

A Minimum Distance guided Genetic Algorithm for Multi-User Detection in a Multi-Carrier CDMA Wireless Broadband System

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Abstract— We propose a novel Minimum Distance guided Genetic Algorithm (MDGA) for Multi-User Detection (MUD) in a synchronous Multi-Carrier Code Division Multiple Access (MC-CDMA) broadband wireless system. In contrast to conventional GAs, our MDGA exploits adequately the output from a bank of Matched Filters as guidance. It starts with a balanced ratio of exploration and exploitation which is maintained throughout the process. A novel replacement strategy is proposed which increases dramatically the convergence rate as compared to the conventional GAs. This allows us to use the simplest form of genetic operators to gain significant reduction in computational complexity as well as near-optimum results. The simulation results demonstrate that our scheme achieves 99.54% and 50+% reduction in computational complexity as compared to the MUD schemes using exhaustive search and conventional GA respectively.

Index Terms — MC-CDMA, Multi-User Detection, Genetic Algorithm, Multiple Access Interference

I. INTRODUCTION

Multi-Carrier Code Division Multiple Access (MC-CDMA) is an emerging broadband wireless transmission technique that combines the advantages of both Orthogonal Frequency Division Multiplexing (OFDM) and Code Division Multiple Access (CDMA) together [1-3]. In MC-CDMA, orthogonal spreading chips from different users are modulated over all the available sub-carriers to achieve high frequency diversity gain. Multi-path problem can be mitigated effectively by using multi-carrier OFDM modulation technique. This system allows all the users to simultaneously share the same frequency band by transmitting data on all sub-carriers at a same time. However, MC-CDMA suffers from a so-called Multiple Access Interference (MAI) problem because in reality spreading codes are not always perfectly orthogonal. To reduce MAI, Verdu [5] proposed a joint detection of all users in CDMA system, called multi-user detection (MUD). The idea of MUD is to treat MAI as a part of information, not noise. In this way, it could improve the system performance significantly. Hence, MUD has received much attention for both CDMA and emerging MC-CDMA systems [4-8].

However, the optimal MUD detector proposed by Verdu becomes impractical due to high computational complexity when there is a large number of users. With the optimal MUD

detector, the receiver should consider all possible combinations of the transmitted signal and check which one could maximize the joint correct decision probability of the bits received from all the users. This is not feasible since the system has to check every possible combination of the bit vector sent. For example, if there are K users in the system, the total number of possibilities becomes 2^K . Hence, the computational complexity of the optimal detector increases exponentially with the increasing number of users. Therefore, recent research work focuses on looking for suboptimal MUD solutions which are feasible in practice.

Genetic Algorithm (GA) [9] is an intelligent technique derived from the principles of genetics and natural selection which can be used to search suboptimal solution with low complexity for multi-objective combinatory optimization problem. GA based suboptimal MUD was first proposed in [10] for CDMA systems showing its capability in approaching single-user performance bound at lower computational complexity than the exhaustive search used in the optimal detector. Later some other GA based MUDs have been proposed (e.g. [1, 11]) with a much better start than that in [10] but gradual convergence towards the optimum solution due to their classic sophisticated replacement strategies. Therefore, a simple intelligent scheme is still required to improve the convergence rate without increasing the complexity of the system. In this paper we introduce a novel and simple search mechanism to increase significantly the convergence speed of conventional GA schemes (e.g. [10, 11]) for MUD application.

The rest of the paper is organized as follows. Section II describes the system model for synchronous MC-CDMA system. The Minimum Distance guided GA is proposed in section III, followed by its performance analysis in section IV. Section V concludes the paper.

II. SYNCHRONOUS MC-CDMA SYSTEM MODEL

We consider a bit-synchronous MC-CDMA system as shown in Fig. 1, where K users simultaneously transmit data bits over an additive white Gaussian noise (AWGN) channel. Assuming that the number of chips is equal to the number of sub-carriers, each user bit is firstly spread by a unique pseudo-random

sequence. Then each chip of the corresponding spread signal is modulated over each of the “M” orthogonal sub-carriers. The k^{th} user’s transmitted signal is given by,

$$s_k(t) = \sqrt{\frac{2E_k}{M}} \sum_{m=1}^M c_{k,m}(t) \cdot b_k(t) e^{j\omega_m t} \quad (1)$$

where, E_k : The transmit power of the k^{th} user ($k = 1, \dots, K$),

M : Number of sub-carriers,

T_b : Data bit duration,

$b_k(t)$: The transmitted bit sequence of the k^{th} user,

$c_{k,m}(t)$: Time-domain representation of the k^{th} user’s spreading sequence over the m^{th} sub-carrier,

