Validation of SAR ATR Performance Prediction Using Learned Distortion Models

Michael Boshra and Bir Bhanu
Center for Research in Intelligent Systems
University of California, Riverside, California 92521

ABSTRACT

Performance prediction of SAR ATR has been a challenging problem. In our previous work, we developed a statistical framework for predicting bounds on fundamental performance of vote-based SAR ATR using scattering centers. This framework considered data distortion factors such as uncertainty, occlusion and clutter, in addition to model similarity. In this paper, we present an initial study on learning the statistical distributions of these factors. We focus on the development of a method for learning the distribution of a parameter that encodes the combined effect of the occlusion and similarity factors on performance. The impact of incorporating such a distribution on the accuracy of the predicted bounds is demonstrated by comparing bounds obtained using it with those obtained assuming simplified distributions. The data used in the experiments are obtained from the MSTAR public domain under different configurations and depression angles.

Keywords: Model-based SAR ATR, performance prediction and validation, learned distortion models, MSTAR data

1. INTRODUCTION

Predicting performance of automatic target recognition (ATR) is critical for the advancement of the field. Our research efforts in this area have been focused on a model-based approach for ATR using synthetic aperture radar data (SAR). Such an approach can be outlined as follows:

1. Each model target is represented by a set of SAR views that sample its signature at a variety of azimuth angles and a specific depression angle.

2. Recognition is performed by matching locations of scattering centers (peaks) extracted from a given data view with those of the model views.

3. Evaluation of a model hypothesis (a model view at a given location relative to the data view) is based on the number of model features consistent with data features.

A statistical framework has been developed for predicting bounds on fundamental performance of the above SAR ATR approach. Such a framework considers data distortion factors such as uncertainty (error in estimating feature locations), occlusion (missing features) and clutter (spurious features). Furthermore, it considers the structural similarity between model views, which plays a fundamental role in deciding the recognition performance.

This paper presents an initial study towards learning the statistical models of data distortion. By incorporating these models in our performance-prediction framework, we expect to obtain performance bounds that are more accurate than those obtained by assuming simplified distributions. In this paper, we focus on the statistical modeling of occlusion. Our previous work assumed a uniform and spatially-independent occlusion model. In particular, given that $O$ features of a model view are occluded, each subset of $O$ features is equally likely to be occluded. Such a simplified assumption ignores the spatial correlation between occluded features. That is, occluded (unoccluded) features tend to be clustered. Incorporating a spatially-correlated occlusion model in our performance prediction framework, summarized below, raises a major source of difficulty, which is the interaction between occlusion and...

Further author information -
Email: {michael, bhanu}@cria.ucr.edu
URL: http://www.cria.ucr.edu
similarity. This is because of the spatial correlation that exists among features that are structurally similar in a pair of model views. Fortunately, in our performance-prediction context, there is a significantly simpler approach. Instead of learning the spatially-correlated distributions of each of occlusion and similarity, and then inferring the interaction between them, we directly learn the distribution of the parameter that encodes the combined effect of both factors on performance.

The remainder of the paper is organized as follows. The next section reviews some of the related research efforts in the area of performance prediction. Section 3 provides a summary of our performance-prediction framework. Section 4 describes the method used to learn the occlusion/similarity parameter described above. The impact of incorporating the learned distribution of such a parameter on the accuracy of performance prediction is demonstrated in Section 5. Finally, conclusions are drawn in Section 6.

2. RELATED RESEARCH

The problem of predicting ATR performance has received significant attention in recent years.\(^{11}\) Approaches for performance prediction can be classified into two categories: empirical and formal. Most approaches belong to the first category, where performance is determined experimentally using either real or synthetic data. For example, Novak et al.\(^{10}\) evaluated the performance of an ATR system using real polarimetric SAR images of camouflaged/uncamouflaged targets, and clutter. The performance metrics estimated included the probabilities of detection and false alarms, in addition to the confusion matrix for three targets and clutter. Catlin et al.\(^4\) used linear regression and neural networks to estimate the function relating the probability of correct identification to aspect and depression angles using real SAR data. Diehl et al.\(^3\) used synthetic imagery, degraded according to a noise model, to determine the relationship between performance and image resolution. Jones and Bhanu\(^6\) empirically estimated a number of metrics for evaluating the performance of a scattering-center-based ATR system using XPATCH SAR data. These metrics included the probability of correct identification, and the confusion matrix for four targets. The model data were distorted by changing model articulations (e.g., changing the orientation of a tank turret), occluding model features, and adding clutter features.

