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Rapid Target Modeling Through Genetic Inheritance Mechanism *Genetically Evolved Target Prototyping (GETP)*

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This report describes a Genetic Evolution Target Prototyping (GETP) methodology for rapid target model development and validation from limited initial sensory and technical data. The Phase I developed methodology generates new target signatures of a given target from an initial signature database by utilizing the power of genetic inheritance. Developed methodology allows for an expansion of the initial signature database and extensive testing of ATR systems over a variety of realistic signatures and situations not seen so far. The methodology utilizes a power of genetic inheritance to generate new signatures of a given target from a limited set of initial signatures. Initial signatures are represented by blob models. They are transformed into a string representation, a representation suitable for the genetic processing. The population of strings obtained from a starting set of signatures is subject to genetic evolution. Crossover and mutation operations are applied during each evolutionary cycle to generate new signatures. New signatures in the population are validated according to closeness to a tuning set of signatures. After a number of evolution cycles, signatures in the current population inherit significant resemblance from the initial and tuning subset of signatures and closely resemble signatures to be interpolated.

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1.0 INTRODUCTION

The objective of this project was to develop a Genetic Evolution Target Prototyping (GETP) methodology for rapid target model development and validation from limited initial sensory and technical data. The Phase I developed methodology generates new target signatures of a given target from an initial signature database by utilizing the power of genetic inheritance. Developed methodology allows for an expansion of the initial signature database and extensive testing of ATR systems over a variety of realistic signatures and situations not seen so far. The methodology utilizes a power of genetic inheritance to generate new signatures of a given target from a limited set of initial signatures. Initial signatures are represented by blob models. They are transformed into a string representation, a representation suitable for the genetic processing. The population of strings obtained from a starting set of signatures is subject to genetic evolution. Crossover and mutation operations are applied during each evolutionary cycle to generate new signatures. New signatures in the population are validated according to closeness to a tuning set of signatures. After a number of evolution cycles, signatures in the current population inherit significant resemblance from the initial and tuning subset of signatures and closely resemble signatures to be interpolated.

This Phase I effort helped to formulate a modified approach which will be presented in the Phase II proposal. During Phase I some concepts developed for target modeling and evolution were tested. It helped to identify missing but required elements of the final approach and provided us with the ability of defining technological limitations and areas of scientific research needed by the Phase II effort. Additionally, contact with potential customer provided valuable help in formulating the requirements for Phase II.

This technology will be extremely applicable to all areas where generation of new realistic entities resembling already existing entities is needed. These areas can range from

the problem of generating new targets to the generation of new scenarios for simulated worlds.

2.0 MOTIVATIONS

Current technology for constructing and validating ground order of battle target models for use in high-frequency, high-resolution, synthetic aperture radar (SAR) template-based and model-based automatic target recognition (ATR) systems is a time consuming, labor intensive process. New, innovative and cost-effective methods for building and validating such models are needed. These methods must radically decrease the amount of time required to create target models and they should incorporate a limited amount of initial realistic data available over the development and validation phases.

3.0 PROJECT OBJECTIVES

There are two major objectives associated with the project as graphically depicted in Figure 1.

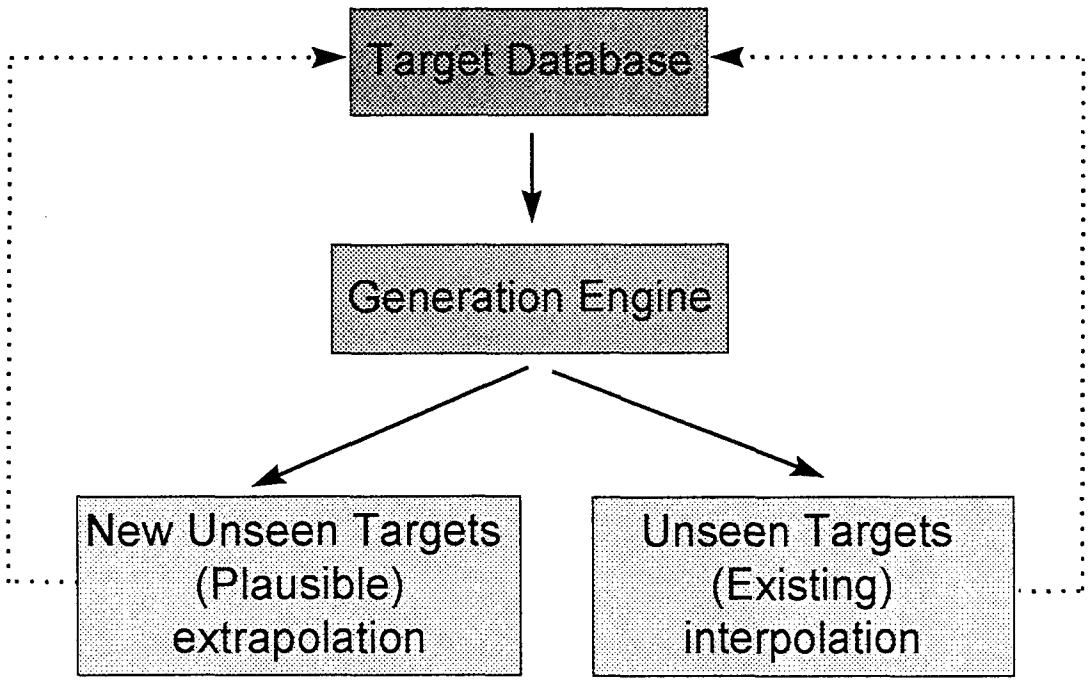


Figure 1. Project Objectives

The first objective is to develop an interpolation technique that generates large number of target signatures in a very close neighborhood of already existing signatures. The new signatures inherit properties and variations from already existing close neighbor signatures.

