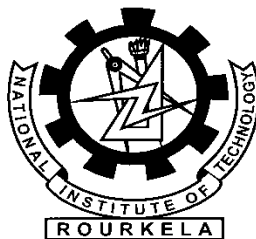


Efficient Design of Pulse Compression Codes Using Multiobjective Genetic Algorithm

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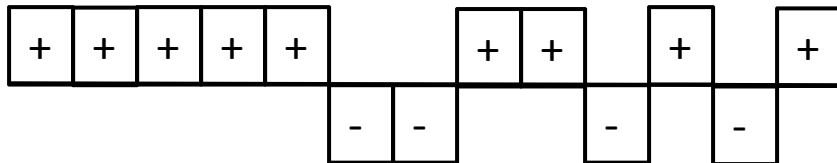
Introduction

- In a pulse radar system the transmitted pulse width should be as long as possible to increase the sensitivity of the system and as small as possible at the receiver for better range resolution.
- In pulse compression technique a long coded pulse is transmitted and the received echo is processed to obtain a relatively narrow pulse.
- Pulse compression technique avoids the transmission of a signal having small pulse width and high peak power for better range resolution.
- The performance of range resolution radar would be optimal, if the coded waveform has impulsive autocorrelation.
- Wide bandwidth, which is necessary for good range resolution, is obtained by modulating phase or frequency of the signal, while maintaining constant pulse amplitude.

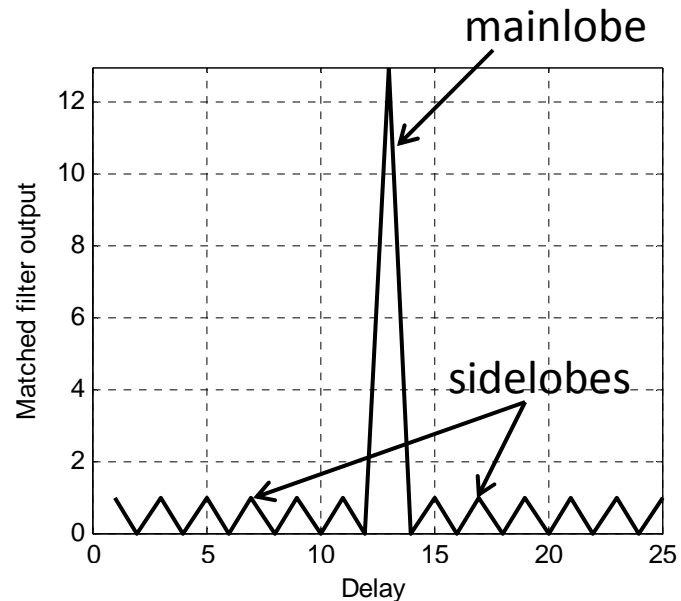
Introduction(Contd...)

- The autocorrelation of phase coded waveforms contain range sidelobes, which have a negative influence on the detection performance of radar.
- A desirable property of the compressed pulse is that it should have low sidelobes in order to prevent a weak target from being masked in the time sidelobes of a nearby stronger target.

barker13=[1 1 1 1 1 -1 -1 1 1 -1 1 -1 1]



Phase Coded Waveform



Multiobjective Formulation

Let an L length binary sequence is given by

$$S = \{s_1 = \pm 1, s_2, s_3, \dots, s_L\} \quad (1)$$

where each element of S has value is either +1 or -1.

The output of the matched filter that is the aperiodic autocorrelation function for positive delays is given as

$$C_k(S) = \sum_{t=1}^{L-k} s_t s_{t+k} \quad (2)$$

where $k = 0, 1, 2, \dots, L - 1$

Multiobjective Formulation(Contd...)

- A significant problem inherent in biphasic pulse compression is that the autocorrelation function does not yield a perfect impulse, that means it does not produce $C_k(S) = 0$ for $k \neq 0$.
- Any non zero value of $C_k(S)$ for $k \neq 0$ is referred to as sidelobe where as the zero-offset correlation value $C_0(S)$ is called the mainlobe.
- The difference between a pulse compression waveform and a simple pulse waveform is in the existence and magnitude of these sidelobes.

Multiobjective Formulation(Contd...)

➤ There are two frequently used sidelobe measures. The first one is the peak sidelobe level(*PSL*) which is the largest sidelobe in the autocorrelation function of the code and is defined as

$$PSL = \text{Max}|(C_k(S))|, k \neq 0 \quad (3)$$

➤ The second is the integrated sidelobe level (*ISL*) defined as the total energy contained in all the sidelobes. As the signal is real valued the autocorrelation is real and symmetric about the zero delay. The *ISL* is represented as

$$ISL = 2 \sum_{k=1}^{L-1} C_k^2(S) \quad (4)$$

The *PSL* and *ISL* is represented as the terms defined in (3) and (4) are simultaneously minimized to achieve desired aperiodic codes.

Nondominated Sorting Genetic Algorithm-II

(1) Population Initialization

The population contains a set of chromosomes. Each chromosome is initialized randomly with binary bits having length same as the code length.

(2) Non-Dominated sort

➤ For each individual p in main population P perform the following

- Initialize the set of individuals dominated by p as $S_p = \emptyset$.
- Initialize the number of individuals that dominate p i.e. $n_p = 0$.