$c_k(t) = \{c_{k,0}(t), c_{k,1}(t), \dots, c_{k,m}(t)\}$: Time-domain representation of the k^{th} user’s spreading code over all sub-carriers,

$\omega_m = 2\pi f_m$, where f_m ($m=1, \dots, M$) are the subcarrier frequencies and $f_m = f_1 + (m-1)\Delta f$, where frequency spacing Δf is $1/T_b$.

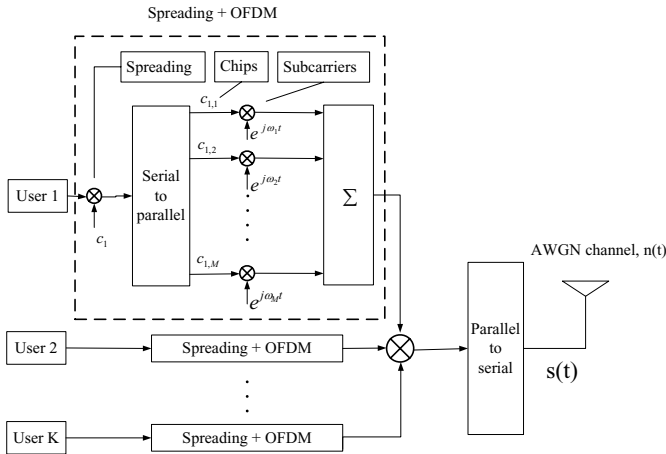


Fig. 1. Transmitter model of MC-CDMA under AWGN uplink channel.

After the spreading and OFDM modulation, the signal is then transmitted over the AWGN channel. Hence, a number of users are able to share all the bandwidth (sub-carriers) simultaneously. The energy of the spreading sequence over a bit period of “ T_b ” for each user is assumed to be “1”. Note that the spreading sequences used may not be perfectly orthogonal to each other in reality due to the cross-correlation product. Assuming perfect synchronization at the receiver, they will have good auto-correlation properties but bad cross-correlation properties.

Fig. 2 shows a simple MC-CDMA receiver followed by a novel GA based MUD. The data carried by each sub-carrier is firstly de-modulated. The demodulated data on the sub-carrier frequency f_1 yields a composite part of the spread signals of all the users, contributed by the 1st chips of their respective spreading sequences. Similarly, for the sub-carriers f_2 till f_M , the contribution is from the set of the 2nd chips till the last set of chips of the spreading sequences from all users respectively. The received signal on the m^{th} sub-carrier is,

$$r_m(t) = \sum_{k=1}^K \left[\sqrt{\frac{2E_k}{M}} c_{k,m}(t) \cdot b_k(t) \right] + n(t) \quad (2)$$

where, $n(t)$ is the AWGN noise added to the signal with two-sided power spectrum density $N_0/2$.

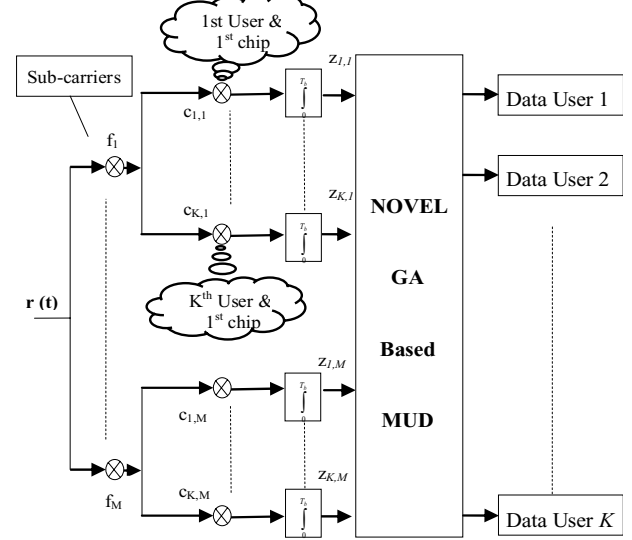


Fig. 2. MC-CDMA receiver model for uplink.