On the other hand, formal approaches attempt to describe data distortion statistically, and then use such a description to predict performance. For example, Grenander et al.\(^7\) used Hilbert-Schmidt bound for estimating fundamental error in template-based ATR. This error was determined for a given image noise model, represented as a probabilistic likelihood function. Irving et al.\(^9\) developed a method for predicting performance of model-based target detection using peak features. This method was based on statistical modeling of data distortion factors, as well as model target views. Doria\(^8\) analyzed the performance of two-class hypothesis testing in model-based ATR using peak features. Performance was analyzed considering a number of factors including model correlation (similarity), and spatial resolution of predicted features.

3. SUMMARY OF PERFORMANCE-PREDICTION METHOD

In this section, we present a summary of our performance-prediction method. More details can be found in References.\(^{2,3}\)

3.1. Problem Definition

We are given the following:

- A set of target views, \(S = \{M_i\}\), of the model targets under consideration, where each view \(M_i\) is represented by a set of discretized point features, \(M_i = \{F_{ik}\}\).
- Statistical models for data distortion factors (uncertainty, occlusion and clutter).

The objective is to predict lower and upper bounds on the probability of correct recognition (PCR) of a given model view as a function of the extent of distortion in it. The applicable transformation in our case is assumed to be the space of 2-D translations,\(^{1,4}\) which is denoted by \(T\). As mentioned earlier, we consider a vote-based criterion for matching.

A model view, \(M_{ik}\), is assumed to be distorted, to form \(\hat{M}_{ik} = \{\hat{F}_{ik}\}\), as follows. Firstly, a subset of \(O\) features is occluded. Secondly, the locations of the remaining \(M_i \neq O\) unoccluded features are randomly perturbed
independently. We assume that the random perturbation follows a uniform distribution, and so it can be represented by an uncertainty region, \( R_u(.) \). Thirdly, a set of spurious features, of size \( C \), is randomly added. We assume that these features are uniformly distributed within some clutter region, \( R_c \), surrounding \( M_i \).

The vote-based criterion adopted in our work is based on the shape of the uncertainty region, \( R_u(.) \). In particular, consider that we are given a data view, \( \tilde{M}_i \), and a model hypothesis, \( M_j^q \), which corresponds to model view \( M_j \) at relative location \( \tau \) with respect to \( \tilde{M}_i \). The number of votes for \( M_j^q \), given \( \tilde{M}_i \), is the number of features in \( M_j^q \) that have at least a data feature within their uncertainty regions.

### 3.2. Estimation of PCR in the Two-Hypothesis Case

In this section, we estimate the probability of correctly recognizing a distorted instance of view \( M_i \), \( \tilde{M}_i \), considering only a single erroneous hypothesis, \( M_j^q \), which is view \( M_j \) at relative location \( \tau \), with respect to \( M_i \).

We start by giving an example to illustrate the combined effects of data distortion and model similarity on the vote process. This example is illustrated in Figure 1. It shows model view \( M_i \) and erroneous hypothesis \( M_j^q \) at various stages of distortion to \( M_i \). The circles associated with the features of \( M_i \) and \( M_j^q \) represent their uncertainty regions. Notice that \( M_i \) and \( M_j^q \) have three feature pairs with overlapping uncertainty regions. In general, we denote the number of similar feature pairs between \( M_i \) and \( M_j^q \) by \( N_{ji}^q \). In addition, we denote the average of the ratio between the area of the overlapping region and that of the uncertainty region by \( P_{ji}^q \). Both parameters, \( N_{ji}^q \) and \( P_{ji}^q \), represent the degree of structural similarity between \( M_i \) and \( M_j^q \). The vote process can be described as follows:

- Initially, with no distortion, \( M_i \) gets five votes (notice that \( |M_i| = 5 \)). On the other hand, \( M_j^q \) does not get any votes, since the uncertainty regions of its features do not contain any features from \( M_i \).

- The first distortion step involves occlusion of two features in \( M_i \). Obviously, this reduces the number of votes for \( M_i \) to three, and contributes no votes to \( M_j^q \).

