Optimization of Radar signals performance using Genetic and Differential Evolution Algorithms

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balance between efficiency and efficacy necessary for survival in many different environments. Genetic

Abstract-**Radar waveform designers have been proposing new sieves for obtaining good non-uniform PRI sequences of radar signal[1], as the exhaustive enumeration method cannot assure to achieve good performance. For improving the performance of radar signal, the use of evolutionary algorithms to design the optimized non-uniform PRI sequences for radar signal waveforms [13]have been reported in this paper.**

Keywords: PRI, PCW,LFM,PSLR, ISLR, GA, DE

I. INTRODUCTION

In the literature, the generation of non-uniform PRI sequences are considered using conventional methods and analysis of the these signals in terms of their performance measures[5] which are Peak Sidelobe Ratio (PSLR) and Integrated Sidelobe Ratio(ISLR) have been presented. The ambiguity analysis of these has also been presented. This paper deals with the application of the genetic algorithm and differential evolution algorithm for the generation of non-uniform PRI sequences for radar signals. As PSLR, PSLR3, ISLR and ISLR3[11] are the main measures of goodness for radar signals, the optimization of these four factors are considered. The PSLR and ISLR are derived from the autocorrelation pattern, PSLR3 and ISLR3 are derived from ambiguity pattern.

II. GENETIC ALGORITHM

Genetic algorithms[14] are search algorithms based on the mechanics of natural selection and natural genetics. A genetic algorithm (GA) is a soft computing technique used to find exact or approximate solutions to optimization and search problems. The central theme of research using genetic algorithms is to achieve robustness, the

algorithms are different from more normal optimization and search procedures because they work with a coding of the parameter set, not the parameters themselves and GA's search is based on population of points but not a single point.

III. GENETIC OPERATORS

Genes are the basic building blocks of genetic algorithms. A gene can be a binary encoding of a parameter and chromosome is an array of genes. The genetic algorithm uses the selection, recombination or crossover and mutation operators on the population of individuals to perform the search.

IV. FITNESS FUNCTIONS

The fitness function, or objective function, is used to assign a fitness value to each of the individuals in the GA and DE population. The fitness function is the only connection between the physical problem being optimized and the genetic GA/DE.. The only constraints on the form and content of the fitness function, imposed by the GA/DE, are that the fitness value returned by the fitness function is in some manner proportional to the goodness of a given trial solution, and that the fitness be a positive value. In some implementations of the GA/DE optimizer, the constraint that the fitness value be a positive value is not even required.

V. PROBLEM FORMULATION

The genetic algorithm starts with several alternative solutions to the optimization problem, which are considered as individuals in a population. Often these solutions are coded as binary strings

called chromosomes. The problem or objective aims here to find a non-uniform PRI sequence that produces the lowest maximum Peak side lobe ratio (PSLR) or Integrated side lobe ratio (ISLR). The Genetic algorithm is applied to PCW, LFM, stepped LFM and Costas pulse trains to achieve the objective. The cost or fitness functions considered here is merit factor. The non-uniform PRI sequence at maximum merit factor is considered. The PSLR, ISLR, PSLR3 and ISLR3 are measured for the optimized non-uniform PRI sequence. Here the chromosomes considered as non-uniform PRI sequences and each bit is represented as PRI.

VI. IMPLEMENTATION

The following steps are followed to optimize meritfactor.

Step.1. Set iteration =1. Generate a population of N individuals which are non-uniform PRI sequences generated by the logistic map in our case. The number of individuals varies depending on the length of the sequence.

Step.2. Evaluate the Fitness value of each individual using the defined objective function in equation 1.15 or equation 1.16

Step.3. Rank-based selection is applied as selection operator, with rank value that decreases linearly from the best to the worst individual. The individuals which are sequences in our problem are ranked from the most-fit to the least-fit, according to the value of the objective function. Unacceptable individuals are discarded, leaving a superior species-subset of the original list.

Step.4.Cross over is performed on the selected parents (sequences) to produce offspring's. Single point crossover is used. The crossover is done between pair of subsequent parent sequences as follows: an integer position k is selected uniformly at random between 1 and the sequence length less one [1,N-1]. Two new strings or sequences are created by swapping all the alphabets between positions k+1 and N inclusively. The offspring's are produced and appended with the selected parents so that the number of parent chromosomes remains constant after each iteration.

