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# A Rejection and Recognition Method Based on Chain Coverage Model in Radar HRRP Target Recognition

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**Abstract:** In this study, an algorithm for chain coverage model is proposed. The proposed algorithm is in accordance with existing out-of-database target rejection techniques in radar target recognition Using High Range Resolution Profiles (HRRP). This algorithm arranges the target samples in order based on the changes of elevation angles to construct a sausage-like coverage area for every two neighboring samples. Then the chain-like coverage model is constructed by connecting each area in proper order. This model depicts a complicated boundary structure of target samples distribution in a high-dimensional space. In this case, each kind of target constructs its own compact coverage area. The judgment with acceptance or rejection is that in terms of test samples whether or not within the target coverage area. If the test sample is accepted by several targets simultaneously, a generalized membership function is put forward to evaluate the strong or weak degree of acceptance samples subject to certain target and realize target identification. The experimental results demonstrate the effectiveness of the algorithm.

**Keywords:** Chain coverage model, generalized membership grade, HRRP, radar target recognition, rejection

## INTRODUCTION

Radar Automatic Target Recognition (RATR) is to extract effective features of target from its radar echoed signatures and to identify the unknown target. High Resolution Range Profile (HRRP) is given by the amplitude of the coherent summations of superposition time returning from target scatterers in each range resolution cell, which represents the projection of the returned complex echoes from target scattering centers onto the radar line of sight (Du *et al*., 2006). Among several kinds of wideband radar target signatures, HRRP is a promising signature which is easier to be acquired. Therefore, identification algorithms based on HRRP has attracted intensive research in the field of RATR (Fu *et al*., 2010).

In practice, RATR mainly deals with uncooperative military targets, which determines that target categories in the database are self-contained while the database shall be gradually enriched and consummated in the process of identification. Hence, when there are test samples belonging to new categories, it is unreasonable to attribute them to any category of the database, which means the samples will be rejected. Therefore, the capability to reject or identify is crucial to evaluate whether an identification system can be put into practice or not.

As regard to the refuse-recognition of RATR, many solutions have been explored. In (Zhou, 2001), given a fixed identification rate, the rejection threshold is calculated as the distance between the training sample and the center of the category to construct distribution histogram of the sample. The generalized confidence degree of the training sample based on the Nearest Neighbor (NN) classifier is calculated in Meng (2005) to determine the rejection threshold by the distribution of confidence. Meanwhile, in Liu *et al*. (2009), taking generalized confidence degree of the sample as indices of system judgment, the rejection threshold is determined by introducing cost factor and designing Fisher discriminant function to evaluate classifier performance. The above methods require a large number of train sets and uniform distribution, otherwise, accurate rejection threshold will be difficult to obtain. In Chai *et al*. (2009), According to multi-modal distribution feature of HRRP, based on Support Vector Description (SVDD) method, the form of linear combination of Gaussian kernels are brought forth

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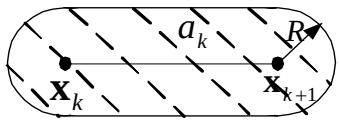
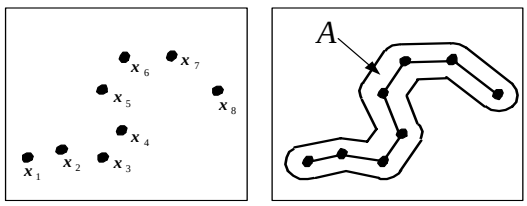
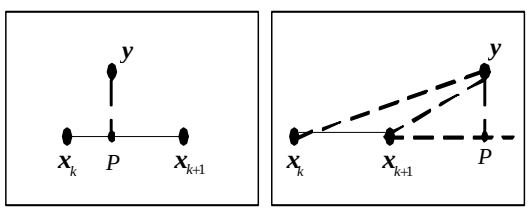



Fig. 1: Local coverage region of two neighboring samples




(a) (b)

Fig. 2: Local coverage region of two neighboring samples (a) two-dimensional target's sample points (b) chain coverage region




(a) (b)

Fig. 3: The distance between the sample and edge (a) pedal lies on the line segment (b) pedal lies on the extension line of the line segment

to establish multi-kernel support vector domain description methods. Hereby, the overlap ranges of samples is obtained if it were described by the minimum hyper-sphere boundary including training samples. However, when the number of samples is small, the superfluous area of spherically shaped boundary founded by this method will be large which deteriorates the rejection performance.

