J. Basic. Appl. Sci. Res., 3(2)302-312, 2013

ISSN 2090-4304
Journal of Basic and Applied Scientific Research
www.textroad.com

Time Reduction on Dispensing Prescription Medicine in Iranian Pharmacies through a Hybrid Approach

Sajad Homayoun, Mohammad Jafar Tarokh

IT Group, Department of Industrial Engineering, K. N. Toosi University of Technology
Tehran, Iran

ABSTRACT

Nowadays with the expansion of information technology (IT) in various fields including medicine, greater improvements in the level of productivity in these fields are expected. One of the processes of everyday life requiring improvement is waiting time for completing the process of dispensing in pharmacies. With regard to the necessity of referring to a physical pharmacy in Iran in order to receive the prescribed medicine. This paper seeks a way to reduce the noted time through proper arrangement of the medicines available on the shelves. While the prescriptions are being dispensed by the pharmacy staff, people have to wait for the completion of the collecting process which will cause the dissatisfaction of the customers. A hybrid framework of data mining & Genetic Algorithm has been designed to reduce the time of dispensing prescriptions in Iranian pharmacies. The prescription data are stored in the pharmacies and the data sets of each prescription are considered as market baskets. First of all, the required knowledge is extracted by using Association Rules method and after that the results are mapped into usable matrices in adaptive-Genetic Algorithm. The fitness function is designed carefully and combined with Entropy methods to achieve appropriate weights. This is among the first studies analyzing prescriptions data through combining Data Mining and adaptive-GA to arrange pharmacies shelves by the purpose of achieving less time in medicines collection process. The framework is examined on a pharmacy's data and the result is simulated and compared to conventional methods of arranging medicines on the shelves. The simulation process showed it is possible to decrease the collecting process time through putting the medicines by better arranging on the shelves according to the past information (prescription sales data which are saved in pharmacy's database).

KEYWORDS: Dispensing Prescriptions, Medicine Arrangement, Data Mining, Association Rules, adaptive-Genetic Algorithm.

INTRODUCTION

In recent years, information technology has shown that it can have an outstanding influence on the development of all fields of studies. Recently, many efforts have been done in using information technology to improve services for humans. Pharmacies are included amongst places which provide services for patients and every person in the society will use these services. Unlike many developed countries that each prescription will be sent to pharmacy via electronic systems and medicine items are received at home, in Iran after the doctor has prescribed medicine, it is brought to pharmacy by the patient or the relatives and after waiting for a few minutes they can receive medicines.

Some hospitals (specifically public hospitals) are very crowded, so waiting hours for dispensing prescriptions increase which would makes patients dissatisfied by these services.

This article proposes a functional framework for finding the best arrangement for medicine items in pharmacy's shelves which directly improves the time spent for the prescription dispensing process. If the distance between shelves for collecting medicine items decrease, the rate of dispensing prescriptions would increase automatically and it will lead to decrease in the whole process time. This framework attempts to analyze the stored data in the pharmacies data base and find a solution with stochastic methods. Finally the results were presented in a case study. It's worth to mention that for solving the arrangement problem we can use many simple ways which examine all possible solutions, but these kinds of methods not work in a timely manner for large scale sets (n) because need to be examined $n!$ Possible answers, thus we use other methods such as stochastic search.

There are two conventional styles to arrange medicines in Iranian pharmacy shelves; 1) Alphabetical, in which medicines are placed according to their names and 2) Classified in medical groups, in which medicines are positioned by medical categories (for example cancer etc.).

The rest of the survey is as follows: Section 1 refers to the literature review. In section 2, the initial methods which are used in designing the framework are mentioned. Section 3 includes the proposed framework for

* **Correspondent Author:** Sajad Homayoun, M.Sc. Student in Information Technology, Phone: +98 9171264179, Email: sajadhomayoun@gmail.com

solving the problem and the case study and the simulation are presented in section 4. Section 5 is involving the conclusion.

1. LITERATURE REVIEW

Although rules of protecting information privacy are essential in today's life, maybe these rules cause some limitations in scientific investigations. Prescriptions' data can be mentioned as one of these fields which encounters some limitations[1], though implementing such investigations (like Data Mining) can lead to discovering new models for improving medications' quality[2] and distribution. It is a must for proposed framework to use the stored data in pharmacies' data base in order to investigate and analyze the pharmaceutical basket of patients. Up to present time, no articles found specifically on the topic of time reduction of dispensing prescription by improving medicine arrangement.

In recent years, the issue of accepting or denying e-prescribing has undergone a challenging matter for governments. Some of them disapprove of e-prescribing because of privacy and security and the rest support it under the advantage of increasing speed and accuracy. Physicians are willing to use new e-prescription systems[2]. By implementing e-prescribing in the state of Massachusetts, two hours has been saved each physician and ten minutes for each patient[3]. By operating e-prescription method, the accuracy of available data in the data base increases and the condition for operating data mining projects are met.

The literature of this research is composed of the literature of two special domains. Market basket analysis (MBA) and product arrangement on the shelves. So many studies have been done on MBA and the authors tried to achieve desirable results by applying techniques such as association rules, clustering and etc. The attained results are usable for marketing managers and sales people. In the other domain studies have been done on arranging products on the shelves.

