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ADAPTIVE GENETIC ALGORITHM ASSISTED MULTI USER DETECTION OF FD-MC-CDMA IN FREQUENCY SELECTIVE FADING CHANNELS

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Abstract:

Multi carrier systems such as OFDM, MC-CDMA (Multi Carrier code division multiple access) exhibits better bit error performances (BER) in frequency selective fading channels, but the main disadvantage of MC CDMA systems is the degradation of its performance due to multiple access interference (MAI). Frequency division multi-carrier code division multiple access (FD-MC-CDMA), exploits the available frequency diversity benefits and reduces MAI. In this paper we proposed maximum likelihood (ML) Multi User detection (MUD) using genetic algorithms for FD-MC-CDMA systems frequency in frequency selective fading channels. Experimental results confirmed that the proposed detection algorithm is effective with less computational load compared to existing estimation algorithms.

Key words: *Multiple Access Interference (MAI), Frequency selective fading channels, FD-MC-CDMA, Adaptive Genetic Algorithm, Bit Error Rate (BER), Signal to Noise Ratio (SNR).*

1. Introduction

For a high data rate transmission, multicarrier code division multiple access (MC-CDMA) attracted a lot of attention as an alternative to a single carrier direct sequence DS-CDMA. In MC-CDMA systems, the total bandwidth is decomposed into a set of disjointed narrow Sub-bands with the same bandwidth. Since the bandwidth of each sub-band is chosen to be less than the coherence bandwidth of the channel, a transmit signal on each sub-band undergoes frequency-flat fading, and MC-CDMA systems are more robust to the distortion induced by frequency selective fading channels than DS-CDMA systems [4].But MC-CDMA systems experience performance degradation due to MAI (multi access interference) caused by up to $N-1$ active users sharing the same N carriers. Typically, the performance of the MC-CDMA system is limited due to the presence of MAI.

Many detectors are proposed to eliminate multiuser interference (MUI) [5]-[8]. While these detectors have been derived from different principles, they usually assume that there is no frequency offset (FO), or the frequency offset is perfectly compensated by the frequency offset estimator. Frequency offset results from mismatch of the carrier frequencies between the transmitter and receiver. This causes inter-carrier interference, which severely degrades the performance of MC-CDMA systems [9]. Frequency Division Multiple Access Scheme (FDMA) [10], [11], completely avoids multi access interference by allocating each user a unique, orthogonal transmission carrier. But in this transmission scheme, no frequency diversity gains are achieved at the receiver. As a result, FDMA systems suffer severe performance degradation in frequency selective fading channels.

In [2] FDMA and MC-CDMA are combined to create the new multiple access technique FD-MC-CDMA. Here, the N subcarriers available in MC-CDMA are divided into groups where each group contains M ($M < N$) non-contiguous subcarriers, maximally separated over the transmit bandwidth and M is selected based on the achievable frequency diversity gain.

In [3] multiuser detection (MUD) using Evolutionary Programming (EP) to detect the user bits based on the maximum-likelihood decision rule was proposed. The major advantage of the proposed detector is that it has lower computational complexity. Genetic algorithms (GAs) [12]–[14] have been employed for solving many complex optimization problems in numerous fields. In [15] the performance of a GA-based multiuser detector employed in an asynchronous CDMA system in conjunction with a modified Viterbi algorithm was studied. It was shown that the GA-based detector achieves the same performance as that of the minimum mean square error (MMSE) multiuser detectors at a lower computational complexity. In [16] and [17] GA-assisted multiuser detector designed for synchronous DS-CDMA system communicating over a flat fading channel with the aid of joint channel estimation was proposed. In [1] genetic algorithm assisted multiuser detection for asynchronous DS-CDMA system transmitting over -path Rayleigh-fading channels was proposed to reduce the complexity and to decrease the detection time. In this paper we propose Genetic-Algorithm-Assisted maximum likelihood (ML) Multi User Detection for FD-MC-CDMA systems in Frequency Selective Fading Channels with reduced complexity and enhanced performance.