The information of any particular bit of a user is carried by all of the sub-carriers at any given time. The matrix representation of the received signal on the m^{th} sub-carrier is as follows:

$$r_m = C_m E b + n \quad (3)$$

where,

$$C_m = [c_{1,m}, \dots, c_{K,m}]$$

$$E = \text{diag} \left[\sqrt{\frac{2E_1}{M}}, \dots, \sqrt{\frac{2E_K}{M}} \right] \quad (4)$$

$$b = [b_1, \dots, b_K]^T$$

$$n = [n_1, \dots, n_K]^T$$

As shown in Fig. 2, the output from the matched filters can be represented in a form of vector “ Z_m ” [1]:

$$Z_m = [z_{1,m}, \dots, z_{K,m}] = R_m E b + n \quad (5)$$

$$\text{where, } R_m = \begin{bmatrix} \rho_{11}^{(m)} & \rho_{12}^{(m)} & \dots & \rho_{1K}^{(m)} \\ \rho_{21}^{(m)} & \rho_{22}^{(m)} & \dots & \rho_{2K}^{(m)} \\ \vdots & \vdots & \vdots & \vdots \\ \rho_{K1}^{(m)} & \rho_{K2}^{(m)} & \dots & \rho_{KK}^{(m)} \end{bmatrix}$$

$\rho_{jk}^{(m)}$ is actually the value of cross-correlation ($j \neq k$) and the auto-correlation ($j=k$) of the spreading sequences contributing on the m^{th} sub-carrier. MAI imposed by the cross-correlation between the spreading codes is the main problem in an MC-CDMA system. The Matched Filter Conventional Detector (CD) for the MC-CDMA system treats MAI as noise. However if we exploit knowledge of the users’ spreading sequences as auxiliaries, the MAI can be substantially reduced [1], resulting

in the corresponding user capacity gains and better BER performance.

The joint optimum decision rule for a K-user synchronous CDMA system was discussed in [1]. That model can be easily extended to a K-user MC-CDMA system model. The discrete-time correlation metric on the m^{th} sub-carrier can be expressed in vector form as:

$$\Omega_m(\mathbf{b}) = 2 \operatorname{Re}[\mathbf{b}^T \mathbf{E} \mathbf{Z}_m] - \mathbf{b}^T \mathbf{E} \mathbf{R}_m \mathbf{E} \mathbf{b} \quad (6)$$

Since the data is transmitted over M orthogonal sub-carriers, the contribution of all the likelihood functions will yield an optimum vector $\hat{\mathbf{b}}$

$$\Omega(\mathbf{b}) = \sum_{m=1}^M \Omega_m(\mathbf{b}) = \sum_{m=1}^M \{2 \operatorname{Re}[\mathbf{b}^T \mathbf{E} \mathbf{Z}_m] - \mathbf{b}^T \mathbf{E} \mathbf{R}_m \mathbf{E} \mathbf{b}\} \quad (7)$$

Hence, the decision rule for the optimum K-user MC-CDMA multi-user detection scheme based on the maximum likelihood criterion is to choose the specific bit combination \mathbf{b} out of 2^K possible combinations, that maximizes the correlation metric of Equation (7). Therefore, it is

$$\hat{\mathbf{b}} = \arg \left\{ \max_{\mathbf{b}} [\Omega(\mathbf{b})] \right\} \quad (8)$$

In the next section, we propose a novel Minimum Distance guided GA for MUD (MDGA-MUD) which provides fast convergence towards near-optimum solutions with low computational complexity.

III. MINIMUM DISTANCE GUIDED GENETIC ALGORITHM

Our proposed novel GA is designed to accelerate the searching speed to find the optimal solution by adequately exploiting the output of a bunch of CDs as guidance. As compared to conventional GA mechanisms for MUD [1, 10, 11], our MDGA proposes two main modifications, M1 and M2. The idea is to keep a balanced search throughout the GA generations: M1 allows us to start the initial search guided by CD's output together with a reasonable amount of randomness derived from general GA theory. M2 is an intelligent replacement strategy that plays the dominant role in providing fast convergence rate. Combining the two modifications together offers our GA a good jumping-off point of search as well as increased convergence with low complexity while keeping the optimum performance. Next, we explain in detail how the MDGA operates.

