An algorithm based on the dichotomy for quickly identifying whether a sequence is a PAPR sequence

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Abstract. With the development of communication technology, OFDM (Orthogonal Frequency Division Multiplexing) technology has become one of the core technologies in the field of wireless communication. Although OFDM has many advantages, it has a problem that the ratio of peak-to-average ratio is too large, that is, the PAPR problem. Despite the achievements in the technical means of suppressing PAPR (Peak to Average Power Ratio), the implementation of new technologies often requires the introduction of excessive IFFT calculations. Based on this situation, this paper proposes a new algorithm based on binary search to solve this problem.

1. Introduction

The special carrier transmission scheme of OFDM can effectively resist the selective fading of frequencies under the multipath[1] channel, so that the inter-symbol crosstalk problem can be well solved, and the complexity is smaller than that of the single carrier system using the equalization technique. At the same time, in the OFDM system, the system can optimize the transmission information bits of each subcarrier according to the signal to noise ratio of each subcarrier[2], thereby significantly increasing the transmission capacity of the system. Since external interference can only affect some carriers in the system, this technology can also resist narrowband interference and improve system reliability.

2. Basic algorithm

2.1Signal predistortion class algorithm

The clipping algorithm is one of the simplest and easiest algorithms to implement. This algorithm mainly performs nonlinear transformation processing on the signal, but the nonlinear ratio transformation causes in-band interference and out-of-band radiation, which degrades the bit error rate performance of the system[3].

2.2Coding class algorithm

The coding class algorithm is a means of high PAPR sequence without distortion suppression signal. Common coding methods include block coding and Gray complementary sequence[4]. The shortcoming
of this algorithm is that it is only applicable to systems with a small number of subcarriers[5], and applications cannot be applied widely.

2.3 Probability class algorithm

Common probabilistic algorithms are SLM and PTS. The SLM algorithm[6] does not need to consider the number of subcarriers and the modulation scheme. It is assumed that the input has several input signals which are independent of each other but contain the same information, and the sequence in which the PAPR is smaller is selected for transmission[7]. Both types of algorithms need to transmit sub-information, which has high computational complexity and a large amount of computation[8].

3. Algorithm flow

The idea of this algorithm can be represented by a flow chart as follows:

![Algorithm flow](Figure 1)

Step 1: Determining the judging threshold. The definition of PAPR for known sequences is as follows:

$$PAPR = 10 \log_{10} \left( \frac{\max \{ |x(t)|^2 \}}{E \{ |x(t)|^2 \} } \right) \text{ dB}$$

It is necessary to firstly determine a threshold for excessive PAPR based on the actual background requirements of the project. In addition, the value should be reasonable and can not be separated from the actual needs, it should meet the actual engineering significance.

Step 2: Selecting the modulation method. Common modulation methods include BPSK, QPSK, QAM, etc. In this paper, BPSK, QPSK, and 8QAM are selected for database establishment.

Step 3: Determining the number of carriers. Since the implementation of the algorithm does not depend on the number of subcarriers and the influence of the modulation mode, the value of the number of carriers is theoretically any positive integer. However, combined with practical considerations, this paper adopts the selection of 4 to 128 carriers to establish a database.

Step 4: Getting the sample sequence. According to the PAPR threshold, modulation mode, and number of carriers determined in the previous stage, the high PAPR sample sequence in the corresponding mode can be calculated.

Step 5: Creating a sample database. According to the high PAPR sample sequence obtained in the previous step, the sample high PAPR sequences in various conditions are stored according to the modulation mode and the number of carriers. Noting that this needs to convert the sample sequence into decimal numbers firstly, in order of storage from large to small or from small to large. The data of the database is finally reflected in the form of a one-dimensional array.

Step 6: Processing the input signal. The input sequence to be determined is binarized into decimal, and the processing form of the sample sequence is finally embodied as a certain number.