1.1. Market basket analysis

There are two approaches in MBA; Exploration which tries to reveal patterns and hidden relationships among available items in customer purchase baskets and Explanation approach detects effects of relationships on marketing variables and etc.

Cavique et al.[4] have tried to make cross-selling strategy automatic. He wanted to simplify analysis of rules and avoid analyzing thousands of output rules from association rules technique. Wong et al.[5] have focused on applying data mining to cross-selling. They proposed a recommendation systems method which exploits association rules in product selection. Cuningham & Frank[6] have tried to classify books by using market basket analysis technique on library data. Their goal was to decline searching average time for each book by placing similar references next to each other. Chena et al.[7] have studied market basket analysis in multi store environments.

Meiwati has tried to analyze marketing baskets of pharmacies' transactional data and find the relationship between medicines which are sold simultaneously[8]. Some articles analyze the relationships among available items in chain stores' customer baskets. Chen et al. analyzed the customer basket in accordance with items' brand in supermarkets and predicted season sales by using time series[9]. Pandit et al. have focused on proposing a model for analyzing customer marketing basket apt to distances which are traversed by customers to collect available items in the list that is prepared in advance[10]. Schwenke et al. simulated the customers' purchase baskets according to their characteristics. Some of these articles are about customer classifications by clustering their marketing baskets[12, 13, 14].

1.2. Product arrangement

Product arrangement is organizing the available products according to the marketing managers desirable goals. According to their goals, appropriate arrangement of products will be in hand by using some algorithms. The objective can be keeping the customer stay on the store for a longer period or decreasing the wasted time for each customer.

Movarei & Vesal[15] have investigated the effects of product arrangement on customers behavior towards new products.

Jiaguo[16] tried to find an optimized product arrangement by using data mining techniques in supermarkets with low physical space.

Buza et al.[17] have tried to attain the optimal products arrangement considering regulatory constraints which are provided by law in each country. They have taken into account constraints like avoiding to place chemical products next to dairy products. They have defined a Constraints Satisfaction Problems (CSP) and tried to arrange the products by introducing an algorithm which solve it.

Matic et al.[18] have introduced a genetic algorithm to solve multi level warehouses arrangement problem. The final goal was to decrease transportation costs for each available item in a multi level warehouse.

Alcazar et al.[19] have proposed a revolutionary and multi objective method to allocate available space on the shelves to the items. They tried to arrange products in shelves according to their categories.

2. PRELIMINARIES

In this paper combination of techniques, such as Association Rules, Genetic Algorithm(GA) and Entropy are used. Association Rules technique looks for items which frequently appeared together and it is a method to analyze customer market baskets[20, 21]. The output from Association Rules involving Support and Rule Support percentages, but they are not enough for interestingness of a rule and we need other measures to evaluate the correlation of every rule[20]. There are many measures to evaluate the correlation of a rule which <Lift> is one of those. GA is a famous technique in solving optimization problems and parallel search in problem space. It was introduced by Holland in 1970s[22]. Adaptive-GA is a kind of GA in which the probabilities of crossover and mutation operators change during the execution of GA[23]. Entropy techniques which quantifies the expected value of the information contained in a message (here a message means a specific realization of the random variable) and it was introduced by Claude E. Shanon in 1948[24].

3. PROPOSED FRAMEWORK

FOR DISCOVERING THE OPTIMIZED MEDICINE ARRANGEMENT IN A PHARMACY, ALL OF AVAILABLE SHELVES ARE CONSIDERED AS A BIG AND UNIFIED SHELF. THIS SHELF WILL BE ENCODED AS A CHROMOSOME IN GENETIC ALGORITHM. After finding the best solution(s) through running GA, the results will decode to achieve the final arrangement. A two phase framework is designed to attain the desirable results. Figure 1 shows the framework.

