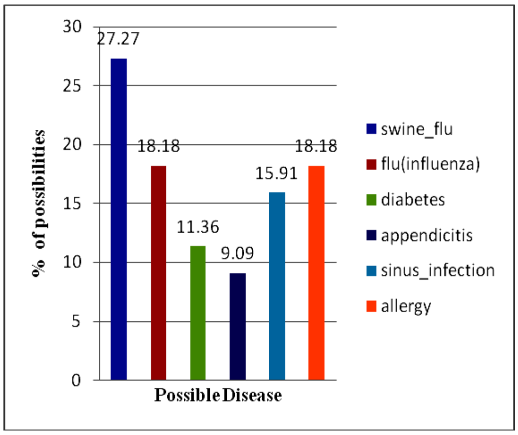

Figure -5 Diseases infection with minimum possibility

Figure-6 depicts a comparative analysis of a patient dataset to predict the percentage of possibilities of disease infections. Where X-axis shows the disease identification numbers as 1, 2, 3, 4, 5, 6, 7, and 8 representing diseases swine_flu, flu(influenza), diabetes, appendicitis, sinus_infection, allergy, strep_throat, common_cold respectively and the Y-axis represents the percentage of possibilities.

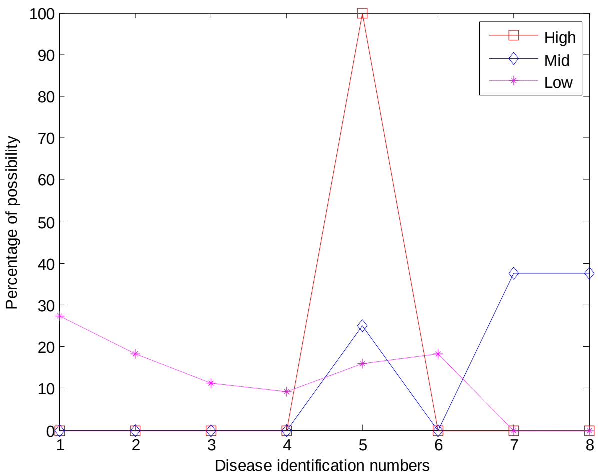

Figure-6 A comparative analysis of possible diseases

VI. Conclusion

In this paper, we have presented a new approach AFIRM which is a fuzzy logic based inference mechanism for association rule mining. This approach was evaluated on a dataset of 1000 patients record which contained symptoms of their different diseases. The goal of this approach is to discover and investigate highly effected disease in a particular season or in a couple of months so that prevention could be conducted by taking important precautions during such season. As per above discussion, overall approach focuses on the inference knowledge discovery by mining the patient record followed by above discussed three step procedure. This approach may play an essential role in the field medical data mining to obtain beforehand recognition and alert about the particular disease to prevent it.

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