Based on literature survey, it can be show that, when the number of train samples is small, it is an effective solution to the outlier target rejection to construct a compact geometric boundary overlay model for the distribution of target samples and then judge whether the test samples locate within the boundary of the overlay model or not. Thus, this study proposes a rejection and recognition method based on chain coverage model. By this algorithm, the target samples of the same category are arranged in order according to changes of attitude angle. Then, a "sausage-like" coverage area is constructed for every two neighboring samples by making use of the continuity of the distribution of HRRP samples next to attitude angle. At last, each area is connected to form a chain-like area which is taken as the coverage model of the target. When the test sample is located out of the boundary of the chain model of certain category of a target, this sample will be rejected, otherwise the sample will be accepted by this target. If the test sample is accepted by multi categories of targets at the same time, this study puts forward a generalized membership function to calculate the strong or weak degree of the acceptance sample subject to this kind of target in order to determine the real category that the test sample belongs to.

## METHODOLOGY

**Construct the chain coverage model:** The attitude angle of radar target refers to the angle between the spindle of the target and radar line-of-sight. For the similar targets, the spatial distribution of attitude angle continuous HRRP samples has a certain continuity property. Therefore, local coverage areas can be constructed by neighboring samples and can be used as a basic unit to establish a complex boundary model for the whole target.

**Determination of local coverage region:** Let $X = \{x_1, x_2, \ldots, x_n\}$ be a HRRP train sample set of a certain target, where n is the number of the samples, $X_i \in R^d$ is the $i^{th}$ HRRP and d is the dimension of the feature. These HRRP samples are arranged in order according to the changes of attitude angle. To connect every two neighboring samples, we can get n-1 connection edges, denoted as $E = \{e_k = (x_k, x_{k+1}) \mid k = 1, 2, \ldots, n-1\}$. A sausage-like local coverage region is created for every connection edges $e_k$. As shown in Fig. 1, the shaded area is the corresponding sausage-like local coverage region $a_k$ of the connection edge $e_k$.

Linking the corresponding local coverage regions of all connection edges yields a chain-like connected region- $A = \left\{ \bigcup_{k=1}^{n-1} a_k \right\}$, which is the target's chain coverage model. Figure 2 shows the chain coverage region of a set of two-dimensional target's sample points. From this figure, we can also see that the chain structure constructs a compact coverage model for the target's complex boundary and effectively characterizes the distribution of the training samples.

**Determination of coverage radius:** During the process of constructing a chain coverage model, the coverage radius R determines the size of the coverage region A. If the sample points of a certain target is very concentrated, a small coverage radius should be taken; Otherwise, a large coverage radius should be used. The distance between samples can be used to evaluate the

concentration of target samples, so we can use the average distance between all adjacent samples as the coverage radius of the target:

$$d_k = \|e_k\| = \|x_{k+1} - x_k\| \quad k = 1, 2, \ldots, n-1$$
$$R = \frac{1}{n-1}\sum_{k=1}^{n-1} d_k \tag{1}$$

**Rejection and recognization based on chain coverage model:**

**Rejection or accpetance of a test sample:** Supposing $y \in R^d$ represents a test sample, whether the sample y belongs to a certain target depends on whether the sample is located within the boundaries of the target chain coverage region. As the chain coverage area of a target is connected by the numerous sausage-shaped local coverage area of adjacent samples, which can be written as $A = \left\{\bigcup_{k=1}^{n-1} a_k\right\}$, whether a sample belongs to a certain target is determined by whether the sample belongs to each local coverage area $a_k$, k = 1, 2, … , n–1.

Firstly, we need to calculate the distance $d(y, e_k)$ between the test sample y and the edge $e_k = (x_k, x_{k+1})$.

