

Application of genetic algorithm with approximation crossover strategy to ambiguity resolution in PD radar

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Abstract: The genetic algorithm (GA) designed as a general optimization method was applied to the ambiguity resolution of pulse Doppler (PD) radar. The fitness, based on squared error for multi-PRF (pulse repeat frequency) consecutive ordered ranges, was designed. The crossover operator and the conditions of ending in GA were discussed. The relations among the probability of ambiguity resolution of this algorithm, the measurement error and the computational efficiency were analyzed. Simulation results show the GA ambiguity resolution algorithm does better than the sliding window algorithm on the probability of ambiguity resolution.

Key words: genetic algorithm; crossover operator; PD radar; ambiguity resolution; sliding window; clustering

A major classification of waveforms deals with ambiguity resolution in range and velocity. Low-PRF (pulse repeat frequency) waveforms are unambiguous in range but ambiguous in velocity, medium-PRF waveforms are ambiguous in both range and velocity, and high-PRF waveforms are ambiguous in range but unambiguous in velocity^[1]. Modern radar systems have multiple PRFs in common. The Chinese remainder theorem is an analytic procedure for calculating ambiguity resolution. These PRFs must be prime to each other but this condition usually can't be met because of the restriction in designing a practical system^[1,2]. In addition, the measurement errors will reduce the probability of ambiguity. Ref.[3] proposed a clustering algorithm to resolve ambiguities. This algorithm was found to be superior to the Chinese remainder theorem for resolving range ambiguities and it is easier for medium-PRF than high-PRF waveforms to resolve all the range-velocity ambiguities. It does not require a specific relationship between the multiple PRFs. However, it is worse at computational efficiency and resolving ambiguity for multiple targets. Based on the clustering algorithm, a sliding window correlator algorithm for resolving the ambiguity in range and velocity is described in Ref. [4]. The probability of ambiguity resolution with the sliding window correlator algorithm can only reach 90% in the case of low or medium PRF for multiple targets in a practical system. As a general optimization method, GA is used to resolve ambiguities in this paper. The changed form of

average squared error $C_R(j)^{[3]}$ is introduced as the fitness function and an approximation crossover strategy is applied in GA. The probability of ambiguity resolution is improved greatly. The computational efficiency is the same level with the clustering and the sliding window correlator algorithms.

1 The Clustering and Sliding Window Correlator Algorithm

The one-dimensional clustering algorithm can be used to resolve either range or velocity ambiguities. Supposing the number of PRFs is m , the ambiguous range measurement for the i -th PRF is R_i , and the unambiguous range for that PRF is $R_{ai} = C/(2\text{PRF})$, C is the speed of light. As shown in Fig.1, all the possible ranges can be expressed as

$$R_{Ki} = R_i + K_i R_{ai} \quad (1)$$

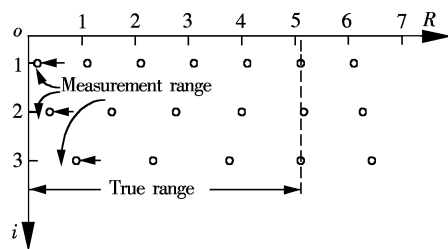


Fig.1 The clustering and sliding window correlator sketch map

If the maximum range of interest is R_{\max} , the integer K_i runs from

$$K_i = 0, \dots, \text{int} \left[\frac{R_{\max}}{R_{ai}} \right] \quad (2)$$

All the possible ranges generated by the m ambiguous measurements are ordered from the smallest to the largest and denoted by R_{oi} . The average squared

Received 2002-12-19.

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error $C_R(j)$ for m consecutive ordered ranges is

$$C_R(j) = \frac{1}{m} \sum_{i=j+1}^{j+m} |R_{oi} - \bar{R}|^2 \quad (3)$$

where \bar{R} is the median value of the m ordered range. The best cluster occurs at that value of j where $C_R(j)$ is a minimum. This happens when all the ambiguous ranges are unfolded correctly and hence all ordered ranges in the subset of m ranges nearly have the same range.

