

Novel Crossover Genetic Artificial Fish Swarm DNA Encoding Sequence Based Blind Equalization Algorithm

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Abstract

A novel crossover genetic artificial fish swarm DNA encoding sequence based weighted multi-modulus blind equalization algorithm(ncGAFS-DNA-WMMA) is proposed to solve the defect that error function doesn't match with the signal constellation model in the multi-modulus blind equalization algorithm(MMA). The proposed algorithm can find the optimal DNA coding sequence through the novel crossover genetic artificial fish swarm algorithm with fast convergence and global searching ability. The initial optimal weight vector of the weighted MMA(WMMA) can be obtained through decoding of the optimization DNA sequence. The simulation results show that the proposed algorithm has the faster convergence speed and smaller mean square error comparison with MMA, WMMA, and AFS-DNA-WMMA(weighted multi-modulus blind equalization algorithm based on DNA encoding sequences optimized by artificial fish swarm algorithm).

Keywords: Weighted multi-modulus blind equalization algorithm (WMMA); Artificial fish swarm algorithm (AFSA); novel crossover DNA genetic algorithm (ncDNA-GA)

Introduction

In order to eliminate inter-symbol interference(ISI) and improve the performance of the communication system, some blind equalization algorithms are used in the receiving terminal to compensate and eliminate ISI of the channels. The multi-modulus blind equalization algorithm (MMA) can effectively eliminate the phase offset and reduce the steady-state mean square error, but its error function doesn't match with the signal constellation model. So, WMMA can be selected to make the error function match with the signal constellation model.

The focus of DNA encoding is to avoid the hybridization of the biochemical reactions among DNA molecules as much as possible. Genetic algorithm (GA) and artificial fish swarm algorithm(AFSA) of the intelligent algorithms can be used to optimize DNA encoding sequences currently. Artificial fish swarm

algorithm(AFSA) is an efficient intelligence algorithm with the fast convergence, but its optimization accuracy is low. DNA genetic algorithm(DNA-GA) can express the genetic operation via DNA encoding method and has a wide searching range. So, DNA encoding sequences can be optimized via fusing AFSA with DNA genetic algorithm.

In this paper, a novel crossover genetic artificial fish swarm DNA encoding sequence based weighted multi-modulus blind equalization algorithm(ncGAFS-DNA-WMMA) is proposed via fusing the advantages of WMMA, DNA-GA and AFSA.

Artificial Fish Swarm Algorithm Based on Novel Crossover DNA Genetic Algorithm

Currently, the crossover operator of DNA genetic algorithm is based on the reorganization of DNA molecules in monotonous form, so in view of the special DNA coding method of genetic algorithm, the novel crossover DNA genetic algorithm(ncDNA-GA) is adopted in this paper to maintain the population diversity via using new crossover operator, and effectively improve the performance of DNA genetic algorithm. Novel crossover operators of DNA genetic algorithm include the permutation crossover operator and translocation crossover operator[1].

In permutation crossover operator, the population is divided into high quality population and inferior in quality of population. Two individuals in the high quality population are selected as the parent bodies. One sequence, which belongs to one parent body, is randomly selected, these two sequences have the same length and are exchanged to come into being two new individuals.

In translocation crossover operator, a sequence in the parent body is randomly cut in a position and inserted into the new position at the same time in the parent body to form a new individual.

In mutation operator, each base of each individual in the group can mutate into another base with a certain probability to form a new population.

Artificial fish swarm algorithm can simulate the artificial fish foraging, cluster, and collision behaviors to achieve the goal of global optimization[2]. The artificial fish swarm algorithm has ability to avoid the local optimal value and obtain the global optimal value. But it also has the disadvantage of slow convergence rate and poor optimization precision. DNA genetic algorithm with a novel crossover operator is to carry out crossover, mutation operation on the DNA coding sequence to obtain high encoding precision. Therefore, the novel crossover DNA genetic algorithm makes up for the defects of artificial fish swarm optimization algorithm.

Novel Crossover Genetic Artificial Fish Swarm DNA Encoding Sequence Based WMMA

Although the MMA can effectively eliminate the phase offset and reduce the

steady-state mean square error(MSE), the steady-state MSE still exists under noise free case[3]. The weighted multi-modulus blind equalization algorithm (WMMA) can get weight factor value via adjusting the MSE. Therefore, it is very important how to select the weight factor λ for the performance of the WMMA. The cost function of the WMMA is defined as

$$J_{WMMA}(n) = E\{(y_R^2(n) - |\hat{y}_R(n)|^{\lambda_R} R_R^2)^2 + (y_I^2(n) - |\hat{y}_I(n)|^{\lambda_I} R_I^2)^2\} \quad (1)$$

where weight factor $\lambda_R, \lambda_I \in [0, 2]$, R_R^2 and R_I^2 are the real and imaginary parts of modulus R^2 , respectively. $\hat{y}_R(n)$ and $\hat{y}_I(n)$ is the quadrature and in-phase component of decision output signal.

