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GA based adaptive receiver for MC-CDMA system

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Abstract: Multicarrier systems like the multicarrier code division multiple access (MC-CDMA) systems are designed for maximum usability of available bandwidth. We use the MC-CDMA system with Alamouti's space time coding in this paper. We propose the genetic algorithm (GA) in order to calculate MC-CDMA receiver weights with two variation schemes. The proposed schemes reduce receiver complexity. The bit error rate and convergence rate are also improved by increasing the number of genes and chromosomes of the GA in both schemes as compared with conventional LMS based receivers of the MC-CDMA system. This is verified via simulations.

Key words: Multiple input and multiple output, multicarrier code division multiple access, space time block coding, genetic algorithm

1. Introduction

The single transmission path between a transmitter and a receiver minimizes the efficient utilization of available bandwidth. The solution to this problem is multiple input and multiple output (MIMO) systems that use more than one antenna at the transmitter and the receiver. This improves the effective utilization of available bandwidth. These systems are effectively used due to a high data rate demand of future generation networks [1].

Multicarrier schemes like multicarrier code division multiple access (MC-CDMA) and multicarrier direct sequence code division multiple access (MC-DS-CDMA) provide an effective solution to high data rate demands of future networks [2]. Alamouti's scheme [3] is one of the plainest space time block coding (STBC) methods that is recommended for attaining transmit diversity gain in future generation networks as in [4,5]. In this paper, we used the MC-CDMA system with Alamouti's STBC scheme.

One of the important causes of poor performance in MC-CDMA based systems is multiuser interference (MI). The multiuser receivers are of two types: optimal and suboptimal receivers. The optimal receivers are much more complex, and so they are not realistic. We used suboptimal receivers as they have low complexity as compared with optimal receivers. The minimum mean square error (MMSE) is one of the well-known suboptimal receivers. In this paper, the filter weights are intended to minimize the mean square error (MSE).

The batch processing system works on groups of data to minimize complications of the receiver in terms of time. The batch processing systems are implemented along with STBC for MC-CDMA and DS-CDMA effectively in [6–8]. The calculation of an inverse autocorrelation matrix on the receiver for each group of data is one of the complications of batch processing systems. The reason is that an inverse autocorrelation matrix

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changes with any change in the channel coefficients and user configuration settings. Another complication is a large filter tap length. Thus, the solution to such problems is to implement the receiver adaptively. One of the adaptive receivers is the least mean square (LMS) receiver. Its traditional version for MC-CDMA is proposed in [9]. However, this receiver does not have a good bit error rate (BER) and convergence rate.

In this paper, we applied the genetic algorithm (GA) to a MC-CDMA receiver for adaptive MMSE weights calculation. The GA is one of the famous optimization algorithms that are suitable for any natural evolution process [10]. In the GA, a new population is produced through mutation. This technique is further compared with a traditional LMS receiver. Our proposed receiver has a better convergence rate and BER by increasing the number of genes and chromosomes in GA. This scheme also reduces the complexity of the receiver.

The paper is organized as follow: Section 2 describes the system model; the batch processing receiver is given in Section 3; MMSE based improved cost function is given in Section 4; Section 5 explains the proposed GA based MMSE weights calculation method; Section 6 explains the simulation results; and Section 7 concludes the paper.

2. System model

We used two transmit and one receive antenna for simplicity as Alamouti's STBC was to be applied to the MC-CDMA system. The number of antennas can be increased as per future requirements.

Figure 1 shows the mth user uplink transmitter for a STBC based MC-CDMA system. Let the two transmit antennas be X and Y, respectively. The two simultaneous symbols $x_m(2i-1)$ and $x_m(2i)$ are transmitted from transmit antenna X and Y at the first symbol interval. In the next symbol interval, $x_m^*(2i)$ and $x_m^*(2i-1)$ are transmitted from antennas X and Y. We used a spreading code pair $(a_{m,1}a_{m,2})$ of size $M \times 1$ for frequency domain spreading from antennas X and Y. The $a_{m,n}$ is given by the following:

