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Comparison and Performance Analysis of DS-CDMA Systems by Genetic, Neural and GaNN (hybrid) Models

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Abstract: Direct Sequence-Code Division Multiple Access (DS-CDMA) technique is used in cellular systems where users in the cell are separated from each other with their unique spreading codes. DS-CDMA has been used extensively which suffers from multiple access interference (MAI) and inter symbol interference (ISI) due to multipath nature of channels in presence of additive white Gaussian noise (AWGN). Spreading codes play an important role in multiple access capacity of DS-CDMA system and Walsh sequences are used as spreading codes in DS-CDMA.

DS CDMA receiver namely genetic algorithm neural network and GaNN (hybrid) based MUD receiver for DS-CDMA communication using Walsh sequences is designed. The performance of the same will be compared among themselves.

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I. INTRODUCTION

In DS-CDMA communication system, users are multiplexed by distinct codes rather than by orthogonal frequency bands or by orthogonal time slots. A conventional DS-CDMA detector follows a single user detection strategy in which each user is treated separately as a signal, while the other users are considered as either interference or noise. Interference such as multiple access interference (MAI) restricts the capacity and the performance of DS-CDMA systems. MAI is the interference between active users, and causes timing offsets between signals. Conventional detectors detect each user separately, and do not take MAI into consideration. Due to this, multiuser detection strategies have been proposed.

Multiuser detection seeks to enhance the performance of non-orthogonal signaling schemes for multiple-access communications by combating MAI caused by the presence of more than one user in the channel. The conventional CDMA is an interference limited system when MAI is increasing with the number of active users, and when signals are received with different power levels due to near-far problem. Conventional single user detection, when optimized for additive white Gaussian noise (AWGN), orthogonal codes and synchronous symbols, depends on power control, which is susceptible to degradation
when the channel condition changes. These factors are taken into account in the simulation with the exception that all active users are assumed to have equal power.

The following sections of this paper, overview of conventional detector, multiuser detectors, and overview of genetic algorithm are presented .The system and the simulation models applied for this work are described. Finally, BER performance results of the same are presented.

II. CONVENTIONAL SINGLE USER MATCHED FILTER

The current CDMA receivers are based on conventional detector, also known as matched filter. In conventional single user digital communication system, the matched filter is used to generate sufficient statistics for signal detection. The detector is implemented as a K separate single-input (continuous-time) single-output (discrete-time) filters with no joint processing at all. Each user is demodulated separately without taking into account to the existence of other (K-1) active users in the system. In other words, other users are considered as interference or noise. The exact knowledge of the users' signature sequences and the signal timing is needed in order to implement this detector.

For *K* direct sequence users in the synchronous single-path BPSK real channel, the baseband received signal is expressed as

$$r(t)=\sum_{k=1}^{K} A_k(t)\, s_k(t)\, b_k(t)+\mathrm{n(t)} \qquad (1)$$

Each code waveform is regenerated and correlated with the received signal in a separate detector branch. The correlation detector, also known as matched filter detector, is implemented through matched filtering, where the interference is from AWGN in a single user channel. The outputs produced by matched filters are the "soft" estimates of the transmitted data. The final output, which is "hard" data decisions ±1, is based on the signs of the soft estimates.
The correlation between the same code waveforms (autocorrelations) is required to be larger than the correlations between different codes (cross-correlation) for successful detection.

III. MULTIUSER DETECTION

There has been great interest in improving DS-CDMA detection through the use of multiuser detectors as proposed. Multiuser detection refers to the problem of detecting transmitted signals by considering all users. In multiuser DS-CDMA systems, detection involves exploitation of the base station's knowledge of signature sequence and the correlation properties contained in MAI to extenuate interference among users and subsequently, suppress noise to better detect each user.

Initially, optimal multiuser detector, or the maximum likelihood sequence estimation detector was proposed by Verdú. As presented in [10-11], this detector is much too complex for practical DS-CDMA systems.