According to Eq.(1), the equalizer tap coefficient vector of the WMMA is updated by

$$\mathbf{W}(n+1) = \mathbf{W}(n) - \mu e_{WMMA}(n) \mathbf{X}^*(n) = \mathbf{W}(n) - \mu(e_{R,WMMA}(n) + j e_{I,WMMA}(n)) \mathbf{X}^*(n) \quad (2)$$

where
$$\begin{cases} e_{R,WMMA}(n) = y_R(n)(y_R^2(n) - |\hat{y}_R(n)|^{\lambda_R} R_{\lambda_R}^2) \\ e_{I,WMMA}(n) = y_I(n)(y_I^2(n) - |\hat{y}_I(n)|^{\lambda_I} R_{\lambda_I}^2) \end{cases} \quad \text{and}$$

$e_{WMMA}(n)$ is the error control function of the WMMA.

The hamming distance between two DNA sequences is the sum of the different characters in all the corresponding position to describe that the two DNA sequences aren't similar degree[4,5]. DNA sequence X and Z are denoted as $X=x_1x_2\dots x_n$ and $Z=z_1z_2\dots z_n$, where n is the number of DNA bases in X or Z, x_m and z_l are the any kind of four bases named as Adenine, Guanine, Cytosine, and Thymine. Their hamming distance is written as $H(X,Z)$ and defined as

$$H(X,Z) = \sum_{i=1}^n h(x_i, z_i) \quad (3)$$

where the value of $h(x_i, z_i)$ is zero if x_i is equal to z_i , else the value is 1.

In the design of DNA encoding, the number of different bases in the sequence X and Y increases with the increase of hamming distance. So, the possibility of hybridization becomes small.

There are two fitness functions in this paper. The first one is used to handle constraints with the weighted average method and defined as

$$Y_1(s_i) = wF(s_i, s_i) = w \cdot \min_{-n < k < n} H(s_i, \sigma^k(s_i^R)) \quad (4)$$

where s_i corresponds to the i th DNA sequence, equal to the i th position vector of artificial fish swarm. w is the weight of the constraint $F(s_i, s_i)$, for simplicity, we use $w=1$.

The second fitness function is defined as the reciprocal of the cost function of the MMA, i.e.

$$Y_2(v_i) = \frac{1}{J_{MMA}(f_i)} = \frac{1}{E[e_R^2(n)] + E[e_I^2(n)]} \quad (5)$$

where $J_{MMA}(f_i)$ is the cost function of the MMA.

Step1: Initialization of DNA sequence. The initial population of DNA sequence $s=[s_1, s_2, \dots, s_N]$, where s_m is the m th DNA sequence and N is the number of DNA sequence. It is equal to the initial position vector of AFS.

Step2: The calculation of the first fitness function. The first fitness function of each artificial fish is calculated according to the Eq.(4). The maximum fitness function and its corresponding position vector are recorded in the first bulletin board.

Step3: DNA coding and the calculation of the second fitness function. The second fitness function of each artificial fish is calculated according to the Eq.(5). The maximum of second fitness function and its corresponding position vector are recorded in the second bulletin board.

Step4: The artificial fish algorithm. Each artificial fish in the fish swarm carries out following behavior. If the following behavior doesn't occur, all fishes carry out swarming behavior. If swarming behavior does also not succeed, all fishes carry out preying behavior.

Step5: The each fish in the artificial fish swarm is sorted from big to small according to the fitness function. The high quality population is formed by the first half of the artificial fish swarm.

Step6: Crossover operation. The position vectors of two DNA sequences are randomly selected as the parent bodies from the high quality population. If a random number within 0 to 1 is less than the permutation crossover probability, permutation crossover operation is carried out. We can obtain two new position vectors of artificial fish swarm. If random number within 0 to 1 is less than the translocation crossover probability, translocation crossover operation is carried out. In this case, we get the new position vector of the artificial fish.

Step7: Mutation operator. The position vector of each artificial fish swarm can be changed when a random number within 0 to 1 is less than the mutation probability. In this case, we can obtain the new position vector of the artificial fish swarm.

Step8: The update of the first bulletin board. The fitness function value of each artificial fish is calculated. The maximum one of them is selected and compared with the previous maximum fitness function value in the first bulletin board. If the maximum one of them is greater than the previous maximum fitness function value, the first bulletin board is updated by the current maximum fitness function value and its corresponding to the position vector.

Step9: DNA coding and the update of the second bulletin board. After the once iteration, the second fitness function of the position vector in the first bulletin board which is obtained by the DNA coding is calculated. The maximum one of them is selected and compared with the previous maximum value of the

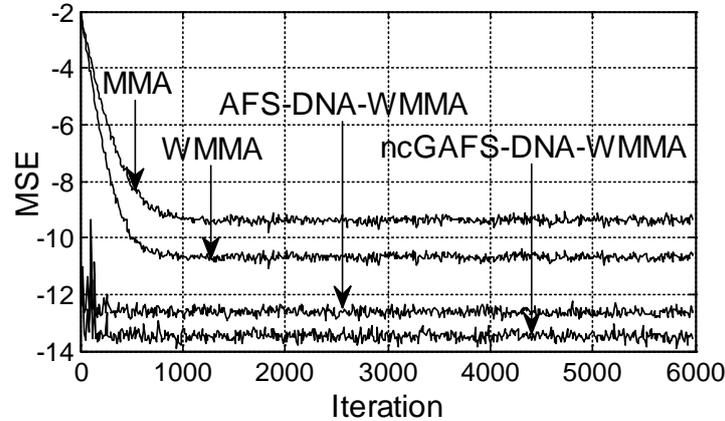
recorded in the second bulletin board. If the maximum one of them is greater than the previous recorded in the second bulletin board, the second bulletin board is updated by the current maximum value and its corresponding to the position vector.