$$a_{m,n} = [a_{m,n,1}, a_{m,n,2}, \ldots, a_{m,n,M}]^T. \tag{1}$$

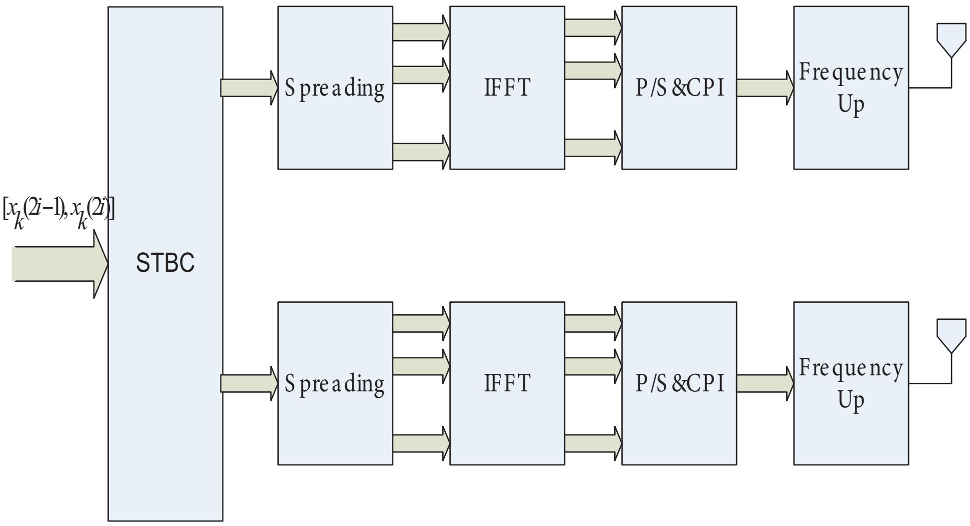

Figure 1. STBC based MC-CDMA transmitter.

The M-point inverse fast Fourier transform (IFFT) is performed where M is the number of subcarriers. It is also added in supposition that the number of subcarriers and that of the processing gain of the spreading code are equal. The IFFT generated signal is further converted from parallel to serial, and then transmitted to the channels. The Rayleigh flat fading channel is implemented using three paths. The fading gains are generated by using complex Gaussian distributions that are normalized such that the average energy of the channel is unity. In all cycles, the channel coefficients as well as the spreading code sequence are constant.

Figure 2 represents the receiver of the STBC based MC-CDMA system. First of all, the cyclic prefixes are eliminated at the receiver. Further, the signal is converted from serial to parallel. The M-point fast Fourier transform (FFT) is applied to this signal. As the multipath reflection results in a delay spread, we supposed that the cyclic prefix length of all users is more than the maximum delay spread. The received signal vector in a frequency domain is given by the following:

$$r\left(2i-1\right)=\sum_{m=1}^{K}\left\{\mathbf{H}_{m,1}\mathbf{a}_{m,1}\mathbf{x}_{m}\left(2i-1\right)+\mathbf{H}_{m,2}\mathbf{a}_{m,2}\mathbf{x}_{m}\left(2i\right)\right\}+\mathbf{z}\left(2i-1\right) \tag{2}$$

$$r\left(2i\right)=\sum_{m=1}^{K}\left\{-\mathbf{H}_{m,1}\mathbf{a}_{m,1}\mathbf{x}_{m}^{*}\left(2i\right)+\mathbf{H}_{m,2}\mathbf{a}_{m,2}\mathbf{x}_{m}^{*}\left(2i-1\right)\right\}+\mathbf{z}(2i)$$

where $\mathbf{H}_{m,n}$ is the frequency domain channel response from the nth transmit antenna of the mth user:

$$\mathbf{H}_{m,n}=diag\left(H_{m,n,0},H_{m,n,1},\ldots,H_{m,n,M-1}\right) \tag{3}$$

Furthermore, $\mathbf{z}\left(\mathbf{l}\right)$ is additive white Gaussian noise with a mean of zero and a covariance matrix $\sigma_s^2 I_{2N}$ with an identity matrix I of size $2M\times 2M$. The mth user's nth information datum $x_m(n)$ is an identically distributed random variable with a mean of zero and a unity variance.

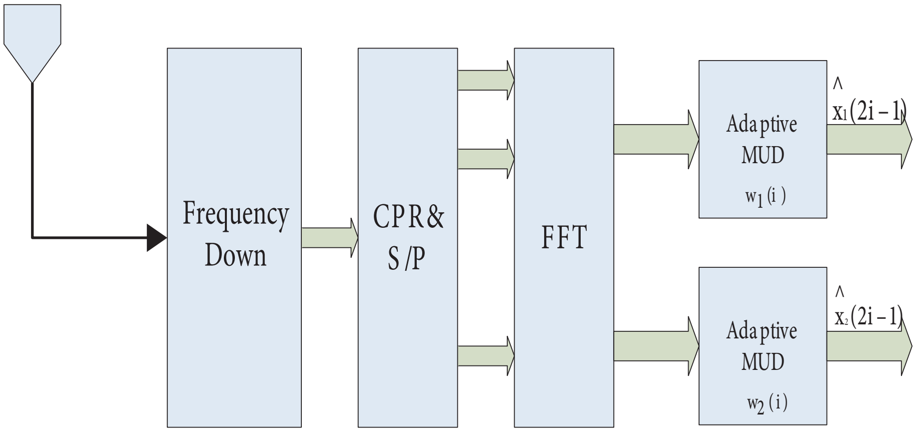

Figure 2. STBC based MC-CDMA receiver.

