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Orthogonal One Twenty Phase Sequence Sets Design Using MGA

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Abstract:
Multi Input and Multi Output (MIMO) radar system and spread spectrum communication system can fundamentally improve the system performance by using a group of specially designed orthogonal signals. In this paper One twenty Phase sequence sets are synthesized using Modified Genetic Algorithm (MGA). MGA is used as a statistical technique for obtaining approximate solutions to combinatorial optimization problems. Some of the synthesized results are presented, and their properties are better than four-phase sequence sets known in the literature. The synthesized One twenty Phase sequence sets are promising for practical application to multiple Radar system and spread spectrum communication. The synthesized sequences also have complex signal structure which is difficult to detect and analyze by enemy electronics support measure. The convergence rate of the algorithm is shown to be good.

Keywords:*Autocorrelation, Hamming scan, Polyphase codes, Genetic algorithm, Radar signal.*

I INTRODUCTION

Polyphase signals have been widely used in radar and communication. But the synthesis of polyphase coded radar signal with good correlation properties is a nonlinear multivariable optimization problem, which is usually difficult to tackle. The Genetic Algorithm (GA) proved to be an efficient and powerful tool to find optimal or near optimal solutions for complex multivariable nonlinear functions. The Hamming Scan Algorithm (HSA) is a traditional greedy optimization algorithm, which searches in the neighborhood of the point in all directions to reduce the cost function[1,2]. The proposed algorithm has fast convergence property of HSA and global minimum capability of GA [3]. This algorithm is used to design orthogonal One twenty Phase coded sequence sets that can be used in netted radar systems (NRS) / multiple radar systems and spread spectrum communication.

II ORTHOGONAL ONE TWENTY PHASE SIGNAL DESIGN

Assuming that an orthogonal One twenty Phase code set consists of L signals with each signal containing N subpulses represented by a complex number sequence, one can express the signal set as follows[5]:

$$\left\{ s_l(n) = e^{j\phi_l(n)},\ n = 1, 2, ..., N \right\},\ l = 1, 2, 3, ...L \quad .. (1)$$

where $\phi_l(n)$ is the phase of bit n of signal l in the signal set and lies between 0 and 2π. If the number of the distinct phases available to be chosen for each subpulses in a code sequence is M, the phase for a subpulse can only be selected from the following admissible alphabets:

$$\phi_l(n) \in \left\{ 0,\ \frac{2\pi}{M},\ 2\frac{2\pi}{M}, ...,\ (M-1)\frac{2\pi}{M} \right\} = \{\psi_1,\ \psi_2, ..., \psi_M\} \quad ... (2)$$

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For example, if M = 4, then values of $\psi_1, \psi_2, \ldots, \psi_4$ will be 0, π/2, π and 3π/2 respectively.

Considering a One twenty Phase code set S with code length N, set size L, and distinct phase number M, one can concisely represent the phase values of S with the following L by N phase matrix:

$$S(L,N,M) = \begin{bmatrix} \phi_1(1) & \phi_1(2) & \phi_1(3) \ldots\ldots & \phi_1(N) \\ \phi_2(1) & \phi_2(2) & \phi_2(3) \ldots\ldots & \phi_2(N) \\ & \vdots & & \\ \phi_L(1) & \phi_L(2) & \phi_L(3) \ldots\ldots & \phi_L(N) \end{bmatrix} \quad ..(3)$$

where the phase sequence in row l $(1 \le l \le L)$ is the One twenty Phase sequence of signal l and all the elements in the matrix can only be chosen from the phase set in (2). The autocorrelation and crosscorrelation properties of orthogonal One twenty Phase codes should satisfy or nearly satisfy the following:

$$A(s_l, k) = \begin{cases} \frac{1}{N} \sum_{n=1}^{N-k} s_l(n) s_l^*(n+k) = 0, & 0 < k < N \\ \frac{1}{N} \sum_{n=-k+1}^{N} s_l(n) s_l^*(n+k) = 0, & -N < k < 0 \end{cases}$$