Step10: Determination of the termination condition. Judge whether the iteration is equal to the maximum value. If the condition doesn't hold, the iteration process goes back to step 4, otherwise, the record in second bulletin board is outputted.

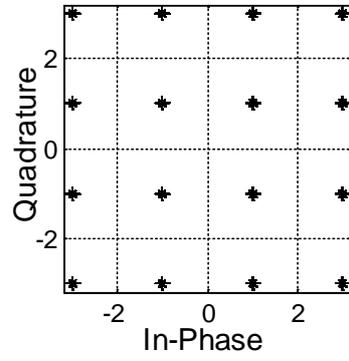
Step11: the record in second bulletin board is used as the real and imaginary parts of initial optimization weight vector to update the weight vector of the WMMA according to Eq.(2).

Test results

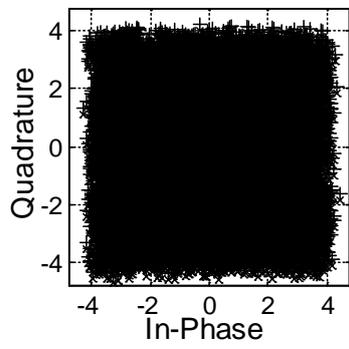
In the simulations, the transmitted signals were 16QAM signals, the channel $h=[0.9656 \ -0.0906 \ 0.0578 \ 0.2368]$, SNR (signal to noise ratio) was 25dB, the number of equalizer weight coefficients $L=11$, the step-size $\mu=0.000005$. The number of AFS $N=10$, crowding factor $\delta=0.5$. Figure 1 is simulated results. Figure 1(a) is the curves of the MSE, (b) is the constellations of the 16QAM, (c) is input of equalizer, (d) is the output constellations of the MMA, (e) is the output constellations of the WMMA, (f) is the output constellations of the AFS-DNA-WMMA. Figure1(g) is the output constellations of the ncGAFS-DNA-WMMA.



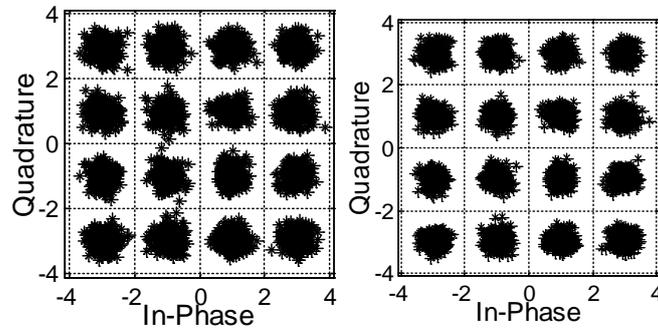
(a)



(b)



(c)



(d)

(e)

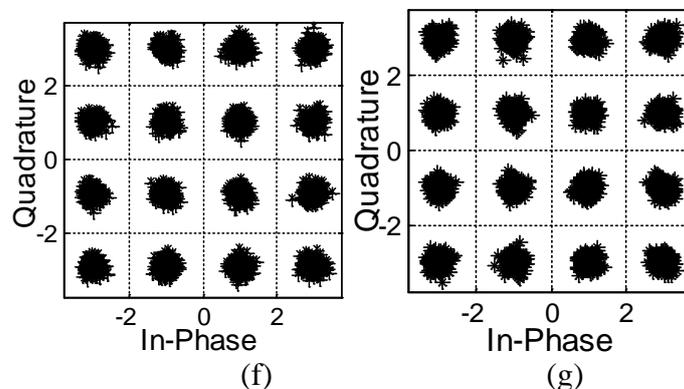


Figure 1: Simulated results

From Figure 1, we can know that the ncGAFS-DNA-WMMA outperforms the AFS-DNA- MMA, WMMA and MMA in improving the convergence speed and reducing MSE. The MSE of the ncGAFS-DNA-WMMA is the smallest and its convergence speed is the fastest. Moreover, the output constellations of the ncGAFS-DNA-WMMA are more compact and clearer than the MMA.

Conclusion

DNA encoding sequences optimized via fusing AFS with DNA-GA are applied to weighted multi-modulus blind equalization algorithm to optimize further the initial weight vector of the WMMA, the novel crossover genetic artificial fish swarm DNA encoding sequence based the WMMA is proposed. The simulation results show that the MSE of the ncGAFS-DNA-WMMA has the fastest convergence rate and lowest MSE, and more compact and clearer output constellations comparison with AFS-DNA-WMMA, the WMMA, and the MMA.

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