The second objective is to develop an extrapolation technique that generates new target signatures from a very limited initial database. The generated target signatures are expected to extrapolate the initial database towards a given direction. This extrapolation is executed over unseen poses which are collected to complete the database.

It was decided during the in-progress project review meeting at DARPA on September 25, 1996, that an interpolation technique will be tested and a solution to the extrapolation will be elaborated. At the time of final reporting, however, we were able to achieve more than originally promised. We carried out experiments with two interpolation techniques and an experiment with one extrapolation approach. These testing experiments helped us to validate elements of developed approaches, elaborate final conclusions, and formulate a final approach to be presented in the Phase II proposal. Other objectives of this effort included:

i. Develop a methodology for rapid target generation from limited initial sensory and technical data,
ii. Investigate the application of the methodology to enhance ATR systems,
iii. Demonstrate feasibility of the methodology through experimental validation,
iv. Investigate commercial potentials, and
v. Transition the Phase 1 effort to Phase 2 by working closely with end-users (e.g. Wright Labs, AAC-1)

The concept of interpolating target signatures over a very close neighborhood is shown in Figure 2. Interpolation assumes the availability of several target signatures obtained under a very small change in pose, for example, obtained for every one degree

resolution. A small subset of these signatures is used to generate a large number of new signatures representing possible variations at these poses. New signatures inherit properties from all provided local signatures and are characterized by a high similarity to these existing signatures. Local constraints are preserved. Properties from neighbors are inherited. In addition, perturbations to inherited properties are introduced.

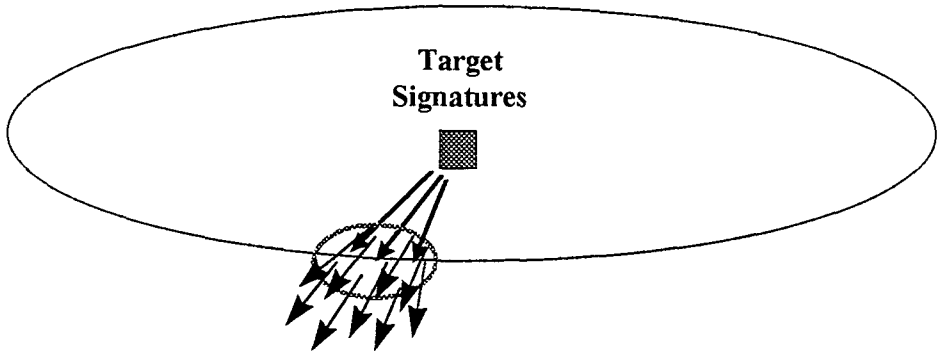


Figure 2. Interpolation of Target Signatures

The concept of extrapolating target signatures from a given single signature towards another (however distant) signature is shown in Figure 3. Extrapolation assumes availability of a very few signatures as an input to the extrapolation process. This process generates new plausible signatures by extending properties of a given single signature toward another distant signature. Resulting new signatures must represent unseen signatures at poses in between.

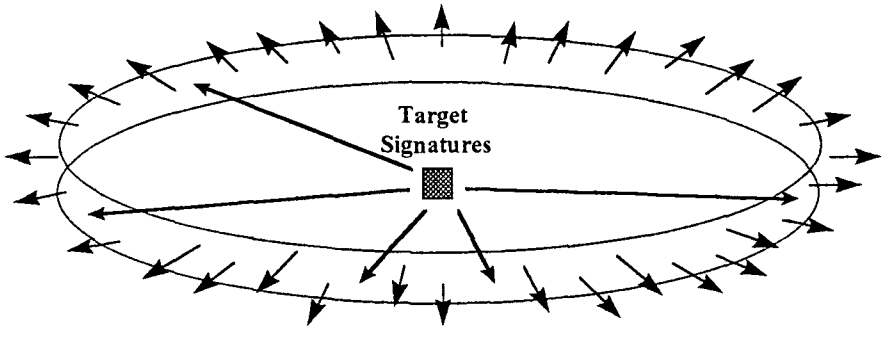


Figure 3. Extrapolation of Target Signatures

Both interpolation and extrapolation concepts can be extended over inheriting articulation properties and inheriting or introducing obscuration properties. This is illustrated in Figure 4. For a given limited number of poses of a target, we assume that available signatures demonstrate articulation changes applied to the target. These input signatures along with the geometrical / functional model of a target are then used to generate a large number of new signatures which extensively share articulation features.