In Fig. 3, lead a perpendicular from sampleY to $\overline{x_k\, x_{k+1}}$, the pedal is P, its coordinate can be calculated by Formula (2):

$$P = x_{t+1} + \frac{\langle y - x_t, x_{t+1} - x_t\rangle}{\langle x_{t+1} - x_t, x_{t+1} - x_t\rangle}\left(x_{t+1} - x_t\right) \tag{2}$$

According to the different relative positions of pedal P and line segment $\overline{x_k\, x_{k+1}}$, the distance $d(y, e_k)$ between sample and the edge $e_k$ can be defined as follows: if the pedal lies on the line segment Fig. 3a, $d(y, e_k)$ is the distance between sample Y and the pedal P; if the pedal lies on the extension line of the line segment Fig. 3b, the $d(y, e_k)$ is the minimum distance between y and the two ends of line segment $\overline{x_k\, x_{k+1}}$ ,summarized as the follows:

$$d(y, e_k) = \begin{cases} \|y - P\|, & y \in \overline{x_k\, x_{k+1}} \\ \min\left(\|y - x_k\|, \|y - x_{k+1}\|\right), & y \notin \overline{x_k\, x_{k+1}} \end{cases} \tag{3}$$

If the distance $d(y, e_k)$ between the sample y and the edge $e_k$ is smaller than the target coverage radius R , we evaluate whether the sample y belongs to the local coverage area $a_k$ via:

$$\begin{cases} y \in a_k,\ d(y, e_k) \le R \\ y \notin a_k,\ d(y, e_k) > R \end{cases} \tag{4}$$

Finally, the rejection rule to determine whether a test sample y belongs to a certain target is given as follows: if the test sample y does not belong to any section of the local coverage area $a_k$, k = 1, 2, …, n–1, it will be rejected to this target. The rule can be written as:

$$\begin{cases} y \notin A,\ y \notin a_1 \cap y \notin a_2 \cap \ldots \cap y \notin a_{n-1} \\ y \in A,\ others \end{cases} \tag{5}$$

**Rejection and recognition:** In a RATR system, firstly we construct the chain coverage areas $\{A_g \mid g = 1, 2, \ldots, G\}$ for each training target, where G is the number of target categories. Then, for every target coverage area $A_g$, reject or accept the test sample y by using the method described in section A:

$$L = \begin{cases} 0\ , & y \notin A_1 \cap y \notin A_2 \cap \ldots \cap y \notin A_G \\ 1\ , & others \end{cases} \tag{6}$$

As in (6), if y is rejected by all type of target $y \notin A_1 \cap y \notin A_2 \cap \ldots \cap y \notin A_G$ , we conclude that the test sample is a new outlier target, represented as L = 0 . If y is accepted by any types of target, we conclude it is an inner target of the database, represented as L = 1.

If a sample is accepted as a inner target of the database (L = 1), we need to further identify the category of this sample and there will be two cases:

- If the test sample is only accepted by one category of target, the test sample can be directly identified as this target.
- If the test sample is accepted by multi categories of targets, it can not be directly identified. For this case, a generalized membership function is proposed to evaluate the strong or weak degree of the test sample belonging to a certain type of target.

If the test sample y is accepted by a certain target, y is definitely located within at least one local coverage areas $a_k$( i.e., $y \in a_k$ and the number of $a_k$ is greater than or equal to 1). At this moment, calculate the membership degree of y with respect to these local coverage areas and choose the maximum value as the generalized membership degree of the test sample relative to this target. Its definition is:

$$f = \max\{\exp(-\frac{\|y - x_k\| . \|y - x_{k+1}\|}{R^2} - \frac{\|y - P\|}{R})|y \in a_k\} \tag{7}$$

where the membership degree $f$ is proportional to the

target coverage radius and inversely proportional to the distance between test sample and the coverage area.

Thus, when a test sample y is accepted by at least one types of target (L = 1), the identification method to this sample is to calculate the generalized membership degree of y with respect to these types of targets and y is belong to the target of the maximum generalized membership degree.

## EXPERIMENT RESULTS

**Experimental data:** We simulate radar backscattering data of six airplanes according to Gorshkov *et al*. (2002) and Shirman (2002) and the parameters of targets and radar are shown in Table 1. As these six airplanes $S_i$ (i = 1, 2,…, 6) are all symmetrical in horizontal, we simulate azimuth 0º~180º at interval 0.5º and elevation angle is initialized as 0º. Note that for each airplane, we get 360 HRRPs. In order to decrease the time-shift sensitivity of HRRP, the power spectrum characteristics of each HRRP will be taken as the training and test sample, its dimension is 128. We choose the 180 HRRPs at integer azimuth as the training subsets (record as $tS_i$) and the corresponding remainders as test subsets (record as $rS_i$).

**Experimental methods:** In practice, the target database of a RATR system is generally incomplete and targets will be gradually added into the database during the process of identification. In order to emulate the practical situation, this test adopts a way by adding one type of new target each time to test and verify the effects of rejection and recognition. For example, if there are two types of target in the target database, input the test samples of all six types of target to test, the samples of two types of target in the database should be accepted and recognized, the samples of the rest four types of target should be rejected.