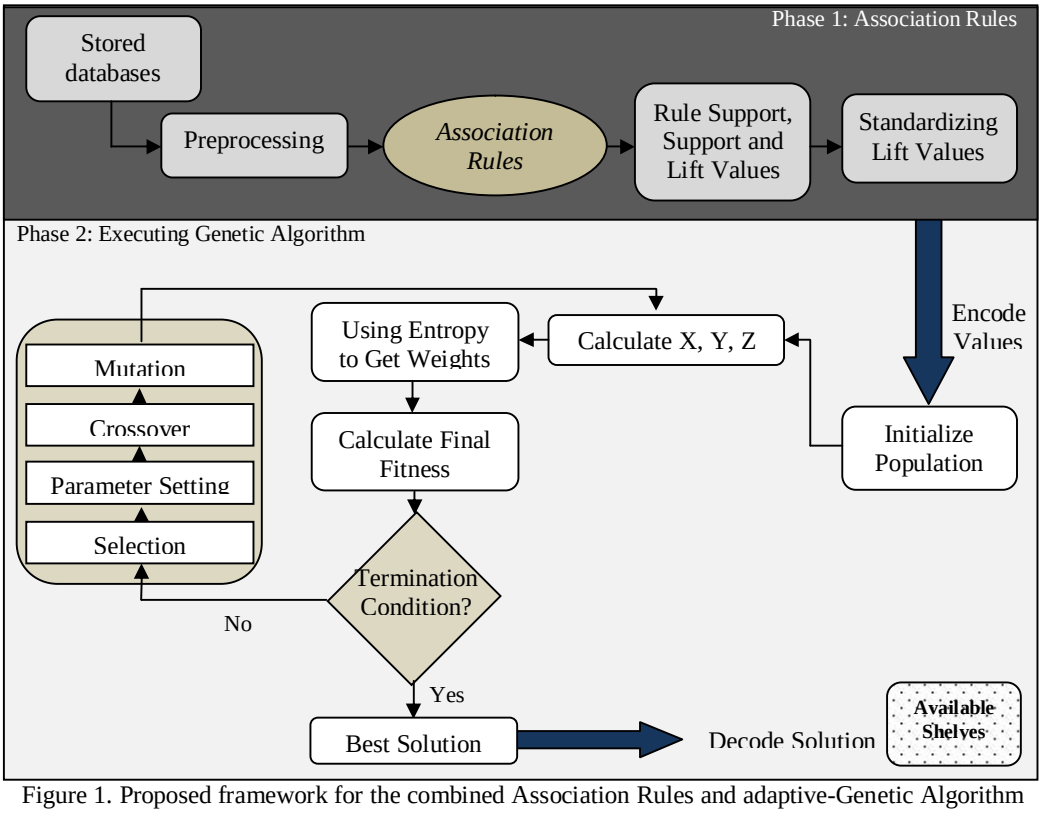

Figure 1. Proposed framework for the combined Association Rules and adaptive-Genetic Algorithm

3.1. Running Phase 1

In this phase of the association rules are made in order. Table 1 shows raw data available in pharmacies database; First, by refining tables, required data is extracted from the data base. After completing the Association Rules, <Support> percentage, <Lift> percentage and <Rule Support> percentage will be in hands. The considerable point in figure 1 is that after implementation of association rules, the final output should be converted into the functional input by Genetic Algorithm. In other words, for implementation of

Genetic Algorithm, encoding of the outputs from phase 1 is essential so that it can be used in the matrices exploited by the program.

Prescription Number	Medicine Code	Type	Date	Medicine Name
…	…	…	…	…
…	…	…	…	…

Table 1. Raw data scheme

The values of <Support> and <Rule Support> can be usable easily, but because <Lift> is not a suitable criterion for measuring the interestingness of a rule, the <Lift> values are standardized in accordance with McNicholas et al. proposed method[25]. Two values of λ^* و υ which are lower bound and upper bound have been calculated by equation 1 and 2. Eventually, amount of $\mathcal{L}^*$ which is the <Standardized Lift> value has been computed based on equation 3.

$$\lambda^* = max\left\{\frac{P(A)+P(B)-1}{P(A)P(B)}, \frac{4s}{(1+s)^2}, \frac{s}{P(A)P(B)}, \frac{c}{P(B)}\right\} \quad (1)$$

$$\upsilon = \frac{1}{max\{P(A),P(B)\}} \quad (2)$$

$$\mathcal{L}^* = \frac{Lift(A\Rightarrow B)-\lambda^*}{\upsilon-\lambda^*} \quad (3)$$

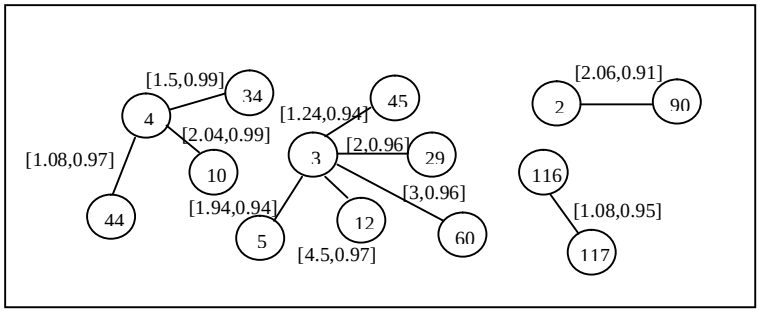

Figure 2. a graph which shows the outputs from phase 1.

Figure 2 displays a graphical example of phase 1 outputs. Numbers of each node represents medicine-code and the weight of edges show the rate of <Rule Support> and the <Standardized Lift> which presented by [RS,SL]. Note that if there is no edge between two nodes, just the rate of <Support> is considered to take effect on the arrangement of those.

3.2. Encoding of Phase 1 results

Permutation coding technique is used in this issue. Every chromosome shows a big shelf which includes permutations of all medicines (n) and each gene contains a medicine code. Exposure of value 101 at gene $D_{1,2}$ represents the existence at the third location in the second row (figure 3).

	0	1	2	3	4	5	6	7	…	c-1
0	$D_{0,0}$	$D_{0,1}$	$D_{0,2}$	$D_{0,3}$	$D_{0,4}$	$D_{0,5}$	$D_{0,6}$	$D_{0,7}$	…	$D_{0,c-1}$
1	$D_{1,0}$	$D_{1,1}$	$D_{1,2}$	$D_{1,3}$	$D_{1,4}$	$D_{1,5}$	$D_{1,6}$	$D_{1,7}$	…	$D_{1,c-1}$
…	.	.	.	.	.	.	.	.	…	.
r-1	$D_{r-1,0}$	$D_{r-1,1}$	$D_{r-1,2}$	$D_{r-1,3}$	$D_{r-1,4}$	$D_{r-1,5}$	$D_{r-1,6}$	$D_{r-1,7}$	…	$D_{r-1,c-1}$

Figure 3. Medicines encoded in a matrix chromosome

To calculate the fitness function, three matrices S, RS, and SL are necessary. Each has been based on the results at the end of phase 1 and used in phase 2. Figure 4 shows how the values are placed. Here Si amount represents the <Support> percentage for the medicine with code i.

