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Wideband Wireless Transmitter Identification Based on Hammerstein-Wiener Model

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Abstract

In recent years, the identification of the same-model wideband wireless transmitter manufactured by a same manufacturer has emerged as a big challenge. In this paper, a model-based approach is proposed for the identification of the same type wideband wireless transmitter. A Hammerstein-Wiener model is adopted for modeling the wideband wireless transmitter and an improved genetic algorithm is proposed for identifying the model. The estimated model parameters are taken as a feature vector for the identification of the wideband wireless transmitter. The simulation results verify the effectiveness of the proposed method. Moreover, the improved genetic algorithm achieves better estimation precision and higher identification rate than the basic genetic algorithm, the classic least squares iteration method, the AWPSO and the neural network algorithm.

Key Words: Transmitter Identification, System Identification, Hammerstein-Wiener Model, Genetic Algorithm

1. Introduction

In recent years, the identification of the wireless transmitter based on radio frequency (RF) fingerprint has become a research focus due to the increasing security threats in wireless networks [1]. It is reported that radio transmitter is employed to deliberately interfere with other transmitters or to illegally use electromagnetic spectrum, resulting in either a security problem or RF traffic jams [2]. So it is crucial to identify radio transmitters. In cognitive radio networks, malicious users are expected to be recognized by the utilization of RF fingerprint, which commonly is the channel information [3]. Likewise the channel information, many other characteristics for the identification of the wireless transmitter have been extracted and studied, including the wavelet coefficients [4], the instantaneous envelope and phase [5]. In [6], the authors proposed a model-based scheme for the identification of specific emitter in multipath channels. In their approach, all the parts of the RF transmitter and the multipath channels were considered as a nonlinear system and were modelled by a Volterra series model and the nonlinear model parameters are extracted as features to identify the emitter. Their results shown that the estimation accuracy increases as the signal-to-noise ratio (SNR) increases. Moreover, the model-based approach is more effective even when the number of samples is small and the SNR is relatively low.

In fact, the RF front end of a wireless transmitter is composed of the cascade of several linear and non-linear blocks such as up-converters, filters, amplifiers, drivers etc. [7]. To well describe the nonlinear behavior of all these blocks needs a suitable model. Various nonlinear models are used in the wireless transmitter modelling, such as the Hammerstein model [8] and the memory polynomial model [9]. As compared to the Hammerstein model and Wiener model, the Hammerstein-Wiener model is obviously more elaborate and it can better mimic strong dynamic non-linear systems. Moreover, it can attain the nonlinear management abilities while maintain a reason-

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ably small number of parameters [7]. Therefore, the Hammerstein-Wiener model is adopted in our scheme.

Once an appropriate model is available, the estimation of the model parameters becomes critical for the identification of the wireless transmitter, since the identification performance is highly depended on the accuracy of the estimation of the parameters. Some of the classical methods, such as the least square iteration method [10], have the disadvantages of low identification accuracy or dissatisfactory convergence. But intelligent algorithms can efficiently cover these demerits. Presently, some intelligent algorithms have been successfully applied to identify the Hammerstein-Wiener model, including the neural network (NN) algorithm [11] and the adaptive weighted particle swarm optimization (AWPSO) algorithm [12].

The method on the basis of the model parameters for the wideband wireless transmitter identification has not yet been studied in the existing works. Motivated by the advantages of the model parameters approach, we put forward a method for the identification of the wideband wireless transmitters by utilizing the intelligent algorithms and the Hammerstein-Wiener model. As a commonly used intelligent algorithm, the genetic algorithm (GA) has a wider applicability compared to the other intelligent algorithms due to the fact that it uses only the fitness function information, without the derivative or other auxiliary information in the search process. In this work, an improved genetic algorithm that has higher prediction accuracy, stronger search ability and better convergence [13], is adopted to identify the parameters of the Hammerstein-Wiener model. The estimated model parameters are then taken as a feature vector for the wideband wireless transmitter identification. The improved genetic algorithm has been experimentally compared with the basic genetic algorithm, the classic least square (LS) iteration method, the AWPSO and the NN in regard to the algorithm complexity and identification performance.