A. Initial Population (M1)

This section explains the first modification – named M1 in this paper. Considering that a good initial estimation of the possible solutions is worthwhile for GA to obtain good performance at low cost of searching progress, the selection of initial population to approach optimal solution is created by mutating the output of a CD.

Let the total population of chromosomes be “ N_p ”, where each chromosome is represented as each row vector in the population matrix. In order to ensure that each bit of a CD's

output experiences change at least once, we generate the initial “K+1” set of population by perturbing the CD's output in such a way that the Hamming Distance (the number of different bits) between the CD's output and the new individual remains 1, which is the essence of our so-called Minimum Distance approach. The CD's output is considered as a robust jumping-off point of search. However, there is a high probability that a search which is guided only by CD's output can get stuck at local optima at high SNR values. In order to ensure a certain proportional searching diversity we make the rest of the population randomly to explore optimum solution in the search space as shown in Fig. 3.

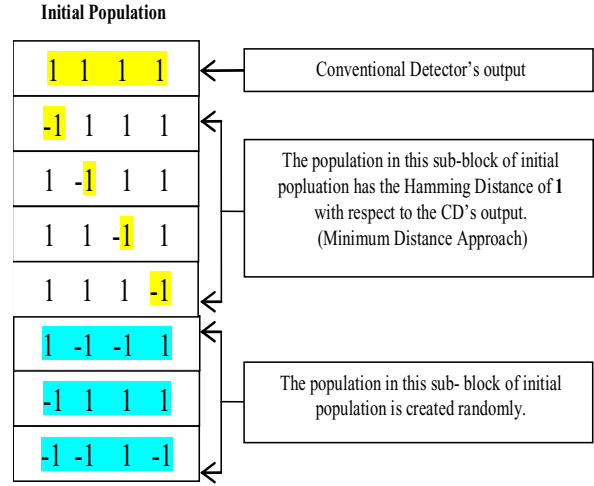


Fig. 3. Formation of Initial pool for the proposed GA.

It is noted here that this modification in the formation of initial population will create some dependency of the population size on the number of users. For example, if the number of users is “K”, then the population size should be chosen in a range of $K < N_p \leq 2K$. So, the algorithm will adjust the population size with the increasing number of users which is actually in accordance with the study carried out by [1]; indicating the need of properly increasing the population size when the number of users in the system is increased.

B. Fitness Function

In general GA, the goal of a fitness function is to evaluate the worth or status of each chromosome. In the MUD problem, the objective of the fitness function is the maximization of the cost (or objective) function, as defined in Equation (7). Each bit in vector “ \mathbf{b} ” actually represents a bit sent by a particular user. The task of MUD is to detect all the users' bits coherently. In order to correctly detect the bit of each user, we need to find such a combination of vector “ \mathbf{b} ” that will maximize the cost function. Hence, GA is invoked in a search for such an optimum solution vector $\hat{\mathbf{b}}$.

C. Replacement Strategy (M2)

After the successful evaluation of the initial pool, truncation selection takes place in which the candidate solutions are ordered by fitness, and according to some selection rate,

“Xrate”. In our case, we set a fixed value $Xrate = 1/2$. The most $\lfloor N_p/2 \rfloor$ fittest individuals in the rank list are selected as candidate parents, where $\lfloor \bullet \rfloor$ stands for floor operator. For example, if the population size is 30, we first select 15 best candidates by the truncation-selection method and then starting from the fittest two parents we form two offspring by performing simple one-point crossover operation. Then, from the next two fittest mating parents we form two more offspring and so on till we form $N_p - (K+1) = 30 - (15+1) = 14$ new offspring. We designed the mating process in a way that in each generation, the number of offspring generated is $K+1 - \lfloor N_p/2 \rfloor$ less than the selected parents, where symbol $\lceil N_p/2 \rceil$ acquires the ceiling value of $N_p/2$.

After successful mating, we replace K prior chromosomes in the rank except fittest mate from the population matrix by performing the same Minimum Distance approach using the fittest mate, i.e. the population matrix will contain the fittest mate on the top along with the “ K ” individuals having Hamming Distance of 1 biased from the fittest and the previously formed “ $N_p - (K+1)$ ” number of offspring. This is how we exploit the information of the best mate (local search) at each generation and how we create a reasonable number of offspring out of the mating pool for exploration.