- The second distortion step involves perturbing the three unoccluded features of \( M_i \) uniformly within their uncertainty regions. Notice that one of the two unoccluded similar features in \( M_i \) moves to the region overlapping with the uncertainty region of the corresponding feature in \( M_j^q \). This results in a single similarity vote for \( M_j^q \), and no change in the votes for \( M_i \).

- The third and final distortion step is to add three spurious features. It can be observed that two of them accidently fall within uncertainty regions of features in \( M_j^q \). This results in two clutter votes for \( M_j^q \), thus increasing the number of its votes from one to three.

The above distortion process results in a "tie" between \( M_i \) and \( M_j^q \), which is a failure in recognition.

The above example gives us the following insight into the vote process. Firstly, the number of votes for \( M_i \), which we denote by \( V_i \), is simply the number of its unoccluded features (we assume here that the case of a clutter feature falling within the uncertainty region of an occluded feature in \( M_i \) is interpreted as no-occlusion/no-clutter case). That is, we have

\[
V_i = |M_i| - O.
\]  

(1)

Secondly, the number of votes for \( M_j^q \), which we denote by \( V_j^q \), is a random variable. These votes come from two sources: 1) view \( M_i \), due to similarity, and 2) clutter features, due to random coincidence. Accordingly, we can express \( V_j^q \) as

\[
V_j^q = V_s + V_c
\]  

(2)

where \( V_s \) and \( V_c \) are random variables corresponding to similarity and clutter votes for \( M_j^q \), respectively. Thirdly, the number of similarity votes, \( V_s \), is bounded by another random variable, \( N_o \), which is the number of unoccluded similar features in \( M_i \) (notice that \( N_o \leq N_{ji}^q \)). In the previous example, we have \( N_o = 2 \), \( V_s = 1 \), and \( V_c = 2 \) (see Figure 1).
The probability distribution function (PDF) of $V^*_{ji}$, which depends on $N_o$, $V_s$, and $V_c$, can be determined as follows. Since $V_s$ depends on $N_o$, we can express the PDF of $V_s$ as

$$P_{V_s}(u_s) = \sum_{n_o} P_{N_o}(n_o) P_{V_s}(u_s; n_o)$$

(3)

where $P_X(x) = \Pr[X = x]$, and $P_{V_s}(u_s; n_o) = \Pr[V_s = u_s; N_o = n_o]$. From (2) and (3), we can express the PDF of $V^*_{ji}$ as

$$P_{V^*_{ji}}(u_{ji}^*) = \sum_{n_o} P_{N_o}(n_o) \sum_{u_s} P_{V_s}(u_s; n_o) P_{V_c}(u_{ji}^* - u_s; n_o, v_c)$$

(4)

where $P_{V_c}(u_c; n_o, v_c) = \Pr[V_c = u_c; N_o = n_o, V_s = u_s]$.

The PDF of $N_o$ and the conditional PDF's of $V_s$ and $V_c$ are determined based on the statistical models of data distortion, and the structural similarity between $M_i$ and $M^*_j$:

- **PDF of $N_o$:** This is the variable that we are interested in learning, as will be discussed in Section 4. If we ignore the spatial-correlation factor, and assume that any subset of $O$ features in $M_i$ is equally likely to be occluded, it can be shown that $N_o$ is expressed by the following hypergeometric distribution:

$$P_{N_o}(n_o) = H_{N_o}(N^T_j - n_o; O, N^T_j \setminus M_i \setminus -N^T_j)$$

(5)
where \( H_X(x; n, a, b) = \frac{\binom{k}{a} \binom{n-k}{b}}{\binom{n}{a+b}} \), and \( K(a, b) = \frac{a^a}{(a-b)! b^b} \).

- **Conditional PDF of \( V_i \):** Based on the assumption of uniform uncertainty model, it can be shown that the conditional PDF of \( V_i \) is represented by the following binomial distribution:

  \[
P_{V_i}(v_i; n_o) = B_{V_i}(v_i; n_o, p^*)
  \]

  where \( B_X(x; n, p) = \binom{n}{x} p^x (1 - p)^{n-x} \).