Let the mth user's useful spreading code for the nth transmit antenna be $\mathbf{b}_{k,m}$, then the received signal is

$$r\left(2i-1\right)=\sum_{m=1}^{K}\left\{\mathbf{b}_{m,1}\mathbf{x}_{m}\left(2i-1\right)+\mathbf{b}_{m,2}\mathbf{x}_{m}\left(2i\right)\right\}+\mathbf{z}\left(2i-1\right) \tag{4}$$

$$r\left(2i\right)=\sum_{m=1}^{K}\left\{-\mathbf{b}_{m,1}\mathbf{x}_{m}^{*}\left(2i\right)+\mathbf{b}_{m,2}\mathbf{x}_{m}^{*}\left(2i-1\right)\right\}+\mathbf{z}\left(2i\right)$$

3. Batch processing receiver

The extended received signal vector for two consecutive symbols is characterized by $\mathbf{y}(i)$;

$$\mathbf{y}\left(i\right)=\left[\mathbf{r}^{T}\left(2i-1\right)\mathbf{r}^{H}\left(2i\right)\right]^{T}=\sum_{m=1}^{K}\left\{\beta_{m,1}x_{m}\left(2i-1\right)+\beta_{m,2}x_{m}\left(2i\right)\right\}+\eta\left(i\right) \tag{5}$$

where

$$\beta_{m,1}=\left[\begin{array}{c}\mathbf{b}_{m,1}\\ \mathbf{b}_{m,2}^{*}\end{array}\right],\beta_{m,2}=\left[\begin{array}{c}\mathbf{b}_{m,2}\\ -\mathbf{b}_{m,1}^{*}\end{array}\right],\eta\left(i\right)=\left[\begin{array}{c}z(2i-1)\\ z^{*}(2i)\end{array}\right] \tag{6}$$

Suppose that the required user is 1. The extended signal $\mathbf{y}(i)$ in Eq. (5) is changed as follows:

$$\mathbf{r}\left(i\right)=\mathbf{A}_{1}\mathbf{x}_{1}\left(i\right)+\mathbf{n}\left(i\right)(7) \tag{7}$$

where

$$\mathbf{A}_{1}=\left[\beta_{1,1}\beta_{1,2}\right]$$

and

$$\mathbf{x}_{1}\left(i\right)=\left[\mathbf{x}_{1}\left(2i-1\right)\mathbf{x}_{1}\left(2i\right)\right]^{T}$$

with $\mathbf{n}\left(i\right)$ denoted by

$$\mathbf{n}\left(i\right)=\sum_{m=2}^{K}\left\{\beta_{m,1}\mathbf{x}_{m}\left(2i-1\right)+\beta_{m,2}\mathbf{x}_{m}\left(2i\right)\right\}+\mathbf{n}\left(i\right) \tag{8}$$

By describing filter weight vectors $\mathbf{w}_1$ and $\mathbf{w}_2$ of size $2M\times 1$, $\mathbf{x}_m\left(2i-1\right)$ and $\mathbf{x}_m\left(2i\right)$ are detected. Then, the mean square error (MSE) at the filter output is as follows:

$$\begin{aligned}C\left(\mathbf{w}_{1},\mathbf{w}_{2}\right)&=E\left[\left|\mathbf{W}^{H}r\left(i\right)-\mathbf{x}_{1}\left(i\right)\right|^{2}\right]\\&=E\left[\left|\mathbf{w}_{1}^{H}\mathbf{r}\left(i\right)-\mathbf{x}_{1}\left(2i-1\right)\right|^{2}\right]+E\left[\left|\mathbf{w}_{2}^{H}r\left(i\right)-\mathbf{x}_{1}\left(2i\right)\right|^{2}\right]\\&=C_{1}\left(\mathbf{w}_{1}\right)+C_{2}\left(\mathbf{w}_{2}\right)\end{aligned} \tag{9}$$

where $\mathbf{W}=\left[\mathbf{w}_1\mathbf{w}_2\right]$ and

$$\begin{aligned}C_{1}\left(\mathbf{w}_{1}\right)&=E\left[\left|\mathbf{w}_{1}^{H}\mathbf{r}\left(i\right)-\mathbf{x}_{1}\left(2i-1\right)\right|^{2}\right]\\C_{2}\left(\mathbf{w}_{2}\right)&=E\left[\left|\mathbf{w}_{2}^{H}\mathbf{r}\left(i\right)-\mathbf{x}_{1}\left(2i\right)\right|^{2}\right]\end{aligned} \tag{10}$$