G.Trunk, et al. have compared the clustering algorithm to the Chinese remainder theorem for ambiguity resolution^[3]. The clustering algorithm indicates the effectiveness of the resolution process by constructing a cost function and has no special restrictions on multiple PRF. Based on the clustering algorithm, Ref. [4] brought forward a sliding window correlator algorithm. In fact, their basic ideas are the same. But the implementation and results are different. The clustering algorithm is relatively well suited for the ambiguity resolution of a single target. The processing burden and false resolution will obviously increase for multiple targets. When using the sliding window correlator algorithm the false resolution only relates to the distribution of targets in unambiguous range and the processing burden only increases slightly when the number of target increases. With some probability of false resolution and limited targets, it may satisfy ambiguity resolution for many targets. The sliding window correlator algorithm is more suited for a practical system than for a clustering algorithm in low or medium PRF for multiple targets.

2 Genetic Algorithms with Approximation Concept Crossover

In the algorithm of clustering and sliding window correlator, ambiguity resolution in range and velocity becomes an optimization, steering the locations of the minimum average squared error $C_R(j)$. The genetic algorithm designed as general optimization method is applied to ambiguity resolution for improving the performances of the probability of ambiguity resolution and processing efficiency. For example, aero radar with X wave band adopts three layers of PRF to resolve ambiguity in range and velocity. The range gate is 75 m, the number of range gates included in each PRF are 85, 101, and 119, the maximal ranges without superposition are $85 \times 101 \times 119$ range gates, supposing 1 000 targets distributed equally in metrical scope and the metrical scope including 0 - 110 km. We just considered the ambiguity within range.

2.1 Fitness function

From Eq.(1), we can get a group of possible ranges:

$$\left. \begin{aligned} R_{K1} &= R_1 + K_1 \times 85 \times 75 \\ R_{K2} &= R_2 + K_2 \times 101 \times 75 \\ R_{K3} &= R_3 + K_3 \times 119 \times 75 \end{aligned} \right\} \quad (4)$$

where R_1, R_2, R_3 are the ambiguous range measurements for the i -th PRF; K_1, K_2, K_3 are random integers of $K_1 \in [0, 17], K_2 \in [0, 14], K_3 \in [0, 12]$, respectively. The average squared error $C_R(j)$ for m consecutive ordered ranges presents the difference of possible range R_{Ki} . In order to convert the minimization problem to a maximization problem, an inverting function is used. The actual fitness function value f assigned to a group R_{Ki} is

$$f = \frac{1}{|R_{K1} - \bar{R}| + |R_{K2} - \bar{R}| + |R_{K3} - \bar{R}|} \quad (5)$$

where \bar{R} is the median value of R_{K1}, R_{K2} and R_{K3} . The mutation is according to the fitness function f .

2.2 Approximation concept in crossover^[5]

Consider the unconstrained maximizing problems with continuous parameters, such a problem can be expressed as

$$\text{Max } f(\mathbf{x}) \text{ with } x_i^L \leq x_i \leq x_i^U \quad i = 1, 2, \dots, N \quad (6)$$

where \mathbf{x} is the parameter vector; x_i^L and x_i^U are the lower and upper bounds of parameter x_i , respectively. There are two main reasons for integrating the approximation concept into the crossover operation: ① Estimate the potential search direction; and ② Increase level of utilization of genetic information provided by the crossover pair.

Without prior knowledge, such a potential search direction usually is not clear. And it is difficult to determine. However, it is possible utilizing the value of fitness function $f(x)$ (or its scaled value) to estimate this direction. In general, the fitness function $f(x)$ between two individuals not only contributes selection pressure during reproduction, but also can be used to indicate a potential direction for generating better quality progeny. Therefore, the procedure to generate progeny (new search points) by the consideration of fitness function difference increases the utilization of genetic information, which is neglected in common crossover operators in general.

