

НЕСОГЛАСОВАННЫЕ ПОЧТИ-ИДЕАЛЬНЫЕ ДВОИЧНЫЕ ПОСЛЕДОВАТЕЛЬНОСТИ

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Двоичные последовательности с хорошими корреляционными функциями широко используются в широкополосной связи, а также радиолокации и гидроакустике. Во многих приложениях требуются последовательности с идеальными и почти-идеальными автокорреляционными функциями. Последовательность называется идеальной, если ее периодическая автокорреляционная функция при всех ненулевых сдвигах равна нулю, и почти идеальной, если ее автокорреляционная функция равна нулю при всех ненулевых сдвигах, кроме одного. В настоящее время известны только одна идеальная двоичная последовательность длины $N=4$, а также семейство почти-идеальных двоичных (АРВ) последовательностей длины $N=2(p^m+1)$.

В. Ипатов для полного подавления боковых лепестков предложил использовать несогласованную фильтрацию последовательностей на основе линейных последовательностей и разностных множеств. Недостатками этого метода являются недвоичный характер весовых коэффициентов несогласованных фильтров, а также фиксированная величина энергетической эффективности η при больших значениях N . АРВ последовательности длины $N=2(p^m+1)$ не имеют этих недостатков, поскольку их эффективность $\eta=1$, а весовые коэффициенты ± 1 .

В этой работе представлены новые сбалансированные двоичные последовательности длины $N=4(p^m+1)$, $p^m-1 \equiv 0 \pmod{4}$, которые, проходя через дискретный несогласованный фильтр с двоичными коэффициентами, создают на его выходе сигнал, имеющий форму почти-идеальной автокорреляционной функции и обладающий энергетической эффективностью, близкой к единице. Последовательности, обладающие такими свойствами, получили название несогласованных почти-идеальных двоичных (МАРВ) последовательностей. Показано, что МАРВ последовательности порождаются из почти-идеальных троичных (АРТ) последовательностей длины $N=4(p^m+1)$ заменой равно отстоящих друг от друга 4-х нулей соответственно элементами 1 -1 1 -1. При этом соответствующая двоичная последовательность весовых коэффициентов фильтра образуется из исходной АРТ последовательности простой заменой нулей на единицы или минус единицы. В работе также получена энергетическая эффективность МАРВ последовательностей и показано, что она асимптотически стремится к 1 с ростом N .

Построенные МАРВ последовательности существенно расширяют множество известных АРВ последовательностей. При этом возможны два случая: когда длина МАРВ последовательностей совпадает с длиной АРВ последовательностей, и когда МАРВ последовательности имеют уникальную длину. Установлено, что в случае равенства длин общее число МАРВ последовательностей длины $4(p^m+1)$ равно общему числу АРВ последовательностей длины $2(p^m+1)$ только когда $m_1=m_2$. Исследуется возможность применения МАРВ последовательностей в широкополосной связи в качестве сигнатурных последовательностей. При этом для устранения ложного захвата за боковой выброс, отстоящий от основного лепестка на $N/2$ тактов, в периодически передаваемой МАРВ последовательности предложено инвертировать каждую k -последовательность.

MISMATCHED ALMOST-PERFECT BINARY SEQUENCES

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1. Introduction

Binary sequences with low correlation are widely used in spread spectrum communication, radar and sonar systems [1-3]. In many applications it is required to have sequences with perfect and almost-perfect periodic autocorrelation functions. Recall that a sequence is called perfect if all its out-of-phase autocorrelation coefficients are zero and one is called almost-perfect if all its out-of-phase autocorrelation coefficients except one are 0 [3-6]. Unfortunately, binary sequences with the perfect autocorrelation are found only for length $N=4$ [3]. Therefore, as a way out mismatched filtering for binary sequences has been suggested [2]. Mismatched filtering provides zero out-of-phase values of the periodic cross-correlation at the filter output but at the same time leads to some loss in signal-to-noise ratio (SNR) with respect to the matched filter [2]. For binary sequences it was shown [2,7,8] that the mismatched filter coefficients form nonbinary sequences with alphabet sizes ≥ 3 and require for their finding nontrivial calculations. Moreover, in most cases the sequence efficiency η , defined as ration of the mismatched filter SNR to the matched filter SNR, tends towards a fixed number $\eta < 1$ when sequence length N tends to infinity [7].

The almost-perfect binary (APB) sequences of length $N=2(p^m+1)$ [4-6] are free from these drawbacks since their efficiency $\eta=1$ and the matched filter sequence is binary. All this, simple design and also a lower cost im-

plementation in comparison with the binary sequences for mismatched filtering with the suppression of all sidelobes make the APB sequences attractive to use in synchronous CDMA and radar systems.