There are two categories of the most proposed detectors: linear multiuser detectors and non-linear detectors. In linear multiuser detection, a linear mapping (transformation) is applied to the soft outputs of the conventional detector to produce a new set of outputs, which hopefully provide better performance. In non-linear detection, estimates of the interference are generated and subtracted out.

Multiuser detection systems for detecting each K user's transmitted symbols from the received signal, which consists of a matched filter bank that converts the received continuous-time signal to the discrete-time statistics sampled at chip rate without masking any transmitted information relevant to demodulation followed by applying multiuser detection algorithm for optimality conditions to produce the soft output statistics. The soft outputs are passed to the single user decoders. With the statistic at the output of the matched filter, an estimate for the transmitted bits that minimizes the probability of error can be found.

IV. GENETIC ALGORITHM ASSISTED DS-CDMA SYSTEMS

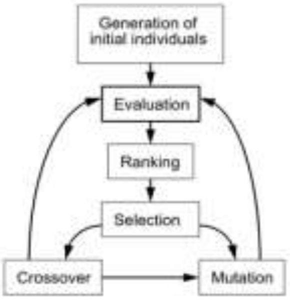


Figure 1: The principle structure of genetic algorithm

A. Components of Binary Genetic Algorithm

The GA begins, like any other optimization algorithm, by defining the optimization variables, the cost function, and the cost. It ends like other optimization algorithms too, by testing for convergence. In between, however, this algorithm is quite different. A path through the components of the GA is shown as a flowchart in Figure 2. Each block in this "big picture" overview is discussed in detail in this section.

B. Selecting the Variables and the Cost Function

A cost function generates an output from a set of input variables (a chromo- some). The cost function may be a mathematical function, an experiment, or a game. The object is to modify the output in some desirable fashion by finding the appropriate values for the input variables. We do this without thinking when filling a bathtub with water. The cost is the difference between the desired and actual temperatures of the water. The input variables are how much the hot and cold spigots are turned. In this case the cost function is the experimental result from sticking your hand in the water. So we see that determining an appropriate cost function and deciding which variables to use are intimately related. The term fitness is extensively used to designate the output of the objective function in the GA literature. Fitness implies maximization problem. Although fitness has a closer association with biology than the term cost, we have adopted the term cost, since most of the optimization literature deals with minimization, hence cost. They are equivalent. The GA begins by defining a chromosome or an array of variable values to be optimized. If the chromosome has Nvar variables (Nvar dimensional optimization problem) given by$P_1,P_2,P_3,\ldots,P_{Nvar}$ then the chromosome is written as an N_{var} element row vector.

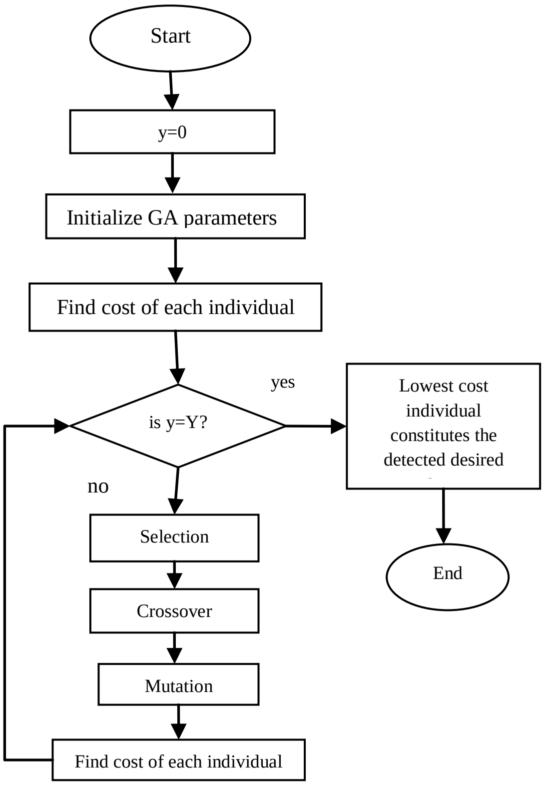


Figure 2. Flowchart of a binary GA.

