



# A novel low complexity multiuser detector based on modified genetic algorithm in direct sequence-code division multiple access communication systems

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## KEYWORDS

Direct Sequence-Code Division Multiple Access (DS-CDMA); Maximum likelihood; Multi-user detection; Genetic algorithm; High dimensional optimization.

**Abstract.** In this paper, we present an efficient evolutionary algorithm for Multiuser Detection (MUD) problem in Direct Sequence-Code Division Multiple Access (DS-CDMA) communication systems. The optimum detector for MUD is the Maximum Likelihood (ML) detector, but its complexity is very high, and involves an exhaustive search to reach the best fitness of the transmitted and received data. Thus, there has been much interest in suboptimal multiuser detectors with less complexity and reasonable performance. The proposed algorithm is a modified Genetic Algorithm (GA) which reduces the dimension of the search space, and provides a suitable framework for future extension to other optimization problems, especially for high dimensional ones. This algorithm is compared with ML and two famous model-free optimization methods: Particle Swarm Optimization (PSO) and Ant Colony Optimization (ACO) algorithms, which have been used for MUD in DS-CDMA. The simulation results show that the performance of this algorithm is close to the optimal detector; it has very low complexity, and it works better in comparison to other algorithms.

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## 1. Introduction

In a DS-CDMA system, the signal is received and detected by a Matched Filter Bank (MFB), which constitutes the conventional detector. This type of receiver is unable to optimally recover the signal, when the channel is contaminated by Additive White Gaussian Noise (AWGN), and suffers from flat or frequency selective fading; because the DS-CDMA signal is affected by Multiple Access Interference (MAI)

and also by the Near-Far Ratio (NFR) [1]. In fact, the signature signals of different users are not completely orthogonal to each other, and cross correlation among these signals results in multiple access interference. Therefore, the conventional matched filter detector, as in single user communication, is no longer effective and causes many problems [2]. In 1986, Verdu in [3] proposed the optimum multiuser detector (OMUD), which consists of a bank of matched filters followed by a Maximum Likelihood Sequence Estimator (MLSE). The MLSE detector generates a maximum likelihood sequence,  $\hat{b}$ , which is associated with the transmitted sequence, as presented in Figure 1 [1]. Vector

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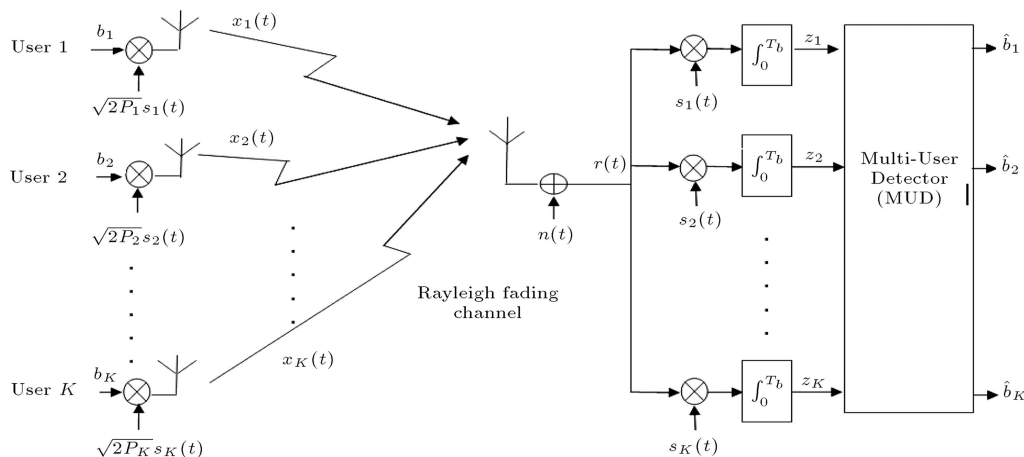


Figure 1. Baseband DS/CDMA block diagram, receiver with MUD [1].

$b$  is estimated in order to maximize the sequence transmission probability, given that  $r(t)$  is received, where  $r(t)$  is extended for all messages, considering all the transmitted messages with the same transmission probability [1]. The OMUD has a computational complexity which grows exponentially with the number of users. Thus, since CDMA systems could potentially have a large number of users, OMUD is unfeasible to implement them. Therefore, many researches have focused on sub-optimum detectors with less complexity and a performance which is almost as high as OMUD. Alternative detectors for OMUD include Decorrelator detector proposed by Verdu in [3] and MMSE detector recommended by Poor and Verdu in [4]. These algorithms have reasonable computational complexity, and their performance is comparable to that of the optimum receiver, but they yield a degraded communication system in the sense of BER [5].

