

Genetic Algorithm Approaches for Improving Prediction Accuracy of Multi-criteria Recommender Systems

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Abstract

We often make decisions on the things we like, dislike, or even don't care about. However, taking the right decisions becomes relatively difficult from a variety of items from different sources. Recommender systems are intelligent decision support software tools that help users to discover items that might be of interest to them. Various techniques and approaches have been applied to design and implement such systems to generate credible recommendations to users. A multi-criteria recommendation technique is an extended approach for modeling user's preferences based on several characteristics of the items. This research presents genetic algorithm-based approaches for predicting user preferences in multi-criteria recommendation problems. Three genetic algorithms' methods, namely standard genetic algorithm, adaptive genetic algorithm, and multi-heuristic genetic algorithms are used to conduct the experiments using a multi-criteria dataset for movies recommendation. The empirical results of the comparative analysis of their performance are presented in this study.

Keywords: Multi-criteria recommender systems, Genetic algorithms, Aggregation function, Evaluation metrics, Prediction accuracy.

1. Introduction

Recommender systems (RSs) are intelligent decision support systems that have been employed extensively over the last few years to assist users in solving various decision-making problems^{43 20}. Several techniques have been deployed to build RSs, and they are mostly used to categorize the systems. Adomavicius and Tozhilin⁵ classified RSs based on the techniques the system used to make meaningful recommendations. They are *collaborative filtering*, *content-based filtering*, and *hybrid-based fil-*

tering that combines the two techniques in different ways. However, as most of the existing RSs used a single rating to represent the opinion of the user, current research has also confirmed that users' preferences for items may depend on several characteristics, which need to be taken into consideration while making recommendations^{44, 11, 18}. Therefore, one of the most outstanding issues in the RSs research community is to overcome the limitations of using just one rating technique to recommend items⁴.

Multi-criteria recommendation techniques are considered as extensions of the single rating tech-

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niques which use multiple ratings from various characteristics of items to model users' preferences and make more accurate and effective recommendations. This is because different users may have different tastes on items subject to numerous features of the items. For example, in a movie recommendation problem, some users may like a movie based on its action or story, while others may like the same movie by its direction, visual effects or any other combinations of the distinct characteristics of the movie. Therefore, measuring similarities between users should be subjected to the tastes of users on several basic features of the items.

While the advantage of considering multi-dimensional ratings has been acknowledged and its accuracy has been tested by the *RSs* community⁴, the challenge now focuses on choosing an efficient modeling approach for predicting users' preferences based on multiple criteria ratings. The aggregation function approach has been used in different ways by many researchers such as Adomavicius & Kwon², Teng and Lee⁴², Lakiotaki et al.³², and most recently by Jannach et al.^{27 26} who used support vector regression to model multi-criteria recommendation problems. However, some of these approaches have some weaknesses. For instance, Teng and Lee proposed the use of data query technique to solve multi-criteria recommendation problems. In their study, recommendation problem was taken to be a query problem, and as such, they employed data query technique to solve multi-criteria recommendation problem. However, as the study did not consider the multi-criteria recommendation problem as an optimization problem, the feature weights of the criteria ratings were not taken into consideration. Similarly, the support vector regression (*SVR*) used by Jannach et al.²⁷, to model the criteria ratings has some drawbacks, as working with the *SVR* requires the choice of appropriate hyper parameters that would allow for sufficient generalization of performance. Also, as the *SVR* uses a kernel trick, choosing a suitable kernel function could be a problem as well⁹. Further, the multi-criteria user modeling approach by Lakiotaki et al., which uses utility additive algorithms (*UTA*)⁴¹ could only work with sufficiently enough ratings available for the active

user. Therefore, more research on modeling multi-criteria recommendation problems are required to improve the accuracy of the systems

Consequently, in 2011, Adomavicius et al.³ challenged the *RSs* research community to use some of the sophisticated machine learning algorithms such as genetic algorithms, artificial neural networks, and the likes to model multi-criteria recommendation using an aggregation function approach. The work of Jannach et al.²⁷ was among the first attempts to follow this challenge. Furthermore, the same people repeated this call after five years while acknowledging the initial efforts to encourage researchers to apply powerful machine learning techniques to address multi-criteria recommendation problems⁴. This challenge engenders our motivation to use genetic algorithms for improving the prediction accuracy of multi-criteria *RSs*.

The goal of this research is to use the standard genetic algorithm and the optimized genetic algorithms (adaptive and multi-heuristic) to enhance the prediction accuracy of multi-criteria *RSs* using the aggregation function approach. We used genetic algorithm because, unlike gradient-based that are required to satisfy certain mathematical properties like differentiability, convexity, and continuity, the genetic algorithm does not have these restrictions in solving many real-life problems. Another advantage of genetic is the use of crossover and mutation operators, which make it popular and more diverse and thus, more immune to being trapped in local minima³⁶. This study aims to contribute to this growing area of research by providing a comprehensive methodological framework that combines genetic algorithms techniques with the single rating collaborative filtering techniques to model multi-criteria rating problems. The study also adds to our understanding of the expected accuracy improvements of the *MCRSs* over single rating techniques. The article consists of five sections, including this introductory section. Section 2 presents a comprehensive overview of the related background. Section 3 elaborates on the research methodology, while section 4 presents the experimental results and discussion, and finally, section 5 focuses on the conclusion and future research directions.

2. Related Background

In this section, we introduce some basic concepts that will be used extensively throughout the paper. In particular, section 2.1 contains an introduction to multi-criteria recommendation and explanations of the two main approaches of modeling multi-criteria ratings. Section 2.2 gives the general overview of genetic algorithms.

2.1. Multi-criteria recommender systems

Traditionally, *RSs* recommend items to users based on a single rating between users and potential items^{16, 17, 19, 22}. Their rating function f measures the degree of likeness of an item by a user as $f : user \times item \rightarrow r_o$, where r_o is the predicted rating. This function is used to calculate r_o between each user-item pair. However, users' interests may depend on several items' characteristics. For instance, as mentioned earlier, a user may prefer to watch a movie by its direction and/or visual effects, while another user may be interested only in the story and/or action of the same movie. This will be difficult if not impossible for a single rating technique to know whether such users are similar or not. Multi-criteria *RSs* (*MCRSs*) constitute a new recommendation technique that uses multiple ratings (criteria ratings) from different characteristics of items to predict the acceptability of an item by the user. Its utility function extends that of traditional techniques to account for multiple criteria ratings, as in the relation presented in (1), for n distinct criteria.

$$f : user \times item \rightarrow r_o, r_1, r_2, \dots, r_n \quad (1)$$

Now that we have seen the utility function of *MCRSs*, how to model the multiple criteria ratings to predict users' preferences remains to be explained. Although many models and approaches for developing *MCRSs* have been suggested, only the aggregation function and heuristic-based approaches are briefly explained here as they are the central part of this study and for making a comparative analysis of their performance.