In this study, the following three indicators will be used to evaluate the performance of the algorithm:

- Correct rejection rate, refers to the rate of the outlier target samples being correctly rejected, record as:

  $P_{t-}$ = The number of outlier target test samples are rejected/The number of outlier target test samples

- Correct acceptance rate, refers to the rate of the inner target samples being correctly accepted, record as:

  $P_{t+}$ = The number of inner target test samples are being accepted/The number of inner target test samples

- Correct recognition rate, refers to the rate of the inner target samples being correctly recognized, record as:

  $P_c$ = The number of inner target test samples are being correctly recognized/The number of inner target test samples

Table 1: Parameters of planes and radar in the simulated experiments

| | | | |
|---|---|---|---|
| Radar parameters | Center frequency | | 5520, MHz |
| | Bandwidth | | 400, MHz |
| | Sampling frequency | | 800, MHz |
| Planes | Length (m) | Width (m) | Scale |
| $S_1$: An-26 | 23.80 | 29.21 | 1:1 |
| $S_2$: B-1B | 44.80 | 23.80 | 2:1 |
| $S_3$: B-52 | 49.50 | 56.40 | 2:1 |
| $S_4$: F-15 | 19.43 | 13.05 | 1:1 |
| $S_5$: Mig-21 | 15.76 | 7.15 | 1:1 |
| $S_6$: Tu-16 | 33.80 | 33.00 | 2:1 |

Table 2: Rejection and recognition result using two targets' HRRPs to train (%)

| | Testing sets | | | | | |
|---|---|---|---|---|---|---|
| Training sets | $rS_1$ | $rS_2$ | $rS_3$ | $rS_4$ | $rS_5$ | $rS_6$ |
| $tS_1$ | 97 | 1 | 2 | 18 | 4 | 13 |
| $tS_2$ | | 0 | 96 | 4 | 6 | 81 |
| New target | 3 | 3 | 94 | 76 | 88 | 86 |
| recognition rate $P_c$ | 97 | 96 | | $\overline{P_c}$ = 96.5 | | |
| Accept rate $P_{1+}$ | 97 | 97 | | + $\overline{P_{1+}}$ = 97.0 | | |
| Refuse rate $P_{1-}$ | $\overline{P_{1-}}$ = 86.0 | | 94 | 76 | 88 | 86 |

Table 3: Rejection and recognition result using three targets' HRRPs to train (%)

| | Testing sets | | | | | |
|---|---|---|---|---|---|---|
| Training sets | $rS_1$ | $rS_2$ | $rS_3$ | $rS_4$ | $rS_5$ | $rS_6$ |
| $tS_1$ | 96 | 1 | 0 | 18 | 4 | 13 |
| $tS_2$ | 0 | 96 | 0 | 5 | 8 | 1 |
| $tS_3$ | 1 | 0 | 96 | 3 | 2 | 0 |
| New target | 3 | 3 | 4 | 74 | 86 | 86 |
| recognition rate $P_c$ | 96 | 96 | 96 | $\overline{P_c}$ = 96.0 | | |
| Accept rate $P_{1+}$ | 97 | 97 | 96 | $\overline{P_{1+}}$ = 96.7 | | |
| Refuse rate $P_{1-}$ | $\overline{P_{1-}}$ = 82.0 | | | 74 | 86 | 86 |

Table 4: Rejection and recognition result using four targets' HRRPs to train (%)

| | Testing sets | | | | | |
|---|---|---|---|---|---|---|
| Training sets | $rS_1$ | $rS_2$ | $rS_3$ | $rS_4$ | $rS_5$ | $rS_6$ |
| $tS_2$ | 96 | 1 | 0 | 1 | 3 | 13 |
| $tS_3$ | 0 | 96 | 0 | 0 | 7 | 0 |
| $tS_4$ | 1 | 0 | 96 | 0 | 1 | 0 |
| $tS_5$ | 0 | 0 | 0 | 97 | 4 | 2 |
| New target | 3 | 3 | 4 | 2 | 85 | 85 |
| recognition rate $P_c$ | 96 | 96 | 96 | 97 | $\overline{P_c}$ = 96.3 | |
| Accept rate $P_{1+}$ | 97 | 97 | 96 | 98 | $\overline{P_{1+}}$ = 97.0 | |
| Refuse rate P1- | $\overline{P_{1-}}$ = 85.0 | | | | 85 | 85 |