The minimum mean square error (MMSE) receiver is attained by the minimization problem in [7]:

$$\begin{aligned}\left[\mathbf{w}_{o,1},\mathbf{w}_{o,2}\right]&=argC\left(\mathbf{w}_{1},\mathbf{w}_{2}\right)\\&=\left\{\mathbf{C}_{1}\left(\mathbf{w}_{1}\right)+C_{\mathbf{2}}\left(\mathbf{w}_{\mathbf{2}}\right)\right.\end{aligned} \tag{11}$$

4. Improved cost function

A relationship between the optimum weights $\mathbf{w}_{o,1}$ and $\mathbf{w}_{o,2}$ is explained in this section. Let $\mathbf{Q}_y$ be given according to its dimensions $M \times M$:

$$\mathbf{Q}_y = \begin{bmatrix} \mathbf{Q}_1 & \mathbf{Q}_2 \\ \mathbf{Q}_3 & \mathbf{Q}_4 \end{bmatrix} \tag{12}$$

The $\mathbf{Q}_y$ has a unique relationship between diagonals [11,12]. It was shown that $\mathbf{Q}_4 = \mathbf{Q}_1^*$ and $\mathbf{Q}_3 = -\mathbf{Q}_2^*$. We used this relationship in the MMSE filter weight vectors in Eq. (10) to derive the improved cost function. The optimal weights vectors $\mathbf{w}_{o,1}$ and $\mathbf{w}_{o,2}$ are as follows:

$$\mathbf{w}_{o,1} = \begin{bmatrix} \mathbf{w}_{1,1} \\ \mathbf{w}_{1,2} \end{bmatrix}, \mathbf{w}_{o,2} = \begin{bmatrix} \mathbf{w}_{2,3} \\ \mathbf{w}_{1,4} \end{bmatrix} \tag{13}$$

The following relationship is fulfilled by these vectors as in [13,14]:

$$\mathbf{w}_{1,2} = \mathbf{w}_{2,3}^*, \mathbf{w}_{1,4} = -\mathbf{w}_{1,1}^* \tag{14}$$

The relationship given in Eq. (14) is justifiable for the weights vectors given in Eq. (13). The convergence rate is increased by only updating those weights vectors satisfying the relationship in Eq. (14). The MMSE cost function in Eq. (11) can be altered as follows:

$$C_N = C_{N1}(\mathbf{w}_d, \mathbf{w}_e) + C_{N2}(\mathbf{w}_d, \mathbf{w}_e) \tag{15}$$

where

$$C_{N1}(\mathbf{w}_d, \mathbf{w}_e) = E[|\mathbf{w}_d^H r(2i-1) + \mathbf{w}_e^T r^*(2i) - d_1(2i-1)|^2]$$

and

$$C_{N2}(\mathbf{w}_d, \mathbf{w}_e) = E[|\mathbf{w}_e^H r(2i-1) + \mathbf{w}_d^T r^*(2i) - d_1(2i)|^2]$$

5. Genetic algorithm explanation

There are many algorithms that are being used in complex nonlinear systems. The GA works effectively in nonlinear problems.

In the GA, the solution is represented as a chromosome. The new population is always generated by breeding and mutation mechanisms [10]. The number of weights required for a solution is $2M$. Each column of the weight matrix is considered to be a gene. The total number of columns in this matrix is M_T. The qth element weight vector is given by:

$$\mathbf{w}_q = [w_{q,1} w_{q,2} \dots w_{q,M_T}]$$

In our proposed scheme, we have applied the GA in order to minimize the cost function given in Eq. (10). Further, the GA is also applied to the improved cost function given in Eq. (15). The GA description is given below in the Table.

Initially, a population of q individuals $\mathbf{W} = [\mathbf{w}_1 \mathbf{w}_2]$ is created randomly. The recursive execution process mechanism is used in the GA after the initialization of the population. One generation is produced in each recursive cycle. Two individuals are picked at random to be the parents of the next generation. These parents give birth to two children. The fitness function is given in Eqs. (10) and (15) for calculating the fitness of children. Furthermore, a new population is produced with genes that give the best answers with the fitness function given in Eq. (10). We continue the process until a threshold value is achieved or a certain number of cycles are completed.

Table. Genetic algorithm (GA) description.