Step.5.Mutation is done by random alteration of bits in the sequences to bring random changes in the chromosomes.

Steps from 2 to 5 are repeated for more number of iterations until a optimum solution or best solution is obtained at each length. For length 9 the number of iterations is chosen as 100. The initial population or the number of parent sequences is varied with the length of the sequence.

An implementation of genetic algorithm begins with a population of (typically random) chromosomes. One then evaluates these structures and allocated reproductive opportunities in such a way that these chromosomes which represent a better solution to the target problem are given more chances to `reproduce' than those chromosomes which are poorer solutions. The 'goodness' of a solution is typically defined with respect to the current population.

VII. DIFFERENTIAL EVOLUTION

GA [14]has poor convergence to reach optimal solution. In this paper, DE[15] Algorithm has been introduced to find out the optimized PRI sequence with good convergence for maximizing the performance measure. DE is a simple real parameter optimization algorithm. It works through a simple cycle of stages, presented in Fig:1
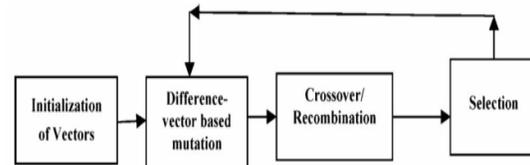

Figure 1 Main stages of the DE algorithm.

VIII. INITIALIZATION

DE searches for a global optimum point in a D-dimensional real parameter space. It begins with a randomly initiated population of *NP D d*imensional real-valued parameter vectors. Each vector, also known as *chromosome,* forms a solution to the multidimensional optimization problem. The ith vector of the population at the current generation:

$$\overrightarrow{X_{i,G}} = \left[x_{1,i,G}, x_{2,i,G}, x_{3,i,G}, ..., x_{D,i,G} \right]$$

The each chromosome parameter there may be certain range within which the value of the parameter should be restricted, because parameters are related to physical components or measures that have natural bounds for example if a parameter is a mass, then it cannot be negative. The initial population cover this range as much as possible by uniform randomizing individuals with in search space constrained by the minimum and maximum

bounds: $\overrightarrow{X_{min}} = \left\{ x_{1,min}, x_{2,min}, ..., x_{D,min} \right\}$

$\overrightarrow{X_{max}} = \left\{ x_{1,max}, x_{2,max}, ..., x_{D,max} \right\}.$

Hence initialize the jth component of the ith vector as

$$x_{j,i,0} = x_{j,\min} + rand_{i,j}[0,1].(x_{j,\max} - x_{j,\min})$$

Where $rand_{i,j}[0,1]$ is a uniformly distributed random number lying between 0 and 1.

IX. MUTATION

Mutation means a sudden change in the gene characteristics of a chromosome. In DE, a parent vector from the current generation is called *target* vector, a mutant vector obtained through the differential mutation operation is known as *donor* vector and finally an offspring formed by recombining the donor with the target vector is called *trail* vector. In mutation operation first create the donor vector for each ith target vector from the current population, three other distinct parameter vectors, say $\overrightarrow{X_{r_1}}$, $\overrightarrow{X_{r_2}}$, and $\overrightarrow{X_{r_3}}$ are sampled randomly from the current population. Where r_1, r_2 and r_3 are mutually exclusive integers randomly chosen from the range[1,NP].

Calculate the difference of any two of these vectors is scaled by a scalar number F (that typically lies in between [0,1] and the scaled difference is added to the third one. Hence we obtained the donor vector $\overrightarrow{V_{i,G}}$, mathematically express as

$$\overrightarrow{V_{i,G}} = \overrightarrow{X_{r_1,G}} + F.(\overrightarrow{X_{r_2,G}} - \overrightarrow{X_{r_3,G}}) .$$

X. CROSSOVER

To enhance the potential diversity of the population, crossover operation comes into play after generating the donor vector through mutation. The donor vector exchanges components with the target vector $\overrightarrow{X_{i,G}}$ under this operation to form the trail vector $\overrightarrow{U_{i,G}} = [u_{1,G}, u_{2,G}, u_{3,G}, ...u_{D,G}]$.