The organization of this paper is as follows. A Hammerstein-Wiener model for wideband wireless transmitters is given in section 2. Then the basic and the improved genetic algorithms are introduced in section 3. In section 4, an identification method that uses a direct comparison of the Euclidean distance between the estimated parameter vector and the real parameter vector is introduced. The process of experiment and simulation is described in detail in section 5. Section 6 summarizes the paper.

2. Hammerstein-Wiener Model

This section provides a brief introduction of the Hammerstein-Wiener model.

The Hammerstein-Wiener model can be regarded as a cascade of the Hammerstein model and the Wiener model. The structure of the Hammerstein-Wiener model is illustrated in Figure 1. The Hammerstein-Wiener model consists of three basic blocks, i.e. two non-linear blocks $f(x)$ and $g(u)$, and a linear block $H(v)$, as shown in the Figure. The $d(n)$ and $y(n)$ are the input and the output signals of the system, respectively. The $v(n)$ and $u(n)$ are the output signals of the first non-linear block $f(x)$ and the linear block $H(v)$, respectively.

The linear filter $H(v)$ serves to capture the dynamic states of the system to be modelled. And it can be modeled by a finite-impulse-response (FIR) filter [7], so the output of $H(v)$, $u(n)$ can be written as

$$u(n) = \sum_{k=1}^{N} h_k v(n-k) \tag{1}$$

where h_k is the filter coefficient and N is the filter order. The input of the filter $v(n)$, which is also the output of the first non-linear block, is represented by a polynomial function, i.e.

$$v(n) = f(d(n)) = \sum_{i=1}^{M} b_{2i-1} d(n) \left| d(n) \right|^{2i-2} \tag{2}$$

where M is the order and b_{2i-1} is the coefficient of the polynomial. In (2), only the odd terms of the polynomial are considered since the even terms will be filtered by the RF filter [14]. Similarly, the output of the second non-linear block $g(u)$ can be described by

$$y(n) = g(u(n)) = \sum_{i=1}^{M'} B_{2i-1} u(n) \left| u(n) \right|^{2i-2} \tag{3}$$

where M' is the order and B_{2i-1} is the coefficient of the

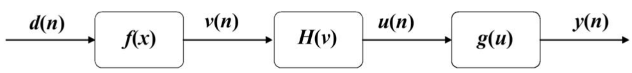

Figure 1. Hammerstein-Wiener model.

polynomial. Consequently, the relationship between the input signal $d(n)$ and the output signal $y(n)$ of the model is

$$\begin{aligned} y(n) &= \sum_{i=1}^{M'} B_{2i-1} u(n) |u(n)|^{2i-2} \\ &= \sum_{j=1}^{M'} B_{2j-1} \left| \sum_{k=1}^{N} h_k \sum_{i=1}^{M} b_{2i-1} |d(n-k)|^{2i-2} d(n-k) \right|^{2j-2} \\ &\cdot \sum_{k=1}^{N} h_k \sum_{i=1}^{M} b_{2i-1} |d(n-k)|^{2i-2} d(n-k) + w(n) \end{aligned} \quad (4)$$

where $W(n) \sim N(0, \sigma^2)$ is the additive Gauss white noise.

In a wideband wireless receiver, the input signal can be viewed as an output signal of a wideband wireless transmitter. We assume that the effects of the wireless channel can be ignored. The nonlinearities of RF front-end of the receiver are also not considered since all the received RF signals, though coming from different transmitters, go through the same RF chain of the receiver and suffer the same nonlinearities. Additionally, the input data of the transmitter, $d(n)$, can be demodulated by the receiver. Based on these assumptions, the data, $d(n)$ and $y(n)$ in (4), are available in the wideband wireless receiver. Therefore, the model parameters can be estimated by utilizing effective system identification algorithms.

3. Basic Genetic Algorithm and Improved Genetic Algorithm

In this section, the basic and the improved genetic algorithms are introduced.

3.1 Basic Genetic Algorithm

The genetic algorithm (GA) is a type of nonlinear optimization method. It builds the overall learning process simulation to a large number of individuals. Each individual represents a result of the giving search space. It starts from an initial population. The fitness based evolution of the population within the search space is iteratively repeated to get better solution. The basic GA has the disadvantages of easy premature convergence and slow convergence speed.