GA algorithm	
S. no.	Steps
1.	Start.
2.	Initialization of weights $\mathbf{w}_q$.
3.	Calculate the fitness function using the cost function given in Eq. (7).
4.	Sort the weights in ascending order as per fitness values.
5.	Select the best parents.
6.	Generate the children using the crossover. (The crossover ration is 3/4 and 1/4 of Parent No. 1 and Parent No. 2).
7.	Mutation process is applied.
8.	Calculate the fitness.
9.	If (Number of cycles) go to step 10, else go to step 3.
10.	Stop.

Let the two parents be $[p_1 p_2]$. We analyzed four different approaches for parent variety: eugenic selection, alpha-male selection, preferred selection, and random selection. In the eugenic selection, the two best parents are: $p_1 = w_1$ and $p_2 \in \{w_k, 2 < k \leq K$. In the preferred selection, p_1 is selected from $p_1 \in \{w_j, 1 < j < k\}$ excluding the finest ones, and p_2 is selected randomly from the outstanding population $p_2 \in \{w_k, 2 < k \leq K$ superior to p_1. In the last strategy of random selection, p_1 and p_2 are selected randomly at each cycle. We find that the preferred selection gives the best result in our analysis. The two selected parents produce two children c_1 and c_2. The c_1 and c_2 have the same genes as the parents altogether. Any of the children, c_1 or c_2 , have the same number of genes from parent p_1 and outstanding genes from p_2.

We observed two crossover ratios: $1/2$, $1/2$ and $3/4$, $1/4$. The crossover of parents with ratios of $3/4$ and $1/4$ gave good results in our case. We chose N individuals that gave us the minimized cost function. We further chose one random index from both columns and rows. We changed the sign of the bit placed in those locations. This new generation was replaced by the following:

$$\min_{x \in \chi} w_1 = \arg C_{N1}(x) \tag{16}$$

$$\min_{x \in \chi} w_2 = \arg C_{N2}(x)$$

This new generation replaced the old generation of W. The population was rearranged in a mounting order of cost after the population had been reorganized. The algorithm moves on to the next generation or ends if the stopping condition is achieved or the number of cycles is completed.

6. Results

The uplink MC-CDMA system is implemented with $M = 32$ subcarriers. The subcarriers are equal to the dimension of the spreading code. The real and imaginary parts of the spreading code are independently chosen from $1/\sqrt{2}$ and $-1/\sqrt{2}$ at random. The Rayleigh flat fading channel is implemented using three paths. The fading gains are generated by using complex Gaussian distributions that are normalized such that the average energy of the channel is unity. In all cycles, the channel coefficients as well as the spreading code sequence are constant. Figures 3 and 4 represent the simulations of the conventional cost function without a relationship with the GA, while Figures 5 and 6 represent the comparison study of the improved cost function with a relationship with the GA and the conventional cost function without a relationship with the GA, respectively.

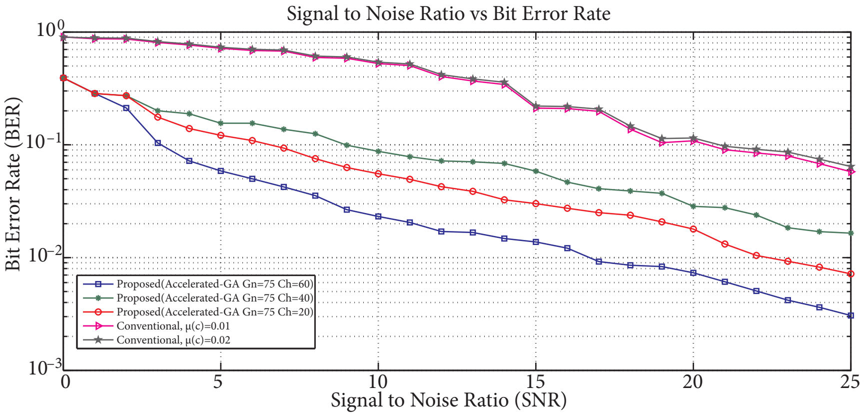

Figure 3. Signal to noise ratio (SNR) vs. bit error rate (BER) with number of genes =75 and a varying number of chromosomes.