S_0	S_1	S_2	. . .	S_{n-1}

Figure 4. Matrix S contains <Support> percentage for each medicine: S_i is the percentage of <Support> for the medicine with code i.

The symmetric matrices, RS & SL (figure 5) which include the <Rule Support> percentage values and the <Standardized Lift> values are formed as illustrated in figure 6.

$$RS = \begin{bmatrix} rs_{0,0} & \cdots & rs_{(n-1),0} \\ \vdots & \ddots & \vdots \\ rs_{0,(n-1)} & \cdots & rs_{(n-1),(n-1)} \end{bmatrix}$$

$$L = \begin{bmatrix} l_{0,0} & \cdots & l_{(n-1),0} \\ \vdots & \ddots & \vdots \\ l_{0,(n-1)} & \cdots & l_{(n-1),(n-1)} \end{bmatrix}$$

Figure 5. RS(Rule Support) and SL(Standardized Lift) matrices

$$RS = \begin{cases} rs_{ij} = rs_{ji} \\ if\ rs_{ij} \neq 0, \quad \text{Rule Support i, j} \\ if\ rs_{ij} = 0, \quad \text{There is no connection between i and j} \end{cases}$$

$$SL = \begin{cases} sl_{ij} = sl_{ji} \\ if\ sl_{ij} \neq 0, \quad \text{Standardized Lift i, j} \\ if\ l_{ij} = 0, \quad \text{There is no connection between i and j} \end{cases}$$

Figure 6. filling the symmetric matrices RS and SL

3.3. Implementation of Phase 2

3.3.1. Calculating Fitness

Fitness function is a criterion to measure how much the solution in each chromosome is close to the optimal solution, although the optimal fitness value is not available here. After implementation, the solution with the highest fitness (equation 4) will be chosen.

The existing Fitness function involves the sum of three different values calculated for all genes. Remember each gene is a medicine code. Ultimate Fitness is the amount calculated in three steps. First, values X, Y and Z are calculated separately for all chromosomes of the current generation (figure 7). Next, the weights of each X, Y and Z are calculated (w_x, w_y, w_z) by using Entropy. Then their effect is determined by the pharmacy manager(λ_x, λ_x, λ_x). They altogether will result in the moderate weight f ($\acute{w}_x, \acute{w}_y, \acute{w}_z$) for arranging medicines. The final values X, Y and Z are calculated through multiplying values $\acute{w}_x, \acute{w}_y, \acute{w}_z$ by values X, Y and Z obtained previously. And finally, the final fitness for each chromosome is obtained. Equation 16 shows the simplified form of equation 8 by using equations 5, 6 and 7.

$$\text{Fitness}_i = \sum_{c=0}^{cc-1} \sum_{r=0}^{rc-1} \left[\left(\sum_{ci=0,}^{c} \sum_{ri=0,(ci \neq c \text{ or } ri \leq r)}^{r} S_{rc} \right) + \sum_{k=0}^{m-1} D_{lk} + \sum_{t=0}^{m-1} P_{lt} \right] \quad (4)$$

$$X_i = \sum_{c=0}^{cc-1} \sum_{r=0}^{rc-1} \left[\sum_{ci=0,}^{c} \sum_{ri=0,(ci \neq c \text{ or } ri \leq r)}^{r} S_{rc} \right] \quad (5)$$

$$Y_i = \sum_{c=0}^{cc-1} \sum_{r=0}^{rc-1} \left[\sum_{k=0}^{m-1} D_{lk} \right] \quad (6)$$

$$Z_i = \sum_{c=0}^{cc-1} \sum_{r=0}^{rc-1} \left[\sum_{t=0}^{m-1} P_{lt} \right] \quad (7)$$

$$\text{Fitness}_i = X_i + Y_i + Z_i \quad (8)$$

	X	Y	Z
$Individual_0$	g_{00}	g_{01}	g_{02}
. . .	. . .	. . .	. . .
$Individual_{p-1}$	$g_{(p-1)0}$	$g_{(p-1)1}$	$g_{(p-1)2}$

Figure 7. Calculated values of X, Y and Z separately

In the proposed framework, three criteria must be considered in arranging the medicines on the shelves:

1) The distance between the dispensing prescription counter and the medicine storage.
2) The distance between medicines which prescribed together frequently.
3) The priority of the medicines that are usually prescribed with the base medicine.