$$\text{Chromosome} = [P_1,P_2,P_3, \ldots, P_{Nvar}] \qquad (2)$$

For instance, searching for the maximum elevation on a topographical map requires a cost function with input variables of longitude (x) and latitude (y)

$$\text{Chromosome} = [x,y] \qquad (3)$$

Where Nvar=2. Each chromosome has a cost found by evaluating the cost function, f , at $P_1, P_2, P_3, \ldots, P_{Nvar}$

$$\text{Cost} = f(\text{chromosome}) = f(P_1, P_2, P_3, \ldots, P_{Nvar}) \quad (4)$$

Putative solutions to the target problem are evaluated using "Cost functions", otherwise known as "Objective functions". Based upon the result of such functions, evolutionary pressures may be applied to a set of solutions. The objective function will obviously be problem specific, but there are certain features which should be avoided forth effective application of a GA. Such unfavorable objective functions are discussed below, but often the problems may be alleviated by choosing a different encoding scheme, by normalizing the input parameters, or by rebasing the function. An advantage of GAs over many search or optimization algorithms is that derivatives of this function are not required. This fact ensures that GAs maybe readily applied on fitness landscapes (or potential surfaces) which contain discontinuities or singularities without any special treatments [7]. Often the cost function is quite complicated, as in maximizing the gas mileage of a car. The user must decide which variables of the problem are most important. Too many variables bog down the GA. Important variables for optimizing the gas mileage might include size of the car, size of the engine, and weight of the materials. Other variables, such as paint color and type of headlights, have little or no impact on the car gas mileage and should not be included. Sometimes the correct number and choice of variables comes from experience or trial optimization runs. Other times we have an analytical cost function [8].

C. The Population

The GA starts with a group of chromosomes known as the population. The population has N_{pop} chromosomes and is an N_{pop}-* N_{pop} matrix filled with random ones and zeros generated using

$$\text{Pop} = \text{round}(\text{rand}((N_{pop}, N_{bits}))) \quad (5)$$

Where the function (N_{pop}, N_{bits}) generates a (N_{pop}, N_{bits}) matrix of uniform random numbers between zero and one. The function round rounds the numbers to the closest integer which in this case is either 0 or 1.Each row in the pop matrix is a chromosome. Next the variables are passed to the cost function for evaluation.

D. Selection

Two chromosomes are selected from the mating pool of N_{keep} chromosomes to produce two new offspring. Pairing takes place in the mating population until $Npop$-N_{keep} offspring are born to replace the discarded chromosomes. Pairing chromosomes in a GA can be as interesting and varied as pairing in an Animal species. GA selection operators perform the equivalent role to natural selection. The overall effect is to bias the gene set in following generations to those genes which belong to the most fit individuals in the current generation. There are numerous selection schemes described in the literature; Roulette wheel selection, tournament selection, random selection, stochastic sampling. These, in essence, mimic the processes involved in natural selection.

E. Mutations

Mutations enable the GA to maintain diversity and also introducing some random search behavior. As for crossover, many types of mutation operator may be conceived depending upon the details of the problem and the chromosomal representation of solutions to that problem. Random mutations alter a certain percentage of the bits in the list of chromosomes. A single point mutation changes a 1 to a 0, and vice versa. Mutation points are randomly selected from the Npop * Nbits total number of bits in the population matrix. Increasing the number of mutations increases the algorithm’s freedom to search outside the current region of variable space.

F. The Next Generation

After the mutations take place, the costs associated with the off spring and mutated chromosomes are calculated.

G. Convergence

The number of generations that evolve depends on whether an acceptable solution is reached or a set number of iterations is exceeded. After a while all the chromosomes and associated costs would become the same if it were not for mutations. At this point the algorithm should be stopped [9].