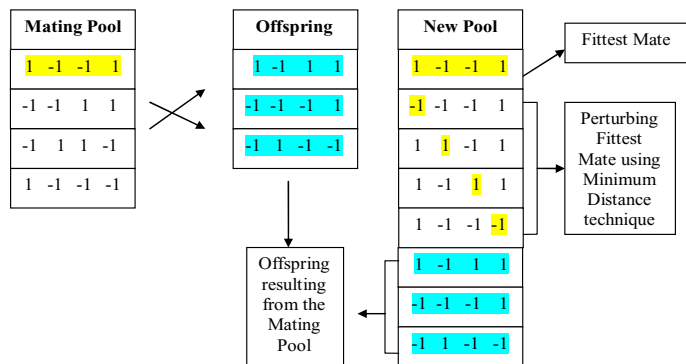


Fig. 4. A Novel Replacement Strategy for MDGA.

In MDGA, the GA is firstly guided by CD’s output and then in the following generations, it is guided by the best mate created from the population matrix in each generation. The fittest-initiated “ $K+1$ ” individuals along with the “ $N_p - (K+1)$ ” offspring generated from the mating pool ensures that the GA would not likely be stuck at the local maximum. The process involved in the replacement strategy is shown in the Fig. 4, with an example population size of 8 chromosomes for a 4-user MC-CDMA system. Note that the crossover point is taken after the 2nd bit.

D. Type of Mutation & Crossover

The new population matrix undergoes mutation process which further ensures that our GA search would not get stuck around local maxima. Usually, the mutation probability is chosen closer to 0 (in our case, it is chosen to be 0.1 which gives the best result from a serial of pretests).

The crossover operator is chosen to be the simplest of its

nature i.e. one-point crossover to reduce computational complexity as compared to conventional GA [11] that uses double or uniform crossover. The crossover probability is chosen to be 1. The population size after each generation remains constant reflecting the simplicity of the algorithm in its implementation.

E. Elitism

The Elitism property is invoked just like in any other conventional GA to preserve the superior chromosome of the fittest individual during mutation process. There is only one best chromosome to be found, and hence, the elitism property is invoked only for one fittest individual out of the total population in every generation. Fig. 5 shows the flow of operations in the proposed GA. In the next section we define the simulation parameters and show the performance and the convergence rate of the highlighted MDGA based MUD.

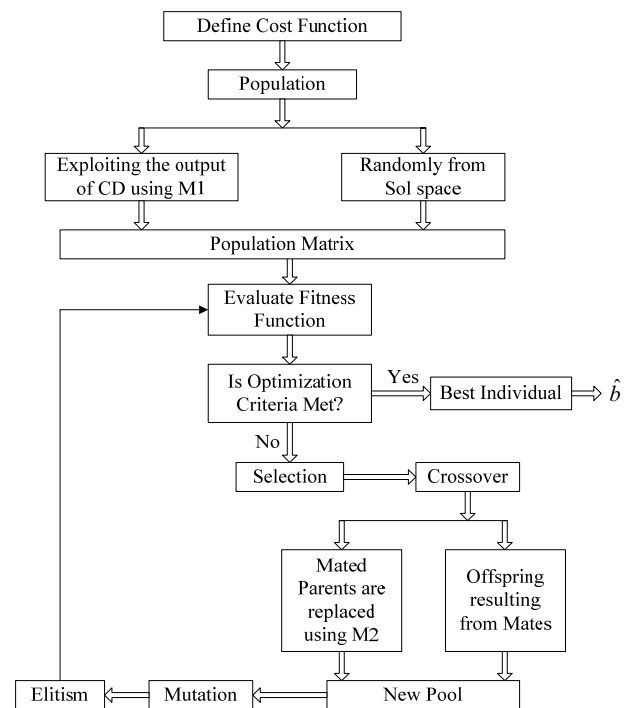


Fig. 5. Flow chart of MDGA-MUD.

IV. SIMULATION RESULTS

The BER, optimum solution detection time and the computational complexity involved are the three main performance criteria to be satisfied. The detection time is governed by the number of generations required to obtain a reliable decision. The computational complexity is determined by the total number of objective function evaluations. Table I shows the configuration parameters used in the simulations. BPSK modulation type is chosen in the system.