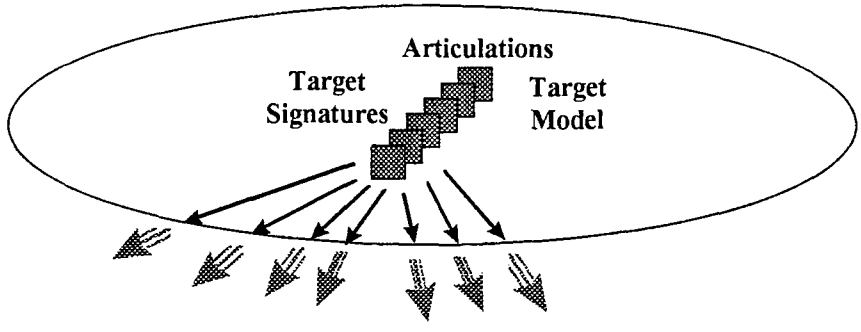


Figure 4. Obscuration of Target Signatures

4.0 APPROACH AND ARCHITECTURE

We have developed a three-step approach for the generation of new target signatures from the existing subset of signatures and from the user defined objectives (interpolation, extrapolation, or articulation). The approach exploits the following three-step procedure arranged into a system as illustrated in Figure 5;

Step 1: Signature Transformation into Blob Representation

Step 2: Blob Based Evolution

Step 3: Signature Synthesis from Blob Representation

In this approach, input real signatures are analyzed and transformed into a higher-level signature model. Model data are then manipulated according to the objectives of interpolation, extrapolation or articulation processes. This manipulation results in a model of a new signature which is next synthesized from fed back model data.

Signature analysis module and signature synthesis module are connected through a database of selected signature sections. These signature sections are generated by the analysis module and used by the synthesis module to reconstruct a new signature. In this way, fragments of raw image data are shared between transformation and synthesis steps, and the structure and parameters of a new signature are generated by the evolution module.

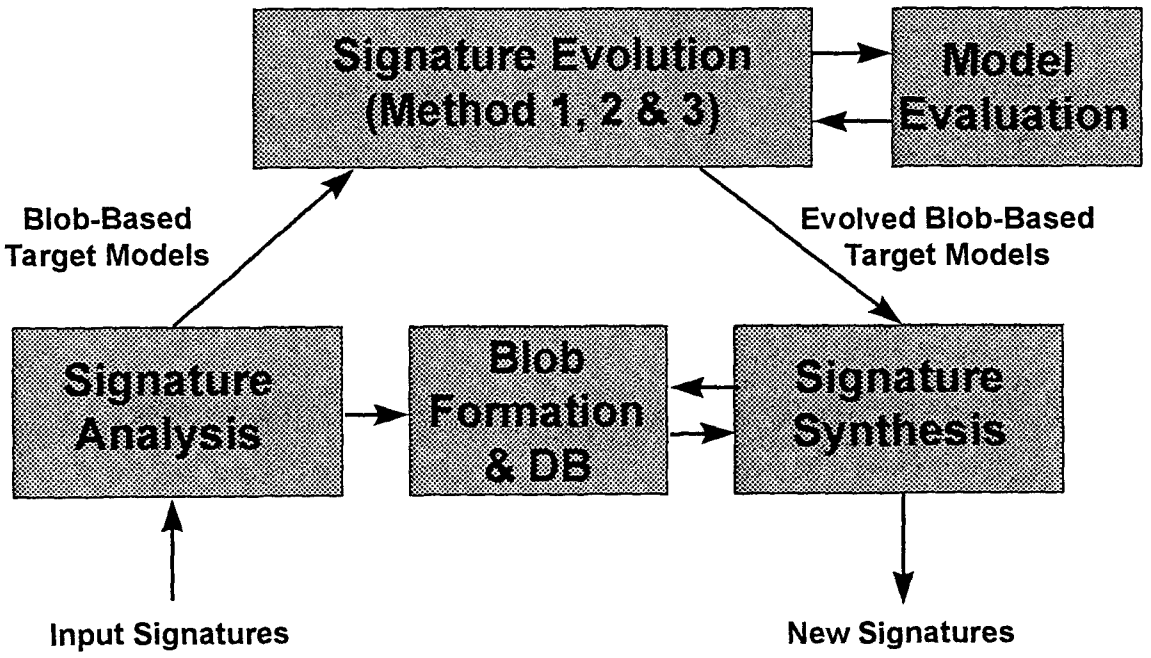


Figure 5. Developed Architecture

4. 1 Signature Analysis

The first step, signature analysis and transformation, aims at the modeling raw signature image data onto a higher abstraction level which could be more suitable for manipulation. At this point, we believe that interpolation or extrapolation processes applied to a higher-level signature representation have a greater chance and flexibility to succeed rather than applied on the row image level.

Signature analysis is focused on the extraction of scattered blobs, distinction of the target area from the background area, formation of a blob graph as the higher-level

signature representation, and formation of blob image sections for cataloging. A blob is defined further as a local energy cluster formed by very few adjacent pixels. Blob center represents local maximum of energy within a given radius.

Processes of signature analysis are shown in Figure 6. Input target signature is processed by the DOG operator (fast approximation of the Laplace operator) to compute energy distribution. Region-of-interest is determined by thresholding the DOG output at zero level. Blob detection is run to determine the center of a blob as a local maximum of the DOG output. Blobs are then extracted from the areas of positive ROI. At the same time, input signature is processed by a RANK filter (similar to the MIT Lincoln Lab filter) which segments the image chip into the target area and the background area. Blobs of target area and blobs of background area are then separated from each other.