- **Conditional PDF of \( V_i \):** Based on the assumption of uniform clutter distribution, it can be shown that the conditional PDF of \( V_i \), \( P_{V_i}(v_i; n_o, v_d) \), is approximated by a binomial distribution. Details about the derivation of the parameters of this distribution can be found in one paper by Boshra and Bhanu.3

3.3. **Estimation of Lower and Upper Bounds on PCR**

Let \( \mathcal{M}_i \) be the set of erroneous hypotheses associated with view \( \mathcal{M}_i \). That is,

\[
\mathcal{N}_i = \{ \mathcal{M}_j' : \mathcal{M}_j \in \mathcal{S}, \text{ and } \tau_i \in \mathcal{T} \text{ s.t. } | \mathcal{M}_j' \cap \mathcal{R}_c | > 0 \} - \{ \mathcal{M}_i' : \tau_i \in \mathcal{T}_{sec} \}
\]

where \( \mathcal{T}_{sec} \subset \mathcal{T} \) represents the extent of tolerance in location error. The probability of misinterpreting a distorted instance of \( \mathcal{M}_i, \mathcal{M}_i' \), as any hypothesis in \( \mathcal{N}_i \), can be expressed as

\[
Pr[\mathcal{N}_i; \mathcal{M}_i'] = \Pr[\exists \mathcal{M}_j' \in \mathcal{N}_i \text{ s.t. } V_j' \geq V_i].
\]  (6)

From (1) and (4), we can determine the probability that the votes for \( \mathcal{M}_j' \) reach or exceed those for \( \mathcal{M}_i \):

\[
Pr[\mathcal{M}_j'; \mathcal{M}_i'] = \sum_{v_j' \geq |\mathcal{M}_i'| - 0} P_{V_j'}(v_j').
\]  (7)

The probability of recognition failure, \( Pr[\mathcal{N}_i; \mathcal{M}_i'] \), can be bounded as follows (refer to (6)):

\[
Pr[\mathcal{N}_i; \mathcal{M}_i'] \leq \sum_{\mathcal{M}_j' \in \mathcal{N}_i} Pr[\mathcal{M}_j'; \mathcal{M}_i'].
\]

The above inequality can be directly used to determine the following lower bound on the probability of correctly recognizing \( \mathcal{M}_i \):

\[
Pr[\mathcal{M}_i; \mathcal{M}_i'] > 1 - \sum_{\mathcal{M}_j' \in \mathcal{N}_i} Pr[\mathcal{M}_j'; \mathcal{M}_i'].
\]  (8)

Our approach for determining an upper bound on PCR is to consider a subset of the erroneous hypotheses, \( \mathcal{N}_{Pt} \subset \mathcal{N}_i \), and assume that the votes for these hypotheses are statistically independent. This enables us to estimate an upper bound on PCR through tractable calculation of the probability that all of the selected hypotheses get less votes than \( \mathcal{M}_i \). In order to obtain a tight upper bound, the hypotheses in \( \mathcal{N}_{Pt} \) are selected to be those which are more "similar" to \( \mathcal{M}_i \) than neighboring ones of the same view in the space of translations \( \mathcal{T} \). The similarity between a hypothesis \( \mathcal{M}_j' \) and \( \mathcal{M}_i \) is measured as the expected number of similarity votes for \( \mathcal{M}_j' \) given a perturbed instance of \( \mathcal{M}_i \) (which is \( N_{j'} P_{j'} \)). Based on such an approach, we can obtain the following upper bound on PCR:

\[
Pr[\mathcal{M}_i; \mathcal{M}_i'] < \prod_{\mathcal{M}_j' \in \mathcal{N}_{Pt}} (1 - Pr[\mathcal{M}_j'; \mathcal{M}_i']).
\]  (9)

4. **LEARNING THE PDF OF \( N_o \)**

In this section, we present a method for learning the PDF of \( N_o \) for a given set of test data \( \mathcal{S} = \{ \mathcal{M}_j \} \). This set is obtained under a condition that is different from the model set (e.g., different configuration, different depression angle). The proposed learning method can be described as follows:
• A subset of the views in \( \mathcal{S}, \mathcal{S}_L \) is selected. In our experiments, \( \mathcal{S}_L \) is chosen to consist of the odd-numbered views in \( \mathcal{S} \).

• For each \( \mathcal{M}_i \in \mathcal{S}_L \), we find the model view in \( \mathcal{S}, \mathcal{M}_i \), corresponding to it. This is done by matching \( \mathcal{M}_j \) with the model views in \( \mathcal{S} \) that are within a difference of \( \pm 3^\circ \) azimuth angles, and selecting the one which generates the largest number of votes. If no views exist within such a range, then \( \mathcal{M}_j \) is assumed to correspond to the model view that is closest in azimuth. Notice that the output of this process is the corresponding model view \( \mathcal{M}_i \) along with the associated relative translation \( \tau_i \) of \( \mathcal{M}_j \) with respect to \( \mathcal{M}_i \).