As shown in Fig. 6, MDGA can converge very close to the optimum within only 5 generations with a population size of 30 when the number of users is 15. This is because that MDGA can not only find a good start point but also achieve a high

convergence rate with each generation due to the proposed two methods (M1 and M2). The number of cost function evaluations taken by MDGA is only 150 till it obtains near-optimum solutions.

TABLE I CONFIGURATION OF THE MDGA-MUD

PARAMETERS	METHODS/VALUES
Population size N_p	30
INITIALIZATION	Initial population generated using M1
Selection Method	Truncation Selection
Selection rate	50%
Crossover operation	Single-point crossover
Crossover Probability p_c	1
NEW POOL	New pool created using M2
Mutation operation	Standard binary mutation
Mutation Probability p_m	0.1
Elitism	Yes
Termination Generation	5
Spreading Factor (SF)	15

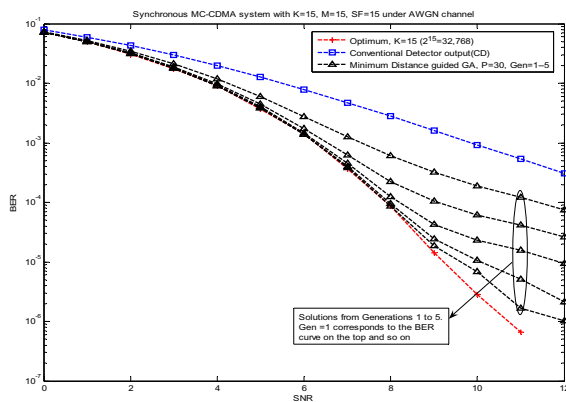


Fig. 6. The BER performance of the first 5 generations of MDGA assisted MUD in MC-CDMA over an AWGN channel. The MDGA-MUD can converge very close to the optimum in as low as 5 generations with a population size of 30 for a 15-user synchronous MC-CDMA system (SF=15 & M=15).

In Fig 7, we investigate the individual impact of each modification. Although the Modification 2 (M2) has a poor start because of the conventional approach used in initializing the GA population which it actually happens in the first generation, but it also provides great deal of convergence in the successive generations due to the novel replacement strategy used in MDGA. Whereas the Modification 1 (M1) has a good start due to the Minimum Distance approach used to initiate the population and poor convergence due to the conventional replacement strategy. Their mutual contribution provides good convergence which is the essential of our proposed scheme.

When SNR increases, the MAI gets higher. This causes the output from CD further away from the optimum. In order to deal with such an issue, the MDGA introduces reasonable amount of randomness in the initial population in order to gain the diversity in the search space at high SNR values. Furthermore, it utilizes the information carried by the best individual in the population matrix in each generation so as to get better and better solutions. It also ensures that the presence

of significant amount of diversity in the new population set by newly producing a number of offsprings from the selected mates. The new comers (offsprings) along with those individuals exploited best mate's by the Minimum Distance approach reacts in our GA to converge very fast towards the optimum. The conventional GA lacks this ability and is more likely to get stuck at local maxima and hence requires an increase in the number of generations before search termination.

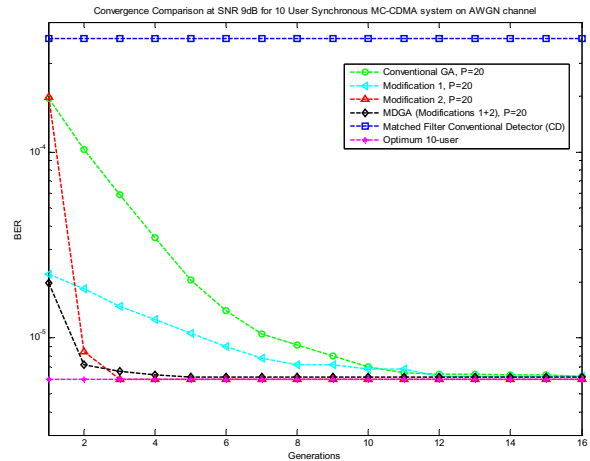


Fig. 7. Convergence comparison of MDGA vs. Conventional GA [11] for 10-User MC-CDMA system under 9dB SNR. It also shows the role played by each modification independently. Please note that the convergence graphs of the two modifications actually cross each other after the first generation.