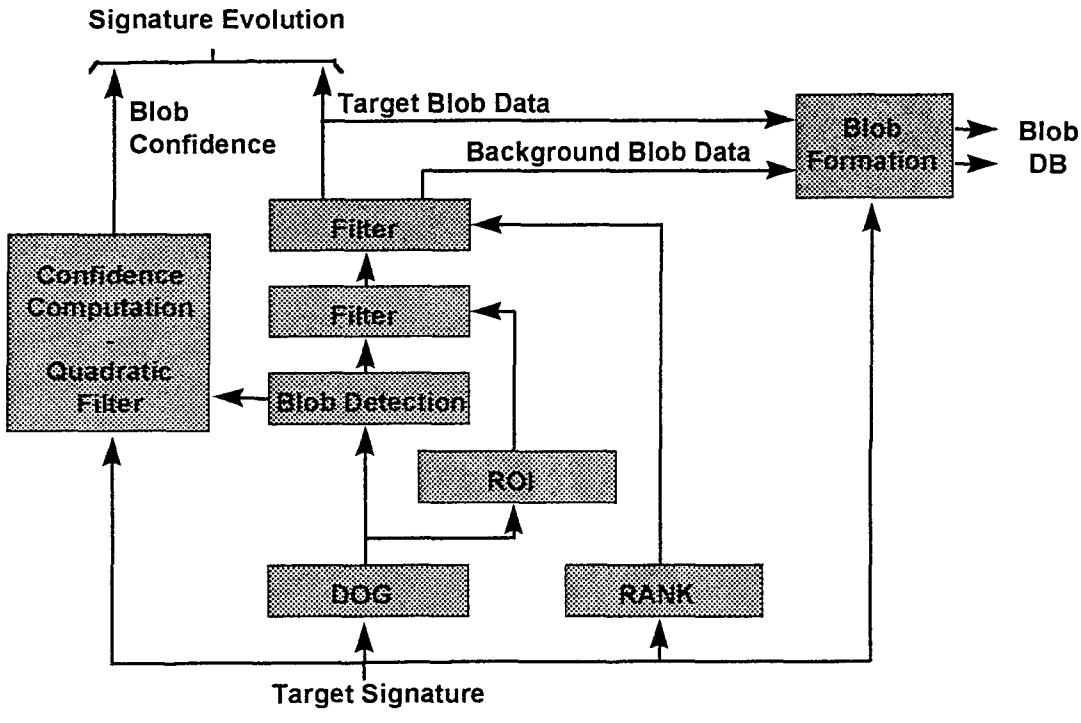


Figure 6. Signature Analysis Process

Intermediate results from the signature analysis are presented in Figure 7. These results were obtained for the relatively large radius of the DOG operator, R=2.4 pixels, which is

appropriate for the target recognition tasks. The large radius captures main energy clusters while the small radius tends to model fine elements of the signature. We later concluded (after final experiments) that for target modeling this radius should be decreased substantially in order to capture fine structures of a signature and improve the quality of the synthesized signature.

The input signature is a HH polarization signature of a T72 tank in 10 degree azimuth. This signature is represented by a 64x32 chip. Results of DOG, RANK and ROI processing are shown for this signature. Resulting blob positions are indicated by "white dots" on the output image. Target blob data is forwarded to the Signature Evolution module (see Figure 6). For each blob position, a corresponding blob window is extracted from the input signature and are provided to the Blob Formation and Data Base module.