Value X represents the optimality of the placement of the repeated items (with higher S values) near the dispensing stand (cell number $D_{0,0}$ in the chromosome(figure 3)). Namely, to increase the amount of fitness, the algorithm tries to place the medicine with higher amounts of S (sell more) near the cell $D_{0,0}$. Y is the optimality of gaps between neighboring agents. Number of medicines taken between the two neighbors should be reduced as much as possible and is calculated by equation 9. RD_{lt} is number of rows between *l* and *t*, and CD_{lt} shows count of columns. RW and CW are weights for row and column, for example if the cells

height are 1.2 times their widths we set RW to 1 and CW to 1.2 to tell the framework length is more important than height.

$$D_{lk} = \frac{cc \times rc}{(RD_{lk} \times RW) + (CD_{lk} \times CW)} \qquad (9)$$

There is another criterion for assessing the optimal arrangement. That is the placement of the neighbors of each medicine in order of preference. For example, if 32, 14 and 9 are neighbors with 83 and Preferred Priority and Current Priority is calculated in Table 2, Preferred Priority will express the source medicine code tends to take the neighbors in order of importance. Ordering the actual sequence neighbors (which is proposed in this chromosome) falls into Current Priority column. The same amount in both columns (such as value 0 for code 14) indicates a good fit into the origin node (e.g. 83). Table 2 states that the medicine code 83 prefers arrangement of the neighbors as 14, 32 and 9, but it is 14, 9 &32 in the current chromosome (the solution).

	Preferred Priority	Current Priority
32	1	2
15	0	0
9	2	1

Table 2 - the preference amount for the medicine with Code 83

P_{lt} value is calculated from equation 10.

$$P_{lt} = \frac{1}{|Preferred\ Priority_{lt} - Current\ Priority_{lt}| + 1} \qquad (10)$$

Preferred Priorities are calculated by equation 11, and greater values of PP illustrate higher prefer priorities.

$$PP_{lt} = RS_{lt} \times (SL_{lt} \times 100) \qquad (11)$$

Fuzzy normalization is used to calculate a unified fitness value for each chromosome and make the possibility of the ultimate fitness' comparison in different generations and finding out how good a solution is in each one of X, Y and Z (equation 12).

$$Normalized\ Value = \frac{Num - Minimum}{Maximum - Minimum} \qquad (12)$$

Five separate programs were written in which the noted fitness function contained only one of the functions X, Y or Z (the relations 13, 14 and 15). Fitness function was carried out both incrementally and decreasingly (for X as a constant value just one program was written for the maximum and minimum values). The Standard Deviation(SD) of the results of each algorithm was calculated. To ensure that the amount of X, Y and Z do not exceed maximum and minimum values in the main fitness function, the global maximum and global minimum are calculated by equations 16 and 17.

$$\text{Fitness}_i = \underbrace{\sum_{c=0}^{cc-1} \sum_{r=0}^{rc-1} \left[\sum_{ci=0,}^{c} \sum_{ri=0,(ci \neq c \text{ or } ri \leq r)}^{r} S_{rc} \right]}_{X} \qquad (13)$$

$$\text{Fitness}_i = \underbrace{\sum_{c=0}^{cc-1} \sum_{r=0}^{rc-1} \left[\sum_{k=0}^{m-1} D_{lk} \right]}_{Y} \qquad (14)$$

$$\text{Fitness}_i = \underbrace{\sum_{c=0}^{cc-1} \sum_{r=0}^{rc-1} \left[\sum_{t=0}^{m-1} P_{lt} \right]}_{Z} \qquad (15)$$

$$Global\ Minimum_{X,Y,Z} = Minimum_{X,Y,Z} - \left(3 \times SD\_Minimum_{X,Y,Z}\right) \qquad (16)$$

$$Global\ Maximum_{X,Y,Z} = Maximum_{X,Y,Z} + \left(3 \times SD\_Maximum_{X,Y,Z}\right) \qquad (17)$$

Crossover & Mutation

With the use of Permutation coding technique to represent each chromosome and the consideration of the absence of duplicate code in each chromosome, an appropriate crossover operator should be designed. Figure 8 shows a horizontal crossover and figure 9 shows the vertical form.

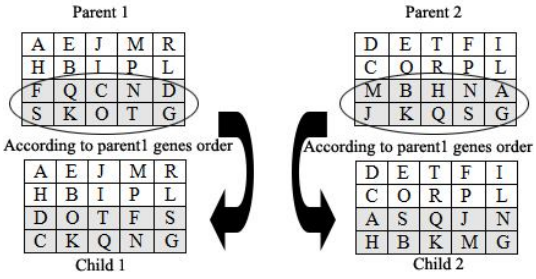

Figure 8. The horizontal crossover operator

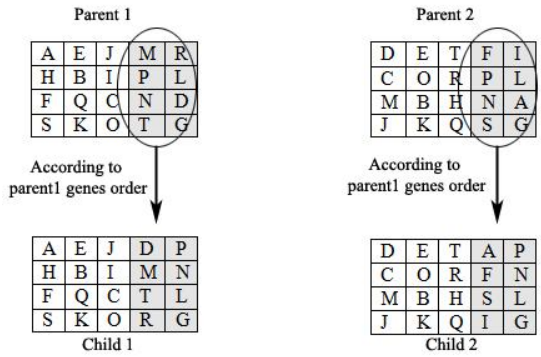

Figure 9. The vertical crossover operator.

Figure 10 shows a function which applies different types of designed mutation methods.