In this work, we present some new balanced binary sequences of length $N=4(p^m+1)$ whose cross-correlation functions with binary mismatched filter sequences have a shape of the almost-perfect autocorrelation functions and their efficiency tends towards 1 with increasing N. We shall say that binary sequences with these properties are mismatched almost-perfect binary (MAPB) sequences.

2. Construction

New binary MAPB sequences are derived from balanced almost-perfect ternary (APT) sequences of length $N=4(p^m+1)$ [9] by replacing their four zeroes with 1 or -1 with alternation from zero to zero. Consider this sequence construction in more detail.

Let $p>2$ be a prime, $n=2m, m\geq 1$ and $p^m-1\equiv 0 \pmod 4$. Let a be a primitive element of $GF(p^n)$ and β be a primitive element of $GF(p^m)$. Then according to [9], a sequence $w=\{w_j\}$ given

$$w_j = \psi(\text{tr}_m^n(a^j)), j=0,1,\dots,4(p^m+1)-1 \tag{1}$$

$$\psi(x) = \begin{cases} (-1)^{\lfloor ((\text{ind } \beta x) \bmod 4) / 2 \rfloor}, & x \neq 0 \\ 0, & x = 0 \end{cases} \quad x \in GF(p^m) \tag{2}$$

where $\text{ind}_{\beta x}$ - the index (logarithm) function x to base β and $\lfloor u \rfloor - \max \{z \mid z \leq u, z - \text{an integer}\}$, is a balanced almost-perfect ternary (APT) sequence of length $N=4(p^m+1)$ with four zeroes and autocorrelation peaks $\theta(0)=4p^m$ and $\theta(N/2)=-4p^m$.

From (2) we can get that $w_j=0$ for $j=(p^m+1)/2, 3(p^m+1)/2, 5(p^m+1)/2$ and $7(p^m+1)/2$. Further, we construct a new binary sequence $b=\{b_j\}, j=0,1,\dots,4(p^m+1)-1$, given by

$$b_j = \begin{cases} 1, & \text{if } j = (p^m + 1)/2 \quad \text{or} \quad 5(p^m + 1)/2 \\ -1, & \text{if } j = 3(p^m + 1)/2 \quad \text{or} \quad 7(p^m + 1)/2 \\ w_j, & \text{in the opposite cases} \end{cases} \tag{3}$$

Note that the sequence b is balanced too.

Now take a binary sequence $c=\{c_j\}$ obtained from the sequence w by replacing all its zeroes with 1 (-1) as the mismatched filter sequence. Obviously, the sequences b and c will differ only in two elements. It is easy to see that the sequences 1111, 1-11-1 and 11-1-1 in pairs are uncorrelated sequences. Using this and also array decomposition properties of APT sequences (1) [9] we get that the cross-correlation function of the sequences b and c completely coincides with the autocorrelation function of APT sequence (1) of the same length.

According to [7,8], the efficiency of mismatched filtering is given by

$$\eta = \frac{R_{bc}^2(0)}{R_{bb}(0)R_{cc}(0)}, \tag{4}$$

where $R_{bc}(j), R_{bb}(j)$ and $R_{cc}(j)$ are periodic cross-correlation and autocorrelation functions of the sequences b and c respectively. Then the efficiency of the sequence b can be calculated as

$$\eta = \frac{p^{2m}}{(p^m+1)^2} \tag{5}$$

From (5) we get that η tends towards 1 with increasing sequence length N . This means that sequences (3) are the balanced MAPB sequences.

3. MAPB sequences of Unique and Non-unique Length

It was shown [10] that the total number of APT sequences (1) of length $4(p^m+1)$ is $M_1 = \frac{\varphi(2(p^m+1))}{m}$

while the total number of the APB sequences of length $2(p^m+1)$ is $M_2 = \frac{\varphi((p^m+1))}{m}$. Consider a case when the

MAPB and APB sequences have the same length, i.e. $4(p^m+1)=2(p^{m_2}+1)$. It is readily seen that $M_1=M_2$ only if $m_1=m_2$. When $m_1 \neq m_2$ there are two cases : 1) $M_1 > M_2 (m_1 < m_2)$ and 2) $M_1 < M_2 (m_1 > m_2)$. We shall say that all MAPB sequences having length which coincides with APB sequence length are non-unique. Parameters of the MAPB sequences of non-unique length $N < 1000$ are shown in Table 1. Also it was found that among all MAPB

sequence lengths $N < 100$ there is only one length $N=72$ for which APB sequence does not exist. In general, there is infinite number of MAPB sequences (3) whose length does not coincide with length of the APB sequences [9]. In this case we say that these MAPB sequences are unique. In particular, as follows from [9] a large number of MAPB sequences (3) with even m and $p > 3$ are unique. Parameters of the unique MAPB sequences for length $N \leq 2088$ are presented in Table 2.