If the search direction d is approximated by a first-order equation, by using the fitness function

difference between parents, the normalized direction is expressed as

$$d = \frac{f_{\text{high}} - f_{\text{low}}}{f_{\text{high}}} \quad (7)$$

where f_{high} and f_{low} indicate the parents with higher and lower fitness function, respectively. Since the working principles of GA are based on scalar fitness function to direct its search, Eq.(7) is a legitimate estimation. Eq.(7) indicates that an individual can improve its fitness function if the individual was moved from one region f_{low} to f_{high} along the direction d . By using Eq. (7), progeny can then be located at the positions of

$$x^{t+1} = x^t + \alpha(x'_{\text{high}} - x'_{\text{low}})d \quad (8)$$

where x^{t+1} represents the location (parameter vector) of progeny at the generation of $t + 1$; $x'_{\text{high}} - x'_{\text{low}}$ is the position difference of parents at generation t ; $\alpha \in [0, 1]$ is a random distance coefficient to determine the location of progeny.

The uses of this linear approximation to establish successive search directions in GA have been discussed by various researchers^[5-7]. Although they differ in ways of selecting candidate parents and modifying parameter vectors, the idea behind these articles is that the linear approximation guides the progeny towards better string structures, which generally represents improved solutions.

Based on the above linear approximation to establish successive search directions, W.B.Liu, et al.^[8] have improved the crossover operation as

$$\begin{cases} x_1^{t+1} = x'_{\text{low}} + \alpha_1(x'_{\text{high}} - x'_{\text{low}})d \\ x_2^{t+1} = x'_{\text{low}} + \alpha_2(x'_{\text{high}} - x'_{\text{low}})d \end{cases} \quad (9)$$

where $\alpha_1 \in [0, 1]$, and $\alpha_2 \in [1, 2]$ are the same as Eq. (8). Where $x_1^{t+1} \in [x'_{\text{low}}, x'_{\text{high}}]$, verse x_2^{t+1} may outside the bound of $x'_{\text{high}} - x'_{\text{low}}$. The improved crossover operation has some characteristics: ① There is no restriction on the positions of progeny; ② It improves the linearization of progeny gene mode. Greater distance $x'_{\text{high}} - x'_{\text{low}}$ between parents and large difference $f_{\text{high}} - f_{\text{low}}$ of fitness function contribute a greater correction; ③ Because of the capability of exploring new points through the modification of parameter vector x of individual strings, new schemata, which do not appear in their parents, can be created as long as all individuals do not have the same fitness function; ④ The new operation maintains genetic diversity in the population, thus avoiding the possibility of premature convergence to local optima.

Besides the above-mentioned characteristics, the crossover operation possesses mutant efficiency. It is

reasonable to omit the operator of mutation. The GA with approximation crossover strategy is applied to the ambiguity resolution of PD radar. The application of other evolutionary algorithms to ambiguity resolution in PD radar still needs to be studied further.

3 Performance Analysis and Results

The probability of correctly resolving ambiguities and generation are the important performances of GA used for ambiguity resolution. The measurement accuracy is an important factor that affects the performance of ambiguity resolution. The measurement accuracy refers to range and velocity cells.

A number of experiments were conducted to provide a reasonable basis for comparison between the clustering algorithm and the GA with the approximation crossover. The stochastic nature of GA search however renders such a comparison study somewhat difficult. To minimize these variations, each function was carried out several times, each with a different random number seed. This is to generate identical initial population and in an effort to avoid the situation where successive random number treated some crossover positions preferentially. The experiments used Matlab 5.3 code running on a PC with Celeron 233 processor and 32M RAM. The parameters are: population is 100; the error coefficient of measurement is variable; the threshold of fitness function (condition of end generation) is variable.

In PD radar system, the precision of the measuring range depends on the range gate and the error coefficient of measurement is about $1/M$, where M is range cells in per PRF. In our example, the precision of the measuring range is 75 m, and the error coefficient of measurement is about 0.84% to 1.2%. As shown in Fig.2, GA with the approximation crossover was used for resolving ambiguity. The fitness function converge infinity after generation 5 with the error coefficient of measurement 4% and the population 100.