Much effort has been devoted to the development of suboptimal detectors with reasonable computational complexity. Generally, the MUD problem is a Non-deterministic Polynomial (NP)-time complete problem, so iterative algorithms and optimum tools are used for its solution. Kechriotis and Manolakos [6,7] proposed implementation of Hopfield neural network for the optimal CDMA multiuser detection, and in [8] generalized regression neural network has been applied. A multistage joint detector is proposed in [9,10] to perform suboptimal maximum likelihood multiuser detection. A multistage detector is proposed in [11] by Varanasy and Azhang. Honig et al. [12] also introduced a blind adaptive interference suppression technique. In [13] a blind multiuser detector, using support vector machine, was applied. The first GA-based multiuser detector (GA-MUD) was proposed by Juntti et al. [14] which assumes a synchronous CDMA system model communicating over an AWGN channel. To improve the convergence rate of GA, Ergun and Hacıoglu used a multistage multiuser detector as a part

of GA procedure in [15]. In [16], Hanzo et al. showed that the convergence of GA is affected by the type of GA operations and the associated system parameters, and GA is not inherently slow.

For better implementation of multiuser detection, some novel techniques such as Particle Swarm Optimization (PSO) [17-21], Space-Time Linear Dispersion [22] and Simulated Annealing [23] have been used recently. In addition, ant colony-based MUD for suboptimal detection is applied in [24-26]. We compare our proposed algorithm with the algorithm in [24], and also with PSO algorithm [20], and we show that the performance of the proposed method is better, and it is more efficient in a high dimensional space and for a system with a large number of users. These algorithms are compared in the sense of complexity as well.

Although genetic algorithm is a strong method in global search, it is known that many kinds of genetic algorithms are not guaranteed to find the global optimum exactly; especially when they encounter large scale problems [27]. It may be a source of inspiration to think about a size reducing algorithm to overcome the so-called “curse of dimensionality”. Our proposed algorithm, which is based on a modified genetic algorithm, reduces the problem of curse of dimensionality.

The remainder of this paper is organized as follows: Section 2 describes our CDMA system model; Section 3 highlights the algorithm used to implement our proposed detector. The simulation results are presented in Section 4, while Section 5 provides comparison of the complexities associated with our algorithm and other methods. Finally, some conclusions are drawn in Section 6.

## 2. System model

We use the equations presented in [1] to describe a DS-CDMA system. We can consider a multiuser detection as an optimization problem. Based on [28],

the objective function for this problem is defined as (Log Likelihood Function (LLF)) [1]:

$$f(B) = B^T r - B^T R B, \tag{1}$$

where  $r$  is the received signal,  $B$  is the bit sequence with  $I$  bits, and  $R$  is the cross correlation matrix. The complete sequence for all  $K$  users can be obtained through optimization of Eq. (1), resulting [1]:

$$\hat{B} = \arg \left\{ \max_{B \in \{-1,+1\}^{IK}} [f(B)] \right\}. \tag{2}$$

OMUD attempts to find the best vector of data bits, but because of high complexity and unfeasible implementation, it is an inefficient method for multiuser detection. Because the optimization associated with OMUD is high dimensional, the dimension of the search space needs to be restricted; hence, all suboptimal algorithms try to find a solution following an objective function, which is able to improve the performance of multiuser detection. These attempts try to reduce the complexity of OMUD and maximize the DS-CDMA mean performance, with  $K$  active users. Most efforts concentrate on approaching the performance of ML algorithm with less complexity and reliable applicability along with the least possible error. In the next section, we propose our algorithm to achieve this goal and compare our algorithm with other efficient algorithms available in the literature.