3.2 Improved Genetic Algorithm

The improved genetic algorithm [15] is capable of well solving the easy premature problem.

The flow chart of the improved genetic algorithm is shown as Figure 2. The dashed box represents the improvement of the GA algorithm, including adaptive crossover, adaptive mutation and niche algorithm.

The improved genetic algorithm includes the following steps:

Step 1. Set the value of maximum gene $P_{\max}$ and minimum gene $P_{\min}$. The gene of the optimal solution meeting the relevant conditions is regarded as the predicted value of the model parameter. More practically, each individual gene value is represented by a floating-point number.

Step 2. Group initialization. The search space for generating the initial group is assumed to be the entire feasible space of the decision variable (model parameters to be identified), and then the initial group with the size as n_0 is randomly generated.

Step 3. Elite reservation strategy. The fitness function values of the initial group are sorted in descending order and then the first N individuals are stored.

Step 4. M individuals are selected for step 5 using the proportional selection algorithm according to the fitness.

Step 5. Adaptive crossover operation. Let x_i^t and x_j^t be the parents of the selected individual, and let x_i^{t+1} and x_j^{t+1} be the offspring of the individual after the adaptive crossover operation. The relationship between them is as follows:

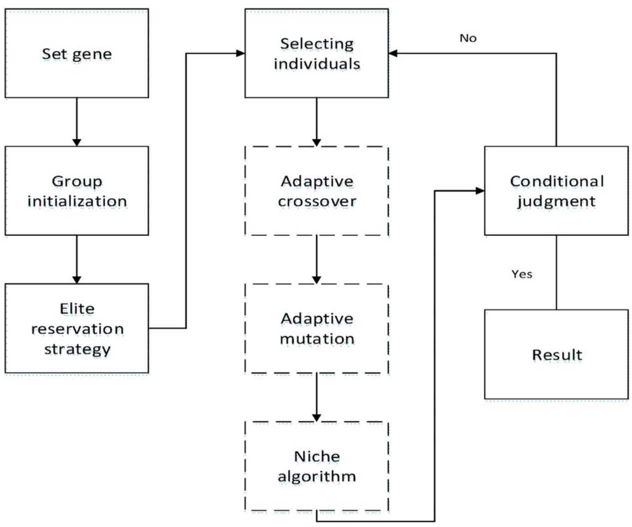

Figure 2. Flow chart of the improved GA.

$$\begin{cases} x_i^{t+1} = P_c x_i^t + (1-P_c)x_j^t \\ x_j^{t+1} = P_c x_j^t + (1-P_c)x_i^t \end{cases} \tag{5}$$

where P_c is expressed by

$$P_c = \begin{cases} P_{c1} - \dfrac{(P_{c1}-P_{c2})(f'-f_{avg})}{f_{\max}-f_{avg}} & f' \geq f_{avg} \\ P_{c1} & f' < f_{avg} \end{cases} \tag{6}$$

In (6), $f_{\max}$ represents maximum fitness in each generation group; f_{avg} is the average fitness value of each generation group; f' stands for the larger fitness value of the two individuals which are selected for crossover operation; P_{c1} and P_{c2} represent the biggest and the smallest crossover probability, respectively.

Step 6. Adaptive mutation. Mutation can maintain high diversity. If the probability of mutation is too large or too small, it will make the GA to become a random search or will make the missing information of the genes unrecoverable. Adaptive mutation can solve these problems. If the individual fitness value is large, its probability of the mutation will be small. But if the individual fitness value is small, its probability of mutation will be high, which can speed up the convergence rate of genetic algorithm. The probability of adaptive mutation can be computed by

$$P_m = \begin{cases} P_{m1} - \dfrac{(P_{m1}-P_{m2})(f_{\max}-f)}{f_{\max}-\bar{f}} & f \geq \bar{f} \\ P_{m1} & f < \bar{f} \end{cases} \tag{7}$$

where P_{m1} and P_{m2} represent the biggest and the smallest probability of mutation, respectively, and $\bar{f}$ represents the average fitness value of each generation group after adaptive crossover operation.