2.1.1. Aggregation function approach

The aggregation function is a model-based approach that builds a predictive model to evaluate and compute unknown ratings through training and learning from a dataset²¹. While other approaches consider the overall rating r_o as another criterion, the aggregation function approach assumes r_o to be an aggregation of the other n -criteria ratings as shown in (2).

$$r_o = f(r_1, r_2, \dots, r_n) \quad (2)$$

The recommended items are then given based on descending values of predicted overall ratings. Various methods can be applied to construct the aggregation function $f(r_1, r_2, \dots, r_n)$. These include domain-specific and heuristic methods, statistical techniques such as linear regression ($r_o^k = \sum_i \omega_i r_i^k$ for k number of training samples and i features), and machine learning methods like artificial neural networks, genetic algorithms, or any other algorithms that can be used to model complex functions.

The basic recommendation operations of the aggregation function approach can be summarized in three steps:

1. Decompose the n -criteria ratings into n separate single rating problems
2. Use any traditional technique to predict new criteria rating $r'_i \forall i \in [1, n]$.
3. Use the proposed aggregation to learn the relationship between r_{is} and r_o as in (2).
4. Integrate step 2 and 3 to predict new r'_o .
5. Recommend items based on the strengths of the r'_o

Furthermore, Fig 1 provides a pictorial description of the execution of the proposed *GA*-based aggregation function models. Each of the proposed models follows this same procedure to predict unknown overall rating r'_o and provide *top-N* recommendations.

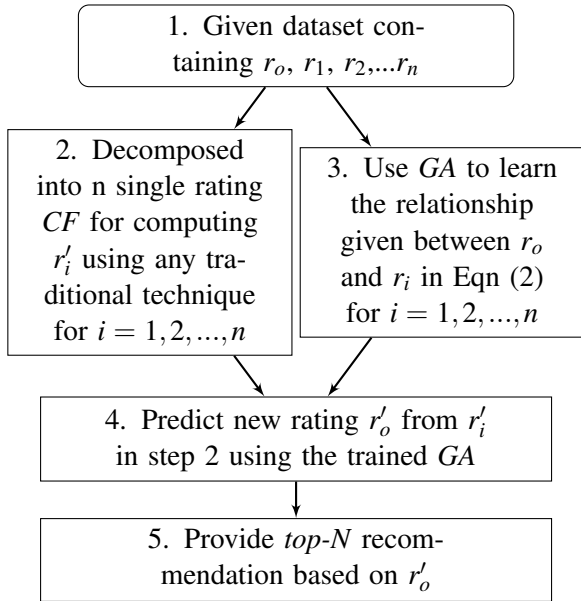


Fig. 1. Operation principles of the GA-based aggregation function models

2.1.2. Heuristic-based Approach

In traditional similarity-based collaborative filtering (CF), a rating r_{ui} of a user u on new item i is estimated using the ratings given by users $v \in U(i)$ who already rated i and have similar opinions with u as shown in (3), where \bar{r}_u is the average of ratings of u and $sim(u, v)$ is the similarity between u and v , which can be calculated using similarity metrics like Pearson correlation similarity in (4).

$$\hat{r}_{ui} = \bar{r}_u + \frac{\sum_{v \in U(i)} sim(u, v)(r_{vi} - \bar{r}_v)}{\sum_{v \in U(i)} |sim(u, v)|} \quad (3)$$

$$sim(u, v) = \frac{\sum_{j \in I(u, v)} (r_{u, j} - \bar{r}_u)(r_{v, j} - \bar{r}_v)}{\sqrt{\sum_{j \in I(u, v)} (r_{u, j} - \bar{r}_u)^2 \sum_{j \in I(u, v)} (r_{v, j} - \bar{r}_v)^2}} \quad (4)$$

Heuristic-based MCRSSs approaches extend the computation of the above mentioned CF technique to account for the criteria ratings. Unlike the aggregation function approach that works based on the criteria ratings, heuristic-based approaches incorporate similarities between users based on individual criteria to predict the overall rating. The

similarities based on each criterion k can be computed as $sim_k(u, v)$ using (4), and the overall similarity can be obtained by modeling the $sim_k(u, v)$ for $k = 1, 2, \dots, n$. Different approaches have been proposed for computing the overall similarities. An average and a worst-case similarity calculation techniques shown respectively in (5) and (6) are among the more commonly used techniques for computing the overall similarity⁴. After calculating the similarity (using either (5) or (6)), the overall rating r_o is estimated the same way the traditional CF estimates r_{ui} in (3).

$$sim_{av}(u, v) = \frac{1}{n+1} \sum_{k=0}^n sim_k(u, v) \quad (5)$$

$$sim_{worst}(u, v) = \min_{k=0, 1, \dots, n} sim_k(u, v) \quad (6)$$

However, even though the efficiency of heuristic-based approach has been proved², one of its major drawbacks is that it can only work with the traditional similarity-based CF.

2.2. Genetic algorithms

In the 1970s, John Holland developed an optimization algorithm called the genetic algorithm (GA for short)²⁴. It is an adaptive and heuristic search technique that mimics parts of natural evolution and genetics. GA was mainly designed to imitate the activities of natural biological systems that are required for evolutionary processes¹⁰, particularly those that follow the postulate of the "survival of the fittest", given initially by Charles Darwin¹⁵. It follows the principle of survival of the fittest between individuals across successive generations for solving optimization problems. Every generation is made up of a population of solutions that are similar to biological chromosomes. Every one of the individuals acts as a point in the search space and represents one possible solution. Then the process of evolution takes place between the individuals in the population.

This optimization technique is much better than conventional artificial intelligence in terms of robustness and its ability to resist slight changes, and it works reasonably well even in the presence of noise. Moreover, it offers significant benefit compared to

older techniques when searching an n-dimensional surface, or a multi-modal or large state-space. To understand the fundamental operations of the GA, some of its basic terminologies need to be understood. The common ones among them are:

- Genes: The elements or building blocks of chromosomes that cannot be further divided.
- Chromosomes: Each chromosome consists of strings of genes, and it represents one possible solution to the problem.
- Population: A collection of chromosomes which can reproduce new chromosomes when genetic operators are applied to them.
- Mutation: A genetic operator that altered the arrangement of genes within a chromosome to produce new traits.
- Crossover: Another genetic operator where some of the genes from two chromosomes are combined to produce new candidate solutions.
- Fitness: A computational value produced by each chromosome that determines the degree to which an individual is considered to be well-fit for solving the problem.
- Selection: A technique of choosing the parent chromosomes that can produce a future population.