1. a random selection gene (medicine) of the chromosome under the name of g.
2. A is the set of all g neighbours.
3. If | A | = 0 go to Step 1.
4. If | A | = 1, change g placement and the only member in place A in chromosome. Now, go to Step 6.
5. If | A | ≥ 2, select 2 members randomly from the set A, and then swap their place in the chromosomes. Now, go to Step 6.
6. End

Figure 10. designed mutation operation

3.3.2. Termination condition:

This condition is designed to produce minimum 100 generations and afterwards the standard deviation of the best fitness' in last 100 generations is the determiner of producing next generation and continuing the genetic algorithm(figure 11). MI will be set by the experts opinion and its value is often between 0.00001 to 0.0001.

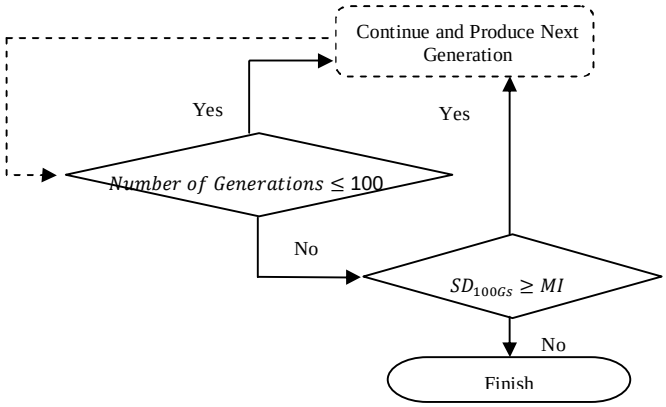

Figure 11. the termination condition for the Genetic Algorithm in the proposed framework; Note, SD_{100Gs} is the standard deviation of last 100 generations.

4. CASE STUDY

To present the proposed framework as a practical one, a pharmacy which stores prescriptions information in a dataset is selected and the framework is applied to the dataset. The selected pharmacy is located in Ahvaz city in Iran.

4.1. Running phase 1

In this phase of the association rules are made in order. First, by refining tables, required data is extracted from the data base. After preprocessing the data records will be in accordance with Table 3. Prescription_ID contains the prescription number and Medicine_Code contains the medicine code. The records with the same Prescription_ID represent the identical prescriptions. For example, according to Table 3, the medicines have together been sold by prescription_ ID 32. It is worthy to mention the first row in table 3 shows the rule 34→4.

Prescription_ID	Medicine_Code
30	2461
31	672
31	274
31	510
32	56
32	54
33	39
…	…

Table 3 - Pharmaceutics sold in any prescription

The implementation of Association rules by data mining software can result in Table 4. Note that, this implementation requires a minimum amount of <Support> and confidence percentages. Namely, the rules that do not satisfy it are removed from the list of results. In this case the minimum <Support> percentage is set to 1% and the minimum confidence is set to 10%. Support column indicates the percentage amount of the medicine with the existing code in the Antecedent Medicine_Code among the entire prescriptions. In other words, some of the percentages of prescriptions contain medicine with Antecedent Medicine_Code code. After executing phase 1, 818 rules discovered which contain 130 medicine in the list. It is worthy to mention the first row in table 4 shows the rule 34→4.

Consequent Medicine_Code	Antecedent Medicine_Code	Support %	RuleSupport %	Lift
4	34	1.51	1.51	13.37
4	44	1.10	1.08	13.31
3	45	1.31	1.29	10.56
117	116	1.13	1.09	77.53
90	2	2.23	2.06	15.94
...	...	...	...	...

Table 4 - Output from the association rules

4.2. Encoding of Phase 1 results:

In this step, the output of phase 1 which showed in Table 4 is encoded to usable matrices for phase 2. First of all, medicines code is mapped to a chromosomes. Then S, RS and SL matrices are filled. (this section has done according to section 4.3)

4.3. Running phase 2:

The Adaptive-GA has been proposed by Srinivas & Patnaik [26] is used in this case. The calculated amounts for each X, Y and Z are shown in Table 5 which are based on equations 13, 14 and 15.

	X	Y	Z
Individual$_0$	14774.96	10382.07	350.27
Individual$_1$	17045.27	10490.06	365.01
. . .	. . .	. . .	. . .
Individual$_{p-1}$	18599.21	10542.75	351.07

Table 5 - Calculated values of X, Y and Z separately

The global maximum and global minimum is calculated by equations 16 and 17. The results are shown in Table 6.

	X	Y	Z
Minimum	5463.08	2872.50	111.46
Minimum Value Deviation	--	4594	5.72
Maximum	24117.30	8037.23	163.25
Maximum Value Deviation	--	746.88	2.04

Table 6. the global minimum and global maximum for X, Y and Z

After setting all the essential parameters in section 3, the framework is used and the final results will be in hands. A snapshot of the final results is shown in figure 12. Note, the final result could be different for each run because the Genetic Algorithm is a non-deterministic algorithm in nature.

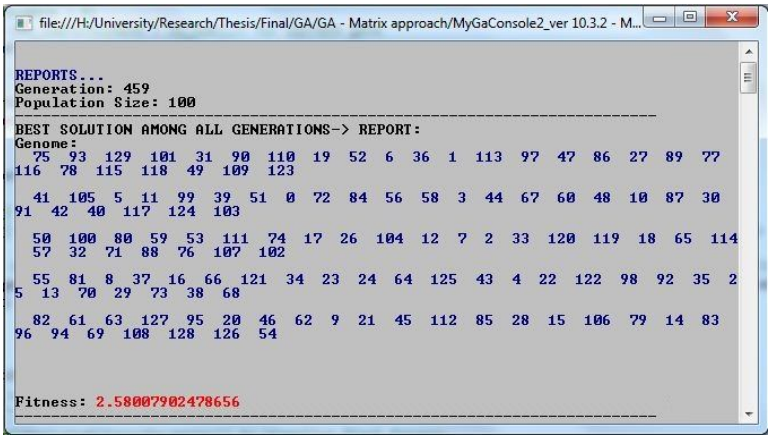

Figure 12. a snapshot of final results

4.4 Simulation

To have faultless simulations, 150 prescriptions are selected randomly from the data base, before executing framework. These prescriptions were not used in the data mining process to avoid logical mistakes in final results.