Step 7: Performing data query. The number obtained in the previous step is searched for the corresponding database according to the previously determined modulation method and the number of carriers. Noting that the dichotomy is used here for data retrieval.
Step 8: Getting the comparison results. According to the search result of the previous step, if the detected data is in the sample library, the input sequence is a high PAPR sequence, and vice versa.

4. Algorithm theory

4.1 Dichotomy

4.1.1 Definition of dichotomy

The dichotomy is a lookup algorithm that retrieves deterministic data in an ordered array, it is often referred to as a halved method. The design idea of the dichotomy is as follows:

1) Firstly ensuring that the arrays have been arranged in the order of large to small or small to large, and then retrieving the comparison from the intermediate data of the array. If the data to be detected happens to be this data, the retrieval ends, and vice versa.

2) If the data to be detected is larger or smaller than the intermediate data, the search is performed in the half of the area where the data is larger or smaller than the intermediate data, and then the step 1) is repeated.

3) If one step finds that the array is empty, the data to be detected is not in the known array.

4.1.2 Calculation of dichotomy

Let the length of the known array be N, then the amount of operation of the dichotomy is $o(\log_2 N)$.

4.2 IFFT algorithm

4.2.1 IFFT definition

The inverse discrete Fourier transform is the inverse of the fast Fourier transform[9]. It is defined as:

$$x(n) = IDFT[X(k)] = \frac{1}{N} \sum_{k=0}^{N-1} X(k)W_N^{-kn}, \quad n = 0,1,\cdots,N-1$$

Where $x(n)$ is a time domain signal and $X(K)$ is a frequency domain signal.

4.2.2 IFFT operation amount

If the length of the sequence to be operated is M, an IFFT operation is performed, and the number of complex multiplications required is $\frac{M}{2} \log_2 M$, the number of additions is $M \log_2 M$.

4.3 Algorithm comparison

Let N be the number of samples in a specific modulation mode of the sample database, and M be the length of the sequence in the corresponding modulation mode, that is, the number of subcarriers. In BPSK, QPSK, 8QAM and other modulation modes, the value must be less than $2^M$.

Therefore, the number of searches for the dichotomy: $\log_2 N < \log_2 2^M = M$

The number of traditional IFFT operations:

the number of complex multiplication + complex addition:

$$\frac{M}{2} \log_2 M + M \log_2 M = \frac{3M}{2} \log_2 M > M > \log_2 N$$

Therefore, the idea of using this algorithm can reduce the amount of calculation and reduce the complexity of the system.
4.4 Algorithm model diagram

Figure 2. Algorithm model diagram

5. Experimental verification

5.1 Experimental verification under BPSK modulation
Taking the number of carriers M=8 and the judging threshold of PAPR as 6dB, firstly, the database is calculated in the early stage, and the sample sequence of high PAPR is obtained. It is found that there are 40 PAPR sequences in 256 sequences, and the two algorithms are compared at this time. The results are as follows:

| algorithm          | Modulation | Number of carriers | Judging threshold | Total number of samples | Number of PAPRs | Number of operations |
|--------------------|------------|--------------------|-------------------|-------------------------|-----------------|---------------------|
| IFFT               | BPSK       | 8                  | 6dB               | 256                     | 40              | 36                  |
| New algorithm      |            |                    |                   |                         |                 |                     |

The analysis of the results of Table 1 is as follows:
1) Using traditional IFFT to judge PAPR:

Multiplication times: \( \frac{8}{2} \log_2 8 = 12 \)

Addition times: \( 8 \log_2 8 = 24 \)

2) Thoughts of finding by dichotomy:
Number of searches (the search process can be regarded as two data for subtraction to determine whether it is 0) / number of additions:

\[ \left\lfloor \log_2 40 \right\rfloor + 1 = 6 \]

Obviously, the algorithm has a smaller amount of computation.