### 3. Proposed algorithm

It is well-known in the evolutionary computation literature that basic genetic algorithms (and even many other modified evolutionary algorithms) have some deficiencies in solution of large scale optimization problems. It is worthwhile to devise a dimension reducing algorithm to surmount the so-called “curse of dimensionality”. One of the most important features of genetic algorithms is their ability to find the global optimum of a cost function [29-31]. Many of the modifications performed on the conventional GA’s have targeted this issue [32]. It is trivial that the optimization algorithm performs better when the number of parameters is fewer. Thereby, decomposition of a large scale problem into small sub-problems is of substantial interest. Such ideas are strong motivations for introducing a novel GA which tries to simplify optimization problems and decompose them into simpler problems, since the probability of finding the solution reduces when the number of parameters increases. To elaborate more, consider the following example [32]:

$$F(\vec{x}) = 0.5 + (\sin^2 |\vec{x}| - 0.5) e^{-0.2|\vec{x}|},$$

$$\vec{x} = (x_1, x_2, \dots, x_l), \tag{3}$$

in which  $\vec{x}$  is the vector of parameters of the problem. Obviously, the global minimum of the cost function is located in  $\vec{x} = 0$  and its value is 0. First, consider  $\vec{x} = x_1$ . As shown in Figure 2, in order to reach the global optimum, it is necessary for an individual to be placed in the best region, which is highlighted in Figure 2. This region occupies a ratio of  $\frac{L_1}{L}$  of the search space, which is a significant part of the space. There are many precise tools which can assist GA to reach this global optimum easily.

Now, consider the following situation:

$$\vec{x} = (x_1, x_2). \tag{4}$$

The function is illustrated in Figure 3. Observe that the portion of the search space occupied by the attraction domain of the global optimum is proportional to  $(\frac{L_1}{L})^2$  rather than  $\frac{L_1}{L}$ . Since  $\frac{L_1}{L} < 1$ , this fact directly causes a reduction in the chance of finding the global optimum. When the number of parameters proliferates, the chance decreases exponentially.

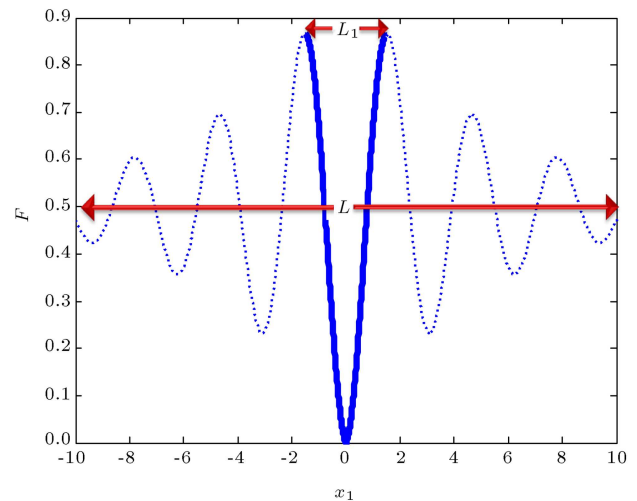


Figure 2. The function  $F(\vec{x})$  in  $\vec{x} = x_1$  [32].

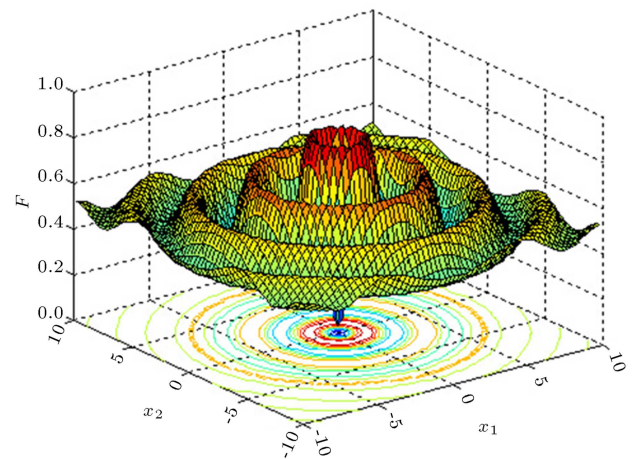


Figure 3. The function  $F(\vec{x})$  in  $\vec{x} = (x_1, x_2)$  [32].

This fact is firstly realized by a naive idea, i.e. neglecting some of the parameters of problem in the optimization procedure. However, in reality, the algorithm allows every parameter to change. The main difference of the algorithm with conventional GA's is that in each iteration, the algorithm is performed over a subset of parameters, while the other parameters are kept constant. In the next iteration, different set of parameters are selected to be constant. The set of changeable parameters are chosen according to a procedure described in the sequel. With a sufficient number of repetitions, one can make sure that an appropriate searching strategy is selected for the whole search space which reduces the dimension of parameters in each iteration of the conventional genetic algorithm. It is heuristically justifiable to initialize the algorithm by a "sufficiently good" solution which is determined by classic detectors, such as the conventional sign detector.