There are two types of crossover methods. The DE family of algorithms can use two kinds of crossover methods—exponential (or two-point modulo) and binomial (or uniform).In exponential crossover, we first choose an integer n randomly among the numbers [1,D]. This integer acts as a starting point in the target vector, from where the crossover or exchange of components with the donor vector starts.

We also choose another integer L from the interval[1,D]. L denotes the number of components the donor vector actually contributes to the target vector. After choosing n and L the trial vector is obtained as

$$u_{j,G} = v_{j,G} \quad for \quad j = \langle n \rangle_D \quad \langle n+1 \rangle_D, .. \langle n+L-1 \rangle_D$$

$$x_{j,G} \text{ for all other } j \in [1,D]$$

Where the angular brackets $\langle \ \rangle_D$ denote a modulo function with modulus D. "Cr" is called the crossover rate and appears as a control parameter of DE just like F. Hence in effect, probability (L =υ) = (Cr)υ - 1 for any positive integer v lying in the interval [1, D]. For each donor vector, a new set of *n* and L must be chosen randomly. The other technique is binomial crossover of the D variables whenever a randomly generated number between 0 and 1 is less than or equal to the Cr value. In this case, the number of parameters inherited from the donor hasa (nearly) binomial distribution. The scheme may be outlined as

$$u_{j,G} = \begin{cases} v_{j,G} & if (rand_j[0,1] \le cr \, or \quad j = j_{rand} \\ x_{j,G} & otherwise \end{cases}$$

where, as before, $rand_j[0,1]$ is a uniformly distributed random number, which is called a new for each jth component of the ith parameter vector. $j_{rand} \in [1,2,..,D]$ is a randomly chosen index, which ensures that trail vector gets at least one component from donor vector. Cr is the approximating the true probability P_{Cr} of the event that a component of the trail vector will be inherited from the donor.

XI. SELECTION

To keep the population size constant over subsequent generations, the next step of the algorithm calls for selection to determine whether the target or the trial vector survives to the next generation, i.e., at G = G + 1. The selection operation is described as

$$\overrightarrow{X_{i,G+1}} = \begin{cases} \overrightarrow{u_{i,G}} & if \quad f(\overrightarrow{u_{i,G}}) \le f(\overrightarrow{x_{i,G}}) \\ \overrightarrow{x_{i,G})} & if \quad f(\overrightarrow{u_{i,G}}) > f(\overrightarrow{x_{i,G}}) \end{cases}$$

Where $f(\overrightarrow{X})$ is the objective function to be minimized. Therefore, if the new trial vector yields an equal or lower valueof the objective function, it replaces the corresponding targetvector in the next generation; otherwise the target is retained in the population. Hence, the population either gets better(with respect to the minimization of the

objective function)or remains the same in fitness status, but never deteriorates.

XII. RESULTS

This section presents the Genetic Algorithm and differential Evolution algorithm optimized PRI sequences and their respective performance measures. PCW, LFM, stepped LFM and Costas pulse trains performance measure (meritfactor) plots using GA and DE are presented and compared for fast convergence. The performance measures of radar signals with the respective optimized non-uniform PRI sequences are quantified by evaluating their corresponding ambiguity functions.

The following non-uniform PRI sequences of the respective radar signals are obtained after applying the optimization techniques and their respective performance measures are tabulated.
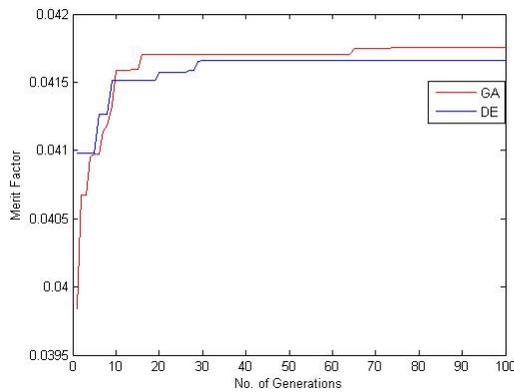