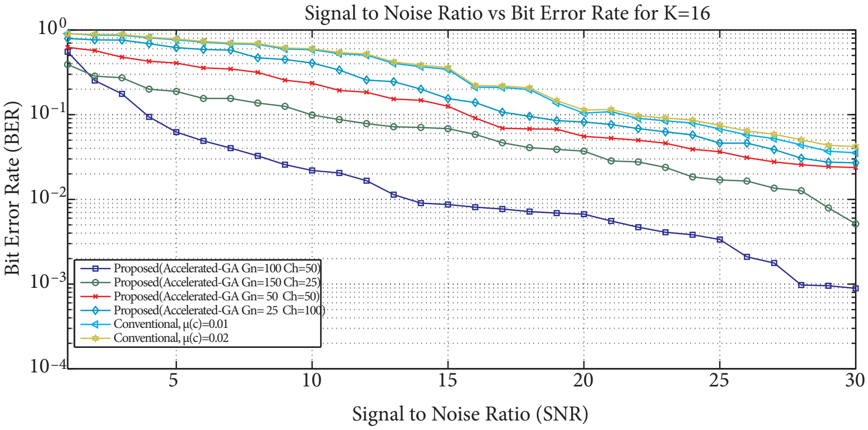

Figure 4. Signal to noise ratio (SNR) vs. bit error rate (BER) with varying numbers of genes and chromosomes.

Figure 3 shows the SNR vs. BER for different variations of the proposed scheme with respect to a fixed number of genes and a varying number of chromosomes. The topmost two curves are for the conventional LMS schemes. It can be easily seen that at SNR = 0 dB, these schemes give a BER of almost 0.9. The BER comes down by increasing the SNR. At SNR = 25 dB, the BER falls nearest to 0.1. The 3rd curve is one of our GA based proposed schemes with 75 genes and 20 chromosome. This scheme gives a BER of 0.4 at SNR = 0 dB. The BER also falls down by increasing the SNR. This scheme gives a BER of 0.1 at a medium SNR. The BER decreases to 0.02 at SNR = 25 dB. The 4th most curve from top to bottom is also proposed, with 75 genes and 40 chromosomes. This scheme also gives a BER of 0.4 at SNR = 0 dB. It gives a BER of 0.06 at a medium SNR. Its BER lowers to 0.01 at SNR = 25 dB. The 5th most curve from top to bottom is also proposed, with 75 genes and 60 chromosomes. This GA based scheme gives the best result. This scheme gives a BER of 0.4 at SNR = 0 dB. It gives BER of almost 0.02 at a medium SNR. The BER falls almost to zero at SNR = 25 dB. Therefore, it can be said that if we fix the number of genes and increase the number of chromosomes of GA, the BER can be minimized.

Figure 4 shows the SNR vs. BER of our proposed scheme with varying number of genes and chromosomes. The top two curves are for the conventional schemes. It can be easily seen that these conventional schemes give a BER of almost 0.9 at SNR = 0 dB. These schemes give a BER of 0.375 at an approximately medium SNR. However, both give a BER of 0.02 at SNR = 30 dB. The third curve of our proposed scheme is with 25 genes and 100 chromosomes. It can be seen that this scheme gives a BER of 0.8 at SNR= 0 dB. Further at a medium SNR, this scheme gives a BER of approximately 0.18. However, this scheme gives a BER of 0.01 at SNR = 30 dB. The fourth curve is also for the proposed scheme with 50 genes and 50 chromosomes. This scheme gives a BER of 0.64 at SNR = 0 dB, and a BER of 0.16 at a medium SNR. However, it gives the same BER of 0.01 at SNR = 30 dB. The fifth curve from the top is from our proposed scheme with 150 genes and 25 chromosomes. This scheme gives a BER of 0.4 at SNR = 0 dB, and a BER of approximately 0.1 at a medium SNR. However, it gives a BER of 0 at SNR = 30 dB. The last curve from the top is for 100 genes and 50 chromosomes. This scheme gives a BER of 0.57 at SNR = 0 dB, and a BER of 0.02 at a medium SNR. This scheme gives a BER of 0 at SNR = 30 dB. Therefore, it can be said that if we fix one of the two, the number of genes or the number of chromosomes, and vary the other one, the same result will be achieved. However, better results can only be achieved by increasing both.

Figure 5 shows the number of users vs. factor of complexity for a fixed number of genes and a varying number of chromosomes. The complexity factor of the GA is calculated by the following:

$$\frac{2^k}{genes \times choromosomes}$$

and a conventional scheme is calculated by $k\,(N-1)\,(N+1)$. We fixed the BER to 0.001 and SNR to 25 dB. It can be seen from the topmost curve that the conventional scheme needs 980 iterations to achieve a 0.001 BER. It can be further seen from the 2nd topmost curve that if we fix the number of genes to 75 and the number of chromosomes to 20, 700 iterations are needed to converge to a 0.001 BER. But if we increase the number of chromosomes from 20 to 40, 350 iterations will be sufficient to achieve the same BER. However, if we increase the number of chromosomes to 60, 235 iterations will achieve the same BER. Therefore, it can be said that if we increase the number of chromosomes with a fixed number of genes, then the convergence rate will be high. Further, it is established that the proposed scheme is much better than the conventional one.