GA implementation starts with a random initialization of the population of chromosomes (or just candidate solutions). Then their fitness will be evaluated to determine the candidate chromosomes that can be chosen to reproduce and generate the next population. The operators mentioned above are to ensure that only the fittest chromosomes and their genes are maintained and combined in a well-defined manner in the future generation. Fig 2 is a flowchart that gives a pictorial representation of the steps involved in GA operations³⁹.

While the process of solving optimization problems using GA follow the same basic concepts, different specifications can cause their implementation to be performed differently. Choosing the right genetic parameters is at the heart of determining how optimal the final solution produced by a particular implementation of the algorithm is. Every GA experiment will have some basic parameters such as

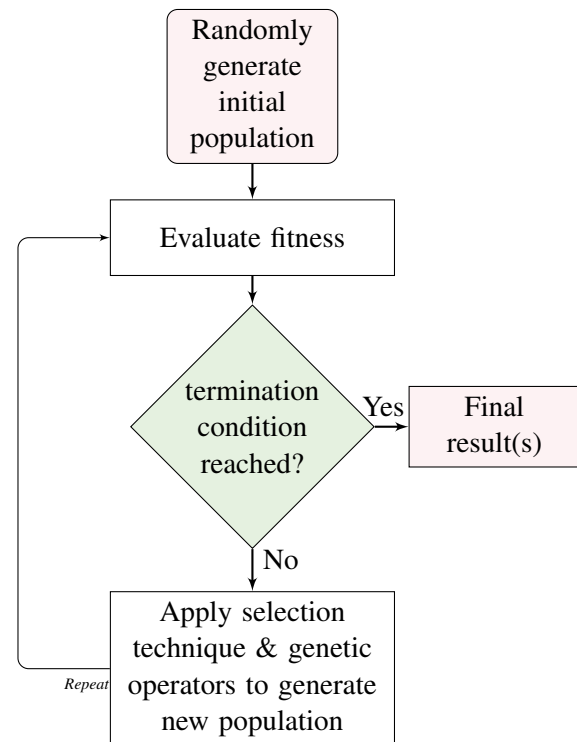


Fig. 2. Basic operations of standard genetic algorithm

the mutation rate, crossover rate, population size, maximum epoch, and elitism number, which are briefly defined below:

- Mutation rate: The probability that determines whether a particular gene in the chromosome will be mutated.
- Crossover rate: The measure of the likelihood of how often the crossover operation will be performed.
- Population size: An integer number that represents the population of candidate solutions at every generation.
- Elitism number: A technique for selecting and retaining the fittest chromosomes called elites, to survive to the next generation. The Elitism number is the total number of elites to be chosen.
- Epoch: The maximum number of training cycles for the experiment.
- Termination condition: A statement that determines when the training should stop.

3. Methodology

The study began with extracting the experimental data set followed by modeling the aggregation function using the *GA* approach. This section consists of the detailed analysis of the data set and the modeling techniques. The explanation of the dataset used for the experiments is given in section 3.1. Section 3.2 shows how to use the three versions genetic algorithm for modeling the criteria rating. Setting the experimental parameters is demonstrated in section 3.3. Finally, the mechanisms on how the overall rating could be predicted and the evaluation metrics used for measuring the accuracy of the systems are contained in sections 3.4 and 3.5 respectively.

3.1. Dataset

A dataset for multi-criteria recommendation problems extracted from Yahoo!Movie website³² was used to test the efficiency of the *GA*-based aggregation function approaches. The dataset contains rating information from users on movies, evaluated on a scale of 13 values from A^+ to F , representing the highest and lowest users' preferences respectively. Four criteria c_1 (action), c_2 (story), c_3 (direction), and c_4 (visual effects) of movies were used as the criteria for recommending movies to users. A rating value $r_i \in [A^+, F]$ for $i \in [1, 4]$ was assigned to each c_i . Similarly, the overall rating is represented by $r_o \in [A^+, F]$. However, the original data set was transformed into a numerical rating matrix with 13 representing A^+ and in a like manner, the number 1 representing F in the original dataset. The dataset was cleaned by removing all cases of incomplete ratings for each criterion and cases of users who rated less than five items to guarantee a sufficient set of items for each user. This compressed the dataset to 62,156 multi-criteria ratings from 6,078 different users on 976 movies.

3.2. Modeling the proposed *GA*-based MCRSSs

As explained in the introductory section, the article proposed three *GA*-based models. This section presents how the criteria ratings are modeled and the methods that each model updates its training

parameters. Sections 3.2.1 discussed the modeling techniques using standard *GA*, while section 3.2.2 contains explanations of the two optimization techniques.

3.2.1. Standard genetic algorithm (SGA)

The experiment has designed an aggregation function that will be used to compute the fitness of chromosomes and the r_o . The proposed aggregation function model is shown in (7), where ω_i are the genes of a chromosome for $i = 1, 2, 3, 4$, since there are four criteria ratings so that each ω_i will measure the significance of r_i in computing r_o . Each ω_i is a randomly generated real number in the interval $[0, 1]$. The numerator in the right-hand side of (7) is the weighted sum ($\sum \omega_i r_i$) of the criteria ratings which is normalized by dividing with the $\sum \omega_i$ to account for the fact the criteria ratings might have different levels of influence in producing the r_o . The constant 1 was added to prevent cases where all the ω_i happened to be zeros. The normalization technique could have a greater importance to the r_i that is closer to r_o .

$$r_o = \frac{\sum_{i=1}^4 \omega_i r_i}{\sqrt{(\sum_{i=1}^4 \omega_i + 1)}} \quad (7)$$

However, as mentioned earlier, training the proposed model using the *GA* requires computing the fitness value of each chromosome in the population. (8) is the fitness function used to calculate the error produced by each chromosome based on the root mean square error (*RMSE*) calculation technique, with k representing a particular feature (k^{th} row of the dataset) in the dataset and r_a^k is the k^{th} overall rating from the dataset.

$$fitness = \sqrt{\frac{1}{N} \sum_{k=1}^N \left(r_a^k - \frac{\sum_{i=1}^4 \omega_i r_i^k}{\sqrt{(\sum_{i=1}^4 \omega_i + 1)}} \right)^2} \quad (8)$$

Now that we have the aggregation and the fitness functions, the *GA*-based approach requires a comprehensive definition for the core genetic operations. A swap operation that picks two genes at random from a chromosome and swapped their positions

(see Algorithm 1) has been used to mutate genes in the chromosomes. The algorithm requires only the current chromosome Ch and its length L as arguments, to randomly generate two different integer indices ($index1$ and $index2$) between 0 and L and use them to swap genes at the generated indices. Additionally, the same mutation operator shown in Algorithm 1 could be presented mathematically as follows. In a chromosome Ch^t of length L during iteration t , with genes $g_i, i = 1, 2, \dots, L$, a randomly selected gene g_j is swapped with another randomly selected gene $g_k, j, k \in \{[1, L] \mid j \neq k\}$. The resulting chromosome $Ch^{t+1} = (g_1, \dots, g'_k, \dots, g'_j, \dots, g_L)$ where g'_k and g'_j were at index j and k in Ch^t respectively.