To simulate the final results, the pharmacy's physical environment and available shelves are designed in computer which is shown in figure 13. Each shelf includes some columns and rows which construct some cells that are equal in height and width, the widths are 1.2 times the heights (in this case).

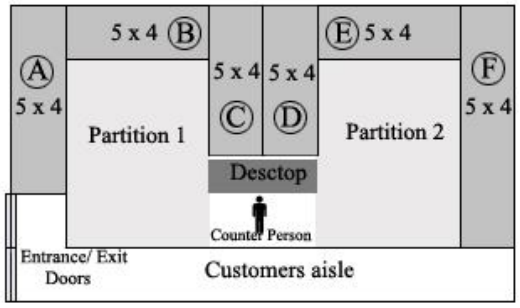

Figure 13 the environment of selected pharmacy designed in computer

The medicines are positioned on the shelves according to two mentioned conventional styles and after that the prescribed items in the 150 selected prescriptions are collected. The final traversed path in column units (for example 16 column units means 16 times the column width) is stored to show the decrease in the traversed path. Next the medicines are placed on the shelves according to new arrangement (Matrix approach). We put the medicines on the shelves by order C, B, A, D, E, F. Then the collecting process is simulated and the final result is compared to the results from two conventional methods. Figure 14 shows a snapshot from final results in simulation process.

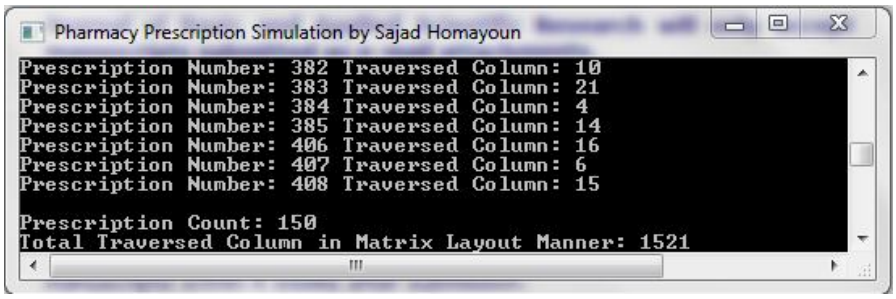

Figure 14 a snapshot of results from simulating New-Matrix approach

Figure 14 shows the traversed columns for each selected prescription all 150 prescriptions in the Matrix approach. Table 7 shows the final results of the simulation process.

Approach	Traversed columns
Alphabetical	2347
Classified	1952
New- Matrix	1521

Table 7 – Final results of simulations

As table 8 shows, there is 35.2 percent improvement in the decrease of traversed columns in comparison with alphabetical arrangement; and there is also 28.08 percent improvement compare to classified method in arranging medicines which could be a significant achievement.

Conventional method	Improvement percent achieved by Matrix approach
Alphabetical	35.2
Classified	28.08

Table 8 – Improvement percentage in New-Matrix method

5. CONCLUSION

In this paper the time reduction of dispensing prescription through using an appropriate medicine arrangement on pharmacy shelves is considered. It is possible to decrease the collecting process time through better arrangement of medicines according to the past information (prescription sales data which are saved in pharmacy's database). The used criteria to arrange medicines are, the distance between medicine location on the shelves and where the pharmacy counter is, the distance between medicines which appeared together frequently and the priority of the medicines that are usually prescribed with the base medicine. First of all, required knowledge is extracted by applying of the Association Rules in phase 1 and the outcomes are directed to phase 2 after the encoding process. Phase 2 executes adaptive-Genetic Algorithm to achieve the best solution. Worthy to mention after finding the best solution, a decoding process must be completed to show the final results. To show the results, a practical case is presented and the final results are displayed. Finally, the output arrangement from the new Matrix approach is simulated and conventional methods are simulated as well. The results show 35.2 percent decrease in traversed path in the new approach compared to alphabetical method. There is also 28.08 percent improvement in compare classified method of arranging medicines on the pharmacy's shelves. There was a need to solve the problem with new approach because if there are n medicines to arrange and the simple and deterministic solving methods are used, it would take a long time to find the optimal solution, because those methods have to examine all the n! possible solutions.

REFERENCES

[1] Smith A., D., Barriers to accepting e-prescribing in the USA, 2006. International Journal of Health Care Quality Assurance, 19(2): 158-180.

[2] Abramson E., L., Patel, V., Malhotra, S., Pfoh, E., R., Osorio, S., N., Cheriff, A., Cole, C., L., Bunce, A., Ash, J. and Kaushal, R., 2012. Physician experiences transitioning between an older versus newer electronic health record for electronic prescribing, International Journal of medical informatics, 8: 539-548.