2. System model

In a traditional MC-CDMA system, at the transmitter the *k*th user's transmission can be given as

$$S^{(k)}(t) = b^{(k)} c^{(k)}(t), \tag{1}$$

where $b^{(k)}$ is k's user information symbol and $c^{(k)}(t)$ is k's user spreading code, which in MC-CDMA refers to

$$C^{(k)}(t) = \sum_{i=1}^{N} \beta_i^{(k)} e^{j2\pi i \Delta f t} g(t), \tag{2}$$

where, N is the total number of narrowband carriers in the MC-CDMA, $\beta_i^{(k)}$ is the i th value in user k's spreading sequence, $i\Delta f$ is the frequency position of the i^{th} carrier component, T_s is symbol duration, to ensure carrier orthogonality. $g(t)$ is a rectangular waveform of unity height which time limits the code to one symbol duration T_s. Fading channels in spread spectrum wireless systems demonstrate an M-fold frequency which can be given by

$$BW = M .(\Delta f) c, \tag{3}$$

where BW is the bandwidth of the MC-CDMA transmission and $(\Delta f)c$ is the coherence bandwidth of the frequency selective fading channel. As proposed in [2] to build a multiple access system exploiting the available M folds diversity while minimizing MAI at the same time, rather than allowing all users to share all the N carriers, small sets of M users sharing sets of M carriers via MC-CDMA are given

Assuming $N/M \in I$, assuming $M = 2^m$

$$\beta_i^{(k)} = \begin{cases} \pm 1, .. & i \in I_1^{(k)}, I_2^{(k)}, ... I_m^{(k)} \\ 0, & otherwise \end{cases} \tag{4}$$

where $I_1^{(k)} = [(k-1)/M] + 1, I_2^{(k)} = [(k-1)/M] + N/M + 1, .. I_m^{(k)} = [(k-1)/M] + (m-1)N/M + 1.$

$|x|$ represents the closest integer less than or equal to x. A total of $N/M = 2^{n-m}$ *sets of* $M = 2^m$ carriers are used concurrently to maintain the total capacity of the system. Different sets of M carriers are frequency division multiplexed such that the M users residing on one set do not interfere with the M users on another set.

The received signal at the receiver can be given as

$$r(t) = \sum_{k=1}^{K} b^{(k)} \operatorname{Re} \times [\sum_{i=1}^{N} \alpha_i \beta_i^{(k)} e^{j(2\pi f_{cc} t + 2\pi i \Delta f t + \phi_i)}] g(t) + \eta(t), \tag{5}$$

where K is the total number of users occupying the system, α_i is the gain, φ_i is the phase offset in the i^{th} carrier due to the channel fade, and $\eta(t)$ represents additive white Gaussian noise. The received signal is first decomposed into its M information-bearing carriers and dispread by user 1's spreading code. The i^{th} carrier generates the decision variable which is given as

$$r_i^{(1)} = \alpha_i b^{(1)} + \alpha_i \sum_{k \in U1\, k \neq 1} b^{(k)} \beta_i^{(k)} \beta_i^{(1)} \tag{6}$$

$$i \in I_1^1, I_2^1, ... I_M^1,$$

where $U1$ is the set of up to M active users in user 1's carrier set, and $\eta(i)$ is a Gaussian random variable with mean zero and variance $\sigma_n^2 = N_0 / 2$. An optimal combining strategy is used to combine all M carriers in user 1's set to best exploit frequency diversity and minimize MAI. To accomplish this we propose a Maximum Likelihood Multiuser Detector Using Genetic algorithm to enhance the performance of detector compared with existing Maximum Likelihood Multiuser Detectors.