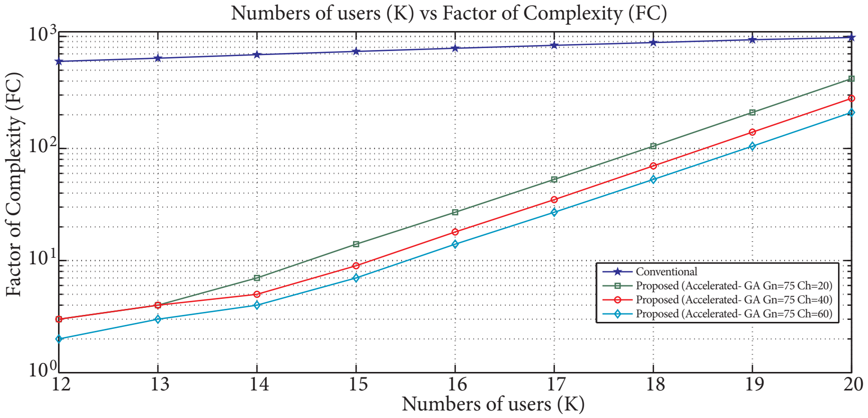

Figure 5. Number of users vs. factor of complexity for a fixed number of genes and a varying number of chromosomes.

Figure 6 shows the number of users vs. factor of complexity for achieving different BERs. It can be seen from the topmost curve that the conventional scheme needs 980 iterations to achieve an approximately 0.001

BER. For the GA based scheme, we have fixed the number of genes to 100 and the number of chromosomes to 50. It can be seen that 420 iterations are needed to achieve a BER of 0.0001 for the topmost curve. Further, the second curve shows that 280 iterations are needed to achieve a BER of 0.001. The third curve shows that it takes 210 iterations to achieve a BER of 0.01. Therefore, it can be said that it takes a higher number of iterations to achieve a low BER.

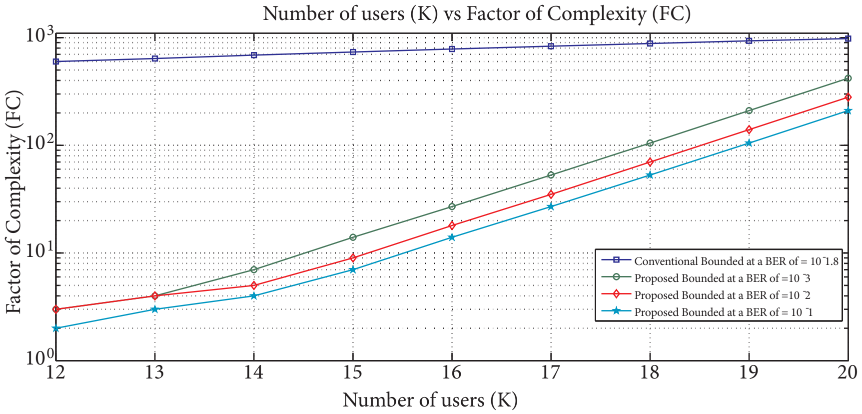

Figure 6. Number of users vs. factor of complexity for achieving different BERs.

Figure 7 shows the number of cycles vs. the mean square error with a fixed number of chromosomes. The SNR is also fixed to 25 dB. The topmost curve shows that the conventional scheme without a relationship converges at the 350th iteration to achieve a BER of 0.03. The second topmost curve shows that the conventional scheme with a relationship converges at the 250th iteration to achieve a BER of 0.03. The 3rd topmost curve represents the proposed accelerated GA without a relationship. The bottom curve represents the proposed accelerated GA with a relationship. It can be seen that the accelerated GA receiver without a relationship converges at the 166th cycle. The accelerated GA receiver with a relationship converges at approximately the 90th cycle. Therefore, it can be said that the accelerated GA receiver with a relationship converges faster than the accelerated GA receiver without a relationship and the conventional schemes.