Step 7. Niche algorithm. The obtained M individuals in step 6 are combined together with N individuals stored in step 4 to obtain a new group containing M+N individuals. For M+N individuals, the Hamming distance between every two individuals is calculated according to the following formula

$$\|x_i - x_j\| = \sqrt{\sum_{k=1}^{Chromlen} (x_{ik} - x_{jk})^2} \tag{8}$$

where $i = 1, 2, \ldots, M+N-1$; $j = i+1, i+2, \ldots, M+N$; and *Chromlen* represents the chromosome length. If $\|x_i - x_j\| < L$ is true, then it is necessary to compare the fitness values of individuals x_i and x_j, and to implement the penalty function ($F_{\min}(x_i, x_j) = Penalty$)) for the individual with smaller fitness in order to further reduce the fitness and eliminate the corresponding individual. Afterwards, the individuals are sorted in descending order according to the new fitness of M+N individuals, and the first N individuals are stored.

For example, Figure 3 shows that there are two chromosomes with two loci and the Hamming distance between the two chromosomes is less than L. Chromosome 2 will be eliminated after step 7.

Step 8. If the program meets the precision requirement or reaches the maximum number of iterations, then terminate; otherwise, return to step 4.

The pseudo code of the improved genetic algorithm is described as follows.

1. *Code* $P_{\max}$, $P_{\min}$; // the float-point encoding method.
2. *Initialization;*
3. **While** ($Fitness(1) > Fit_{\max}$ & $k \geq k_{\max}$)
4. P = *sort Fitness*(); // individual is sorted according to the fitness function value from high to low.
5. $N = P(1{:}N)$; $P' = P(N+1{:}n_0)$; // Save the former N individual.
6. Selection behavior;
7. if (rand(0, 1) < p_c)
8. Adaptive crossover;
9. if (rand(0, 1) < p_m)
10. Adaptive mutation behavior;
11. for $i = 1{:}M-1$
12. for $j = i+1{:}M$
13. if $Distance[p'(i)\, p'(j)] < L$
14. $Fitness_{\min}[p'(i)\, p'(j)] = Penalty$;
15. k++;
16. **End While**
17. Output result

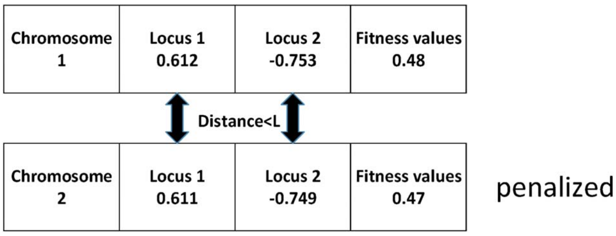

Figure 3. An example of niche algorithm.

4. Identification Method

In this section, a method for the identification of the wideband wireless transmitters that uses a direct comparison of the Euclidean distance between the estimated parameter vector and the real parameter vector is introduced.

Firstly, the identification system establishes an objective function according to a certain criterion using the available input data $d(n)$ and the output data $y(n)$. Then the system solves the objective function to obtain the estimated vector $\hat{\theta}$ of system model parameters. The minimum mean square error (MSE) criterion is adopted, and the objective function for identifying the Hammerstein-Wiener model can be expressed by

$$E(\hat{\boldsymbol{\theta}}) = \frac{1}{K}\sum_{k=1}^{K}\left|y(n-k) - \hat{y}(n-k)\right|^2 \tag{9}$$

where K is the signal sample length, $y(n)$ is the true output and $\hat{y}(n)$ is the estimated output that is related to the model parameter vector $\hat{\theta}$. In order to get the optimal model parameter vector, it is necessary to minimize the objective function (9). Hence, the nonlinear system identification problem is transformed into a minimum value problem in the parameter space. The minimum value of the formula (9) is obtained by using the improved genetic algorithm. And the fitness function is defined as

$$f = \frac{1}{E(\hat{\boldsymbol{\theta}})} \tag{10}$$

Two same types of wideband wireless transmitters produced by a same manufacturer are assumed and are named as No. 1 and No. 2. They are modeled by the Hammerstein-Wiener model and their model parameter vectors are θ_1 and θ_2. In order to evaluate the similarity between the two model parameter sets, the cosine of the angle between the two vectors is adopted and is calculated by

$$\cos\alpha = \frac{(\boldsymbol{\theta}_1^H \boldsymbol{\theta}_2)}{|\boldsymbol{\theta}_1||\boldsymbol{\theta}_2|} \tag{11}$$

where $(\cdot)^H$ is the conjugate operator, and α is the angle between $\theta_1$and θ_2. If θ_1 is very similar to θ_2, then the angle α will be very small.