3. Multiuser Detection Using Genetic Algorithm

Genetic Algorithm (GA) is a famous probabilistic search technique based on the principles of biological evolution. Similar to biological organism which evolves to adapt to its environment, Genetic Algorithm follows a path of analysis from which a design evolves, one that is optimal for the environmental restrictions placed upon it. Genetic Algorithm uses probabilistic transition rules to select someone to reproduce or to die so as to guide their search toward regions of the search space with likely improvement. Thus, Genetic Algorithm is a powerful and globally stochastic search and optimization technique and is widely used in optimization problems.

First, we define the trial data vector in our proposed Genetic Algorithm based on Multiuser Detector as $\hat{b} = [\hat{b}_1, \hat{b}_2, ... \hat{b}_k]$ for k users then

$$\hat{r}(t) = \sum_{k=1}^{K} \sqrt{E_k}\, \hat{b}_k\, s_k(t) \otimes h_k(t) \tag{7}$$

where E_k is signal energy per bit of k^{th} user, b_k is the k^{th} user's data modulated by binary phase shift keying (BPSK), and $s_k(t)$ is the k^{th} user's spreading waveform and $h_k(t)$ is the frequency selective fading channels response. Fig. 1 shows a flow chart of the proposed Genetic Algorithm based on Multiuser Detector used in FD-MC-CDMA system. The proposed GA based MUD process will return optimum or near-optimum estimated value $\hat{b}_k$ of b_k for the kth user.

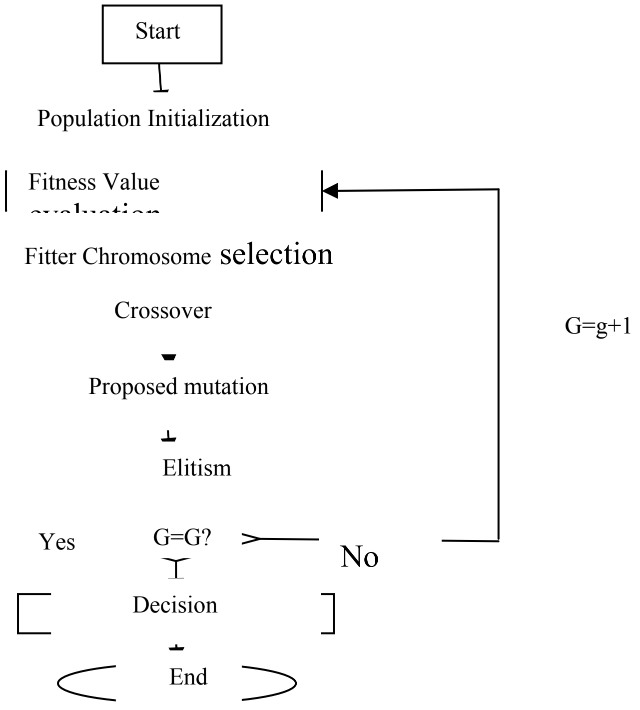

Fig.1 Flow chart of the proposed Genetic Algorithm assisted Multiuser detection scheme

The steps involved in implementing Multiuser detection using genetic algorithm is described below.

Step 1. Start with encoding

To start Genetic Algorithm, the trial data vector $\hat{b}$ must first be encoded into binary string form. The encoded binary string is regarded as a chromosome in Genetic Algorithm and its elements are regarded as genes. Thus, the MUD can be treated as a multi-objective optimization solution that finds the most likely combination of the binary bits. Without loss of generality, BPSK modulation has already been employed in the transmission model. Thus, the chromosome encoding procedure is unnecessary. The number of genes in a chromosome, which is the number of bits in a trial data vector for BPSK, is the number of users. If the transmission signals are modulated by QPSK, namely two bits per symbol, the chromosome must have two bit genes. In general, the number of bits in a symbol is equal to the number of bits in a gene.