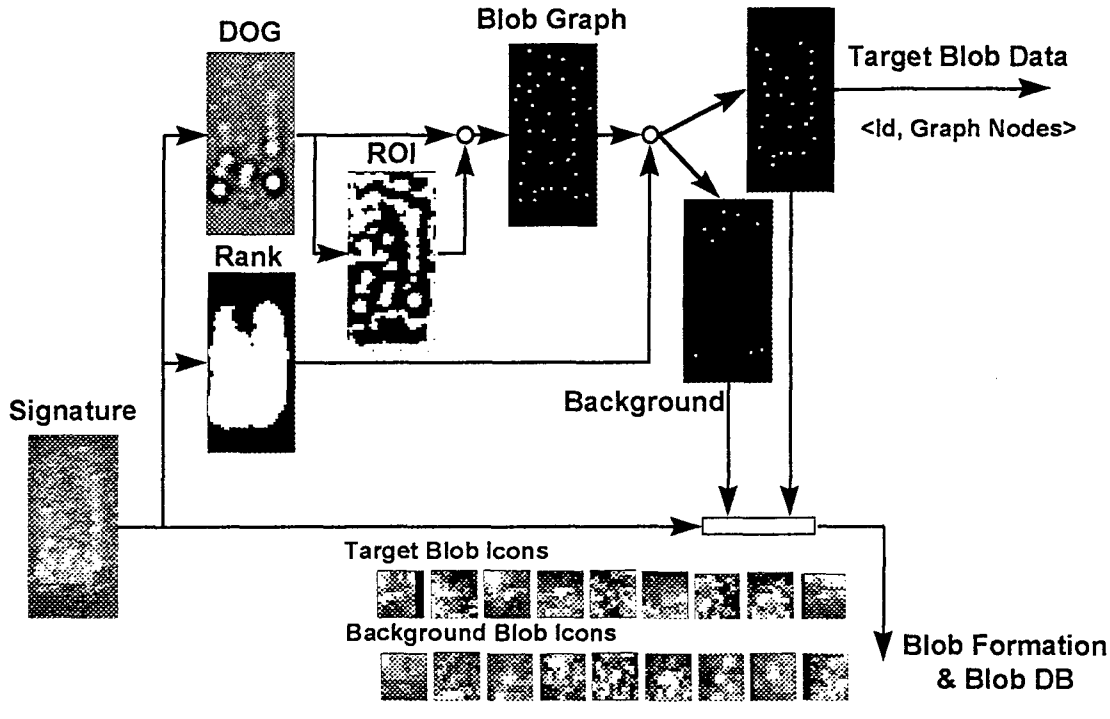


Figure 7. Signature Analysis Image Transformation

Next, a relative confidence of a blob is computed. A single value confidence was used to balance the strength and the spread of a blob. It was achieved by a low pass filtering process. Figure 8 shows the input signature and its cross-section, filter cross-

section, and a resulting confidence image, and its cross-section. Confidence values were scaled to the interval from 0 to 100. A blob with confidence of 100 was allocated as the blob with the maximum function value on a given filtered signature image. Any other blob of the signature had allocated confidence as a percentage of the interval from 0 to this maximum extracted. Blob confidence values were then provided to the Signature Evolution module.

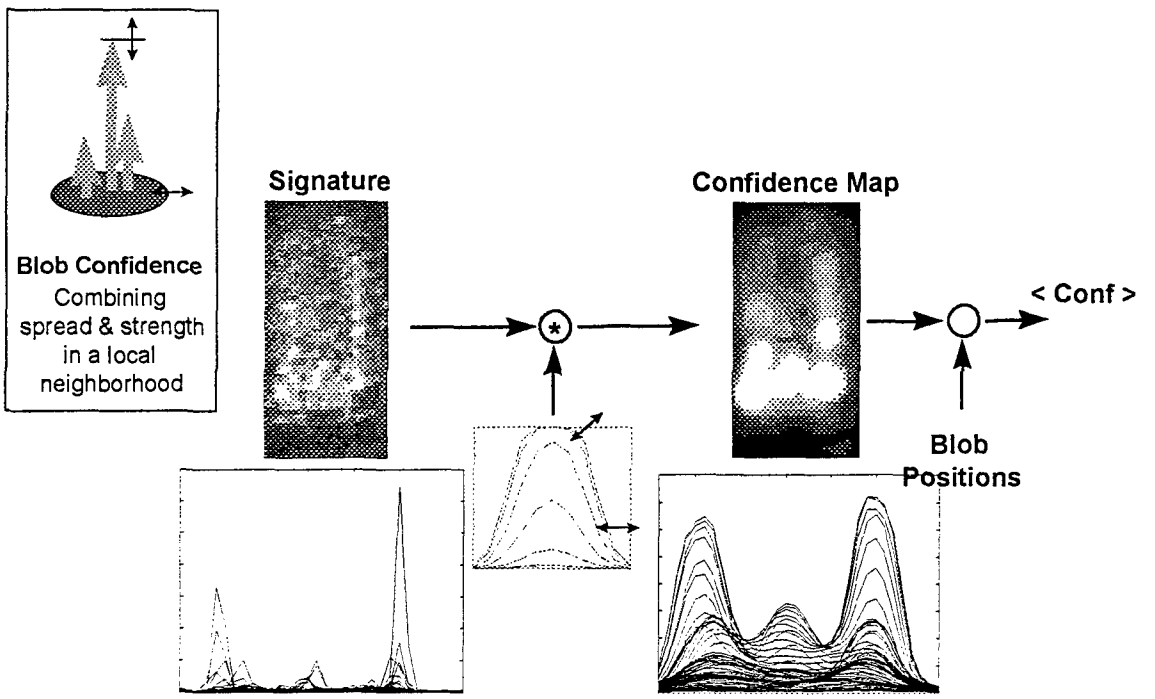


Figure 8. Confidence Computation

4.2 Blob Formation

Blob images extracted by the Signature Analysis module are processed to form a catalog of blobs. The blob formation process aims at the isolation of a single blob (central to the image section) from any other closely positioned blob. In addition, each blob image is normalized to a common reference level. These blob formation processes and resulting blob images are shown in Figure 9.

It is important to notice that example blob sections on the left hand side have other very closely positioned adjacent blobs. The blob formation process was able to reduce

these adjacent blobs as is shown when comparing corresponding left hand side and right hand side blob images. Also, each blob image was normalized to the same average energy unit.