Since the parameters have been estimated by the improved genetic algorithm, an intuitive method for wideband wireless transmitter identification can be utilized, which is a direct comparison of the Euclidean distance between the estimated parameter vector and the real parameter vector. The decision rule can be written as

$$\left|\hat{\boldsymbol{\theta}} - \boldsymbol{\theta}_1\right| \underset{H_1}{\overset{H_0}{\gtrless}} \left|\hat{\boldsymbol{\theta}} - \boldsymbol{\theta}_2\right| \tag{12}$$

where the hypothesis H_0 means that the received signal is from the wideband wireless transmitter No. 2, and the hypothesis H_1 represents that the signal is transmitted by the No. 1 transmitter.

5. Simulations

To verify the effectiveness of the improved GA and the Hammerstein-Wiener model for the identification of the wideband wireless transmitters, comprehensive simulations are carried out. For performance comparison, simulations are also performed using the basic genetic algorithm, the AWPSO, the NN and the LS iteration method.

5.1 Parameters Configuration

Suppose two wireless transmitters, No. 1 and No. 2, are to be identified and both of them have the same bandwidth of 20 MHz. Assuming the orders of the three blocks of the Hammerstein-Wiener are 7, 3 and 5, respectively, and they can concisely be written as 7-3-5. In this special case, the parameters of the model form a vector $\theta = [b_1, b_3, b_5, b_7, h_0, h_1, h_2, B_1, B_3, B_5]$.

The parameters b_1, h_1 and B_1 are set to be 1 so that the uniqueness of the system identification is ensured. The parameters of the two wideband wireless transmitters are designated in Table 1. The cosine value between the two parameter vectors is 0.9995 and the angle is 1.8221°, which means a high similarity.

The SNR is ranged from 2 dB to 30 dB with a step of 4 dB, and each algorithm is executed 2000 times at each SNR. The maximum number of iterations for the LS iteration method is 1000. The population size for both the

Table 1. Parameters configuration

	Parameters ***b*** of the nonlinear subsystem				Parameters ***h*** of the linear subsystem			Parameters ***B*** of the nonlinear subsystem		
Transmitter	$b1$	$b2$	$b3$	$b4$	$h1$	$h2$	$h3$	$B1$	$B2$	$B3$
No. 1	1	-0.0135	-0.0086	-0.0017	1	0.0628	0.0079	1	-0.08551	-0.00814
No. 2	1	-0.0187	-0.0053	-0.0019	1	0.1163	0.0194	1	-0.09061	-0.00974

improved GA and the basic GA are set to be 50. The selected parameters for the improved GA and the basic GA are as follow:

Improved GA:
$Penalty = 0.001$, $L = 0.05$, $P_{m1} = 0.05$,
$P_{m2} = 0.001$, $P_{c1} = 0.8$, $P_{c2} = 0.6$, $N = 10$
Basic GA:
$P_c = 0.6$, $P_m = 0.05$

In order to evaluate the performance of the model identification, the normalized mean squared error (NMSE) is defined as

$$NMSE = 10\log_{10}\frac{\sum_{n=1}^{K}\left|y(n)-\hat{y}(n)\right|^2}{\sum_{n=1}^{K}\left|y(n)\right|^2} \tag{13}$$

where $y(n)$ and $\hat{y}(n)$ represent the real and the predictive outputs, respectively, and K is the number of samples.

5.2 Performance Comparison of the Algorithms

In the following simulations, the average runtime and the NMSE of the model identification algorithms are compared.