Next, let us take a closer look at the objective function. Considering Eq. (1); the objective function is comprised of two terms:  $B^T r$  and  $B^T R B$ . For maximizing the  $B^T r$  part, considering the fact that each element of  $B$  can only take the values of either 1 or -1, it is enough for each element of  $B$  to be either 1 or -1, according to the sign of corresponding member in  $r$ . Since the  $B^T R B$  term is a square matrix, if the non-diagonal elements were small, it would practically be equal to  $B^T B$ . In this case, it is indifferent if the values of elements of  $B$  are either 1 or -1. The main problem is that in most cases, some non-diagonal matrix elements are not considerably small and cannot be assumed as negligible. Because the matrix  $R$  is symmetric, these elements add terms of type  $2R_{ij}B_i^T B_j$  to the objective function. In this case, if  $R_{ij}$  is negative, the fact that  $B_i^T$  and  $B_j$  bear the same sign helps to increase the value of the objective function, and if  $R_{ij}$  is positive, their difference in sign helps this fact. In other words, the problem variables are no longer independent, and their interaction is influential. The variable showing more interaction with other variables is considered to be a more significant variable. We propose the following criterion as below:

$$id_k = \sum_{j=1}^K abs(R_{kj}), \tag{5}$$

where  $K$  is the number of transmitted bits (assuming BPSK modulation). Any element of  $B$  for which  $id$  takes a higher value is a more significant and effective variable, since it has high interaction with other variables, and influences the convergence of algorithm more. As discussed, a number of variables (say  $M$ ) are selected for optimization in the proposed algorithm, and the rest ( $K - M$ ) are kept constant at the previous value. As we discussed, those variables with lower  $id$  are more likely to be at their optimal value, provided

by the conventional detector (initial value). Thus, it is better to take advantage of a probabilistic algorithm for selection of  $M$ , so that the variables with higher  $id$  are more likely to be selected. Accordingly, the Roulette Wheel algorithm can be used in each iteration for selection of variables with a probability proportional to their  $id$  value. However, we take advantage of a method with less computational cost. This is done through selection of a random number for each variable, having uniform distribution between zero and the  $id$  corresponding to that variable. Then, the  $M$  variables possessing larger random numbers are picked out. This action, on one hand, makes all the variables likely to be selected, and on the other hand, makes those variables with higher  $id$  more likely to be chosen. In the next step, a chromosome is created using these  $M$  variables, and the conventional genetic algorithm is performed on it once. Subsequently, the best response is saved as the new values of these  $M$  variables, and this process continues again for the other set of variables. This process repeats until the selection of all variables. After several iterations, all variables are converged to their optimal value. The parts of this conventional genetic algorithm are as follows.

**3.1. Fitness function evaluation**

In each generation, the fitness values are computed for each chromosome. The fitness function is determined by Eq. (1).

**3.2. Selection**

In order to preserve better chromosomes (solutions) to yield better offspring, we employ the truncated selection scheme, through retaining only some of the parent chromosomes in the population, which possess larger fitness values, and reproduce them in the mating pool from which the two parent chromosomes are randomly selected for the following crossover step [29,31].

**3.3. Crossover**

The bits of the parent vectors are then exchanged using the uniform crossover process in order to produce two offsprings. The process of uniform crossover invokes a crossover mask, which is a sequence consisting of randomly generated 1s and 0s [29,31]. Figure 4 illustrates an example of the crossover process.

**3.4. Mutation**

The mutation process [29,31] refers to the alteration of the value attributed to a bit in the offspring from 1 to -1 or vice versa, with a probability  $pm$ . Here, we set

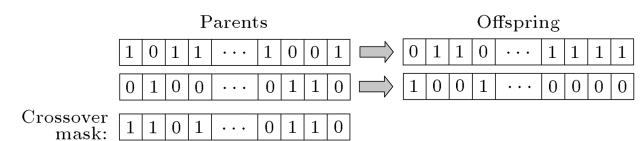


Figure 4. Crossover process [29,31].

$pm = 1/K$ , such that, on average, only one bit in each individual is mutated. Figure 5 displays an example of this process.

The flowchart of the proposed algorithm is provided in Figure 6.