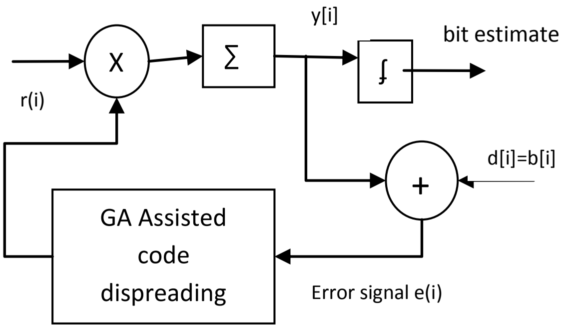


Figure 3: GA-Assisted DS_CDMA systems

V. NEURAL NETWORK ASSISTED DS-CDMA SYSTEMS

Neural networks imitate nervous systems found in biological organisms. It is built of data processing units (neurons) connected via adjustable connection weights. Neurons are arranged in layers, an input layer, hidden layer(s), and an output layer. There is no specific rule that dictates the number of hidden layers. The function is mainly based on the connections between different neurons. In the input layer, each neuron is designated to one of the input parameters. The network can work as pattern detector, function approximator and so on. The network learns to adjust its weight adaptively by certain algorithm. This is done in 3 stages, training, validation and testing. A neural network detection network for 2 users is shown in Fig.4.

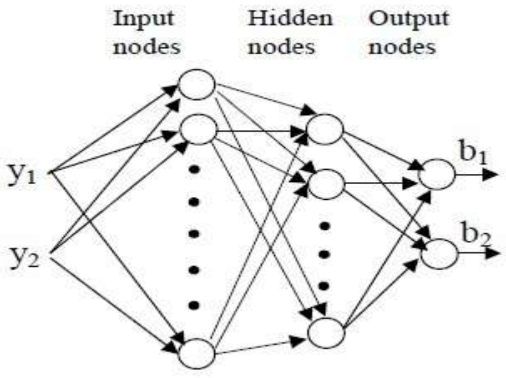


Figure 4. Neural network

For working as a receiver the number of nodes is set as number of users. The matched filter output is set as the input to the neural network. The performance of the neural network as a detector for multiple access technique and the abilities of the simulating environment to mimic the realistic communication is given in [2]. The network is trained with Levenberg-Marquardt algorithm [14]-[15] for back propagation in the present work.

A. *Multilayered Perceptrons (MLPs)*

The MLPs [13-14] are the simplest and therefore most commonly used NN architectures. NN consists of neurons that are connected to each other with weights and works parallel. Function of the network is determined by connections between neurons. The network can do some certain functions by adjusted weight factors between neurons. Adjusting the weight factors is called as training. During the training, weights are changed until the certain outputs are obtained for the defined inputs. After the training, NN processes the inputs to get desired outputs. MLPs consist of input, hidden and output layers and they have feed forward connections between neurons. Neurons in the input layer only act as buffers for distributing the input signals to neurons in the hidden layer. There are various activation functions that are used in neurons. Weights are changed with various learning algorithm for getting proper output. *P* inputs are applied to the first layer by multiplying *W1* weight matrix. The outputs of the first layer are applied to the second layer by multiplying *W2* weight matrix. Finally, the outputs of the second layer are applied to the third layer (output layer) by multiplying *W3* weight matrix. Here, the Levenberg-Marquardt algorithm is used as learning algorithm for MLPs.

VI. GaNN (hybrid model) ASSISTED DS-CDMA SYSTEMS

Both the advantages of GA and NN can be obtained.

The application of genetic algorithm on neural network makes hybrid network where the weights of the neural network are calculated using genetic algorithm approach.

The general idea of combining GA and NN is illustrated in figure 5. Information about the neural network is encoded in the genome of the genetic algorithm. At the beginning, a number of random individuals are generated. The parameter strings have to be evaluated, which means a neural network has to be designed according to the genome information. Its performance can be determined after training with back-propagation. Then, they are evaluated and ranked. The fitness evaluation may take more into consideration than only the performance of the individual. Finally, crossover and mutation create new individuals that replace the worst members of the population.