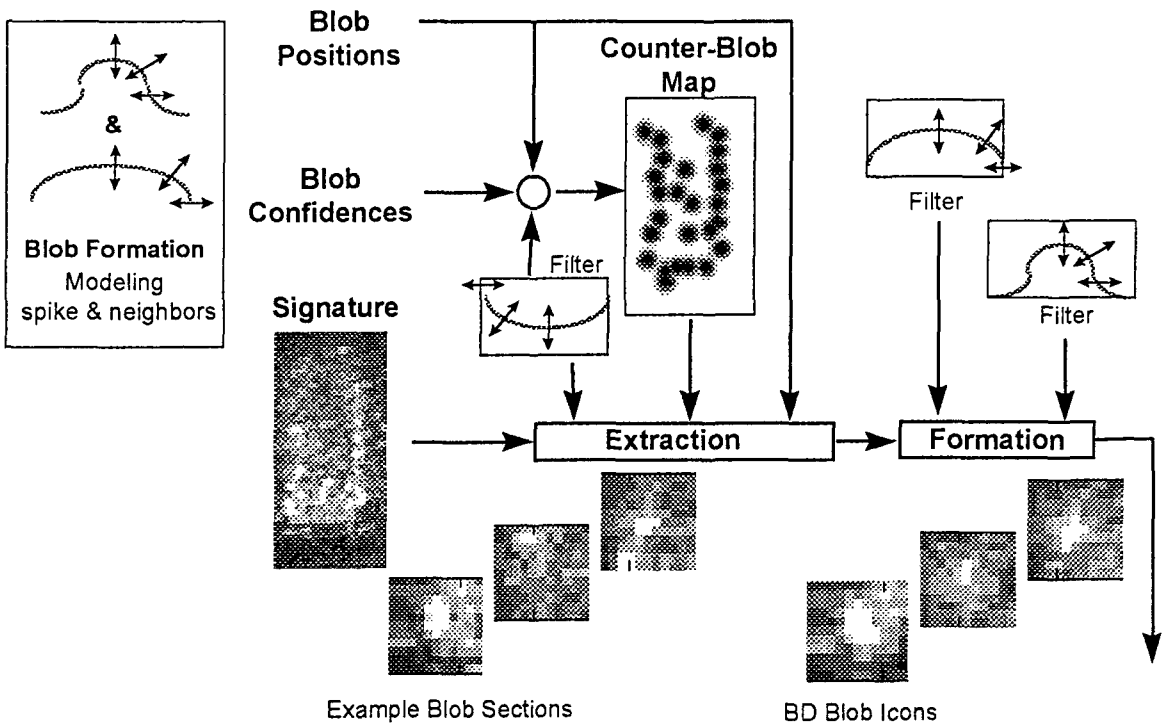


Figure 9. Blob Formation

4.3 Signature Synthesis

This section presents signature synthesis and a demonstration of integrated analysis-synthesis process. An experimental evaluation of the analysis-synthesis part of the system was needed before connecting the Signature Evolution module.

4.3.1 Signature Synthesis Processes

Processes of signature synthesis are presented in Figure 10. Signature synthesis aims at the generation of a new target signature from a given blob model of a target and an image catalog of blobs. Input to the synthesis is determined as a vector of blob identifiers,

positions, and confidence values. There are two phases in signature synthesis; 1) target area synthesis, and 2) background area synthesis.

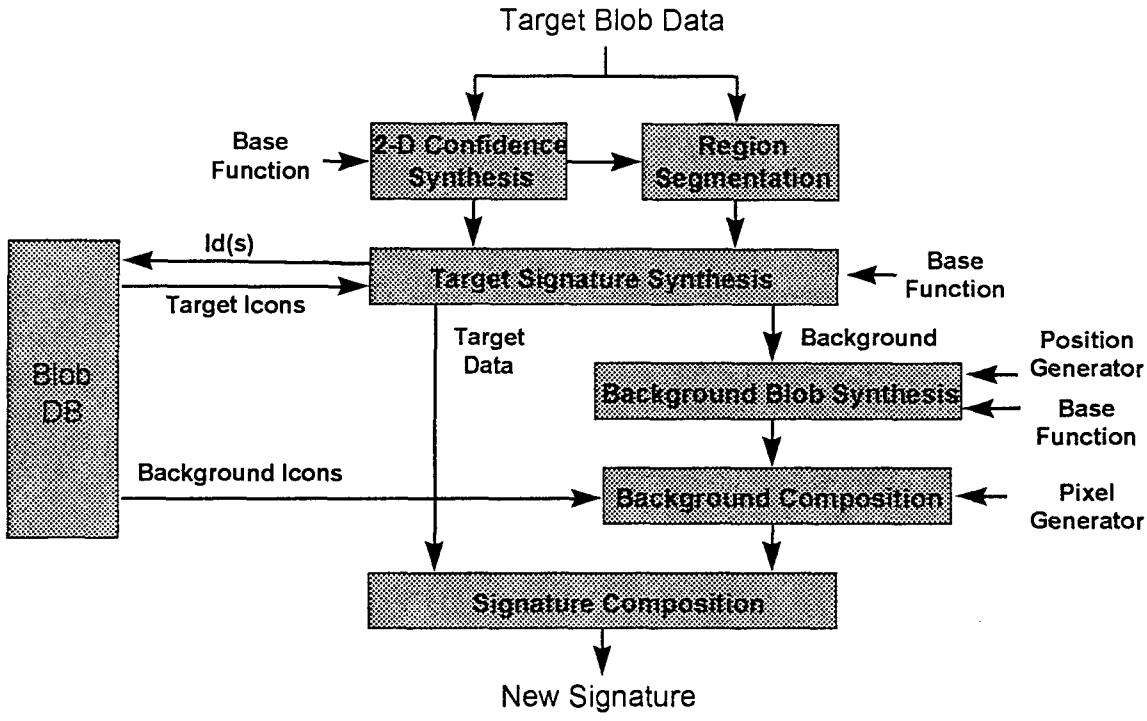


Figure 10. Signature Synthesis

First, a 2-D confidence map is synthesized from provided blob positions and blob confidence values. This map is then segmented onto an image of blob identifiers (see Figure 11). Blob identifiers activate the Data Base to retrieve corresponding blob image sections. Amplitude of each blob image is adjusted by the confidence value, then blob image sections are inserted into a synthetic image.