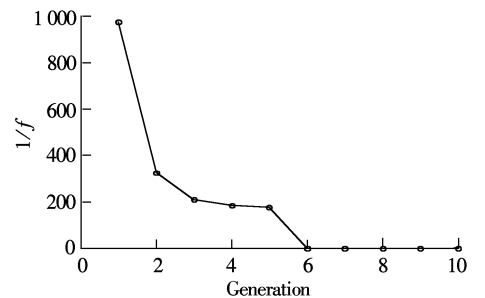


Fig.2 Convergence of GAs with the approximation crossover used for resolving ambiguity with the error coefficient of measurement 4%

The threshold of fitness function is one of the important factors, which affects the probability of resolving ambiguity and computational efficiency. This tendency can be observed from Tab.1 and Tab.2. Tab.1 presents the error coefficient of measurement versus the probability of resolving ambiguity (%) and average time using GA as the population is 100; the times of run for every sequence number (SN) is 1 000; the error coefficient of measurement is variable; the threshold of fitness function is 1/800. Tab.2 presents the error coefficient of measurement versus the probability of resolving ambiguity (%) and average time using GA as the population is 100; the times of run for every SN is 500; the error coefficient of measurement is variable; the threshold of fitness function is 1/450. Greater threshold of fitness function can lessen the computational time, but the probability of resolving ambiguity is lower. The error coefficient of measurement is another important factor, which affects the probability of resolving ambiguity and the computational efficiency. With the increment of the error coefficient of measurement, the probability of resolving ambiguity declines, and the computational time increases.

Tab.1 The error coefficient versus the probability and average time using GA with 1 000 times and $f = 1/800$

SN	The error coefficient of measurement/%	The probability of resolving ambiguity/%	Average time/s
1	2	99.8	0.575 5
2	4	99.2	0.571 0
3	6	93.2	0.519 1
4	8	93.4	0.603 5
5	10	unconverge	unconverge

Tab.2 The error coefficient versus the probability and average time using GA with 100 times and $f = 1/450$

SN	The error coefficient of measurement/%	The probability of resolving ambiguity/%	Average time/s
1	2	100	0.569 4
2	4	100	0.492 7
3	5	unconverge	unconverge
4	6	unconverge	unconverge

Tab.3 expresses the results of resolving ambiguity using the sliding window correlator algorithm, the average of the probability of resolving ambiguity is 91.67%, and the average time is 0.165 7 s. Compared Tab.1, Tab.2 with Tab.3, the probability of resolving ambiguity using the approximation crossover GA is higher than that of using the sliding window correlator algorithm. The computational time using the approximation crossover GA is 4 to 6 times of that of using the sliding window correlator algorithm.

Tab.3 The probability versus average time using the sliding window correlator algorithm with 100 times

SN	The probability of resolving ambiguity/%	Average time/s
1	93	0.122 6
2	88	0.175 8
3	94	0.174 7
4	94	0.173 5
5	91	0.173 7
6	90	0.174 2

4 Conclusion

The paper presents a GA with approximation crossover used on ambiguity resolution of PD radar. This genetic crossover integrates design space approximation to facilitate the searching of GA. A higher probability of resolving ambiguity was achieved. Although the computational efficiency using the approximation crossover GA is lower than that of using the sliding window correlator algorithm, with the development of DSP technology, this shortage can be overcome.

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逼近交叉策略的遗传算法 在 PD 雷达解模糊中的应用

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摘 要 遗传算法作为一种通用的寻优方法, 本文将其用于 PD (pulse Doppler) 雷达的解模糊处理. 基于多重 PRF (pulse repeat frequency, 脉冲重复频率) 之间所有可能距离的均方误差, 设计了适应度函数; 讨论了基于逼近交叉策略的遗传算法在 PD 雷达解模糊中的应用, 并通过仿真分析了解模糊正确率、测量误差、计算效率等之间的关系. 仿真结果证明该方法的解模糊正确率与滑窗相关器算法比较有了较大的提高.

关键词 遗传算法; 交叉算子; PD 雷达; 解模糊; 滑窗; 聚类

中图分类号 TN958