



Specific Emitter Identification Using IMF-DNA with a Joint Feature Selection Algorithm

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Abstract: Specific emitter identification (SEI) is a technique to distinguish among different emitters of the same type using weak individual characteristics instead of conventional modulation parameters. The biggest challenge in SEI is to not only distinguish the different emitters with close modulation parameters but also to identify a specific emitter when its modulation parameters change significantly. For this paper, individual differences in pulse envelopes were investigated and four types of pulse envelopes were modeled. To exploit the individual features along with the pulse envelope for the identification of a specific emitter, an intrinsic mode function distinct native attribute (IMF-DNA) feature extraction algorithm and a joint feature selection (JFS) algorithm were proposed, which together constitute the final proposed SEI technique. Compared with four other feature selection methods, the proposed feature selection algorithm performed better for finding the most useful features for classification, which greatly helps in the reduction of feature dimension. Compared with radio frequency DNA (RF-DNA), IMF-DNA had a far superior correct emitter identification rate under similar conditions. A real data verification method was developed to verify the performance of IMF-DNA for specific emitter identification. The method achieved a correct identification rate of 85.3% at a sampling rate of 200 MHz and had an estimated signal-to-noise ratio (SNR) of approximately 10 dB.

Keywords: specific emitter identification; IMF-DNA; feature selection; pulse envelope; support vector machine

1. Introduction

Specific emitter identification (SEI) is a widely applied practical technique for electromagnetic environmental perception, both in modern electronic warfare and many civilian scenarios [1,2]. In modern electronic warfare, radar emitter recognition (RER), which is an important research area of electronic reconnaissance, has faced some challenges in recent years, such as the intentional and random variation of modulation parameters [3–5]. SEI was proposed to solve these problems. However, it is difficult to ensure the valid and reliable performance of SEI if only some conventional characteristic parameters are extracted and used for SEI. There is an urgent need for new features that can indicate individual minor differences between different devices of the same type with the same or similar traditional characteristics. In fact, the practical demand of SEI comes not only from the military, but also from many civilian areas, such as information forensics and security [6–9].

In recent decades, a radio frequency distinct native attribute (RF-DNA) fingerprinting technique has been proposed to identify ZigBee devices. This technique computes some statistics from the time series of device emissions and can be regarded as a physical layer-based security measure [6,7,10–15]. The research team of Michael A. Temple is well known for exploiting RF-DNA to identify emitters;



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their prominent and impressive work began in 2008 [16], and greatly inspired the presented research in this paper. RF-DNA fingerprinting can be extended to other domain features, such as fractal features [17–21], and can be used to characterize native attributes. The method can also be extended to sub-bands of different frequencies using signal decomposition methods such as empirical mode decomposition (EMD) [22], variational mode decomposition (VMD) [23], and the empirical wavelet transform (EWT) [24]. After a feature selection process, the features with anti-noise ability and greater robustness can be selected for the final specific identification [10].

EMD, VMD, and EWT are multi-component signal analysis algorithms which can decompose a signal into several components, called intrinsic mode functions (IMFs) [22-24]. Extracting individual features from IMFs instead of the original RF signal has recently attracted the interest of numerous researchers [9,25–30]. Several spectral features, including spectral flatness, spectral brightness, and spectral roll-off, have been exploited to improve the identification accuracy compared with other existing temporal feature-based methods [25]. For instance, in [9], an SEI technique using the entropy and the first- and second-order moment features extracted from the Hilbert-Huang transform (HHT) spectrum was presented; impressively, the proposed algorithm is also applicable to fading channels. Additionally, in [27], a VMD-based SEI algorithm using mean and variance features extracted from each component (i.e., IMF) was proposed. In [28], a fusion frequency feature extraction method based on VMD, duffing chaotic oscillator (DCO), and permutation entropy was proposed to identify underwater acoustic signals. Moreover, in [29], a regression variational mode decomposition (RVMD) algorithm was used to decompose radar signals, and an SEI algorithm using the first IMF and a deep belief network (DBN) was finally proposed. VMD has been used for the attenuation of random seismic noise, and greatly improves the signal-to-noise ratio (SNR) of seismic data [30]. Signal decomposition algorithms are capable of representing the original signal in several sub-bands of different frequencies, which allows them to remove noise and consequently improves the SEI performance.