5.2 Experimental verification under QPSK modulation
Taking the number of carriers M=1024 and the judging threshold of PAPR as 6dB, firstly, the database is calculated in the early stage, and the sample sequence of high PAPR is obtained. It is found that there
are 15 PAPR sequences in $2^{2048}$ sequences, and the two algorithms are compared at this time. The results are as follows:

Table 2. Experimental verification under QPSK modulation

| Algorithm    | Modulation | Number of carriers | Judging threshold | Total number of samples | Number of PAPRs | Number of operations |
|--------------|------------|--------------------|-------------------|-------------------------|-----------------|---------------------|
| IFFT         | QPSK       | 1024               | 6dB               | $2^{2048}$              | $2 \times 10^{615}$ | 15360               |
| New algorithm|            |                    |                   |                         |                 | 2045                |

The analysis of the results of Table 2 is as follows:

1) Using traditional IFFT to judge PAPR:
   Multiplication times: $\frac{1024}{2} \log_2 1024 = 5120$
   Addition times: $1024 \log_2 1024 = 10240$

2) Thoughts of finding by dichotomy:
   Number of searches/number of additions:
   $\left[ \log_2 2 \times 10^{615} \right] + 1 = 2045$
   Obviously, the algorithm has a smaller amount of computation.

6. Performance analysis

6.1 Advantages and disadvantages analysis

The main advantage of the algorithm is that the operation amount of identifying the unknown sequence is PAPR sequence is significantly reduced, the capacity of the sample sequence can be flexibly adjusted, and the accuracy of the recognition sequence can be controlled by increasing or decreasing the sample sequence capacity, as long as the relevant requirements are met. Under the condition, the amount of calculation required for recognition can be further reduced by reducing the number of sample capacities, that is, reducing the accuracy of recognition.

The shortcomings of the algorithm: Although the algorithm greatly reduces the complexity of the operation, it requires a large amount of sample data to be calculated and stored in advance, which increases the workload of the previous period. That is, the increase in the complexity of the sample sequence is exchanged for the decrease in the amount of computation when the unknown sequence is identified later.

6.2 Relationship between sequence length and judging accuracy

6.2.1 Performance experiment under BPSK

In the BPSK modulation mode, taking the number of subcarriers as 8 and the decision threshold as 6dB, the performance of the algorithm is shown in Table 3:

Table 3. Performance experiment under BPSK

| Modulation | Number of carriers | Judging threshold | Total number of samples (original) | Number of PAPRs | Number of database samples (current) | Judgment correct probability |
|------------|--------------------|-------------------|-----------------------------------|-----------------|-------------------------------------|-----------------------------|
| BPSK       | 8                  | 6dB               | 256                               | 40              | $K(0 < K \leq 40)$                   | $1 - (40 - k) \times \left(\frac{1}{2}\right)^8$ |
6.2.2 Performance experiment under QPSK

In the QPSK modulation mode, taking the number of subcarriers as 1024 and the decision threshold as 6dB, the performance of the algorithm is shown in Table 4:

| Modulation | Number of carriers | Judging threshold | Total number of samples (original) | Number of PAPRs | Number of database samples (current) | Judgment correct probability |
|------------|--------------------|-------------------|-----------------------------------|-----------------|--------------------------------------|----------------------------|
| QPSK       | 1024               | 6dB               | $2^{2048}$                        | $2 \times 10^{615}$ | $K(0 < K \leq 2 \times 10^{13})$ | $1 - \frac{(2 \times 10^{13} - K) \times (1024)^{2}}{2^{2048}}$ |

7. Conclusion

This paper proposes an algorithm based on the dichotomy to quickly identify high PAPR sequences, which effectively reduces excessive computation when using the traditional IFFT method, reduces the computational complexity of the recognition sequence, also reduces the complexity of the system, improves the effectiveness of the system. At the same time, the algorithm requires highly construction of the previous sample database, and it is more complicated to implement the database that meets the requirements. There are still many technical means to restrain high PAPR. It is believed that with the deepening of research, this algorithm can achieve improvement and more efficient in building database. At last it can ensure faster recognition of high PAPR sequences and provide some technical support for methods that restrain high PAPR sequences.

Acknowledgment

This work is supported by the National Natural Science Foundation of China (No.61671471 and No.61601512) and Natural Science Foundation of Jiangsu Province (No. BK20160770)

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