• For the matched pair \( (\mathcal{M}_j, \mathcal{M}_i) \), we construct the "occluded" view of \( \mathcal{M}_i \) assuming it corresponds to \( \mathcal{M}_j \). Notice that, according to our distortion model (see Section 3.1), \( \mathcal{M}_j \) is obtained from \( \mathcal{M}_i \) after being translated, occluded, perturbed, and cluttered. We are interested in obtaining a "snapshot" of \( \mathcal{M}_i \) after being distorted by occlusion only. This snapshot, denoted by \( \mathcal{M}_i \), is obtained by eliminating features of \( \mathcal{M}_i \) that are not consistent with any feature in \( \mathcal{M}_i \).

• For each erroneous hypothesis \( \mathcal{M}_i \) \( \in \mathcal{M}_t \) \( \in \mathcal{N}_i \) \( \in \mathcal{N}_t \), we calculate the number of similar feature pairs between \( \mathcal{M}_i \) and each of \( \mathcal{M}_i \) and \( \mathcal{M}_i \), \( N_f \) and \( N_f \), respectively. The parameter \( \bar{N}_f \) represents the number of unoccluded similar feature pairs, which is the parameter of interest to us, \( N_o \).

• The values of \( \bar{N}_f \) for all \( \mathcal{M}_f \) \( \in \mathcal{N}_f \) are used to estimate the PDF of \( N_o \) as follows. From Section 3.2, it can be observed that the PDF of \( N_o \) depends on three parameters: \( \bar{O} = |\mathcal{M}_i| - |\mathcal{M}_f|, \bar{N}_f \) and \( |\mathcal{M}_i| \). Accordingly, the values of \( \bar{N}_f \) for each unique combination of \( |\mathcal{M}_i|, \bar{O}, \) and \( \bar{N}_f \) are accumulated in a separate histogram. The corresponding PDF of \( N_o \) is then obtained by simply normalizing the histogram.

In the next section, we demonstrate the impact of using the learned PDF of \( N_o \) on the accuracy of the estimated performance bounds.

5. EXPERIMENTAL RESULTS

In this section, we compare the accuracy of performance bounds obtained by assuming a uniform spatially-independent occlusion model with those obtained by using the learned PDF of \( N_o \). The performance metric used here is PCR as a function of occlusion and clutter rates.

1) Model Set: We consider a model set consisting of three military targets: T72, BMP2 and BTR70. These targets are represented by 231, 233, and 233 views, respectively, at depression angle 17°. Examples of these views along with associated peaks are shown in Figure 2. Each model view is represented by the 30 peaks that are strongest in magnitude of radar returns.

2) Test Sets: We have chosen three sets of test views. The first set, \( \mathcal{S}_1 \), is obtained by introducing synthetic distortion to each model view as follows:

- A randomly-selected subset of \( \mathcal{O} \) features is occluded.
- Occluded features are perturbed, where the uncertainty region, \( R_u(\cdot) \), is chosen to be the four-neighbor region.
- A set of \( C \) spurious features is uniformly added, where the clutter region, \( R_c \), is chosen to be the convex hull of the model features.

The values of \( \mathcal{O} \) and \( C \) are chosen to be the same. The range of these values is \( \{9, 10, \ldots, 20\} \). Notice that since \( \mathcal{O} = C \), the test views have the same number of features as the model ones (30 features). For each \( \mathcal{O}/C \) value, every model view is distorted four times. Accordingly, for a model set of size \( N \) and a specific \( \mathcal{O}/C \) value, the size of the corresponding test subset is \( 4N \). The other two sets involve real distortion. The second set, \( \mathcal{S}_2 \), is a variant of \( \mathcal{S} \) obtained under different configurations (e.g., difference in number of fuel barrels, different flash lights). The third one, \( \mathcal{S}_3 \), is a variant of \( \mathcal{S} \) obtained under a different depression angle (15°, versus 17° for model views). As is the case with model views, each test view is represented by the strongest 30 scattering centers. We assume that \( R_u(\cdot) \)
Table 1. Description of the test sets used in the experiments.