Individual differences between devices of the same type are mainly caused by the individual attributes of the physical components, which are stable for a long period of time or may even be permanent, such as frequency drift [31], power amplifier amplitude response [9,32], and phase noise [33,34]. In general, once an emitter is activated, the signals transmitted from the emitter have unique characteristics and can be used as a "fingerprint" to clearly identify the emitter. Previously proposed SEI algorithms and their applications are mainly based on the use of such unique individual characteristics. In SEI research, the work of Kawalec and Dudczyk is also well known, and their prominent and impressive research into SEI can be dated back to 2004 [18,35–38]. Their work is a continuation of the pioneering work of Kawalec on emitter recognition. The impressive work of Kawalec and Dudczyk in SEI research is mainly focused on systematically developing new methods which fully use abundant traditional pulse parameters.

SEI is mainly used to find specific views and representations of emitters, and has been used to obtain views of emitters in different domains, such as the time domain [9,39], the frequency domain [26,32,40,41], and the fractal domain [17–21]. Figure 1 shows a schematic timing diagram of a receiver and an emitter presented in [31]. Most of the studies mentioned above mainly focus on inter-pulse or intra-pulse information [18,20,36–38,42–45], which are in pulse level shown in Figure 1. Another of our papers focused on the phenomenon of frequency drift in an emitter start-up process which happens in the observing time window (OTW) level shown in Figure 1. For this paper, we focused on individual differences in the pulse envelope, which are in pulse level and can reflect the signatures of digital-to-analog converters (DACs), filters, and power amplifiers. Four types of pulse envelopes were modeled after analyzing the effect of physical devices on the pulse envelope. To exploit individual features along with the pulse envelope for SEI, an IMF distinct native attribute (IMF-DNA) feature extraction algorithm and a joint feature selection (JFS) algorithm were proposed, which constitute the final proposed SEI technique. Simulations and real data verification were used to verify the practical performance of the proposed SEI algorithm.



Figure 1. The schematic timing diagram of a receiver and an emitter. OTU, observing time unit; A/D, analog/digital.

The rest of this paper is organized as follows: the signal modeling, modulated with four types of envelopes, is presented in Section 2; the proposed SEI algorithm for feature extraction from pulsed emitter signals and the joint feature selection algorithm are presented in Section 3; the simulation results and analysis are presented in Section 4; the real data verification is presented in Section 5; and conclusions and a summary of the results of the simulation and the whole work of this paper are presented in Section 6.

2. Signal Modeling

For signal modeling, we mainly consider the influence of phase envelopes, which are a typical emitter signature. The characteristics of a pulse envelope are mainly produced by the following factors: (1) the pulse envelope may be distorted by the inertia of the device during the DAC conversion of a digital signal to an analog signal; (2) the pulse envelope may be distorted by individual differences in the pass band flatness of the low-pass filters and the bandpass filter; this is more obvious for broadband signals, such as linear frequency modulation (LFM) signals; and (3) the pulse envelope can also be distorted by individual differences in frequency response at different frequencies in the pass band of intermediate frequency amplifiers, power amplifiers, etc. The above factors may lead to unsatisfactory envelopes of the pulsed signals from different emitters, which can be regarded as unique signatures of different emitters [26].

A typical envelope of a real pulsed signal is shown in Figure 2. This paper focuses on rising-edge modeling. Both the falling edge and the rising edge are assumed to have a symmetrical shape, and the top envelope is set at a constant level.

Four types of pulse envelopes were built for this paper, namely, linear envelope (LE), tangent envelope (TE), quadratic envelope (QE), and sigmoid function envelope (SE). The expression for the LE is as follows:

$$LE(\lambda) = \begin{cases} \frac{1}{\lambda'T}t & 0 \le t \le \lambda T\\ 1 & \lambda T < t \le T - \lambda T\\ \frac{1}{\lambda'T}(T-t) & T - \lambda T < t \le T \end{cases}$$
(1)

where λ is the time percentage of the pulse width occupied by the rising edge, which is the same as that occupied by the falling edge $\lambda' = \lambda$ if no overshooting occurs.

The expression for the TE is as follows:

$$TE(\lambda) = \begin{cases} \tan\left(\frac{\theta}{\lambda'T}t\right) & 0 \le t \le \lambda T\\ 1 & \lambda T < t \le T - \lambda T \\ \tan\left(\frac{\theta}{\lambda'T}(T-t)\right) & T - \lambda T < t \le T \end{cases}$$
(2)

where θ is used to adjust the degree of curvature of the rising edge. Generally, we can set $\theta = 0.25\pi$. $\lambda' = \lambda$ if no overshooting occurs.