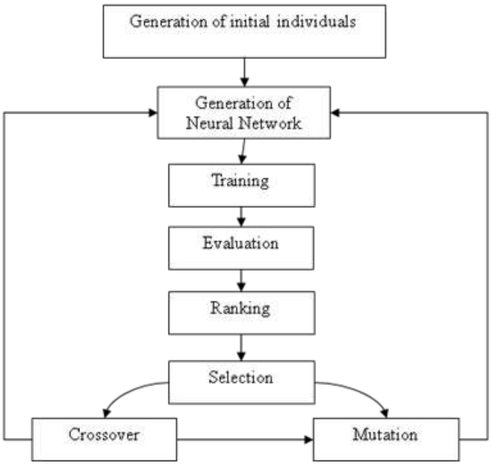


Figure 5. General structure of GaNN system

A WORKING OF GaNN

A multilayer perceptron (MLP) based on feed-forward ANN was applied to build the predictive model. The network consists of an input layer, hidden layer and an output layer. The Inputs for the network are outputs from the matched filter. In this network, data always flow in a forward direction, i.e. from input layer to output layer. The connection between inputs, hidden and out-put layers consist of weights (w) and biases (b) that are considered parameters of the neural network (NN). The neurons in the input layer simply introduce the scaled input data via w to the hidden layer. The neurons in the hidden layer carry out two tasks. First, they sum up the weighted inputs to neurons, including b, as shown by the following equation:

$$\text{sum} = \sum_{i=1}^{n} x_i w_i + b$$

Where x_i is the input parameter. The weighted output is then passed through a transfer function. The most used transfer functions to solve non-linear and linear regression problems are hyperbolic tangent sigmoid (tansig), log-sigmoid (logsig) and linear (purelin). Here, tansig is used as transfer function between input and hidden layer, while purelin is used as transfer function between hidden and output layer, shown by the following equations:

$$\text{purelin(sum)} = \text{sum}$$

$$\text{tansig(sum)} = \frac{1 - \exp\ (-\text{sum})}{1 + \exp\ (-\text{sum})}$$

The output produced by hidden layer becomes an input to out-put layer. Neurons in the output layer produce the output by the same method as that of neurons in the hidden layer. An error function is carried out based on predicted output and actual output. Training an ANN model is an iterative process which pre-specified error function is minimized by adjusting the 'w' appropriately. The commonly used error function the mean squared error (MSE) is employed in this work which is defined as

$$\mathrm{MSE} = \frac{1}{N}\sum_{i=1}^{N}(Y_t - Y_N)^2$$

Where Y_t is the target output, Y_N is the predicted output and N is the number of points. There are various types of training algorithms. One of the most employed classes of training algorithms for feed-forward neural network (FFNN) is the back-propagation (BP) method. Training of ANN by means of BP. BP algorithm is an iterative optimization process where the MSE is minimized by adjusting the w and b appropriately. There are many variations of BP algorithm for training NNs. During training step the 'w' and 'b' are iterative updated by LM algorithm until the convergence to the certain value is achieved.

Once a generalized ANN model was developed, the input space is optimized by the genetic algorithm (GA). The input vector containing of input parameters of model converts the decision parameter for the GA. The GA is the optimization strategies developed based on the principles of natural selection. This algorithm begins with a population of represented random solutions. After that, a number of operators are repeatedly used, until convergence is gained.

The development of the GA follows some steps as initialization of solution populations identified as chromosomes, fitness computation based on objective function, selection of best chromosomes, and genetic propagation of chosen parent chromosomes by genetic operators like crossover and mutation. Crossover and mutation are implemented to produce the new and better populations of chromosomes.

V. SIMULATION RESULTS

In order to validate the proposed GA and NN for DS-CDMA applications, extensive simulation studies were conducted. All the simulations are done in Mat lab.