Second, for remaining unfilled spaces of a new signature, background blob data (identifiers, positions, and confidence values) are generated randomly. Then the same procedure is used to synthesize background blobs. If there are still pixels of undefined value, their value is determined randomly with a given distribution (in our case Gaussian distribution was selected). Finally, a synthetic image is formed as an 64x32 chip.

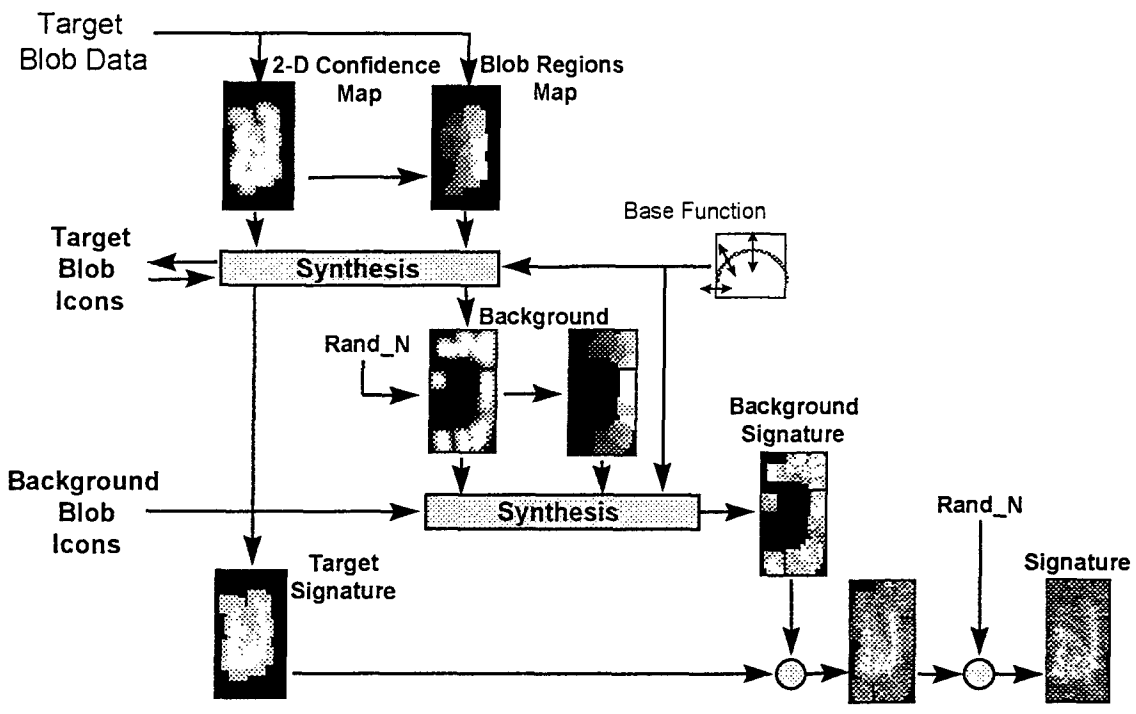


Figure 11. Image Formation During Synthesis Process

4.3.2 Signature Analysis-Synthesis Demonstration

Since signature analysis decomposes a signature and represents it as a model on a higher abstraction level and then signature synthesis transforms the model data back into a new signature, we had to test the composition of both transformations. The experiment was designed to validate both analysis and synthesis schemes and their integration. Architecture for this experiment is shown in Figure 12. The input signature was transformed into the blob model data and forwarded to the signature synthesis without any manipulation of the model. At the same time, blob images extracted by the blob formation module were stored in the Data Base as a catalog of blob images. Model data and the database were used to support signature synthesis to generate a synthetic signature.

Both the input signature and the synthetic signature are shown in Figure 13. Unfortunately, due to the use of a histogram equalization technique there is a slight change in the gray scale of both signatures. We investigated the similarity of signatures by

comparing signature cross-sections. The comparison showed the same cross-section patterns over the target area. The signatures differ, however, over the background area. This is because background is synthesized using randomly generated background data rather than data provided from the input signature. In addition, we observed that in the future the analysis process should apply a DOG operator of a smaller radius value.