The expression for the QE is as follows:

$$QE(a,b,\lambda) = \begin{cases} \frac{at^2 + bt}{a\lambda'^2 T^2 + b\lambda' T} & 0 \le t \le \lambda T\\ 1 & \lambda T < t \le T - \lambda T\\ \frac{a(T-t)^2 + b(T-t)}{a\lambda'^2 T^2 + b\lambda' T} & T - \lambda T < t \le T \end{cases}$$
(3)

where *a* and *b* are used to adjust the degree of curvature of the rising edge. $\lambda' = \lambda$ if no overshooting occurs.

The expression for the SE is as follows:

$$SE(\lambda) = \begin{cases} \frac{1+e^{-\sigma}}{1+e^{\sigma-\frac{2\sigma t}{\lambda'T}}} & 0 \le t \le \lambda T\\ 1 & \lambda T < t \le T - \lambda T \\ \frac{1+e^{-\sigma}}{1+e^{\sigma-\frac{2\sigma t}{T-\lambda'T}}} & T - \lambda T < t \le T \end{cases}$$
(4)

where σ is used to adjust the "*S*" shape of the rising edge. Generally, we can set $\sigma = 5$. $\lambda' = \lambda$ if no overshooting occurs.

Figure 3 shows the four types of pulse envelopes when $\lambda = 0.25$, $\theta = 0.25\pi$, a = 1000, b = 0.001, and $\sigma = 5$.



Figure 2. A typical envelope of a pulsed signal.



Figure 3. The four types of pulse envelopes used in this study.

The differences in the rising edges for different emitters are so small that they can hardly be distinguished considering the transport channel noise, as can be seen from the distance between the different envelopes shown in Figure 3. By inference, SEI will not perform optimally if only some individual features are extracted in the time domain. Therefore, we attempted to extend the time-domain signal in the frequency direction using a signal decomposing algorithm; this can simultaneously increase the dimension of the feature vector in cost and reduce the redundancy of features, which in turn can decrease the feature dimension. As a result, we propose a novel specific emitter identification algorithm which uses individual envelope characteristics. This work was mainly inspired by the distinguished work of Michael A. Temple's team [6,10–15].

3. Proposed Algorithm

The new algorithm developed in the present study is shown in Figure 4. The algorithm decomposes the original time-domain signal into several IMFs, segments the IMFs into separate time series, and extracts the features that will be used for identification from each IMF. Unlike the RF-DNA algorithm, our algorithm uses features from different IMFs, whose amplitude (*a*) sequences and frequency (*f*) sequences are exploited in order to identify specific emitters. Consequently, our algorithm involves far fewer signal segmentations (eight) than the RF-DNA algorithm (80 in [10]). Considering that the feature sources are IMFs, the proposed SEI algorithm is named IMF-DNA.



Figure 4. The comparison of the process flows of the proposed specific emitter identification (SEI) using the intrinsic mode function distinct native attribute (IMF-DNA) algorithm and the radio frequency DNA (RF-DNA) algorithm.

3.1. Signal Decomposition

A pulsed signal s(t) can be decomposed into

$$s(t) = \sum_{i=1}^{K} c_i(t) + r_K(t),$$
(5)

which is a cumulative sum of multiple intrinsic mode functions $\{c_i(t)\}, i = 1, \dots, K$ and a residual trend $r_K(t)$ according to a local feature timescale of the signal, where *K* is the number of modes. This is the basic idea of EMD, which was proposed by Huang [22]. Recently, it has been shown that the VMD

signal decomposing algorithm [23], which is similar to EMD, can also transform a signal into a group of IMFs. Either of these two signal decomposing algorithms is practical for our technical framework. The quantity of IMFs (*k*) used for fingerprint feature extraction is usually an empirical value depending on the decomposition result, and was set as 3 in the present study. The proposed technical framework also works for the EWT [24].