Step 2. Population initialization

After encoding, an initial population consisting of *P* members, called individuals, is created. In our proposed Genetic Algorithm, each individual or chromosome in the population is represented by a vector including *K* bits. In the vector, each bit is a trial data belonging to one of the *K* users. The p^{th} individual which is the estimated value of $b = [b1, b2, ..., b_k]^T$ in Eq. (1) is defined as

$$\hat{b}_p^{(g)} = [\hat{b}_{1,p}^{(g)}, \hat{b}_{2,p}^{(g)}, ..., \hat{b}_{3,p}^{(g)}]^T,\ p = 1,2,3,4,...P \quad , \tag{8}$$

where superscript *g* (*g*=1, 2, …, *G*) denotes the g^{th} generation and $\hat{b}_{k,p}^{(g)}$ denotes the k^{th} (*k*=1, 2, …, *K*) gene of the p^{th} individual at the g^{th} generation. After initialization of the population of *P* individuals the optimization process starts, in which the initial generation *g* is 1.

Step 3. Fitness evaluation

In the procedure of this fitness evaluation, Genetic Algorithm exploits an objective function (OF) to evaluate the fitness of each individual in the population, which represents how closely each individual matches the optimum individual. The optimum individual can maximize the objective function value. We will now discuss how to find the objective function. The solution of optimum detection is the most likely trial data vector $\hat{b}_{opt}$ that minimizes $\| r(t) - \hat{r}(t) \|_2$

$$\hat{b}_{opt} = \arg\{\min \| r(t) - \hat{r}(t) \|_2\}, \tag{9}$$

where $\hat{b}_{opt} \in \{\hat{b} = [\hat{b}_1, \hat{b}_2, \hat{b}_3 ..., \hat{b}_k]^T\}$, $\hat{b}_k \in \{-1,1\}, k \in \{1,2..,k\}$, and $\| . \|_2$ denotes Euclidean norm or Euclidean distance. To consider the likelihood function

$$f[r(t), 0 \le t \le T_s \mid \hat{b}]| = \exp\{-\int_{T_s} [r(t) - \hat{r}(t)]^2 dt/(2\sigma^2)\} . \tag{10}$$

Analyzing the differential part of the right hand side of Eq. (10), we find it to be an expression of the distance. From equations. (9) and (10), the solution of optimum detection selects $\hat{b}$ that can also maximize the likelihood function above or, ignoring the term which is independent of $\hat{b}$ equivalently maximizes

$$\Omega(\hat{b}) = 2\int_{T_s} \hat{r}(t) r(t) dt - \int_{T_s} r(t)^2 dt. \tag{11}$$

By substituting Eq. (7) into Eq. (11), we obtain

$$\Omega(\hat{b}) = 2\int_{T_s} [\sum_{k=1}^{K} \sqrt{E_k}\, \hat{b}_k\, s_k(t) \otimes h_k(t)] r(t) dt - \int_{T_s} [\sum_{k=1}^{K} \sqrt{E_k}\, \hat{b}_k\, s_k(t) \otimes h_k(t)]^2 dt . \tag{12}$$

We define

$$s_k(t) = \sqrt{E_k} s_k(t) \otimes h_k(t) \text{ - (13)}$$

Then Eq. (12) can be rewritten as

$$\Omega(\hat{b}) = 2\int_{T_s} (\sum_{k=1}^{K} \hat{b}_k\, s_k(t)) r(t) dt - \int_{T_s} (\sum_{k=1}^{K} \hat{b}_k\, s_k(t))^2 dt . \tag{14}$$

The transmitted signal generated by Kth user is given by

$$X_k(t) = \sqrt{E_k} b_k s_k(t)$$

Substituting X$_k$(t) and (7) into Eq. (14), we obtain

$$\Omega(\hat{b}) = 2\int_{T_s} (\sum_{k=1}^{K} \hat{b}_k\, s_k(t))(\sum_{k=1}^{K} \hat{b}_k\, s_k(t)) dt + 2\int_{T_s} (\sum_{k=1}^{K} \hat{b}_k\, s_k(t)) n(t) dt - \int_{T_s} (\sum_{k=1}^{K} \hat{b}_k\, s_k(t))^2 dt$$