[3] Ranjan, J., 2009. Data mining in pharma sector: benefits, International Journal of Health Care Quality Assurance, 22(1): 82-92.

[4] Cavique, L., Next-Item Discovery in the Market Basket Analysis, 2005. Proceeding of IEEE conference on Artificial intelligence, Portuguese, pp: 198-199.

[5] Wong, R. C., Fu, A. W., and Wang, K., 2005. Data Mining for Inventory Item Selection with Cross-Selling Considerations, Kluwer Academic Publishers: 1-38.

[6] Cuningham S J and Frank E, 1999. Market Basket Analysis of Library Circulation Data, Proceeding of the 6th conference on Neural Information Processing(ICONIP), pp: 825-830.

[7] Chena, Y. L., Tangb, K., Shena, R. J. and Hua Y H, 2004. Market basket analysis in a multiple store environment, Decision Support Systems, 40: 339– 354.

[8] Meiwati, L., Applications using data mining association rules with priori method for analysis of data on the market basket pharmacy sales transactions, http://papers.gunadarma.ac.id/index.php/computer/article/view/840, retrieved on the 6th of January at 09:01 PM.

[9] Chen, J., Yang, X., Chen, L., Dong, L., Fu, Y., 2010. An Analysis of Shopping Basket in a Supermarket, Proceeding of International Conference on Information Management and Engineering (ICIME), pp: 486-489.

[10] Pandit, A., Talreja, J., Agarwal, M., Prasad, D., Baheti, S. and Khalsa, G., 2010. Intelligent Recommender System Using Shopper's Path and Purchase Analysis, Proceeding of International Conference on Computational Intelligence and Communication Networks, pp: 597-602.

[11] Schwenke, C., Vasyutynskyy, V. and Kabitzsch, K., 2011, Analysis and Simulation of Sales Receipt Data in Supermarkets, IEEE ETFA, pp: 1-8.

[12] Reutterer, T., Mild, A., Natter, M. and Taudes, A., 2006. A Dynamic Segmentation Approach for Targeting and Customizing Direct Marketing Campaigns, Journal of Interactive Marketing, Wiley Periodicals, 20(3): 43–57.

[13] Y. Boztug and T. Reutterer, 2008. A combined approach for segment-specific market basket analysis, European Journal of Operational Research, 187: 294–312.

[14] Hahsler, M. and Hornik, K., 2007. Building on the arules infrastructure for analyzing transaction data with R, in R. Decker, H. J. Lenz (eds.), Advances in Data Analysis, Proceedings of the 30th Annual Conference of the Gesellschaft für Klassifikation, (Springer , Berlin), pp: 449-456.

[15] Movarrei, R. and Vessal, S. R., 2010. Mysteries of New Product Promotion; Effects of Layout on Buyer Behavior, Proceeding of IEEE International Conference on Management of Innovation and Technology (ICMIT), Singapore, pp: 468-473.

[16] Jiaguo, L., 2010. A Solution based on Data Mining to Shelf Space Allocation, Proceeding of the 3rd IEEE International Conference on Computer Science and Information Technology (ICCSIT), pp: 282-285.

[17] Buza, K., Buza, A. and Kis, P. B., 2010. Towards Better Modeling of Supermarkets, Proceeding of IEEE International Joint Conferences on Computational Cybernetics and Technical Informatics (ICCC-CONTI), Romania, pp: 499-503.

[18] Matic, D., Filipovic, V., Savic, A. and Stanimirocic, Z., 2011. Kragujevac Journal of Mathematics, 35(1): 119-138.

[19] Alcazar, A. I. E., Garcia, A. I. M., Guillem, J. M. A., Palmer, M. E. G., Merelo, J. J., Sharman, K. C., and Cid, E. A., 2008, A Multiobjective Evolutionary Algorithm for the Linear Shelf Space Allocation Problem, Proceedings of ACM the 10th international conference on Parallel Problem Solving from Nature: PPSN X, Germany, pp: 1001-1010.

[20] Hann J., Kamber M., 2006. Data Mining Concepts and Techniques, 2nd ed., Morgan Kaufman Publishers, San Francisco, pp: 261-262.

[21] Agrawal, R., Imielinski, T. and Swami, A., 1993, Mining association rules between sets of items in large databases. Proceeding of ACM-SIGMOD International Conference on Management of Data (SIGMOD'93), pp: 207–216.

[22] Holland, J., 1975, Adaptation in Natural and Artificial Systems, University of Michigan.

[23] Back, T., 1992, Self-adaptation in Genetic Algorithms. In: Varela and Bourgine (eds) Proceeding of the First European Conference on Artificial Life, (The MIT Press, Cambridge, MA), pp: 263-271.

[24] Shannon. C. E., 1948. A Mathematical Theory of Communication, Bell System Technical Journal, 27(3): 379–423.

[25] McNicholas, P. D., Murphy. T, B., O'Regan, M., 2008, Standardising the lift of an association rule, Computational Statistics and Data Analysis, 52(10): 4712–4721.

[26] Srinivas, M. and Patnaik, L. M., 1994. Adaptive Probabilities of Crossover Genetic in Mutation and Algorithms, IEEE Transactions on System, Man and Cybernetics, 24(4): 656-667.