3.2. IMF Segmentation

In the IMF-DNA algorithm, the IMFs are segmented into several time series, as in the RF-DNA algorithm. The enframe function in the MATLAB software (MathWorks, Natick, MA, USA), which is commonly used for signal windowing and framing in speech signal processing, is a useful tool to segment time sequences, and can be designed as a sliding window to resample the original signal time sequence. Its calling syntax is "y = enframe(x, w, s)", where *x* represents the signal to be framed, *w* is the frame length or window width, and *s* indicates the step size or sliding window offset. For *n* segments, we obtain the following:

$$s = \left\lceil \frac{\text{length}(x) - w}{n} \right\rceil,\tag{6}$$

where the function $\lceil \cdot \rceil$ is the ceiling function, which maps a real number *x* to the least integer. The returned value *y* of the enframe function is an *n* × *w* matrix, so the fractal dimension needs to be calculated row by row. In this study, the number of segments was 8. The segmentation methodology was presented in our previous paper [21].

3.3. Feature Extraction from IMFs

Following [10], we assume that the individual characteristics for a frequency are duplicates of the features for phase (φ). Therefore, the features are only extracted from the amplitude sequence and the frequency sequence, and the feature structure can be expressed as follows:

$$\begin{cases} \mathbf{F}_{C_{i}} = \left[\mu_{C_{ij}} \sigma_{C_{ij}}^{2} \gamma_{C_{ij}} \kappa_{C_{ij}} \right]_{1 \times 4} \\ \mathbf{F}^{a|f} = \left[\mathbf{F}_{C_{1}} \vdots \mathbf{F}_{C_{2}} \cdots \mathbf{F}_{C_{k}} \right]_{1 \times N_{c}} , \\ \mathbf{F} = \left[\mathbf{F}^{a} \vdots \mathbf{F}^{f} \right]_{1 \times N_{F}} \end{cases}$$
(7)

where $N_c = 4 \times nk$ denotes the number of features extracted from all components (i.e., IMFs) from the amplitude sequence or frequency sequence, respectively; $N_F = N_c \times 2$ is the final feature dimension of IMF-DNA; μ denotes mean value; σ^2 denotes variance; γ is skewness; and κ is kurtosis. In this paper, the final feature dimension of IMF-DNA was 96, compared to a value of 90 for RF-DNA.

3.4. Dimensional Reduction Analysis and the Proposed Joint Feature Selection Algorithm

A previous study [10] used two pre-classification dimensional reduction analysis (DRA) feature selection methods—namely, the Kolmogorov–Smirnov test (KS test) and the F test—and two post-classification DRA feature selection methods—namely, generalized relevance learning vector quantized improved (GRLVQI) relevance and Wilks's lambda ratio. In the present study, we propose a joint feature selection (JFS) algorithm based on these four feature selection methods (Algorithm 1). This JFS is a voting algorithm and can select the features which contribute most to the classification. The ranking results obtained using the KS test, F test, GRLVQI relevance, and Wilks's lambda ratio are denoted as *K*, *F*, G, and W, respectively.

Algorithm 1: Joint feature selection (JFS) algorithm

Initialize the ranking results obtained using each of the four feature selection algorithms (the

Kolmogorov–Smirnov test, the F test, GRLVQI relevance, and Wilks's lambda ratio) as $K_{1\times NF}$, $F_{1\times NF}$, $G_{1\times NF}$, and $W_{1\times NF}$, which stores the feature index number; i = 0; the vote counting result NVC = $\mathbf{0}_{1\times NF}$, any element of which is less than or equal to the number of all voting members (4 in this paper); the index number of a group of features selected FS, index number of a group of features to update FS_update

Repeat

i = i + 1

Count the votes of each feature from the first *i* numbers of $K_{1 \times NF}$, $F_{1 \times NF}$, $G_{1 \times NF}$ and $W_{1 \times NF}$, and update NVC

Search the elements of NVC and find the feature index members which obtained votes greater than or equal to T_{voting} , and denote the result as FS_temp

Check the elements of FS_temp, find the new members which do not appear in FS, and denote these new members as FS_update

```
if FS_update is blank
continue
else
FS ← {FS, FS_update}
Clear FS_temp
FS_update ← 0
```

until $i = N_F$

where T_{voting} is a preset threshold value, which is usually more than half the number of all voting members. The degree of feature dimension reduction is denoted as N_d , which refers to the first N_d features of the total number of N_F features.