The usual crossover operation that mates two parents to produce two offspring was used throughout the experiments. Although different permutations can be formed since the genes are selected randomly from parents, Fig 3 gives some basic combinations of parents' genes to produce offspring. The operation chooses half of the total number of genes from each parent at random to form two new chromosomes.

The crossover operator could be formulated mathematically, given two parent chromosomes $Ch_1 = \{e_1, e_2, \dots, e_L\}$ and $Ch_2 = \{g_1, g_2, \dots, g_L\}$, each of length L , then a chromosome $Ch_3 = \{h_1, h_2, \dots, h_L\}$ is said to be the resulting offspring of the crossover between Ch_1 and Ch_2 if and only if every $h_i \in Ch_3$ equals atleast one of the correspon-

Algorithm 1: Mutation operation

```

procedure SWAPGENE(int L, Chromosome
Ch)
   $index_1 \leftarrow random(0, L)$ 
   $index_2 \leftarrow random(0, L)$ 
  while  $index_1 == index_2$  do
     $index_2 \leftarrow random(0, L)$ 
  end while
   $flag \leftarrow Ch(index_1)$ 
   $Ch(index_1) \leftarrow Ch(index_2)$ 
   $Ch(index_2) \leftarrow flag$ 
end procedure

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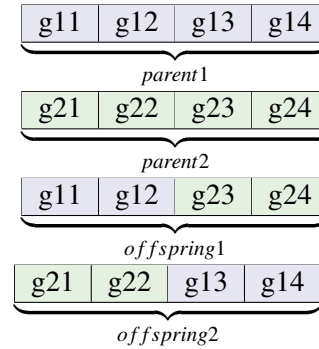


Fig. 3. Sample of the crossover operation

ding genes (e_i and g_i) in c_1 and Ch_2 respectively. That is $\forall i : h_i \in \{e_i, g_i\} \Leftrightarrow Ch_3 \in [Ch_1, Ch_2]$. Also, the crossover operator can be expressed as a probabilistic mapping $A : Ch_1 \times Ch_2 \xrightarrow{r} Ch_3$, where r is the probability (rate) that specifies the likelihood of which corresponding genes will be interchanged. The technique used in this study was to produce two resulting offspring by crossing two parents. This means for the two parents $Ch_1^t = \{e_1, e_2, \dots, e_L\}$ and $Ch_2^t = \{g_1, g_2, \dots, g_L\}$ selected for the crossover at position k and during iteration t , the resulting offspring to be used for iteration $t+1$ are $Ch_1^{t+1} = \{e_1, \dots, e_k, g_{k+1}, \dots, g_L\}$ and $Ch_2^{t+1} = \{g_1, \dots, g_k, e_{k+1}, \dots, e_L\}$, where $k \in [1, L]$. Furthermore, as chromosomes are to be selected from the population for reproduction, the issue now is how to choose the parent chromosomes so that only the best one will survive and produce new offspring. To date, various methods have been introduced and used to measure the chromosomes' fitness and select the fittest to generate a new population. These methods include rank selection, steady-state selection, roulette wheel selection, and a tournament selection. The roulette wheel selection technique has been demonstrated in much GA-based research²⁹ and its efficiency has been established. Therefore, for this study, the roulette wheel selection was used during the selection operation. It works based on fitness values to select the parent chromosomes so that fittest chromosomes will have the chance to be selected (survival of the fittest). To reveal the process of roulette wheel selection, assume that the roulette wheel where all chromosomes are placed is represented by a circle and the area occupied by an individual chromosome depends on its fitness value (see

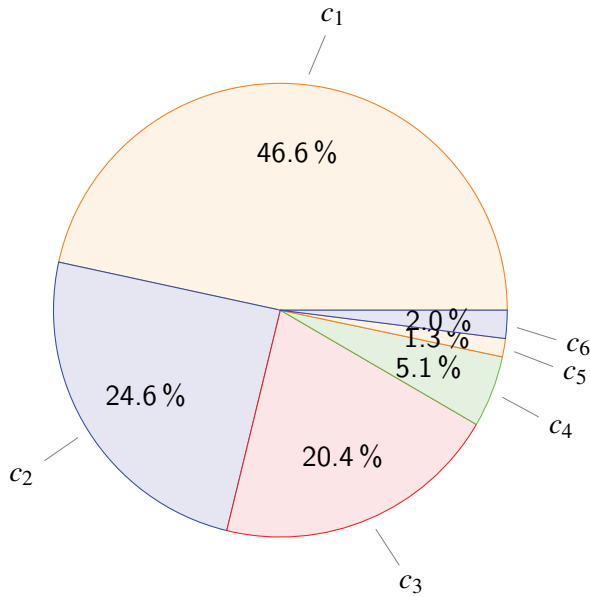


Fig. 4. Roulette wheel selection

Fig 4), and a die is thrown at random onto the surface of the circle to select a chromosome. It is evident that chromosome c_1 occupying 46.6% of the surface will have a high chance of being selected. In addition to its easiness in implementation, the roulette wheel selection technique was used because, as we can see from the figure, the fittest chromosome can be selected many times. This is good since we are not selecting chromosomes of the next generation but the parents, and it is possible for one chromosome (especially the fittest ones) to be parents multiple times.

3.2.2. Optimization of GA-based approach

The experiment did not only used the standard genetic algorithm (SGA) technique to train and learn the aggregation function, other subsets of the GA have been considered as well. This becomes necessary due to the large volume of the dataset and various complex computations required to complete the operations explained above. The optimization techniques are mainly for improving the computation speed and the general performance of the SGA. The two additional techniques used are explained as follows.

- *Adaptive genetic algorithm (AGA)* Traditionally,

SGA needs trial and error method to choose the best training parameters that might produce an optimal solution. AGA is one of the two subsets of the GA used in this study to improve the performance of the usual operations of the SGA. It works by adjusting the training parameters automatically while the training is in progress, with a hope that it may lead to choosing the best parameters at any given time. AGA uses information about the fitness of individual chromosome, the current fittest value, an average of the population's fitness, and the current parameters to dynamically calculates the best parameters to use in the next iteration. This can help to determine how well each of the chromosomes is performing by comparing its fitness with that of the fittest individual so that chromosomes with the poor performance can be dropped and those with better performance can be retained. This dynamic update of parameters is the most preferred way to enable the algorithm itself to adaptively make the necessary updates. Moreover, it increases the operational performance of the algorithm when the population begins to converge, and chromosomes start to come closer to a particular point in the search space. In such a situation, the increase in rates can allow the chromosomes to reach other points in the solution space.

To formulate this technique, let f_b , f_μ , f_c and r_i represent the best population's fitness, the average fitness of the population, the fitness of the current chromosome, and the initial parameter value (e.g., mutation rate) respectively. (9) computes the best rate that was implemented in this study to update the crossover and mutation rates.