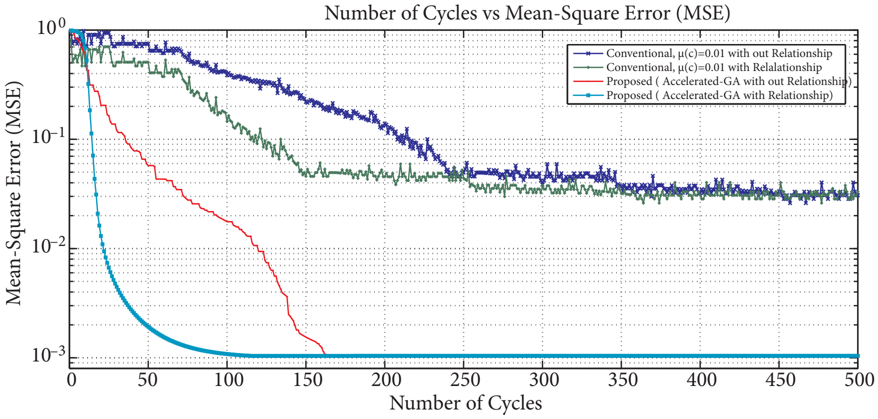

Figure 7. Number of cycles vs. the mean square error with a fixed number of chromosomes.

Figure 8 shows the number of users vs. factor of complexity with varying number of chromosomes and BER. The curve representations from top to bottom are as follows:

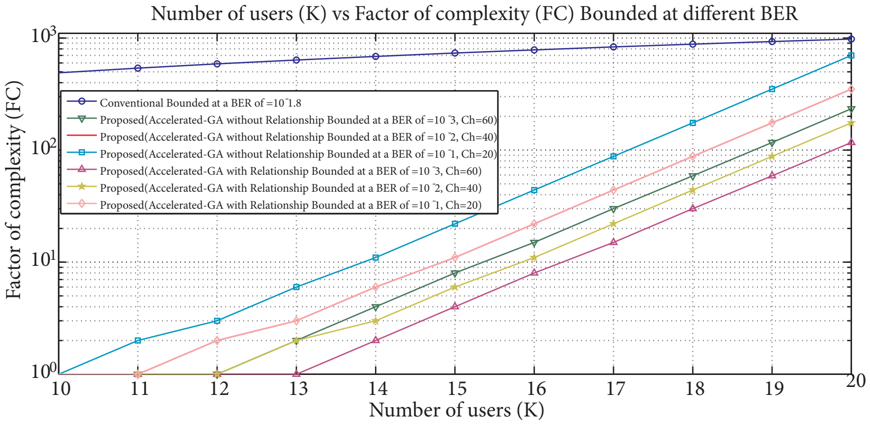

Figure 8. Number of users vs. factor of complexity bounded at different BERs.

- It can be seen from the topmost curve that the conventional scheme needs 980 iterations to achieve an approximate BER of 0.001.

- The 2nd curve is for the accelerated GA without a relationship bounded at BER $= 10^{-1}$ and the number of chromosomes = 20. It is noted that it needs 700 iterations for K = 20 in order to achieve a BER = 10^{-1}.

- The 3rd curve is overlapped by another curve as well. This other curve is for the accelerated GA with a relationship bounded at the same BER and number of chromosomes, and the 3rd curve is for the accelerated GA without a relationship bounded at BER $= 10^{-2}$. It is noted that both schemes need 350 iterations for K = 20 in order to achieve the mentioned BER.

- The 4th curve is for the accelerated GA without a relationship bounded at BER $= 10^{-3}$ and the number of chromosomes = 60. It is noted that it takes 235 iterations for K = 20 in order to achieve a BER = 10^{-3}.

- The 5th curve is for the accelerated GA with a relationship bounded at BER $= 10^{-2}$ and the number of chromosomes = 40. It is noted that it takes 175 iterations for K = 20 in order to achieve the BER = 10^{-2}.

- The 6th curve is for the accelerated GA with a relationship bounded at BER $= 10^{-3}$ and the number of chromosomes = 60. It is noted that it takes 117 iterations for K = 20 in order to achieve a BER = 10^{-3}.

Therefore, it can be said that the accelerated GA receiver with a relationship requires a smaller number of iterations to achieve any BER for a number of users K as compared with the accelerated GA receiver without a relationship.

7. Conclusion

Multicarrier systems like MC-CDMA systems are designed for maximum usability of on-hand bandwidth. We used MC-CDMA with Alamouti's space time coding in this paper. We proposed a GA with two variations for the MC-CDMA system in order to calculate MMSE weights in this paper. The variations on the receiver were either without a relationship or with a relationship. We found that this scheme gives a better BER and convergence rate than the conventional LMS based MC-CDMA receiver. It can be seen that if we increase the number of genes and chromosomes with the same effect, these receivers have a better convergence rate and a better BER. Further, it is observed that the accelerated GA calculation scheme with a relationship converge faster than the accelerated GA scheme without a relationship. However, the BER remains steady.

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