$$l = 1,2,\ldots..L. \qquad \ldots\ldots \qquad (4)$$

and,

$$C(s_p, s_q, k) = \begin{cases} \frac{1}{N} \sum_{n=1}^{N-k} s_p(n) s_q^*(n+k) = 0, & 0 \le k < N \\ \frac{1}{N} \sum_{n=-k+1}^{N} s_p(n) s_q^*(n+k) = 0, & -N < k < 0 \end{cases}$$

$$p \ne q, \quad p,q = 1,2,\ldots L \qquad \ldots. \quad (5)$$

where $A(s_l, k)$ and $C(s_p, s_q, k)$ are the aperiodic autocorrelation function of One twenty Phase sequence s_l and the cross-correlation function of sequences s_p and s_q respectively, the asterisk denotes the complex conjugate, and k is the discrete time index. The design of an orthogonal One twenty Phase code set is equivalent to the construction of a One twenty Phase matrix S(L,N,M) in (3) with the autocorrelation and crosscorrelation constraints in (4) and (5). It seems to be very difficult to algebraically design a set of three or more sequences with low crosscorrelation between any two sequences in the set. Alternatively, a more practical approach to design a One twenty Phase code set with properties in (4) and (5) is to numerically search the best One twenty Phase sequences by minimizing a cost function that measures the degree to which a specific result meets the design requirements. For the design of orthogonal One twenty Phase code sets used in NRS, the cost function is based on the sum of the square of maximum autocorrelation sidelobe peaks and the square of maximum crosscorrelation peaks. Hence, from (4) and (5), the cost function can be written as

$$E = \sum_{l=1}^{L} (\max_{k \ne 0} |A(s_l, k)|)^2 + \lambda \sum_{p=1}^{L-1} \sum_{q=p+1}^{L} (\max_{k} |C(s_p, s_q, k)|)^2 \quad \ldots.(6)$$

where λ is the weighting coefficient between autocorrelation function and crosscorrelation function in the cost function. With given values of N, M, and L, the minimization of cost function in (6) generates a group of One twenty Phase sequences that are automatically constrained by (4) and (5). In other words, the objective is that the autocorrelation sidelobe peaks and the crosscorrelation peaks for all lags of S must be as small as possible.

III. 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. 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 One twenty phase sequence is ψ_m $(1 \le m \le 120)$, i.e., one term in eq. (6), it is replaced with phase ψ_i, i =1, 2,…, 120, i ≠ 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 (6). This process is recursively applied to the matrix until no phase changes are

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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. 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.

IV. 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 [3]. 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.

V. MODIFIED GENETIC ALGORITHM (MGA)

Modified Genetic Algorithm is used as a statistical technique for obtaining approximate solutions to combinatorial optimization problems. This 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. 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.

