

Phase Coded Sequences Design for Pulse Compression Radar

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Abstract

Sequences with good autocorrelation property are useful for pulse compression Radar Systems. in this paper different phase coded sequences are synthesized using a Modified Genetic Algorithm (MGA). This algorithm is a combination of Genetic Algorithm (GA) and Hamming Scan algorithms. It combines the good properties of the two algorithms like global minimum converging property of GA and fast convergence rate of Hamming scan algorithm. The synthesized phase coded sequences with good autocorrelation property are presented in this paper.

Key words: Autocorrelation, Hamming scan, Polyphase codes, Pulse compression, Genetic algorithm, Radar signal

Introduction

Sequences with good autocorrelation property are useful for pulse compression radar systems, and spread spectrum communication applications. The aperiodic autocorrelation function (ACF) of sequence S of length N is given by,

$$A(k) = \begin{cases} \sum_{n=0}^{N-k-1} s_n s_{n+k}^* ; & 0 \le k \le N-1 \\ \sum_{n=0}^{N+k-1} s_n s_{n-k}^* ; & -N+1 \le k \le 0 \end{cases}$$
 (1)

If all the sidelobes of the ACF of any polyphase sequence are bounded by

$$|A(k)| \le 1, \ 1 \le |k| \le N-1$$
 ... (2)

then the sequence is called a generalized Barker sequence or a polyphase Barker sequence.

Barker introduced binary sequences for lengths N = 2,3,4,5,7,11, and 13, fulfilling the condition in eq. (2)[1]. The binary Barker can be regarded as a special case of polyphase Barker sequences. If the sequence elements are taken from an alphabet of size M, consisting of the Mth roots of unity,

$$S_{m} = \exp\left\{2\pi i.\frac{m}{M}\right\} =: \exp(i\phi_{m}) \qquad 0 \le m \le M - 1 \qquad \dots \qquad (3)$$

the sequence is alternatively named an M-phase Barker sequence. In 1965, Golomb and Scholtz [2] first investigated generalized Barker sequences and presented six phases Barker sequence of lengths $N \le 13$. In [3], sixty-four phase Barker sequences up to length 18 were reported later near by sixty phase barker sequences

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upto length 26 was reported[4], in [5] polyphase Barker sequences of lengths 46-63 were presented, wherein, an alphabet size of 2000 had to be used. In[6] Ninety-Six Phase sequences are synthesized using Modified Genetic Algorithm (MGA). Fixed alphabet of 360 coded sequences is used in [7]. However, polyphase Barker sequences for larger lengths require larger alphabets and the possibility for exhaustive search diminishes. Unfortunately, Barker sequences are very rare. The synthesis of polyphase codes with good correlation properties is a nonlinear multivariable optimization problem, which is usually difficult to tackle. The Genetic Algorithm (GA) technique proved to be an efficient and powerful tool to find optimal or near optimal solutions for complex multivariable nonlinear functions but has slow convergence rate. The concept of Hamming scan algorithm has been employed for obtaining the pulse compression sequences at larger lengths with good correlation properties [8-9]. This algorithm has fast convergence rate but has demerit the viz., the tendency to be stuck with local minima. The MGA has global minimum estimation capability of GA algorithm and fast convergence rate of Hamming scan algorithm [6].

Binary code is one of the most commonly used radar pulse compression signals due to the easy signal generation and processing [10-13]. Polyphase signal has larger main lobe-to- peak sidelobe ratio over binary signal of the same code length. In addition, polyphase waveforms have a more complicated signal structure and thus, are more difficult to detect and analyze by an enemy's electronic support measures (ESMs)[10-12]. With the maturity of digital signal processing, the generation and processing of polyphase signals has become easy and less costly. Therefore, polyphase code is increasingly becoming a favorable alternative to the traditional binary code for radar signals and can be used as the basic code for radar signal design. In this paper, MGA has been used for the design of sixty-four phase sequences with good correlation properties.

Phase Coded Sequences

The phase coded sequences of length N bits is represented by a complex number sequence

$$\left\{ s(n) = e^{j\phi_m(n)}, n = 1, 2, ..., N \right\}$$
... (4)

Where $\phi_m(n)$ is the phase of nth bit in the sequence and lies between 0 and 2π . If the number of the distinct phases available to be chosen for each bit in a code sequence is M, the phase for the bit can only be selected from the following admissible values:

$$\phi_{m}(n) \in \left\{0, \frac{2\pi}{M}, 2\frac{2\pi}{M}, ..., (M-1)\frac{2\pi}{M}\right\}.$$
(5)
= $\{\psi_{1}, \psi_{2}, ..., \psi_{M}\}.$