Figure 2. PCW pulse train meritfactor maximization plot using GA and DE
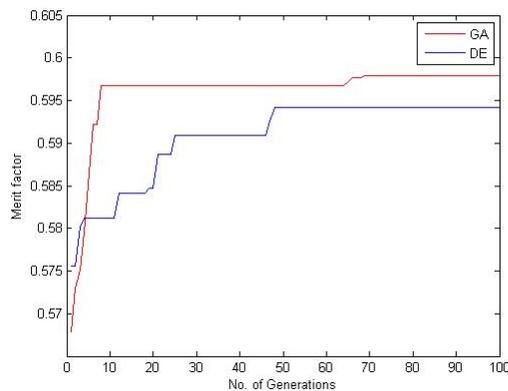

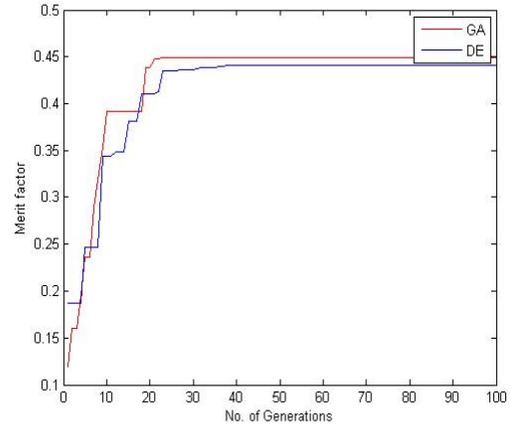Figure 3. LFM pulse train meritfactor maximization plot using GA and DE

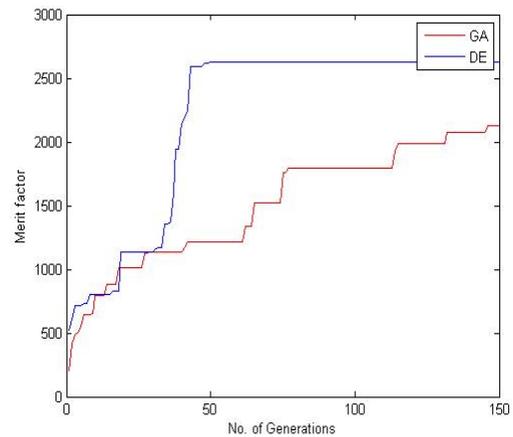Figure Costas pulse train meritfactor maximization plot using GA and DE

Figure 4. Costas pulse train meritfactor maximization plot using GA and DE

Non-uniform PRI	No. of pulses N	PCW			
		PSLR (dB)	ISLR (dB)	PSLR3 (dB)	ISLR3 (dB)
GA	9	-0.953	3.4953	-0.9538	13.79
DE	9	-0.95	3.673	-0.95	13.8

Table 1: Performance measures of PCW pulse train

Non-uniform PRI	No. of pulses N	LFM			
		PSLR (dB)	ISLR (dB)	PSLR3 (dB)	ISLR3 (dB)
GA	9	-2.99	-12.6	-2.9901	2.233
DE	9	-2.99	-12	-2.99	2.26

Table 2: Performance measures of LFM pulse train

Non-uniform PRI	No. of pulses N	Costas			
		PSLR (dB)	ISLR (dB)	PSLR3 (dB)	ISLR 3 (dB)
GA	9	-18.75	1.2791	-18.75	3.479
DE	9	-18.5	1.3777	-18.5	3.55

Table 3: Performance measures of Costas pulse train

Non-uniform PRI	No. of pulses N	Stepped LFM			
		PSLR (dB)	ISLR (dB)	PSLR3 (dB)	ISLR3 (dB)
GA	9	-42.30	-38.11	-42.301	-33.872
DE	9	-43.6	-37.8	-43.62	-34.2

Table 4: Performance measures of stepped LFM pulse train

XIII. CONCLUSION

From the results obtained, it can be concluded that the performance measure, meritfactor is optimized for less number of generations in the DE for all the signals. The four performance measures, PSLR, ISLR, PSLR3 and ISLR3 of radar signals with optimized non-uniform PRI are tabulated in the respective tables for the comparision and stepped LFM found to be superior.

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