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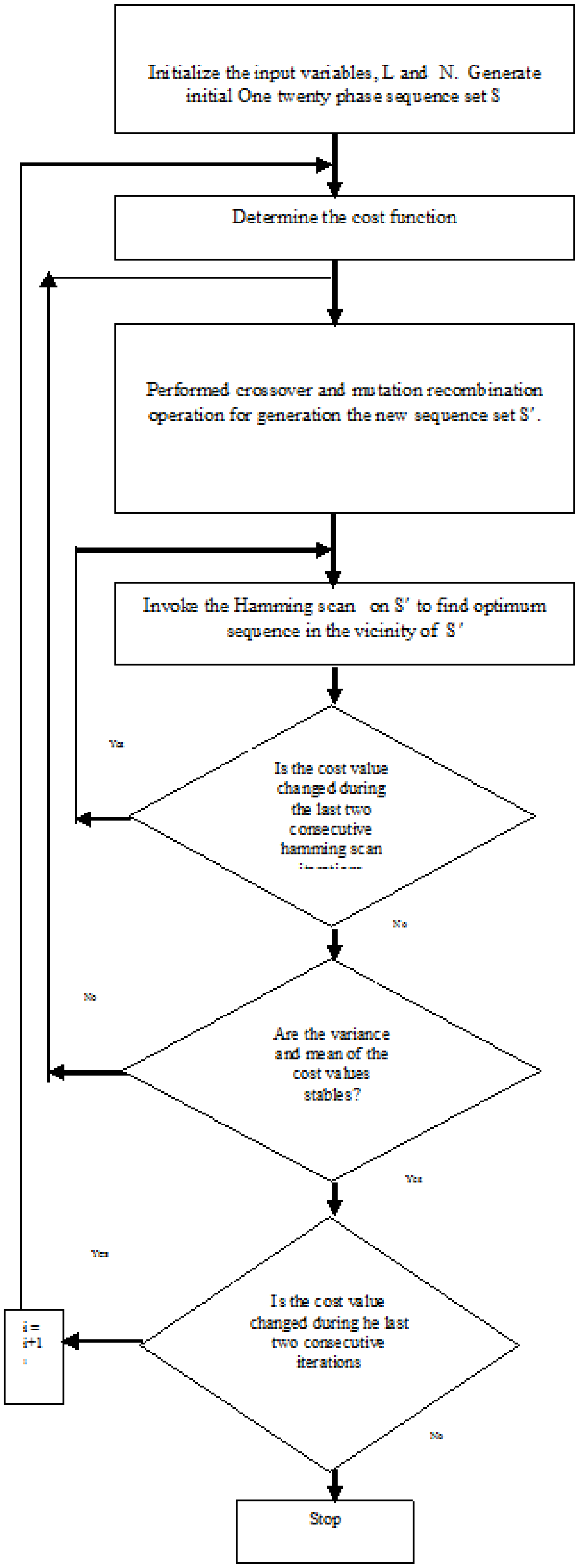

Fig.1 Flow chart of MGA

VI. DESIGN RESULTS

A variety of One twenty Phase code sets are designed using the proposed algorithm. The cost function for the optimization is based on (6), and the value of λ in the (6) is chosen as 1. In this work all the autocorrelation sidelobe peak (ASP) values and Cross-correlation Peaks (CP) values are normalized with respect to sequence length, N and all the design examples are single realizations. Some of the synthesized results are presented which have better correlation properties than four- phase sequences available in literature [5]. Tables I & II show the comparison between our results and the results reported in the reference [5]. In table I, columns 2 and 3 show maximum ASP and average of the ASPs respectively, columns 4 and 5 show maximum CP and average of CPs respectively. From table I, it is observed that normalized value of maximum ASP in literature is 0.182 while synthesized value is 0.109 and maximum CP in literature is 0.212 while synthesized value is 0.145, both values are better than the values reported in literature. Similarly, average of ASPs is also better as indicated. Table II shows the same correlation properties as table I but for different values of L and N. From table II, it is observed that normalized value of maximum ASP in literature is 0.095 while synthesized value is only 0.059. Similarly average of ASPs and maximum CP are also lower. All the synthesized results are one-time optimization results although better designs might have been obtained by repeatedly applying MGA. Fig. 2 shows the autocorrelation and fig. 3 shows the cross-correlation between any possible pair of sequences of One twenty-phase designed sequences of set L = 3 and N = 150. As shown in the fig.3 the cross-correlation functions between possible pairs of sequences are very low which indicate that designed sequences are orthogonal. The proposed optimization algorithm for One twenty Phase sequence set design is indeed very effective, especially when the code length is large. As expected, the autocorrelation sidelobe energy and the cross-correlation energy of the sequence sets are nearly uniformly distributed among all possible locations. For conventional radar pulse-compression signals such as polyphase sequences or Frank polyphase sequences [6-8], the autocorrelation sidelobe peak decreases at the rate of 1/√N. Similarly, One twenty Phase sequence sets designed in this work also decrease at the rate of 1/√N.

Table I Comparison between ref [5] values and synthesized values (M = 120, L= 4 & N = 40).

Particulars	Max (ASP)	Avg (ASP)	Max (CP)	Avg (CP)
Literature values (M= 4)	0.182	0.152	0.212	0.198
Synthesized Values	0.109	0.102	0.145	0.143

Table II Comparison between ref [5] values and synthesized values (M= 120, L=3 & N=128).