5.2.1 Average Runtime

Table 2 shows the average runtimes of the four algorithms using the Hammerstein-Wiener model. The runtimes of the improved GA and the basic GA are longer than that of the LS-iteration method and the AWPSO. The reason is that the LS-iteration algorithm and the AWPSO are easier to fall into a local optimal solution, whereas the intelligent algorithms contain multiple intelligent behaviors of multiple individuals at each run. Due to an additional operation of niche elimination, the running time of the improved GA is slightly longer than the basic GA. Since the NN algorithm needs an additional training phase, the runtime of the NN is not listed.

Table 2. Algorithm average runtime

Algorithms	Improved GA	Basic GA	AWPSO	Ls-iterative
Runtime (s)	483.25	302.07	86.45	52.13

5.2.2 NMSE

Figure 4 illustrates the NMSE versus SNR curves with order 7-3-5. It shows that the NMSE curves of the five algorithms are decreasing with the increase of the SNR. Moreover, we can see that the improved GA has the lowest NMSE. The NMSE of the two intelligent algorithms are much smaller than others. The reason is that those iterative methods are more sensitive to noise. In the NN algorithm, the number of training samples is set to 20000. The performance of the NN is good at low SNR, but with the rise of the signal to noise ratio, its effect is not very obvious upgrade.

Figure 5 demonstrates the prediction error curves of the two GA methods when SNR is 16 dB. The figures show that the average prediction error of the improved GA is lower than 0.05.

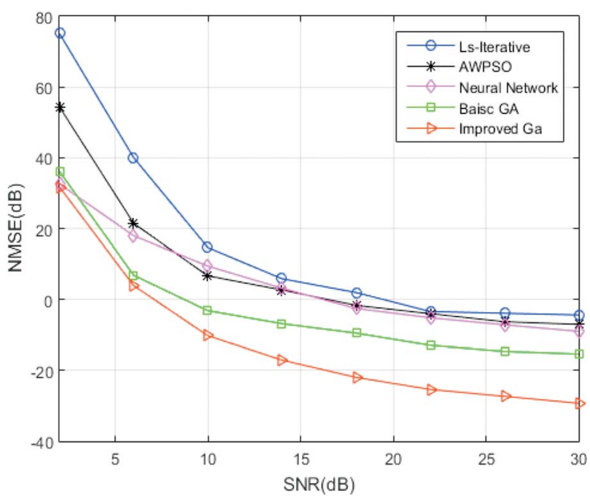

Figure 4. NMSE of five algorithms using the Hammerstein-Wiener model with order 7-3-5.

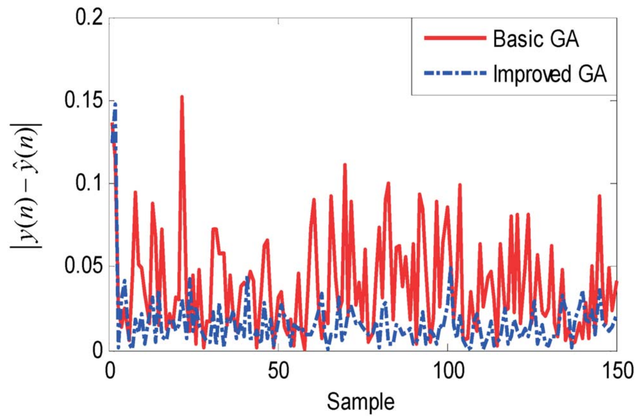

Figure 5. The prediction error between the expected and the prediction outputs using the Hammerstein-Wiener model.

These results evidently show that the improved GA is more accurate than the other algorithms.

5.2.3 Order Selection

Simulations are also performed to get the relationship between the order of the model and the NMSE when SNR is 16 dB.

The order of the Hammerstein-Wiener model reflects the nonlinear distortion degree of the transmitter, so the model order influences the prediction precision of the improved genetic algorithm. Table 3 shows that when SNR is 16 dB the prediction error is smallest when the Hammerstein-Wiener model order is 7-3-5, which means that the order 7-3-5 is the best among all the orders listed in Table 3.

5.3 Wideband Wireless Transmitter Identification

In the following, the identification of the model parameters and the transmitters are performed by using the Hammerstein-Weiner model with the order 7-3-5.