The algorithm seems to have another advantage. Fine tuning algorithms for GA's such as Tabu search

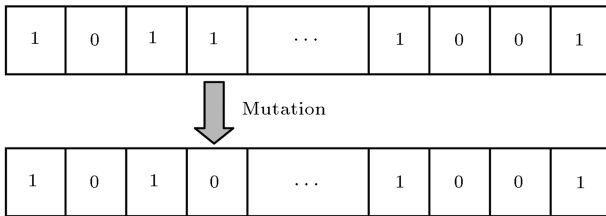


Figure 5. Mutation process [29,31].

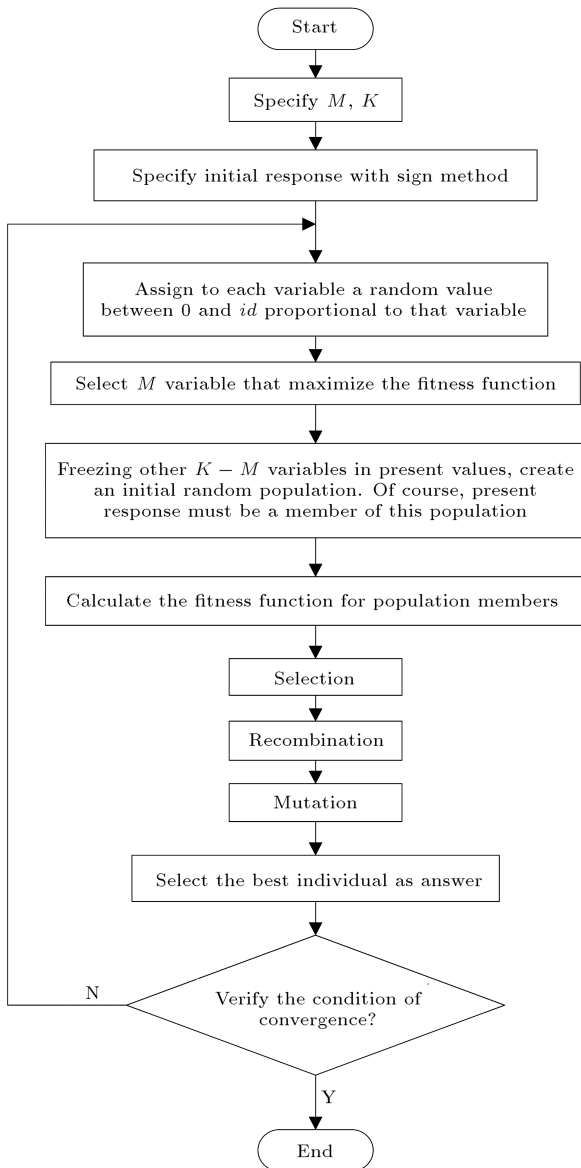


Figure 6. The flowchart of proposed algorithm.

and other types of local search are more efficient in escaping from the local minima when the dimension of the search space is low. Thereby, this algorithm is more likely to perform better when combined with fine-tuning algorithms.

#### 4. Numerical results

In this section, the performance of the algorithm described in Section 3 is compared with two optimization-based algorithms, PSO and ACO, considering BER as the main figure of merit. The convergence of each algorithm versus optimization parameters is also provided. It is assumed that the communication system is asynchronous DS-CDMA MUD, over slow Rayleigh fading AWGN channel. The numerical results were obtained based on the averaging of 1000 simulation runs; these results were attained in identical systems and channel conditions in order to provide fair comparison to other algorithms. Our results are presented in form of examples. In all examples, the simulation parameters are as shown in Table 1.

The spread sequences are selected as Pseudo-Noise (PN)  $m$ -sequence; the number of active asynchronous users in the system is  $K = 20$  and we set  $M = 4$ ; the processing gain is  $N = 63$ . In all examples, it was assumed that the phases, amplitudes, channel gains and random delays of all users are perfectly known in the receiver, and users' power is:

$$E \left[ \sum_{l=1}^L |a_{k,l}^{(i)}|^2 \right] = 1, \quad \text{for } k = 1, 2, \dots, K. \quad (6)$$

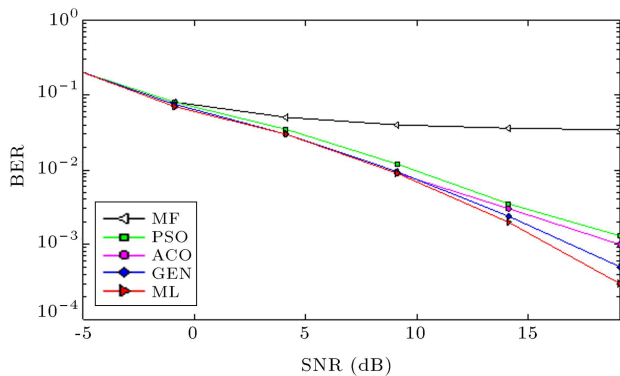
In all simulations, the population of PSO, ACO and the proposed genetic algorithm has been selected as 20, and the iteration has been chosen as 100 for all methods.