$= \Omega(\hat{b}) = 2\hat{b}^T SS^T + 2\hat{b} n - (\hat{b}^T S)(\hat{b}^T S)^T$ which is simplified as $2\hat{b}^T Rb + 2\hat{b} n - \hat{b}^T R\hat{b}$ further it is simplified as

$$\Omega(\hat{b}) = 2\hat{b}^T (Rb + n) - \hat{b}^T R\hat{b} , \tag{15}$$

where $n = \int_{T_s} S_k(t)n(t)dt$ and $n = SS^T$ is an auto and cross correlation matrix. We define $y = Rb + n$ which can be treated as the output of the matched filter (MF). So, we treat $\Omega(\hat{b})$ as the objective function which is simplified as

$$\Omega(\hat{b}) = 2\hat{b}^T y - \hat{b}^T R\hat{b} \ . \tag{16}$$

Thus, the solution of optimum or near-optimum detection is the one that maximizes the objective function value in Eq. (16), and $\boldsymbol{y}$ is the input of the proposed GA. The standard of fitness evaluation of the individuals is that the greater is the objective function value of an individual, the fitter is the individual.

Step 4. Selection

To evolve the population, some excellent individuals will be chosen to constitute a future population for reproduction. The fitter individuals with better genes are more likely to be selected to produce the descendant individuals. So, the rule of selection is based on their fitness or objective function values. The selection probability of the p^{th} individual is given by

$$P_P = \frac{\Omega(b_P{}^{(g)}) - \hat{\Omega}_W{}^{(g)} + 1}{\sum_{P-1}^{P} (\Omega(b_P{}^{(g)}) - \hat{\Omega}_W^{(g)} + 1)} \ , \tag{17}$$

where $\Omega(b_P^{(g)})$ the objective is function value of the p^{th} individual at the g^{th} generation and $\Omega_W^{(g)}$ is the worst objective function value at the g^{th} generation.

Step 5. Crossover

Crossover is the operation by which the selected individuals exchange their genes to produce pairs of descendants. The crossover operation randomly chooses one cutting point or many cutting points and exchanges the binary strings of individuals before or after the cutting points. For example, after a cut in the first bit in each of the two strings 0011 and 1010, these two strings are crossed over to produce a new pair of descendants 0010 and 1011. Since the offspring inherit the merits of their parents, they are expected to be superior to their parents.

Step 6. Mutation

Mutation is the proposed complementary error function to increase the diversity of the population, this mutation operation randomly changes some of the crossover result genes. Without mutation, the GA's search falls into local optima. Thus, the mutation operation is crucial to the success of Genetic Algorithm. A mutation probability $p_m^{(i,j)}$ which is relative to a signal-to-noise ratio (SNR) from i to j is defined. It can be calculated with the help of a complementary error function which can be given by.

$$erfc(x) = \frac{2}{\sqrt{\pi}} \int_x^{\infty} e^{-t^2} dt, x \geq 0 \ . \tag{18}$$

Step 7. Elitism

An elitism operation is used to avoid losing excellent individuals which have higher fitness or greater OF values from one generation to another. The operation copies a small part of the best parent individuals, and replaces the worst offspring.

4. Adaptive Population Sizing Genetic Algorithm

Genetic Algorithm is convergent, but the degree of convergence depends on the number of generations G and/or the population size P [25]. As stated above, if P and/or G are sufficiently large, our proposed Genetic Algorithm based Multi User Detection approaches the optimum maximum likelihood detection results. However, increasing P increases the computational complexity of the Multi User Detection system. It is impractical to pursue a slightly higher degree of convergence or a slightly lower Bit Error Rate performance at the expense of much more computational complexity. So, we employ adaptive population sizing genetic algorithm to solve the complexity problem. Besides the reduction of computational complexity, the proposed adaptive population sizing genetic algorithm can improve BER performance [26]. In [27] Population Resizing based on Fitness Improvement Genetic Algorithm was proposed. The proposed algorithm is similar to a traditional Genetic Algorithm but at the end of the typical selection, reproduction, and mutation steps, the population size can grow or shrink based on an improvement of the best fitness contained in the population.