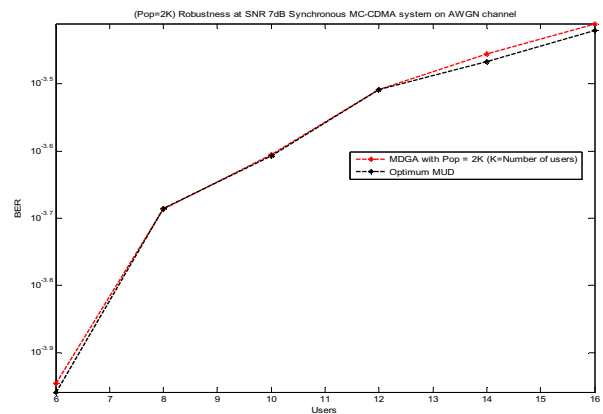


Fig. 8. MDGA is robust with the increasing number of users in the MC-CDMA system.

The population size in MDGA is dependent on the number of users "K" in the system. The simulation results in Fig. 8 show that with the increasing number of users in the system, MDGA still closely inosculates the optimum solution. This shows that the fixed relationship between Population size and the number of users (Pop = 2K) with the Termination Generation = 5 is true for all user scenarios and hence, our scheme is robust with the increasing number of users in the system.

In this paper, the computational complexity is defined as the number of cost function evaluations needed to reach the optimum solution [1]. The percentage of complexity involved

is $\left(\frac{Pop \times Gen}{2^K}\right) \times 100\%$. As shown in Fig. 9, MDGA can give

the near-optimum solution within only 150 cost function evaluations (Gen = 5, Pop = 30) as compared to 2^{15} (32,768) evaluations taken by exhaustive search. Hence, it achieves 99.54% reduction in complexity as compared to ML-MUD. Also from Fig. 7, as compared to conventional GA [11] with 240 (Gen = 12, Pop = 20) cost function evaluations, the MDGA reaches the optimum in only 100 (Gen = 5, Pop = 20) cost function evaluations, ensuring 58.3% complexity reduction in terms of cost function evaluations.

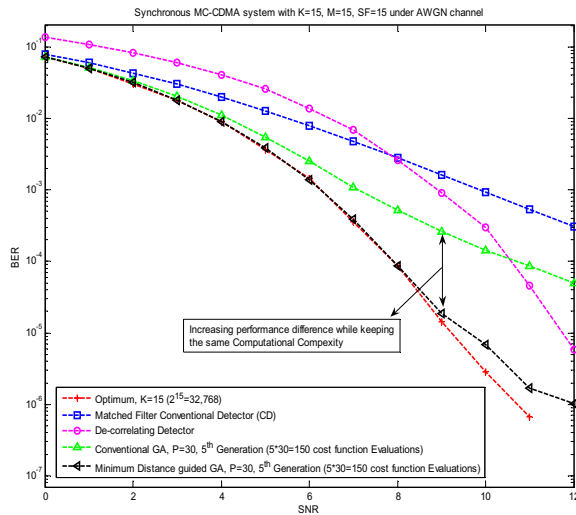


Fig. 9. BER Comparison of MDGA vs. Conventional GA [11] with the same computational complexity (P=30 and Gen=5) vs. De-Correlating. The MDGA based MUD in 15-User synchronous MC-CDMA (SF=15 & M=15) system, outperforms Conventional GA with significant reduction in the BER.

The relation between the population size and the number of users in MDGA helps us to further generalize the computational complexity in terms of number of users. For constant termination generation (e.g. Gen = 5), the number of cost function evaluations are $Pop \times Gen = 2K \times 5 = 10K$.

Hence, the complexity becomes $\left(\frac{10K}{2^K}\right) \times 100\%$. The amount

of computational complexity introduced is ten times the number of users, i.e. the number of evaluations = $10K$, where $K = (1, 2, 3, \dots, K_{max})$.

V. CONCLUSIONS

Our MDGA scheme carried out a balanced search based on an equal amount of exploration and exploitation within each step of the GA. The Minimum Distance technique is used effectively along with a novel replacement technique. The two techniques together have shown their significant improvement on the convergence rate as well as dramatic reduction on the computational complexity as compared to the existing GA assisted MUDs. Our scheme is less complex than the other genetic algorithms because it is realized based on simple genetic operators and features (standard bit mutation, one-point

crossover & fixed population size).

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