Each simulation is presented as an example. In these examples, as will be seen, our proposed method is more effective and better in comparison to the two other algorithms presented before.

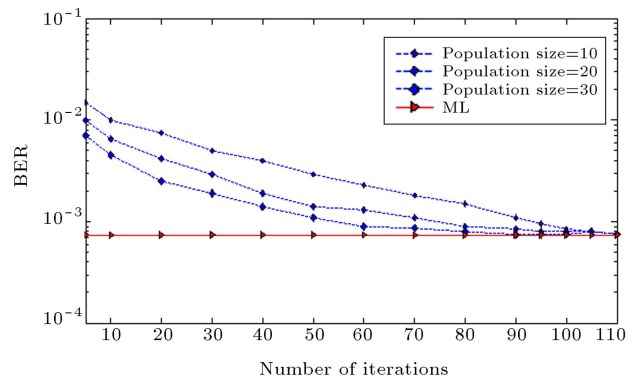
**Example 1.** In this example, the main parameter of each communication system, BER, is discussed. In Figure 7, the BER of the proposed algorithm is compared with the two other algorithms, and also with the comprehensive search in the space of parameters known as ML and the worst case detector as Matched filter. It is revealed that although in low SNR there is no main difference among the methods, the proposed genetic algorithm in high SNR converges to optimum MUD, and the BER of this method is less than ACO and PSO methods. The proposed algorithm has better performance since it decomposes the MUD problem to several simpler problems, and causes better convergence and less BER. Figure 7 shows the unsuitability of the matched filter form, MUD.

**Table 1.** Simulation parameters.

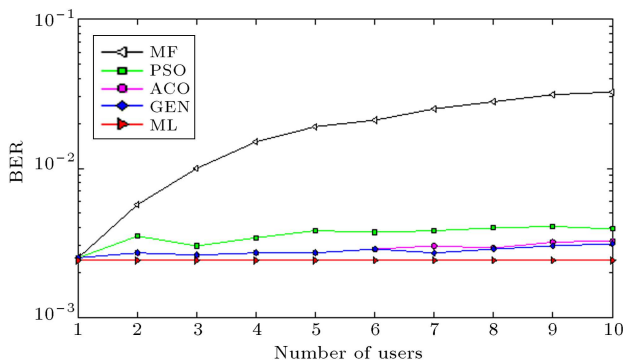
Modulation	BPSK
Spreading code	<i>m</i> -sequence with 63 chips
Communication system	Uplink asynchronous CDMA
User number ( <i>K</i> )	20
Channel	AWGN with slow Rayleigh fading
<i>M</i> (number of higher <i>id</i> variables in proposed algorithm)	4
Path number ( <i>L</i> )	4
Path loss variance	-5 dB



**Figure 7.** BER of the proposed algorithm in comparison to other methods versus SNR.



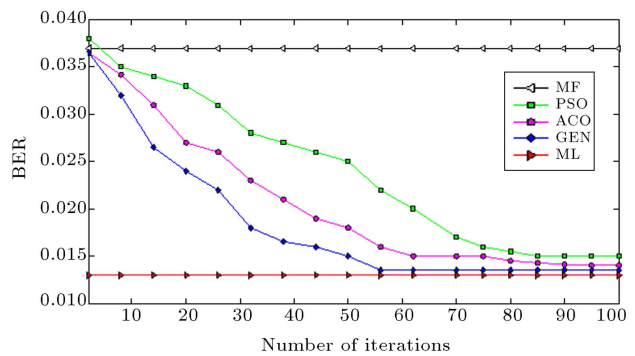
**Figure 9.** BER of the proposed genetic algorithm versus number of generations in different population sizes,  $p = 10, 20, 30$ . SNR is fixed at 15 dB.



**Figure 8.** BER of the proposed algorithm versus number of users in comparison to other methods. SNR is fixed at 12 dB.