3.5. Recognition Process Using a Support Vector Machine

Support vector machines (SVMs) have been widely used and have generally proven to be powerful and robust classification tools. Therefore, in this study, a classifier based on an SVM was applied for the final emitter identification of SEI. SVMs are machine learning algorithms that are based on statistical learning theory [46] and usually use a kernel function $k(x_i, x_j)$ to measure the similarity between two samples x_i and x_j , which can map the nonlinear separable data to a high-dimensional space where the classifier can linearly separate the samples. The decision function for an SVM classifier can be written as follows:

$$f(\mathbf{x}) = \operatorname{sgn}\left(\sum_{i=1}^{N} \alpha_i y_i \mathbf{k}(\mathbf{x}_i, \mathbf{x}) + b\right),\tag{8}$$

where x_i denotes the *i*-th sample, i = 1, ..., N is the sample index of the training data, and $y_i = \{\pm 1\}$ is the label of each sample. The typical kernels used for SVMs are the Gaussian radial basis function (RBF) kernel, the polynomial kernel, and the sigmoid kernel [47].

SVMs are conventional classifiers for binary classification; however, they can be extended to multiple classification using some algorithms, such as the one-against-all technique. In this study, we exploited a multi-classifier based on the LIBSVM machine learning library [48] to implement the final specific emitter identification, in which a general Gaussian RBF kernel is applied.

4. Numerical Results and Analysis

4.1. Signal Simulation and Feature Extraction

The numerical experiment simulated two emitters, E_1 and E_2 , and three types of primary signals, giving a total of six signal sources, as shown in Table 1. The envelope types could be replaced by QE or SE. The original signal sources can be expressed as follows:

$$\begin{cases} s_{1i}(t) = A_i(t) \exp[j(2\pi f_0 t + \pi k t^2 + \varphi_{1i})] \\ s_{2i}(t) = A_i(t) \exp[j(2\pi f_0 t + \varphi(t))] \\ s_{3i}(t) = A_i(t) \exp[j(2\pi f_0 t + \varphi_{3i})] \\ A_1(t) = LE(\lambda) \\ A_2(t) = TE(\lambda) \end{cases}$$
(9)

where $i = 1, 2, A_i(t)$ is the envelope function designed in Section 2, the initial frequency f_0 is 20 MHz, the bandwidth *B* is 5 MHz, the chirp period *T* and the pulse width T_w are both 20 µs, and the sampling rate F_s is 1000 MHz. The frequency modulation rate k = B/T, $\lambda = 0.15$, and the parameter θ in $A_2(t)$ is 0.25π , which can be found in Equation (2). In the equation for $s_{2i}(t)$, $\varphi(t)$ is the phase modulation function for binary phase shift keying (BPSK) signals, and can be written as follows:

$$\begin{cases} \varphi(t) = \pi B[\lfloor \frac{t}{T_c} \rfloor] \\ B[n] = \{1111100110101\}, n = 0, \cdots, N_c - 1 , \\ T_c = \frac{T}{N_c}, N_c = 13 \end{cases}$$
(10)

where B(n) denotes a Barker code, N_c is the length of the Barker code, and T is the pulse width, which is 20 µs.

Table 1. The signal parameters used for different pulse envelopes. LE, linear envelope; TE, tangent

envelope; LFM, linear frequency modulation; BPSK, binary phase shift keying.

Emitter Envelope Type ______Primary Signal Type

Emitter	Envelope Type	Primary Signal Type		
		LFM	BPSK	Single Tone
E ₁ E ₂	LE TE	s ₁₁ s ₁₂	s ₂₁ s ₂₂	s ₃₁ s ₃₂

The channel noise type is additive white Gaussian noise, and the number of samples for each emitter and each primary signal type is 1000, resulting in a total of 6000 samples. The signal segmentation number for IMF-DNA is 8, the number of IMFs used for feature extraction is 3, and the feature vector dimension for each IMF segments is 2 with skewness and kurtosis removed. Therefore, the final feature vector dimension is 96. For comparison, the feature vector dimension of RF-DNA is 90 (10 signal segments and 9 features for each segment).

The signal decomposing algorithm used in this paper was VMD, which can effectively separate and suppress the noise component. The key parameter for decomposition, namely K (the total number of modes), was set as 3, and the parameter α , which imposes the tightness of the band limits, was set as 1800. The parameter optimization is mainly based on other parameter optimization algorithms, such as particle swarm optimization, which will be presented as a separate work in the future. In this paper, the values of the parameters were obtained by empirical investigation. More details about VMD can be found in [23].