Particulars	Max (ASP)	Avg (ASP)	Max (CP)	Avg (CP)
Literature values(M= 4)	0.095	0.089	0.118	0.111
Synthesized Values	0.059	0.056	0.089	0.085

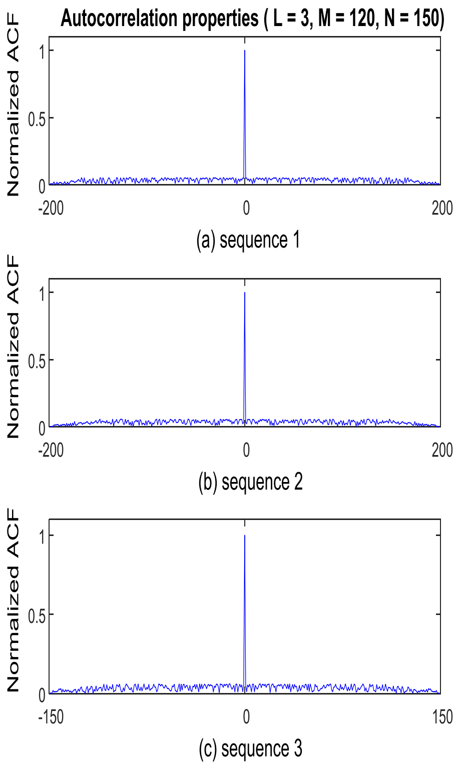

Fig.2Normalizedautocorrelationfunctionsof(a)sequence1, (b)sequence2,and(c)sequence3ofthedesigned120-phase sequencesof setwithL=3and N=150.

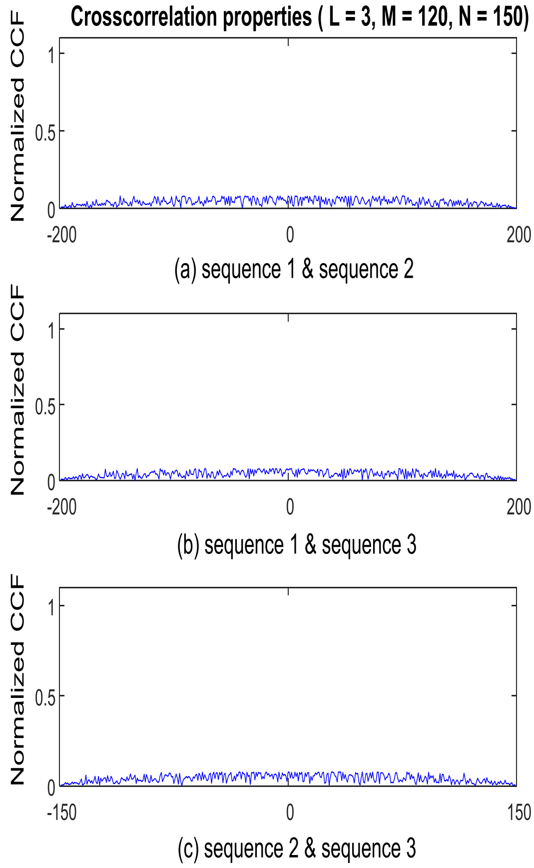

Fig.3 Normalizedcrosscorrelationfunctionsof (a)sequences 1and2(b)sequences1and3,and(c)sequences2and3,of 120-phasedesignedsequencesof setL=3andN=150.

VII. CONCLUSIONS

An effective MGA has been developed for the design of One twenty Phase code sets used in radar and spread spectrum communication for significantly improving performance of the system. This new approach includes the GA and HSA and provides a powerful tool for the design of Orthogonal One twenty Phase Sequence Sets for Radar Systems with requirements imposed on both autocorrelation and crosscorrelation functions. From the design results, it is found that for large code lengths, both average autocorrelation side lobe peak and average crosscorrelation peak approximately decrease at the rate of 1/√N with code length N. This property conforms to those of other well-known polyphase sequences designed through algebraic methods. The synthesized sequence sets have correlation properties better than four-phase sequences reported in the literature.

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