During the training period the receiver parameters were optimized/trained with1000 random samples and the parameters so obtained were averaged over 50 experiments. The parameters of the receiver were fixed after the training phase. Bit error rate (BER) was considered as the performance index. In this section, the BER performance of the conventional MUD receiver using Walsh spreading sequences is done and the performance is compared with GA assisted DSCDMA receiver. In all the experiments randomly generated +1/- 1samples were transmitted for each user. These samples were spread using Walsh sequences to each of the users.

After spreading, the sequences were added and transmitted through the non-dispersive channel. The channel corrupted the transmitted signal with AWGN. The channel output was fed to the receiver structures. The tests were conducted for different levels of SNR. Additionally tests were also conducted by varying number of active users in the system for fixed value of SNR.

For neural networks, simulations have been carried out using Levenberg-Marquardt method, resilient backpropogation, Batch Gradient Descent with Momentum, GD with adaptive learning rate.

Table 1: The basic simulation parameters used by the GA assisted MUD DS-CDMA system

Parameters	**Value**
Modulation scheme	BPSK
Spreading code	WALSH
No. of users Npop	16
GA's selection method	Fitness-proportionate
GA's mutation method	Standard binary mutation
GA's crossover method	Uniform crossover
GA's mutation probability *pm*	0.1
GA's crossover probability *pc*	1
Mating pool size *T*	5
Elitism	Yes

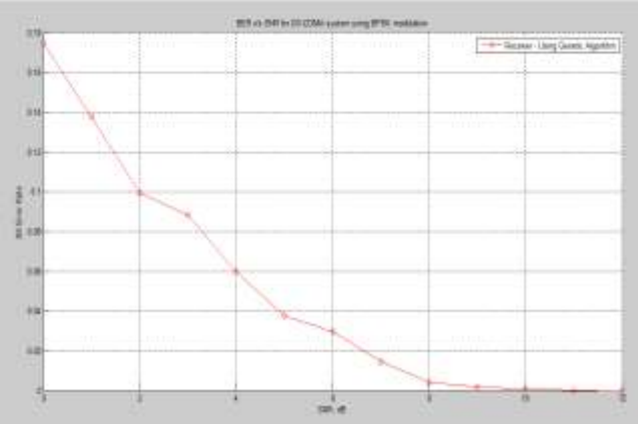


Figure6. SNR v/s BER plot of GA assisted DS-CDMA

Table 2: The basic simulation parameters used by the NN assisted MUD DS-CDMA system

Parameters	**Value**
Modulation scheme	BPSK
Spreading code	WALSH
No. of users	16
epochs	1000
goal	0.001
Learning rate	0.05
show	50

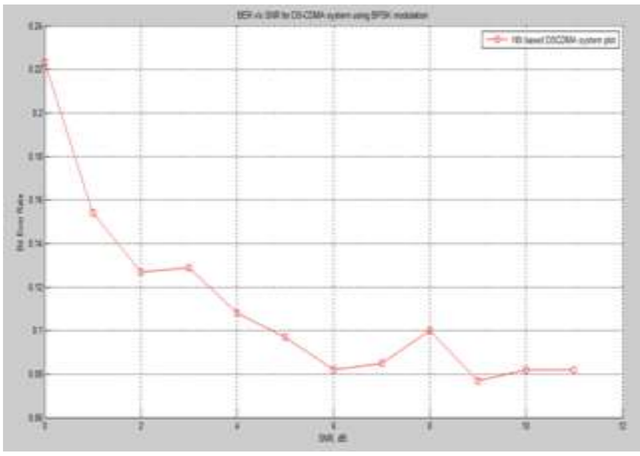


Figure7. SNR v/s BER plot of NN assisted DS-CDMA using Levenberg-Maruardt (trainlm)