**Example 2.** In Figure 8, the effect of the increasing number of users on BER is analyzed for the classic algorithms and optimization-based techniques such as ACO and the proposed genetic algorithm. From this figure, the BER of the proposed algorithm does not considerably increase with the increasing user numbers. This simulation is done for SNR=12 dB.

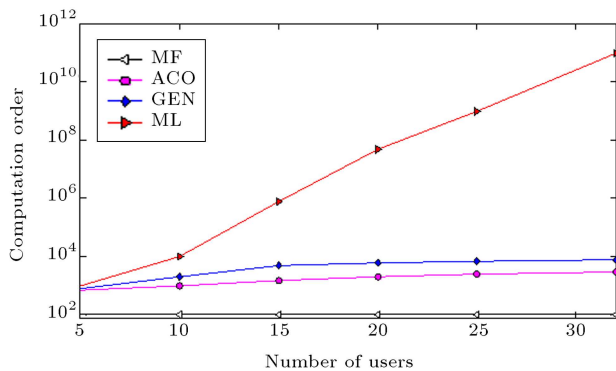
**Example 3.** In Figure 9, the proposed algorithm, with different population sizes, is implemented, and the numerical results are depicted. It is observed that with the population size 30, the algorithm converges to optimum MUD. Of course, this fact happens also



**Figure 10.** BER versus the number of iterations in proposed algorithm and ACO, PSO, ML and Matched Filter methods; SNR=7 dB.

for population sizes 20 and 10, but with delay in convergence. As could be observed in the figure, after approximately 70 iterations, the proposed algorithm operates very well, and the convergence of this case is quite satisfactory. This simulation is carried out with SNR=15 dB.

**Example 4.** In Figure 10, BER versus the number of iterations is illustrated, and it is revealed that the proposed algorithm converges faster and more accurately in comparison to ACO and PSO, because the proposed approach reduces the probability of being trapped in



**Figure 11.** Computation order of the proposed method versus the number of users; comparison to ACO, ML and Matched filter methods.

the local minimum. This property is very important, as the complexity of calculations is decreased to a great extent, and noticeably, the cost of the detector and hardware is minimized. ACO and PSO algorithms are very efficient and applicable in MUD, and this figure shows that our algorithm is comparable with these algorithms, and even in some cases, it works better, and its convergence is faster with lower complexity. This simulation is conducted in SNR=7 dB.

## 5. Computational complexity

A common form in order to compare algorithms' complexities can be done through the O notation, which means the order of magnitude associated with the algorithm complexity. But, comparing algorithms with only O can be insufficient. In order to express the complexity of the analyzed algorithms, it is essential to determine which instructions are carried out and how many times they are processed [1]. If the number of transmitted bits is  $I$  and the number of users is  $K$ , complexity is in the order of  $(KI)^2$  as most genetic algorithms [11]. This relation is because both the number of Generations and the number of Populations are proportional to  $KI$ , and the complexity of genetic algorithms is proportional to the product of these two parameters. For OMUD, the number of operations increases exponentially with the number of users, i.e.  $2^{KI}$ .

Figure 11 shows that the complexity associated with our proposed algorithm is much less than ML and is comparable with ACO. Of course, because of the decomposition in our proposed algorithm and repetition of the calculations for the parameters of modified Genetic Algorithm, the complexity is increased a little and it is more than the ACO complexity.

## 6. Conclusions

In this paper, multiuser detection based on the modified genetic algorithm was implemented, and through

presentation of a new search method, the desirable optimization method was achieved. When compared with sub-optimal algorithms, such as ACO and PSO, the new algorithm shows better performance, and in some cases, rapidly approaches the optimal ML algorithm. This algorithm is quite efficient with good initial guesses and fine tuning of parameters, and shows acceptable performance. The present paper is novel from two viewpoints: First, we have invented a new modified genetic algorithm which is powerful against high dimension problems. This is very important, since we know that the curse of dimensionality is the main cause of failure in large scale optimization problems. Second, we have defined a way to find more important variables in DS-CDMA systems, i.e. we have proposed that users with higher cross-correlation have more important role in the final fitness function. The proposed method presents the selection criteria of more important parameters that influence the convergence of the genetic algorithm. So the optimization procedure should be applied first to them and then to others. In the field of evolutionary computation there are no powerful analytical studies on algorithms. However, that is a very difficult work. We suggest interested and capable readers to try that on the current method.

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