$$r_{new} = \begin{cases} \frac{(f_b - f_c) * r_i}{f_b - f_\mu} & f_c > f_\mu, \quad f_b \neq f_\mu \\ r_i & otherwise. \end{cases} \quad (9)$$

Furthermore, it is interesting to present the step by step workflow of the optimized GA. Fig 5 in the next page shows a flowchart that contains the execution steps of the AGA. As we can see from the figure, the AGA works with the average of the fitness values of the population f_μ , the fitness of the fittest chromosome f_b , and the fitness value of individual chromosome f_c . To avoid division

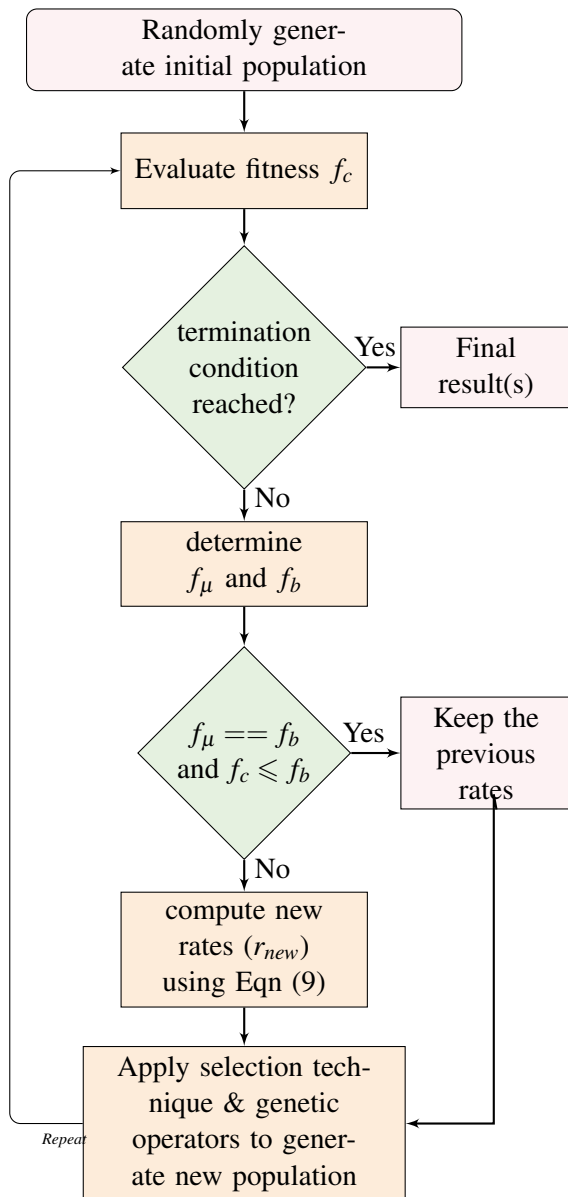


Fig. 5. Basic operations of AGA

by zero in (9) and to prevent losing chromosomes with the high fitness values, the algorithm updates the rates of only individuals whose fitness values are strictly less than f_b .

- **Multi-heuristic genetic algorithm (MGA)** The second optimization technique used for achieving remarkable performance improvements was the multi-heuristic approach¹⁰, which combines the principal features of two or more heuristic approaches to form a single algorithm for enhancing

the prediction performance. This phase of the experiment integrates the SGA with a hill climbing technique that was aimed to decrease the rate of accepting the worse chromosomes. A simulated annealing was the heuristic used which is a member of local search techniques alias threshold algorithms¹. Implementing multi-heuristic technique help in preventing premature convergence²⁵ to improve the search process. Similar to the adaptive method, multi-heuristic was implemented to update the crossover and mutation rates, which are to be set initially at a high rate and the technique will reduce the rate slowly as the algorithm is executing. However, since this technique requires some additional parameters known as starting temperature T_o , and the slow rate S_r , for slowing down the rates so that the crossover and mutation rates will be updated from r_i to r_{new} and cool the T_o using (10).

$$r_{new} = r_i * T_o \tag{10}$$

$$T_o = T_o * (1 - S_r)$$

Additionally, Fig 6 summarizes the execution steps of MGA, where it extends the SGA by applying some heuristics to update the rates automatically. The main difference between SGA and MGA is the cooling state shown in the figure that computes r_{new} from the current rate r_i using the additional parameters (T_o and S_r).

3.3. Setting the experimental parameters

In an experiment involving the use of GA and other evolutionary algorithms, selecting suitable experimental parameters would improve the computation time and the solution accuracy. The population size is one of the key GA parameters that determine the convergence of the search space and an approximate number of iterations (epoch) to be used to produce optimal solutions. Other relevant parameters such as the mutation and crossover probabilities are required to be carefully selected to prevent jumping over the solutions they are close to and prevent getting stuck in local minima. Many research on optimal parameter settings in GA have been conducted^{12, 13, 6}

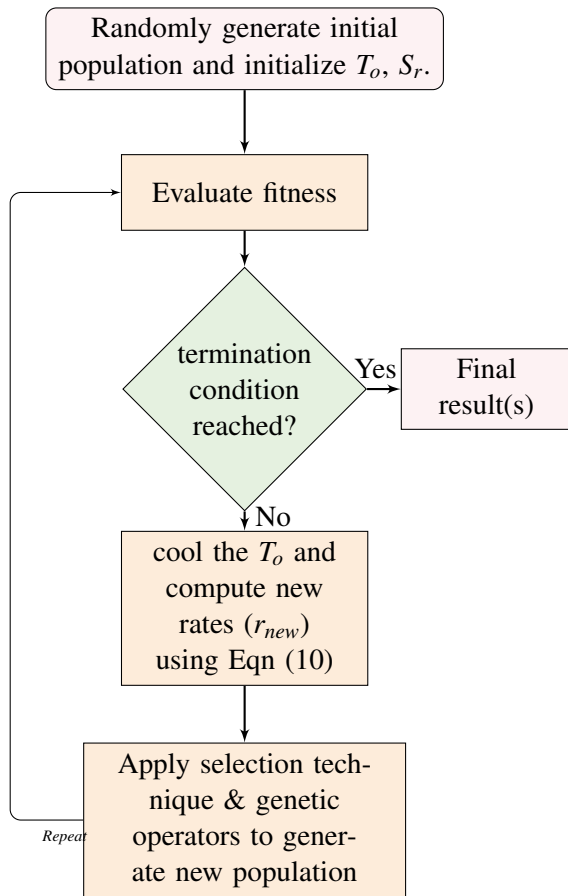


Fig. 6. Basic operations of MGA

and presented the ways and benefits of choosing the optimal experimental parameters. As it was investigated by Alajmi and Wright⁶, selecting a small population size, high crossover probability, and low mutation rate are considered to be the most appropriate control parameters that could provide optimal solutions. Therefore, in our experiments, the same population size $N = 100$ chromosomes has been used in all the GA-based models. Other common parameters are the elitism number $n = 5$, the maximum number of iterations epoch = 200, the minimum (target) error $e = 0.01$, and the termination condition depends on the epoch and e . In SGA, we set the crossover and mutation probabilities to 0.85 and 0.2 respectively. These parameters were chosen after several trial and error experiments. Similarly, the 0.85 and 0.2 were used to initialize the crossover and mutation rates in AGA, and the values keep updating as the algorithm

† latent factor is a measure of common characteristics of items

is running.

To recap, the MGA works by starting with high (hot) crossover and mutation probabilities and cools the values slowly as the algorithm runs. We initialized T_o to 1.00, and S_r to 0.012. The crossover rate begins at 1.00, and the mutation rate was initialized to 0.50.

3.4. Overall rating prediction

Before using any of the GA techniques to estimate the overall rating r_o , the n-dimensional rating problem was decomposed into n separate single-rating recommendation problems so that each criterion will be treated independently as a traditional recommendation problem. This indicates that a traditional collaborative filtering technique is required to estimate $r_i \forall i \in [1, n]$ as $f : user \times item \rightarrow r_i$ ². The current study uses two popular model-based collaborative filtering techniques to conduct several experiments and compare their performance with the proposed GA-based approaches. A singular value decomposition (SVD) and a slope one algorithm were used as the traditional techniques for predicting r_i during the experiments.

SVD is a matrix factorization model that maps items and users to k-dimensional joint latent factors[†]space to model user-item relationships as an inner product in that space³⁰. According to the SVD technique, each item is related with a vector $V_i \in \mathbb{R}^n$. Also, each user is related to another vector $V_u \in \mathbb{R}^n$, so that for any given item i , the entries of V_i determine the degree to which the item possess those latent factors. Similarly, entries of V_u determine the extent at which a user u is interested in the top-level items on the corresponding factors. Therefore, $\sum_{m=1}^n V_{im} \cdot V_{um}$ is the dot product $(V_i^T V_u)$ that represents the interactions between u and i . Further reading on SVD algorithm and also the step-by-step procedure of its implementation are explained extensively in^{30 28}.