For example if M = 4, then values of $\{\psi_1, \psi_2, \psi_3 \text{ and } \psi_4\}$ will be 0, $\pi/2$, π and $3\pi/2$ respectively. Considering a phase coded sequence S with code length N, one can concisely represent the phase values of S with the following 1 by N phase matrix:

$$\mathbf{S} = \begin{bmatrix} \phi_{\mathrm{m}}(1), & \phi_{\mathrm{m}}(2), & \phi_{\mathrm{m}}(3), \dots & \phi_{\mathrm{m}}(N) \end{bmatrix} \dots (6)$$

where all the elements in the matrix can only be chosen from the phase set in eq. (5). A more practical approach to design sixty-four phase sequences with properties in eq. (2) is to numerically search the best sixty-four phase sequences by minimizing a cost function that measures the degree to which a specific result meets the design requirements. For the design of sixty-four phase sequences used in radar and communication the cost function is based on the sum of square of autocorrelation side lobe peaks. Hence, from eq. (1) the cost function can be written as,

$$E = \sum_{k=1}^{N-1} |A(k)|^2 \qquad \dots \qquad (7)$$

The minimization of cost function in eq. (7) generates a phase coded sequences that are automatically constrained by eq. (2). In this optimization we have minimize the autocorrelation sidelobe energy.

Discriminating Factor (DF)

The discriminating factor (DF) as defined by Golay is ratio of mainlobe peak value to the magnitude of sidelobe peak value of Autocorrelations function of sequence S. The DF, mathematically is defined as follows[14].

$$DF = \frac{A(0)}{\max_{k \neq 0} |A(k)|} \qquad \dots \qquad (8)$$

The denominator is a measure of the peak sidelobe value and is related to the L_{∞} norm of the sidelobes.

Hamming Scan Algorithm

The Hamming scan algorithm is a traditional greedy optimization algorithm, which searches in the neighborhood of the point in all directions to reduce the cost function and has fast convergence rate [15]. This algorithm mutates element of sequence one by one. The Mutation is a term metaphorically used for a change in an element in the sequence. For example if a phase value of a M phase sequence is ψ_m ($1 \le m \le M$), i.e., one term in eq. (6), it is replaced with phase ψ_i , i =1, 2,..., M, i $\ne m$, and the cost for each ψ_i change is evaluated. If the cost is reduced due to a change in phase value, the new phase value is accepted; otherwise, the original phase value is retained. The same procedure is performed for all phase values of sequence, i.e., every term of eq. (6). This process is recursively applied to the matrix until no phase changes are made. A single mutation in a sequence results in a Hamming distance of one from the original sequence. The Hamming scan algorithm mutates all the elements in a given sequence one by one and looks at all the first order-Hamming neighbors of the given sequence [16]. Thus, Hamming scan performs recursively local search among all the Hamming-1 neighbors of the sequence and selects the one whose objective function value is minimum[6-7].

Genetic Algorithm (GA)

GA technique, introduced by John Holland at University of Michigan proved efficient and powerful tool to find optimal or near optimal solutions for complex multivariable nonlinear functions. The major advantage of the GA algorithm over the traditional "greedy" optimization algorithms is the ability to avoid becoming trapped in local optima during the search process.

The genetic algorithm creates a population of solutions and applies genetic operators such as crossover and mutation to evolve the solutions in order to find the best one(s). The three most important aspects of using genetic algorithms are: (1) definition of the objective function, (2) definition and implementation of the genetic representation, and (3) definition and implementation of the genetic operators. Once these three have been defined, the generic genetic algorithm should work fairly well. But the limitation of GA is slow convergence rate. This limitation is overcome by in modified Genetic algorithm.

Modified Genetic Algorithm (MGA)

Modified Genetic Algorithm is proposed as a statistical technique for obtaining approximate solutions to combinatorial optimization problems. The proposed algorithm is a combination of Genetic Algorithm (GA) and Hamming Scan algorithms. It combines the good methodologies of the two algorithms like global minimum converging property of GA algorithm and fast convergence rate of Hamming scan algorithm[8-10]. The demerit of Hamming scan algorithm is that it gets stuck in the local minimum point because it has no way to distinguish between local minimum point and a global minimum point. Hence it is sub-optimal. The drawback in Genetic algorithm is that it has a slow convergence rate because even though it may get closer to the global minimum point, it may skip it because of the methodology it employs. The MGA overcomes these drawbacks.

It is quite effective to combine GA with Hamming Scan (HSA) Algorithm. GA tends to be quite good at finding generally good global solutions, but quite inefficient at finding the last few mutations to find the absolute optimum. Hamming Scan are quite efficient at finding absolute optimum in a limited region. Alternating MGA improve the efficiency of GA while overcoming the lack of robustness of HSA. MGA are introduced as a computational analogy of adaptive systems. They are modeled loosely on the principles of the evolution via natural selection, employing a population of individuals that undergo selection in the presence of variation-

inducing operators such as mutation and recombination. A fitness function is used to evaluate individuals, and reproductive success varies with fitness.

Ambiguity Function

The radar signal design is actually based on the ambiguity function and cross ambiguity function rather than autocorrelation functions. The ambiguity function of transmit waveform specifies the ability of the sensor to resolve targets as a function of delay (τ) and Doppler (ν). The ideal transmit signal would produce an ambiguity function with zero value for all non-zero delay and Doppler (i.e., a "thumbtack"), indicating that the responses from dissimilar targets are perfectly uncorrelated. It is well known that if the ambiguity function is sharply peaked about the origin, then simultaneous range and velocity resolution capability is good.