• for each individual q in P

* if p dominates q then

$$\cdot S_p = S_p \cup \{q\}$$

* else if q dominates p then

$$\cdot n_p = n_p + 1$$

NSGA-II(Contd...)

• If $n_p = 0$ then p belongs to the first front and rank of individual p i.e. $p_{rank} = 1$. Update the first front F_1 by adding p to front one i.e. $F_1 = F_1 \cup \{p\}$

➤ This is carried out for all the individuals in main population P .

➤ Initialize the front counter $i = 1$

➤ Perform the following if i^{th} front is nonempty i.e. $F_i \neq \emptyset$

• $Q = \emptyset$. The set Q is used to store the members of the next front.

• for each individual p in front F_i

* for each individual q in S_p

· $n_q = n_q - 1$, decreament the domination count for individual q

· if $n_q = 0$, set $q_{rank} = i+1$. Update q i.e. $Q = Q \cup q$.

• $i = i + 1$.

• set Q is the next front and hence $F_i = Q$

NSGA-II(Contd...)

(3) Crowding Distance Assignment

Once the non- dominated sorting is complete the crowding distance is assigned

➤ For each front F_i , n is the number of individuals.

- Initialize the distance for all individuals to be zero i.e. $F_i(d_j) = 0$, where j corresponds to an individual in front F_i .

- for each objective function m

- * Sort the individuals in front F_i based on objective function m i.e $I = \text{sort}(F_i, m)$.

- * Assign infinite distance to boundry values for each individual in F_i i.e $I(d_1) = \infty$ and $I(d_n) = \infty$

- * for $k = 2$ to $(n - 1)$

$$I(d_k) = I(d_k) + \frac{I(k+1).m - I(k-1).m}{f_m^{max} - f_m^{min}}$$

where $I(k) \cdot m$ is the value of the m^{th} objective function of k^{th} individual in I

NSGA-II(Contd...)

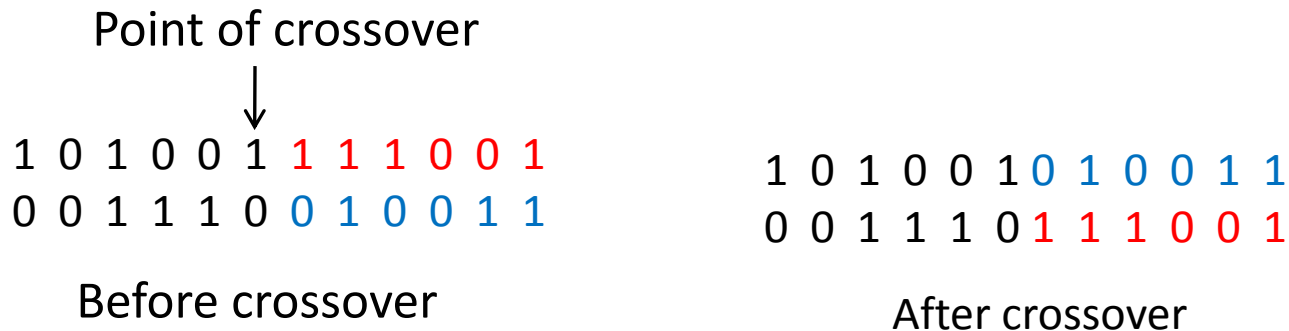
(4)Selection:

The individuals are selected using a binary tournament selection. The selection is carried out as follows.

- (a) An individual is selected if its non domination rank is smaller than the other.
- (b) If both the individuals belong to the same front i.e both have same non domination rank then the individual having higher crowding distance is selected

(5)Genetic Operators

Single point crossover and mutation operations is used in NSGA-II.



NSGA-II(Contd...)

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 0 | 0 | 1 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | 1 |
| 0 | 0 | 1 | 1 | 1 | 1 | 0 | 1 | 0 | 0 | 1 | 1 |

Mutation

(6)Recombination and Selection:

The offspring population is combined with the current generation population and the total population is sorted based on nondomination. The new generation is filled by chromosomes from each front subsequently until the population size exceeds the current population size N .

Simulation results

The population size N is taken as 200 and the number of generations varied from 150 to 200

The crossover and mutation probability used are 0.8 and 0.1 respectively

| Seq Len | [Neural Network] | | NSGA-II | |
|---------|------------------|-----|---------|-----|
| | PSL | ISL | PSL | ISL |
| 49 | 5 | 688 | 4 | 560 |
| | 5 | 688 | 5 | 472 |
| 50 | 5 | 674 | 5 | 658 |
| 51 | 5 | 618 | 5 | 594 |
| 52 | 5 | 708 | 5 | 604 |
| 53 | 5 | 700 | 5 | 604 |
| 54 | 5 | 750 | 5 | 702 |
| 55 | 5 | 902 | 5 | 830 |

Conclusion

- The search for optimum sequence depends on the selection of the initial population of parent sequences.
- It observed from the simulation result that NSGA-II method gives better result in terms of ISL and/or PSL compared to Neural Network method.
- The quality of solution improves with increase in the number of generations.

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Thank You