In 2005, Lemire et al. presented a paper³³ that proposed a collaborative filtering algorithm called slope one algorithm that was considered to provide a high prediction accuracy than other similarity-based recommendation techniques. Slope one algorithm is a

single rating technique that intuitively works based on the principle of “popularity differential” between items for users³⁴. It is a collaborative filtering technique based on predictors of the form $f(y) = y + a$, which was the reason for the name “slope one”⁷. It predicts any missing rating by computing the average deviation in rating $\bar{\Delta}_{i,j}$ between any pair of items i and j in only two steps: pre-computation and rating prediction steps. Pre-computation step computes the value of $\bar{\Delta}_{i,j}$ using (11), where $N_{i,j}$ is the number of users who rated i and j . Finally, the unknown rating of item k by the user u is predicted from (12).

$$\bar{\Delta}_{i,j} = \frac{\sum_n (r_{n,i} - r_{n,j})}{N_{i,j}} \quad (11)$$

$$r_{u,k} = \frac{\sum_{i/i \neq k} (\bar{\Delta}_{k,i} + r_{u,i}) N_{k,i}}{\sum_{i/i \neq k} N_{k,i}} \quad (12)$$

3.5. Methods of measuring ratings prediction accuracy

Different accuracy metrics have been used in various literature to empirically measure the prediction and recommendation accuracy of RSs by estimating how well the systems can predict nearly exact ratings between every user-item pair. This study evaluates the accuracy of the systems based on the popular metrics broadly classified by Herlocker et al.²³ into three classes: the predictive, the classification and the correlation metrics. The predictive accuracy metrics are to estimate how similar are the predicted ratings with the actual user ratings from the data set. Two metrics that measure statistical differences between the predicted and the actual ratings are used to establish the significance level of prediction accuracy of the proposed GA-based aggregation function approach. A mean absolute error (also known as *MAE*) was used to estimate the average absolute differences between predicted and the actual ratings. The second metric that is related to *MAE* is the root mean square error (*RMSE*) that squares the error differences. It was used in addition to *MAE* so that emphasis on significant errors can be determined. Furthermore, regarding determining how often the systems could precisely make the right decision concerning whether or not an item is good for the rec-

ommendation. *Precision*, *recall*, and F_1 measures are among the popular candidate metrics recommended for measuring top-N ranking accuracy³¹, and they are therefore used in a similar passion as used in several collaborative filtering research works, such as the work of Sanwar et al.⁴⁰.

Additionally, three evaluation metrics for measuring the ranking accuracy of RSs have been used to differentiate between the relevant and non-relevant recommendations carefully, and also to evaluate the ranking accuracy of the algorithms. The area under the curve (*AUC*) of a receiver operating characteristics (*ROC*), the normalized discounted cumulative gain (*NDCG*), and the fraction of concordant pairs (*FCP*) were used to ensure the correct measurement of the ranking accuracy. Finally, a Pearson correlation coefficient was used to measure the linear relationships between the actual from the data set and the predicted ratings.

4. Results and Discussions

Before experimenting the proposed GA-based approaches, we tested and analyzed the efficiency of each of the two traditional collaborative filtering algorithms. Therefore, the experiments are divided into four parts, and results of each experiment are demonstrated in the following subsections.

4.1. Single-rating techniques

As mentioned in section 3.1, each row of the dataset contains the criteria ratings and the overall rating, this experiment considered the overall ratings as the single rating between for a user to the corresponding item and uses them to learn the relationships between users and items. This was done to monitor their execution time and analyzed their performance regarding prediction, ranking, and classification accuracy. Although the *SVD* has high training complexity than the slope one algorithm⁸, it can be seen from the data in Table 1 that the *SVD* technique reported significantly more accuracy than slope one algorithm. In other words, from this result, we can see that the *SVD* technique shows lowest values of *MAE* and *RMSE* and highest values for all the remaining

Table 1. Evaluation results of traditional *SVD* and Slope one techniques.

Evaluation metric	<i>SVD</i>	Slope one
<i>MAE</i>	2.031	2.131
<i>RMSE</i>	2.857	3.048
F_1	0.793	0.786
<i>FCP</i>	0.767	0.739
<i>NDCG</i>	0.927	0.925
<i>AUC</i>	0.755	0.720

metrics. Note that, despite the low performance of the slope one algorithm shown in this table, the subsequent experiments were conducted with both *SVD* and slope one technique to see the performance of each of the *MCRSs* and to analyze the result subject to the traditional *CF* used. This could be interesting as it will show whether there is a high dependency between *MCRSs* and the single rating technique that was used to model the systems.

4.2. *SGA-based Approach*

Recall that both the traditional *SVD* and slope one-based *RSs* used only the overall ratings to learn users' behavior and predict ratings to new items. However, the *SGA-based MCRS* determines the relationships between criteria ratings to estimate the weights ω in (7) and uses them to calculate r_o . The purpose of the *SGA-based* experiment is first, to determine how much the accuracy of the system could be improved compared to the corresponding traditional *SVD* and slope one *RSs*. Secondly, to use the results for comparison with the remaining optimization techniques and possibly with some of the previous methods proposed in the literature for modeling the criteria ratings.