The population size changes when 1. There is an improvement in best fitness, or 2. There is no improvement in the best fitness for a “long time”. If neither of the above occurs, the population size shrinks by a small percentage (1-5%). The motivation behind the algorithm is to use large population sizes for exploration and small population sizes for exploitation. In their work, the growth rate X for a population is given by,

$$X = increaseFactor \times (MaximumEvalNum - CurrentEvalNum) \times$$
$$\times \frac{\max imumFitness_{new} - \max imumFitness_{old}}{initial \max fitness} ,$$

where *increase Factor* is a parameter in the interval (0,1), *MaximumEvalNum* is the maximum number of fitness evaluations allowed for the whole run *currentEvalNum* is the current evaluation number, and $maximumFitness_{new}$, $maximumFitness_{old}$, and *initialmaxfitness*, are the best fitness values in the current, previous, and initial generation. The initial population size, as well as a minimum and maximum population sizes in which the algorithm must operate should be specified. In our proposed Genetic Algorithm based Multi User Detection experiments, we used *initialPopSize*=20, *increaseFactor*=0.1, *V*=500, *decreaseFactor*=0.4, *minPopSize*=5, *maxPopSize*=100.

5. Simulation Results

Simulations were conducted to evaluate the performance of our proposed Adaptive Genetic Algorithm based Multi User Detection for a FD-MC-CDMA based communication system simulated in MATLAB in a Rayleigh fading channel for which $N = 32$ carriers, $M = 4$ users, BPSK modulation and Convolution coding of order ½ . The proposed adaptive Genetic Algorithm employs *initialPopSize*=20, *increaseFactor*=0.1, *decreaseFactor*=0.4, *minPopSize*=5, *maxPopSize*=100. The performance and complexity of proposed Adaptive Genetic Algorithm based Multi User Detection was compared with successive interference cancellation (SIC), parallel interference cancellation (PIC) and Genetic Algorithm based Multi User Detection methods. Figure 2 shows the bit error rate performance comparison of proposed scheme with existing matched filter, SIC method, PIC method and conventional genetic algorithm. Simulation results confirmed that the proposed method outperformed and its BER performance superior compared to existing matched filter, SIC method, PIC method and MUD using conventional genetic algorithm

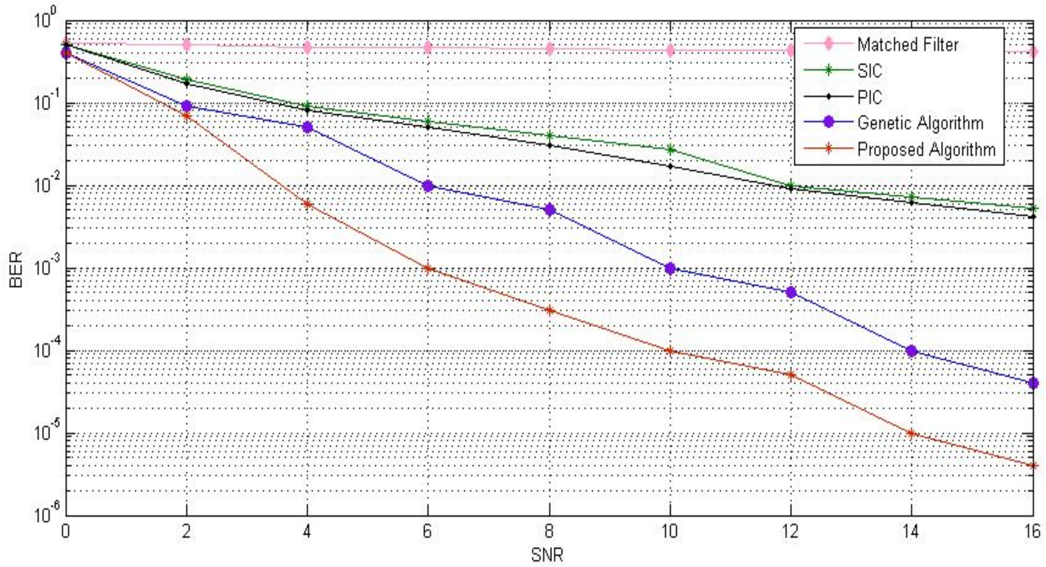

Figure.2. Bit error rate performance comparison of proposed scheme with existing matched filter, SIC method, PIC method and conventional genetic algorithm