Ambiguity function $|\chi(\tau, \nu)|$ can be defined a[12]

$$\left|\chi(\tau,\nu)\right| = \left|\int_{\infty}^{\infty} u(t) u^{*}(t-\tau) \exp(j2\pi\nu t) dt\right| \qquad (9)$$

where u(t) is the transmitted signal.

$$|v|T < 0.5$$
 .. (10)

where T is the signal time duration equal to Nt_b , where t_b is the duration of sub pulse. Therefore, if eq (9) is satisfied, the Doppler effect on the processing result is negligible; otherwise, the correction processing must be conducted. A simple way to minimize the Doppler effect is to select the signal time duration such that eq (9) is satisfied for all expected target speeds. Another approach for overcoming the Doppler Effect is to use a bank of Doppler-matched filters for every signal. Each of the Doppler-matched filter is designed to match a different Doppler-shifted version of the signal. Target detection is based on the maximum output from the Dopplermatched filter bank. The Doppler shift frequencies and the number of the matched filters are chosen such that the signal loss is limited to a tolerable level (such as 3 dB) for all possible target speeds.

Results Analysis

Different phases sequences are designed using the MGA, the length of the sequence, N, is varied from 16 to 256. The cost function for the optimization is based on eq. (7). In this paper all, the DF values are single realizations obtained using I7, processor. Table I shows the synthesized results of different phase coded sequences. In table I, column 1 shows sequence length, N, column 2 shows the autocorrelation DF values of well-known Frank codes, column 3 shows the autocorrelation DF values of 16-phase coded synthesized sequences, column 4 shows the autocorrelation DF values of 32-phase coded synthesized sequences, column 5 shows the autocorrelation DF values of 64-phase coded synthesized sequences column 6 shows the autocorrelation DF values of 128-phase coded synthesized sequences.

Fig (1) shows the comparison of autocorrelation Discrimination Factors of 16 phase, 32 phase, 64 phase and 128 phase coded synthesized sequences with sequence length, N varying from 16 to 256. From fig (1) and table (1) it can be shown that design sequences have better DF than well-known Frank codes of same length. In this paper the effect of alphabet size on DF is demonstrated. It can be shown that as number of phases or alphabet size is increases as multiple of two and started phases from 16 to 128 phases and found that DF value is also increased.

Fig (2) and (3) show signal phase structure and Ambiguity function of 16-phase synthesized sequence of length N = 256. Fig (4) and (5) show signal phase structure and Ambiguity function of 128- phase synthesized sequence of length N = 256. As shown in the fig (3) and (5) ambiguity function synthesized sequence has thumbtack shape. If ambiguity function has thumbtack shape then radar range resolution and parameter measuring accuracy will be good and measurement will be unambiguous. The design polyphase sequences are very useful for pulse compression radar and low probability of intercept radar. The synthesized sequences have good autocorrelation and ambiguity function properties. The synthesized sequences also have more complicated signal structure which is difficult to detect and analyze by an enemy's electronic support measures (ESMs).

Sequence Length(1)	Discrimination Factors				
	Frank codes(2)	16-phase codes (3)	32-phase codes (4)	64-phase codes (5)	128-phase codes (7)
16	11.3	16	16	16	16
25	15.5	16.59	21.58	25	26.8
36	18	19.7	23.15	27.7	28.61
49	21.8	22.38	25.77	28.8	31.3
64	24.4	25.38	29.8	33.68	35.63
81	28.1	26.4	33.09	35.21	37.91
100	30.86	28.32	38.11	41.66	42.84
121	34.47	31.64	39.09	42.03	44.37
144	37.31	35.03	40.94	46.29	48.91
169	40.82	39.7	44.32	48.94	52.29
196	43.65	41.3	46.7	49.05	55.24
225	47.07	45.6	49.92	52.81	56.41
256	49.94	60.4	64.02	68.5	71.03

Table 1: Comparison of Autocorrelation Discrimination Factors of 16, 32, 64 and 128 phase codedsynthesized sequences with sequence length, N varying from 26 to 256



Fig 1: Comparison of Autocorrelation Discrimination Factors of 16, 32, 64 and 128 phase coded synthesized sequences with sequence length, N varying from 26 to 256



Fig 2: Phase structure of 16-phase design sequence of length N =256



Fig 3: Ambiguity function of 16- phase synthesized sequence of length N =256







Fig 5: Ambiguity function of 128- phase synthesized sequence of length N =256

Conclusion

An effective Modified Genetic algorithm has been used for designing the different phase coded sequences with good Discrimination factors. The synthesized sequences can be used in pulse compression radar systems and spread spectrum communications for significantly improving performance of the system. The 16, 32, 64 and 128 phases sequences are designed upto a length of 256. The synthesized results presented in this paper not only have better correlation properties than well known Frank codes but also have more complicated signal structure which is difficult to detect and analyze by an enemy's electronic support measures (ESMs). Hence, it can be concluded that the design results are very useful for radar as well as spread spectrum communication systems.

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