The T_{voting} parameter of the proposed feature selection algorithm was set as 4 (i.e., the total number of feature selection methods used for joint selection), and the most recently updated members in one loop were not intentionally ranked again.

4.2. Recognition of Emitters

For the analysis of the classification performance of IMF-DNA and the proposed joint feature selection algorithm, the following three experiments were carried out:

- Experiment 1: Classify the six signal sources into six classes, which means the emitters are identified as six emitters. The experiment was designed to prove that the proposed fingerprint algorithm can also be used for modulation classification;
- Experiment 2: Classify s₁₁, s₁₂, s₁₃ as Emitter E₁ and s₂₁, s₂₂, s₂₃ as Emitter E₂, that is, identify two different emitters. The experiment was designed to determine the influence of the pulse envelope and primary signal on the proposed fingerprint algorithm;
- Experiment 3: Classify s_{11} as Emitter E_1 and s_{21} as Emitter E_2 , which removes the influence of the primary signal and can be used to verify the performance of the SEI using pulse envelope characteristics.

Figure 5 shows the SVM classification performance for six classes for Experiment 1 using the IMF-DNA algorithm. The results proved that the proposed algorithm can effectively distinguish between different modulations with minor differences in individual pulse envelopes. It has previously been shown that the final reduced dimension does not significantly affect the final classification performance [10]. The main reason for this may be that the differences in modulation are large enough to allow correct classification.



Figure 5. The performance of the support vector machine (SVM) classification for six classes using IMF-DNA. (**a**) $N_d = 10$. (**b**) $N_d = 30$. (**c**) $N_d = 50$. (**d**) $N_d = 80$.

For Experiment 2, simultaneously considering the differences in modulation and the differences between envelopes, it was attempted to use the classification to distinguish the emitters by locating the individual differences between envelopes using the proposed feature selection algorithm. The results are shown in Figure 6. Because features related to the rising edge and falling edge are observed

first and the features related to modulation are observed later in the feature selection process, the classification performance is excellent when the reduced dimension is low. As the number of features used for classification increases, during which the ratio of other features related to the modulation also increases, the performance decreases significantly as the difference between the two classes becomes less and less. Especially when SNR increases (Figure 6c,d), the influence of modulation increases rapidly, and consequently the classification performance decreases significantly. Additionally, the full dimension line shown in Figure 6a,b is below 85% and out of the display range of the y-axis, which can be seen in Figure 6c,d.



Figure 6. The SVM classification performance for two classes using the IMF-DNA algorithm. (**a**) $N_d = 10$. (**b**) $N_d = 30$. (**c**) $N_d = 50$. (**d**) $N_d = 80$.

Experiment 3 was designed to remove the influence of the primary signal. Figure 7 shows the results for this experiment in terms of the SVM classification performance for LFMs with different envelopes being classified into two classes using the IMF-DNA algorithm. The result shown in Figure 7a verifies the superior performance of the proposed joint feature selection algorithm compared to the KS test, F test, GRLVQI relevance, and Wilks's lambda ratio methods. All the primary signals used for classification were LFMs, which means that the differences between primary signals are removed, and the classification performance increases, especially in lower reduced dimensions, such as $N_d = 10$ (see Figures 5a and 7a). The superior performance of IMF-DNA proves that it can select the ideal features which make the largest contribution to the classification. As the number of features used for the classification increases, the classification performance stays stable, with no differences being observed between primary signals. The above analysis proves the inferences and conclusions in experiment 2 as a supplement.



Figure 7. The performance of the SVM classification for linear frequency modulations (LFMs) with different envelopes being classified into two classes using IMF-DNA. (**a**) $N_d = 10$. (**b**) $N_d = 30$. (**c**) $N_d = 50$. (**d**) $N_d = 80$.

From the results of experiments 1 to 3, the following conclusions can be made: first, the proposed joint feature selection algorithm performs better than the KS test, F test, GRLVQI relevance, and Wilks's lambda ratio methods; second, the proposed IMF-DNA algorithm performs excellently for specific emitter identification; and finally, if some primary signal suppression algorithm can remove the influence of the primary signal on the specific emitter features, the SEI performance will increase more robustly, which can prevent the performance reduction observed in Experiment 2. Future work will involve exploiting a primary signal suppression algorithm for SEI.