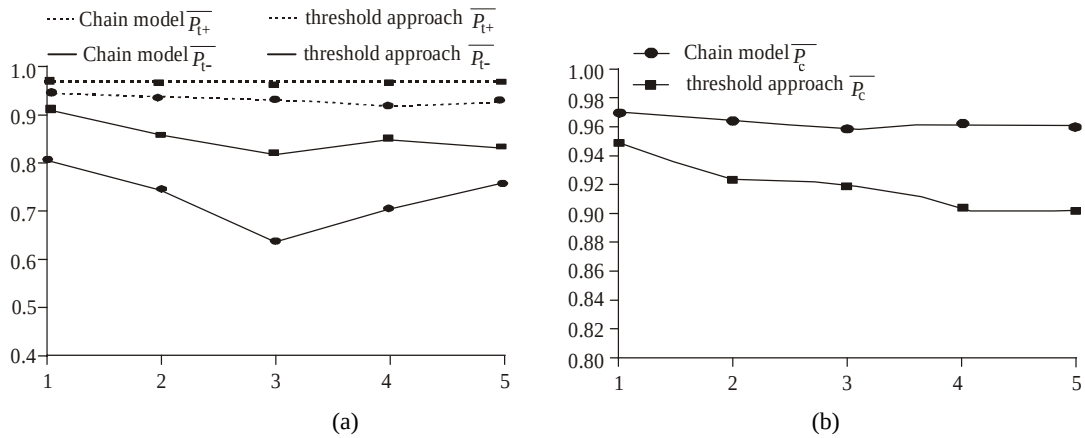



Fig. 4:The compare of chain coverage model algorithm and threshold approach. (a) the average correct acceptance rate $\overline{P_{1+}}$ and the average correct rejection rate . $\overline{P_{1-}}$ (b) the average correct recognition rate $\overline{P_c}$

**Experimental results and analysis:** When the number of types of the targets in-database increases from two to four, Table 2 to 4 display the correct rejection rate, correct acceptance rate and correct recognition rate after identifying all the six types of test samples, respectively.

Take Table 3 for example, the type of the targets in-database is three. In this experiment, the feature database is created by using the train samples of three types of target ($tS_1$:An-26 $tS_2$:B-1B $tS_3$:B-52), input all the six types of test samples to identify. At this time, except the test samples of the three targets in-the-database ($rS_1$, $rS_2$, $rS_3$) should be accepted, the remaining test samples should be rejected and considered as new targets.

The experimental results of Table 2 to 4 show that this algorithm achieves not only higher correct rejection rate (above 82%), but also higher correct acceptance rate (above 96%) and correct recognition rate (above 96%).

To further verify the effect of this algorithm, we use the method in (Zhou, 2001), where the rejection threshold is determined by the distribution histogram of the sample, to identify the same sample sets. The results of the threshold approach and our chain coverage model algorithm are shown in Fig. 4. Figure 4a shows the average correct acceptance rate $\overline{P_{t+}}$ and the average correct rejection rate $\overline{P}_{1-}$ of two algorithms and Fig. 4b shows the average correct recognition rate $\overline{P_c}$ , where X-coordinate is the number of targets of a experiment. Figure 4 indicates that the proposed algorithms are better than the threshold approach.

## CONCLUSION

In accordance with out-of-database target rejection existing in radar target recognition system of HRRP, a target rejection and recognition algorithm based on the chain coverage model is proposed in this study. The algorithm uses the basic assumptions of biomimetic pattern recognition theory for reference and makes use of the continuity of the samples distribution of same target to build a compact chain-like coverage boundary for the distribution of target samples. The judgment with acceptance or rejection is that in terms of test samples whether or not within the target coverage area. When the test sample is repeatedly covered, a generalized membership to judge the category of the sample is defined. The chain coverage model has the advantages of more compact boundary, smaller superfluous area and more simple calculation. The results of simulation verify validity of the proposed algorithm. For the proposed algorithm, the selection of target coverage radius has great impact on the results of rejection. If the coverage radius increases, the target coverage area will be enlarged. Correspondingly, the correct rejection rate will increase, while the correct acceptance rate will decrease. Therefore, in the future work, we may define the loss function through analyzing the cost of false alarm and missing report and determine the size of the coverage radius based on practical demand.

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