Table 1. Parameters of all non-unique MAPB sequences with length $N \leq 488$

p_1	m_1	p_2	m_2	N	M_1	M_2
5	1	11	1	24	4	4
3	2	19	1	40	4	8
13	1	3	3	56	12	4
29	1	59	1	120	16	16
41	1	83	1	168	24	24
53	1	107	1	216	36	36
3	4	163	1	328	20	80
89	1	179	1	360	48	48
113	1	227	1	456	72	72
11	2	3	5	488	60	24

Table 2. Parameters of all unique MAPB sequences with length $N \leq 2088$

p	m	N	M_1	η	p	m	N	M_1	η
17	1	72	12	0,8920	277	1	1112	276	0,9928
5	2	104	12	0,9246	17	2	1160	112	0,9931
37	1	152	36	0,9481	313	1	1256	312	0,9936
7	2	200	20	0,9604	317	1	1272	208	0,9937
61	1	248	60	0,9680	337	1	1352	312	0,9941
73	1	296	72	0,9732	7	3	1376	112	0,9942
97	1	392	84	0,9797	349	1	1400	240	0,9943
101	1	408	64	0,9805	353	1	1416	232	0,9944
109	1	440	80	0,9819	19	2	1448	180	0,9945
137	1	552	88	0,9856	373	1	1496	320	0,9947
149	1	600	80	0,9867	389	1	1560	192	0,9949
157	1	632	156	0,9874	397	1	1592	396	0,9950
13	2	680	64	0,9883	401	1	1608	264	0,99503
181	1	728	144	0,9890	409	1	1640	320	0,99513
193	1	776	192	0,9897	421	1	1688	420	0,99527
197	1	792	120	0,9899	433	1	1736	360	0,99540
229	1	920	176	0,9913	449	1	1800	240	0,99556
241	1	968	220	0,9918	457	1	1832	456	0,99564
257	1	1032	168	0,9923	461	1	1848	240	0,99568
269	1	1080	144	0,9926	521	1	2088	336	0,99617

4. Example

Let $p=17$, $n=2$, $m=1$ and x^2+x+3 be a primitive polynomial over $GF(17)$. According to (1), we construct a balanced APT sequence of length 72: -111-1-11-1-1-1-1011-111111-11-1-11-11-11011-1-111111-1-11 1-11110-1-11-1-1-1-11-111-11-11-10-1-111-1-1-1-1 with peak 68. Evidently, it is a case of the unique sequence length. Using (3), we get the following MAPB sequence of unique length 72: -111-1-11-1-1-1111-111111-11-1-11-11-11-111-1-111111-1-111-11111-1-11-1-1-1-1-11-111-11-1-1-1-111-1-1-1-1 with the efficiency $\eta=0,8920$.

5. Some applications

In spread spectrum communication systems the usage of the periodical MAPB sequences for the channel synchronization generates a problem caused by a peak autocorrelation ambiguity since during time acquisition there is the probability (1/2) of the false lock-in by the sidelobe peak having the same absolute value as the mainlobe peak. To overcome this shortcoming we shall use a fact that the odd-periodical cross-correlation function of the sequences **b** and **c** have zero value at shift $N/2$ between them. Therefore, one sequence (marker) of the periodical transmitted MAPB sequence is periodically multiplied by -1 . In a result there are two successive zero values instead of two peaks at the correlator output. After the detecting of this state the sampling times of the correlator output should be shifted by $N/2$ chips to the left (the right). Opposite, when during the acquisition process the mainlobe is chosen the marker produces only one negative peak at the correlator output. For more reliable discrimination of the false lock-in a signal consisting of three MAPB sequences BPSK modulated with a data $-11-1$ can be chosen as the marker.

6. Conclusions

In this paper, using the APT sequences with two zeroes and mismatched filtering, some new MAPB sequences of length $N=4(p^m+1)$ with high efficiency are proposed. The MAPB sequences essentially enlarge a set of known almost-perfect binary sequences. There are two cases: when MAPB sequence length coincides with length of the APB sequences and when MAPB sequences have unique length. It was found that in the case of their length coincidence the total number of the distinct MAPB sequences of length $4(p^m+1)$ is equal to the total number of the distinct APB sequences of length $2(p^{m_2}+1)$ only when $m_1=m_2$. The MAPB sequences can be used in spread spectrum communication, radar, and sonar systems.

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