<table>
<thead>
<tr>
<th>Set</th>
<th>Distortion Type</th>
<th>Uncertainty Region</th>
<th>Clutter Region</th>
<th>Occluded/Clutter Features</th>
<th>Size</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\mathcal{S}_1$</td>
<td>synthetic</td>
<td>4-neighbor region</td>
<td>convex hull</td>
<td>9, 10, \ldots, 20</td>
<td>$4 \times 697 \times 12$</td>
</tr>
<tr>
<td>$\mathcal{S}_2$</td>
<td>configuration change</td>
<td>4-neighbor region</td>
<td>convex hull</td>
<td>estimated</td>
<td>464</td>
</tr>
<tr>
<td>$\mathcal{S}_3$</td>
<td>depression-angle change</td>
<td>4-neighbor region</td>
<td>convex hull</td>
<td>estimated</td>
<td>581</td>
</tr>
</tbody>
</table>

and $R_c$ are the same as in the first set. The occlusion and clutter parameters are obtained through finding the best matching model view, as explained in Section 4. These selected sets are summarized in Table 1.

3) Generation of Actual and Predicted Plots: Actual PCR plots are determined using a recognition system that examines all the relevant subspace of the 2-D translation space, for each pair of test and model views (the relevant subspace is the bounding box on the translations that lead to at least a single pair of consistent test and model features). Accordingly, its performance is optimal, for the given vote-based criterion. The predicted PCR plot is obtained as described in Sections 3 and 4. We only consider the exact location of the view to be acceptable; i.e., $\mathcal{T}_{acc} = \{0\}$. In addition, since the shape of $R_c$ in the test sets (the convex hull of model features) is view dependent, we consider the area of $R_c$ to be the average of clutter-region areas of the model views. This average is found to be 532 pixels.

4) Results: We start by presenting the results corresponding to the synthetically-distorted set, $\mathcal{S}_1$. Figure 3 shows the actual PCR plot along with the predicted bounds for $\mathcal{S}_1$. From this figure, we observe that the proposed method succeeds in predicting tight bounds on performance. This is because the assumed distortion models are similar to the actual (synthetic) ones. Next, we compare actual and predicted performance when the assumed distortion models are different from the actual ones. Figures 4(a) and 4(b) show actual PCR plots for sets $\mathcal{S}_2$ and $\mathcal{S}_3$, respectively, along with bounds predicted under the assumption of uniform distortion models. In these figures, we observe that the predicted bounds overestimate performance. This is mainly attributed to ignoring the spatial correlation between occluded features in the interaction between occlusion and similarity. Figures 5(a) and 5(b) show actual PCR plots for sets $\mathcal{S}_2$ and $\mathcal{S}_3$, respectively, along with predicted bounds when using the learned PDF of $N_o$. From these figures, we observe that the predicted bounds become considerably more accurate. This demonstrates the
Figure 3. Actual PCR plot versus predicted lower and upper bounds for set $\mathcal{S}_1$.

Figure 4. Actual PCR versus predicted bounds obtained under the assumption of uniform distortion models: (a) set $\mathcal{S}_2$; (b) set $\mathcal{S}_3$.

significance of the occlusion and similarity factors on performance, and, accordingly, the importance of accurately characterizing them. We also observe that some minor discrepancies remain between the actual PCR plots and the predicted bounds. These discrepancies are expected to be eliminated through: 1) learning of the remaining distortion parameters (in particular, the shape of the clutter region), and 2) development of an upper-bound prediction method that does not rely on a statistical-independence assumption that is used by the current method.$^2$

6. CONCLUSIONS

This paper continues our efforts in the area of ATR performance prediction. Our focus has been on statistical modeling of occlusion and its effect on performance. The difficulty of modeling occlusion is in the need of considering the spatial correlation between occluded features. This is further complicated by the need to analyze the combined effect of occlusion and another spatially-correlated factor, similarity, on performance. This difficulty has been avoided by directly learning the distribution of the parameter which encodes the combined effect of occlusion and similarity on performance. The impact of using this learned distribution on the accuracy of performance prediction has been demonstrated using MSTAR data obtained under different configurations and depression angles.
Figure 5. Actual PCR versus predicted bounds obtained using the learned PDF of \( N_0 \): (a) set \( S_2 \), (b) set \( S_3 \).

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