Figure.3.compares the computational complexity involved for Multi User Detection using proposed algorithm and conventional genetic algorithm. Simulation results confirmed that the complexity of the proposed adaptive population sizing genetic algorithm based multi user detector is very less compared to conventional genetic algorithm based multi user detector. The complexity of the conventional genetic algorithm based multi user detector increased with number of generations, but the complexity of proposed adaptive genetic algorithm based multiuser detector doesn't increase so much with number of generations.

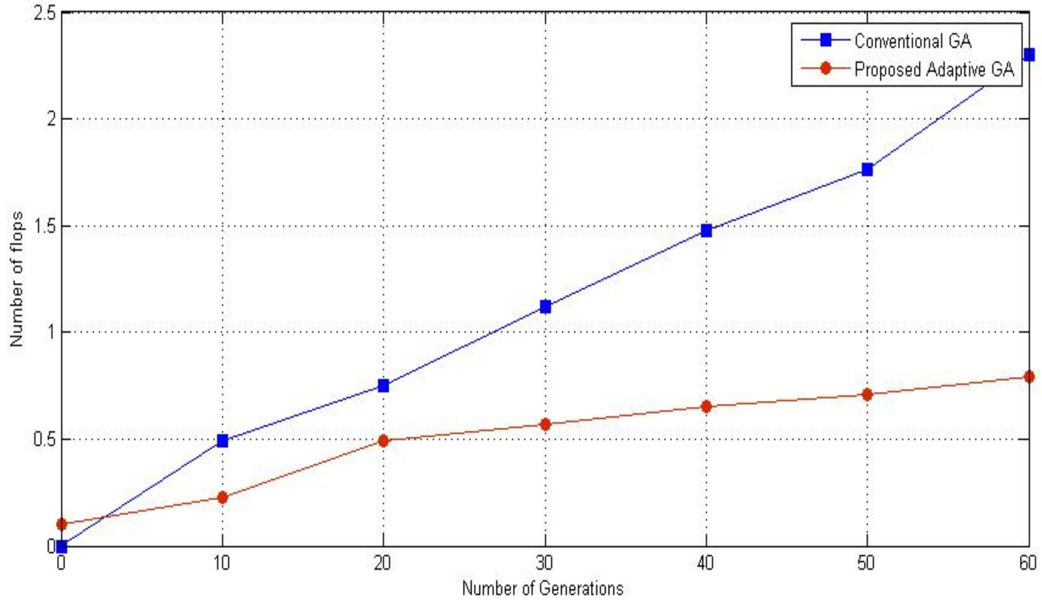

Figure.3. Comparison of computational complexity of proposed algorithm and conventional genetic algorithm.

6. Conclusion

In this paper we proposed an adaptive genetic algorithm assisted multi user detection of FD-MC-CDMA in frequency selective fading channels, the proposed system is simulated in MATLAB and the performance of the proposed adaptive genetic algorithm assisted multi user detector is compared with existing successive interference cancellation (SIC), parallel interference cancellation (PIC) and conventional genetic algorithm based multi user detectors. Simulation results shown that the bit error rate performance of the proposed adaptive genetic algorithm based multi user detector is superior compared to the performance of the existing multi user detectors. Further the computational complexity of conventional genetic algorithm based multi user detector is compared with the proposed adaptive genetic algorithm based multi user detector. Simulation results confirmed the computational complexity of proposed adaptive genetic algorithm based multi user detector is very less compared to conventional genetic algorithm based multi user detector.

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