4.3. Comparison between IMF-DNA and RF-DNA

For a final performance comparison, the RF-DNA feature vector was designed as a 90-dimensional vector, consisting of 10 signal segments each containing 9 feature vector members. This high dimensional vector was reduced into 10 or 30 dimensions using the proposed joint feature selection algorithm. The final performance comparison between IMF-DNA and RF-DNA is shown in Figure 8.

As can be seen from Figure 8, the performance of the IMF-DNA algorithm is much better than that of RF-DNA, especially for lower SNR. The main reason why IMF-DNA performs better is that the VMD algorithm can decompose the original signal into several IMFs and the original minor differences in envelope will be distributed in different IMFs, which makes it possible for some differences to become more outstanding when other components are removed. At the same time, an efficient feature selection algorithm was applied to find the features which contribute most to the classification, which maximizes the distance between classes.

When using the proposed algorithm, we found that the sampling rate also affects the classification performance. Specific emitter identification performs better with a higher sampling rate, which requires more calculation.



Figure 8. A comparison of the identification performance of the RF-DNA and IMF-DNA algorithms for LFMs with different envelopes being classified into two classes and all the signal sources being classified into two classes.

5. Verification Using Real Data

To verify the performance and practicality of the proposed algorithm, the emitted signals from two signal sources of the same type were sampled. To suppress the influence of the sampling equipment, this study used an M9703A high-speed digitizer/wideband digital receiver (Keysight Technologies, Inc., Santa Rosa, CA, USA), which had been regulated within the last year, to sample the signal sources. The real signal sampling experiment is described in Figure 9. The sampling work was presented in our previous paper [21].



Figure 9. Real signal sampling experiment. (**a**) Sampling the signals from two emitters. (**b**) Process of signal sampling and signal processing.

The carrier frequency of the two emitters was 425 MHz, the modulation bandwidth was 5 MHz, and the pulse width was 130 μ s. The sampling rate was 2 GHz and the digital down-conversion process moved the spectrum to the intermediate frequency of 25 MHz. A total of 1000 samples for each emitter with similar values of estimated SNR were selected. Other real radar emitter sampling data, with a sampling rate of 200 MHz, were incorporated into the identification process. Therefore, the down-sampling rate for the first two signal sources was also set to 200 MHz. A total of 1000 pulses from the real radar emitter were selected for identification at the same time. Figure 10 presents the feature distribution of the three different real emitters after normalization; the data have a mean value of zero and a variance of 1.



Figure 10. The feature distribution of three different real emitters after normalization. (a) Emitter 1. (b) Emitter 2. (c) Emitter 3 (real radar emitter).

As shown in Figure 10, Emitters 1 and 2 are signal sources with more stable parameters, which makes the feature distribution more stable and the spectrum purer. Emitter 3 is a real radar emitter with more outliers distributed at both ends, especially in features 1 to 6, which indicates strong dispersion characteristics.

For the final identification, 30% of the samples were used for training and the rest of the samples were used for testing. The SNR was estimated to be approximately 10.0 dB, and the correct identification rate was 85.3% using the proposed SEI algorithm, which consists of the IMF-DNA fingerprint algorithm and a joint feature selection algorithm. For comparison, the correct identification rate using RF-DNA under almost the same conditions was 83.3%. The final correct identification rate is different from the simulation result shown in Figure 8, which is mainly due to the sampling rate.

6. Conclusions

In this paper, individual differences in pulse envelopes were analyzed and four types of pulse envelopes were modeled. After the signal modeling, a specific emitter identification algorithm using IMF-DNA and a joint feature selection algorithm was proposed. Compared to four other feature selection methods, the proposed feature selection algorithm performed better, finding the most useful features for classification, which significantly helped with the reduction of feature dimension. Three experiments were used to verify the practical performance of IMF-DNA for modulation recognition and specific emitter identification. Compared with RF-DNA, IMF-DNA achieved a higher correct emitter identification rate under similar conditions in simulation experiments. IMF-DNA has significant advantages over RF-DNA, especially for lower SNRs (e.g., below 0 dB). On the other hand, for SNRs above 0 dB, the performances of the two algorithms rapidly converged, and they eventually became equal. However, for real data verification, the correct identification rate of IMF-DNA was only marginally higher than that of RF-DNA, which was mainly due to the sampling rate. Real data

verification proved that the practical performance of IMF-DNA for specific emitter identification is excellent; the algorithm achieved a correct identification rate of 85.3% at a sampling rate of 200 MHz and an estimated SNR of approximately 10 dB.

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