Table 2 presents the breakdown of the performance of *SGA-based MCRSs* according to the same measures of accuracy used in subsection 4.1. In the table, there is a clear trend of decreasing errors (*MAE* and *RMSE*), which is by far, better than the accuracy observed previously in Table 1. The lower errors indicate that the predicted ratings of this technique are much closer to the actual ratings than the traditional

 Table 2. Evaluation results of *SGA-based MCRSs*.

Evaluation metric	<i>SVD-based</i>	Slope one-based
<i>MAE</i>	1.218	1.335
<i>RMSE</i>	1.747	1.931
F_1	0.869	0.864
<i>FCP</i>	0.908	0.866
<i>NDCG</i>	0.994	0.994
<i>AUC</i>	0.912	0.894

techniques. Furthermore, the increase in values of the other six evaluation metrics shows the ability of *SGA-based MCRSs* to make correct decisions about whether an item is suitable for the recommendation or not.

One other significant finding is that comparison between Table 1 and Table 2 showed that the same way *SVD-based* in Table 1 has better accuracy than slope one-based. The *SGA-based MCRSs* that worked with *SVD* algorithm has high accuracy than the one that was modeled using the slope one algorithm.

4.3. *MGA-based Approach*

The difference between *MGA-based* and *SGA-based MCRSs* was that instead of using trial and error to chose parameters for the genetic operators (crossover and mutation) in *SGA-based* technique, the *MGA-based* uses heuristics (simulated annealing in this case) to cool down the parameters as the algorithm was executing. The rationale behind this experiment is to find out whether using the *MGA-based MCRSs* could provide higher performance than the *SGA-based* system. Table 3 shows the results obtained from the preliminary analysis of the performance of *MGA-based MCRSs*. As expected, the *MGA-based MCRSs* show significant improvement to the *SGA-based MCRSs*. The only single point where the two systems showed the same accuracy is the *NDCG* of the slope one-based *MCRSs*. With regards to the comparison of this result with that of single techniques in Table 1, the performance of *MGA-based MCRSs* accords with our earlier observations in section 4.2, which showed that the *MCRSs* has the highest accuracy and also the per-

Table 3. Evaluation results of *MGA*-based *MCRSs*.

Evaluation metric	<i>SVD</i> -based	Slope one-based
<i>MAE</i>	0.961	1.190
<i>RMSE</i>	1.396	1.670
F_1	0.896	0.881
<i>FCP</i>	0.913	0.867
<i>NDCG</i>	0.996	0.994
<i>AUC</i>	0.916	0.896

 Table 4. Evaluation results of *AGA*-based *MCRSs*.

Evaluation metric	<i>SVD</i> -based	Slope one-based
<i>MAE</i>	1.164	1.199
<i>RMSE</i>	1.691	1.670
F_1	0.879	0.869
<i>FCP</i>	0.911	0.867
<i>NDCG</i>	0.996	0.994
<i>AUC</i>	0.913	0.894

formance is subject to the single rating techniques used. The results also provide further support for the assumption that optimizing the *GA* could achieve significant performance improvements. Furthermore, the results in this section indicate that the *AGA*-approach in the next section would possibly provide another promising performance.

4.4. *AGA*-based Approach

The *AGA* approach uses information about the fitness of the individual chromosome to update the mutation and crossover rates.

The *AGA* is another method analogous to *MGA* that are among the more practical ways of improving the accuracy of *SGA*. The main reason for this particular experiment is to establish whether the *AGA* could be better than the two previous approaches, especially the *MGA* approach that has already shown significant improvement over the *SGA*. The results of the performance analysis of *AGA*-based *MCRSs* are presented in Table 4. Although no difference greater than *MGA*-based *MCRSs* was observed from this table, there was a significant improvement compared to the performance of *SGA*-based technique illustrated in Table 2. Furthermore, a comparison of the two results in Tables 3 and 4 reveals that based on slope one algorithm, the *MGA*- and *AGA*-based *MCRSs* have the same values of *RMSE*, *FCP*, and *NDCG*. Turning now to the experimental evidence from *SVD* algorithm, the *MGA*-based *MCRSs* outperforms the corresponding *AGA*-based *MCRSs* on all the evaluation metrics except on *NDCG* where they all have the same value.

4.5. Comparative analysis

Together, the results in Tables 1, 2, 3, and 4 provide important insights into the kinds of traditional technique to use while modeling multi-criteria rating problems using an aggregation function approach, and they also show the effectiveness of using the optimized genetic algorithms (*MGA* and *AGA*). The results in Table 1 are consistent with those of Cacheda et al. ⁸ whose findings showed that *SVD*-based *RSs* are more efficient than the slope one-based *RSs*. Furthermore, the findings confirmed to us that there is an association between performance of *MCRSs* that are designed using aggregation approach and the performance of the corresponding single-rating technique. In summary, these results indicate that *MCRSs* that were developed and integrated with the *SVD*-based traditional techniques are more efficient than the slope one-based approaches, and specifically, the *MGA*-based approach has the highest accuracy. These findings are further supported by Table 5, which shows the percentage of inter-correlations between the actual ratings of the users from the dataset and the predictions of each approach. The first part column of the table contains the correlation between the predicted values of all the slope one-based techniques and the true ratings, while the second column is for the *SVD*-based techniques. From this data, we can see that *MGA*-based *MCRSs* resulted in the highest correlation with the true users' ratings. The present study confirms previous findings and contributes additional evidence that suggests that crossover and mutation operators are the most important driving factors that determine the accuracy of *GA*-based systems. Furthermore, to highlight the significance of introducing the optimization