5.3.1 Parameters Identification

Table 4 presents the true values and the estimated values using the improved GA. The relative error is employed to evaluate the identification performance and it is defined as

$$\sigma = \frac{|d - \hat{d}|}{|d|} \cdot 100\% \tag{14}$$

where d is the true value, $\hat{d}$ is the estimated value, and σ is the relative error.

Table 4 shows that the average relative error of the parameters is 5.83%, which means the estimation precision is relatively high.

5.3.2 Identification Performance of Wideband Wireless Transmitter

As shown in Figure 6, the recognition rates of the improved GA and the basic GA are increasing with the increase of the SNR. The SNR of the improved GA is nearly 3.5 dB lower than the basic GA when the recognition rate is higher than 90%. The recognition rate of the improved GA is 6.01% higher than the basic GA on average, due to the fact that the basic GA is unable to fully traverse the entire solution space and to carefully search the global optimum point in the feasible solutions area. Also, we can see that the AWPSO and the NN have better identification performance than the LS-iteration algorithm, but they have worse identification performance than the GA

Table 3. NMSE of different orders

Order	7-3-3	7-3-5	7-5-3	3-7-5	5-3-7	5-7-3	3-5-7
NMSE (dB)	-19.64	-20.03	-19.89	-19.62	-19.92	-19.58	-19.96

Table 4. Parameters identification of No. 1 transmitter

SNR = 16 dB	Parameters ***b*** of the 1st nonlinear subsystem				Parameters ***h*** of the linear subsystem			Parameters ***B*** of the 2nd nonlinear subsystem		
No. 1 transmitter parameters	*b*1	*b*3	*b*5	*b*7	*h*1	*h*2	*h*3	*B*1	*B*3	*B*5
True values	1	-0.0135	-0.00860	-0.00170	1	0.0628	0.00792	1	-0.0855	-0.00874
Estimated values with improved GA	1	-0.0141	-0.00912	-0.00184	1	0.0617	0.00786	1	-0.0913	-0.00762
Relative error	0	4.44%	6.05%	8.24%	0	1.75%	0.76%	0	6.78%	12.8%

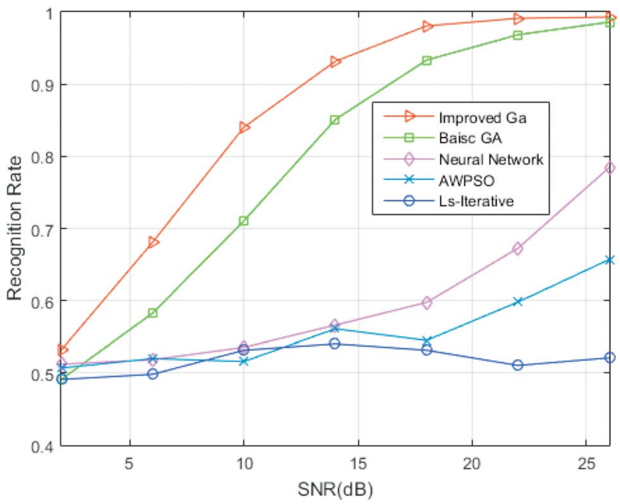

Figure 6. Recognition rate vs. SNR.

and the improved GA. The NN algorithm has a certain classification ability when SNR is high, but it highly relies on system training. The AWPSO algorithm has a poor performance when SNR is low.

The simulation results have clearly proven that the identification approach with the improved GA is much more effective than other four algorithms, even for relatively low SNRs.

6. Conclusion

In this paper, the wideband wireless transmitter is modeled with a Hammerstein-Wiener model and the improved GA is proposed to identify the wireless transmitters. In order to verify the performance, the improved GA is compared with the basic genetic algorithm, the LS-iteration method, the NN and the AWPSO algorithm. The experimental results show that the improved genetic algorithm has the best identification performance of the five algorithms while the LS-iteration algorithm has the worst. The recognition rate of the improved genetic algorithm is 6.01% higher than the basic genetic algorithm on average. Despite it takes a longer average runtime, the improved GA has less average relative error and better recognition performance.

Acknowledgement

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