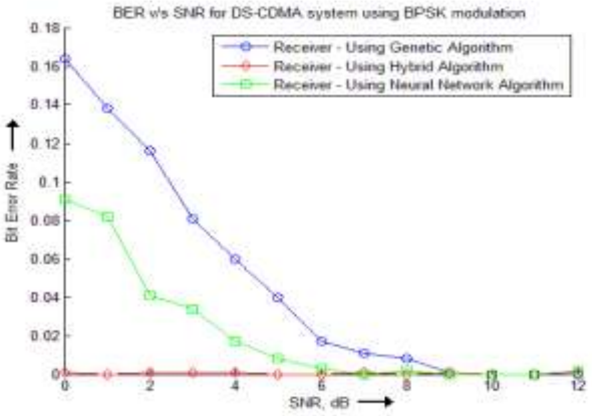
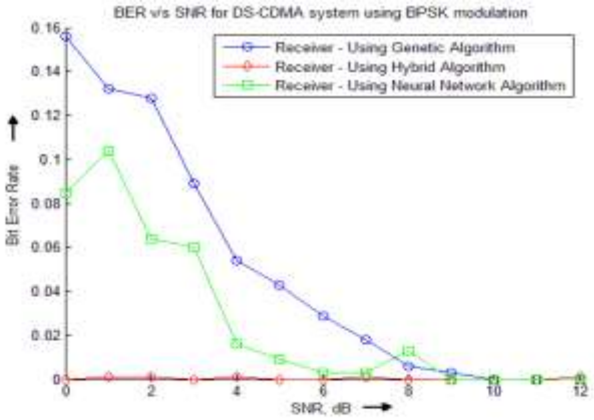


Figure8. BER v/s SNR Comparison of all the 3 algorithms for 7 users



BER v/s SNR Comparison of all the 3 algorithms for 10 users

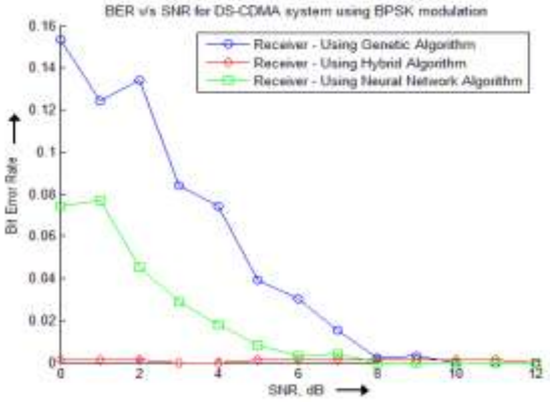


Figure9. BER v/s SNR Comparison of all the 3 algorithms for 16 users

Table 3: SNR v/s BER comparison for 7 users

SNR (dB)	BER		
	Genetic algorithm	Neural network	Hybrid (GaNN)
2	0.1380	0.0820	0
4	0.0870	0.0340	0.001
6	0.0400	0.0080	0
8	0.0110	0.0030	0.001
10	0	0.0020	0.001

Table 4: SNR v/s BER comparison for 10 users

SNR (dB)	BER		
	Genetic algorithm	Neural network	Hybrid (GaNN)
2	0.1320	0.1040	0.001
4	0.0890	0.0600	0.001
6	0.0430	0.0090	0
8	0.0180	0.0030	0.001
10	0.0020	0	0

Table 5: SNR v/s BER comparison for 15 users

SNR (dB)	BER		
	Genetic algorithm	Neural network	Hybrid (GaNN)
2	0.1240	0.0770	0.001
4	0.0840	0.0290	0
6	0.0390	0.0080	0.001
8	0.0150	0.0040	0.001
10	0.0020	0.0003	0

VI. CONCLUSION AND DISCUSSION

In conclusion, performance of DS-CDMA MUD receiver is successfully simulated and evaluated using different algorithms for 16 users (max). Among these algorithms GaNN hybrid combination based receiver resulted in the minimum BER.

In the future, investigation is to simulate and evaluate the performance of the DS-CDMA systems using these algorithms for more number of users, using Raleigh fading channel and using different user signals like walsh sequence, gold sequences.

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