techniques, Table 6 gives the percentage differences between the *SGA* and the *MGA* and *AGA* with respect to the traditional *CF* techniques.

Moreover, it is encouraging to compare these results with that of the heuristic-based approach that uses similarities between users based on individual criteria to compute the overall rating. To do this, a separate experiment was conducted using a heuristic-based multi-criteria rating approach described in section 2.1.2. We used the worst-case similarity computation in (6) which has been proved to be among the best-performing techniques of measuring the similarity between users^{2 27}. We used item-based *CF* technique with the number of neighbor $k=40$. The decision of using item-based comes after considering that our dataset contains more users than the number of movies (see section 3.1), which could prevent a situation where some users may not have neighbors due to the limitations in the number

Table 5. Percentage correlations between actual ratings and predicted values for each technique

Techniques	SVD-based	Slope one-based
<i>SGA</i>	89.18	85.37
<i>MGA</i>	92.57	89.86
<i>AGA</i>	90.30	86.85

Table 6. Percentage improvements of *MGA*- and *AGA*-based *MCRSs* over the *SGA*-based approach.

Evaluation metric	SVD-based		Slope one-based	
	<i>MGA</i>	<i>AGA</i>	<i>MGA</i>	<i>AGA</i>
<i>MAE</i>	21.10	4.43	10.86	10.19
<i>RMSE</i>	20.09	3.21	13.52	13.52
F_1	3.11	1.15	1.97	0.59
<i>FCP</i>	0.55	0.33	0.11	0.11
<i>NDCG</i>	0.20	0.20	0.00	0.00
<i>AUC</i>	0.44	0.11	0.22	0.00

Table 7. Results of heuristic-based approach

<i>MAE</i>	<i>RMSE</i>	F_1	<i>FCP</i>	<i>NDCG</i>	<i>AUC</i>
1.354	1.934	0.865	0.862	0.9716	0.881

of movies. Table 7 provides the results obtained from the heuristic-based *MCRSs*. As it can be seen from this table, no increase in accuracy was found compared with our *GA*-based approaches.

In addition to the comparison with heuristic-based multi-criteria rating approach, it is also interesting to compare the result of the study with the previous works that use other machine learning and statistical techniques to model the criteria ratings. Although direct comparison may not be possible due to the differences in the data set and the choice of the single rating techniques, we can make this comparison by taking the percentage improvement of proposed *MCRSs* in each study with respect to the single rating technique used to model the system. For instance, in terms of improvements with regard to prediction accuracy, the *MGA* in Table 3 column one has $MAE = 0.961$ and $RMSE = 1.396$, and the corresponding single rating *SVD* in Table 1 has $MAE = 2.031$ and $RMSE = 2.857$, the percentage decrease in $MAE = \frac{2.031-0.961}{2.031} \times 100 \approx 52.68\%$ and similarly, the percent decrease in $RMSE = 51.14\%$.

This is far better than the 16% decrease in MAE of support vector machine approach that was investigated by Fan and Xu¹⁴, not to talk of a linear regression method, which only reduces the error by 15%³⁵. The same comparison can be made with other approaches such as the fuzzy-based approach³⁸, the hybrid approach³⁷ which combined self-organizing map (*SOM*) with fuzzy techniques to improve the prediction accuracy, Jannach et al.²⁷ who proposed a support vector regression method

for improving the accuracy of multi-criteria, and so on. It is also important to note that these comparisons can be made not only on MAE and $RMSE$, the performance based on the remaining metrics can be done as well.

5. Conclusion and Future work

The present study was designed to determine the effectiveness of various genetic algorithms techniques for improving the accuracy of *MCRSs*. The experiment was conducted on the *SGA* which its parameters are set using trial and error, and two additional techniques that update their parameters dynamically when the experiment is executing. The two optimized *GA*-based techniques are the *AGA* that uses fitness values of the population to update the learning parameters and the *MGA* technique that uses the concept of a simulated annealing algorithm to cool down the learning parameters to avoid premature convergence. Each of these techniques has been used in conjunction with two separate collaborative filtering techniques to model the criteria. The two traditional single rating techniques used are the singular value decomposition (*SVD*) and the slope one algorithm. A total of six *MCRSs* have been developed in addition to the two single rating *RSs*. The preliminary results of the eight experiments have been investigated and presented in this paper. The results of this investigation show that the proposed techniques are by far better than the corresponding traditional recommendation techniques, the heuristic-based methods, as well as other aggregation-based approaches that have been developed using some machine learning and statistical techniques. These were confirmed by making a comparative analysis between the proposed *GA*-based techniques and the state-of-the-art in multi-criteria rating problems. According to the experimental findings of the current study, *MGA*-based *MCRSs* achieved the most significant performance improvements. This evidence has further suggested that the *MGA*-based approach is the efficient way of modeling *MCRSs* problems.

However, the *GA* is only one among the most popular types of evolutionary algorithms that could be applied to solve multi-criteria optimization problems, similar algorithms such as an ant colony, a particle swarm optimization, gravitational search algorithms, and so on, need to be tested to investigate the degree to which they might improve the prediction accuracy of *MCRSs*. Another, area for future research might be to explore the use of *GA* to train ar-

tificial neural networks or a hybrid of *GA* with other popular training algorithms like the gradient-descent backpropagation algorithms to train the network. Moreover, a greater focus on combining fuzzy-based approaches⁴⁵ with *GA*, to estimate the overall rating could provide impressive results.

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