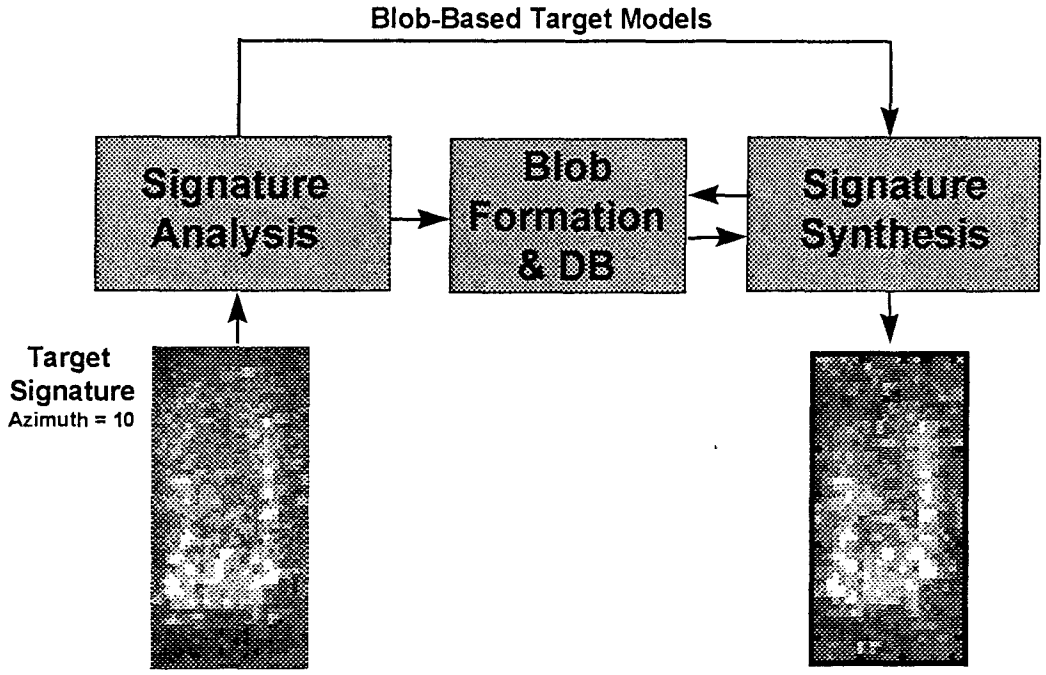


Figure 12. Analysis-Synthesis Demonstration

4.4 Stochastic Evolution

We have developed a stochastic evolution method for signature interpolation. This method aims at the population of a given target signature at a given pose or several signatures over a very small pose interval. This process can generate a huge number of signatures at different levels of confidence. This type of data can then be used by the ATR community to evaluate the sensitivity of the ATR algorithms. Also, this method can be refined and applied during the Phase II research for properties inheritance/sharing between two adjacent signatures.

Application of stochastic evolution is shown in Figure 13. This type of evolution can be applicable for: 1) sharing blobs and/or blob properties between two or more adjacent signatures, 2) modifying blob positions in x-y coordinates, and 3) modifying blob confidences. Stochastic evolution is guided by the underlying distribution, which has been set to the Gaussian distribution for our experiments.

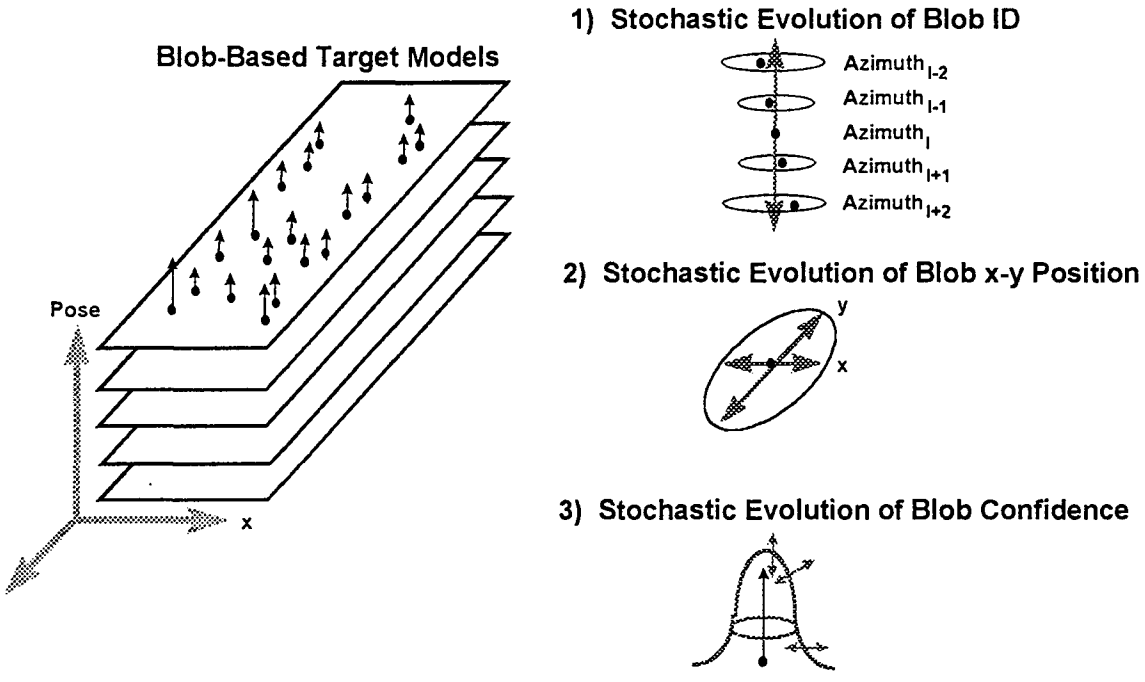


Figure 13. Stochastic Evolution

Experimental results for stochastic distribution were carried out for a single signature and are shown in Figure 14. The degree of blob position and blob confidence adjustment was increased gradually and evaluated on the synthesized images. This type of evolution seems particularly useful for sharing properties between signatures and for introduction of disturbances simulating obscurations and different type of camouflage. Also, since some researchers envisioned SAR phenomenology as somehow related to stochastic processes, it makes sense to consider some elements of this evolution type to be integrated with, for example, traditional linear or polynomial interpolations.

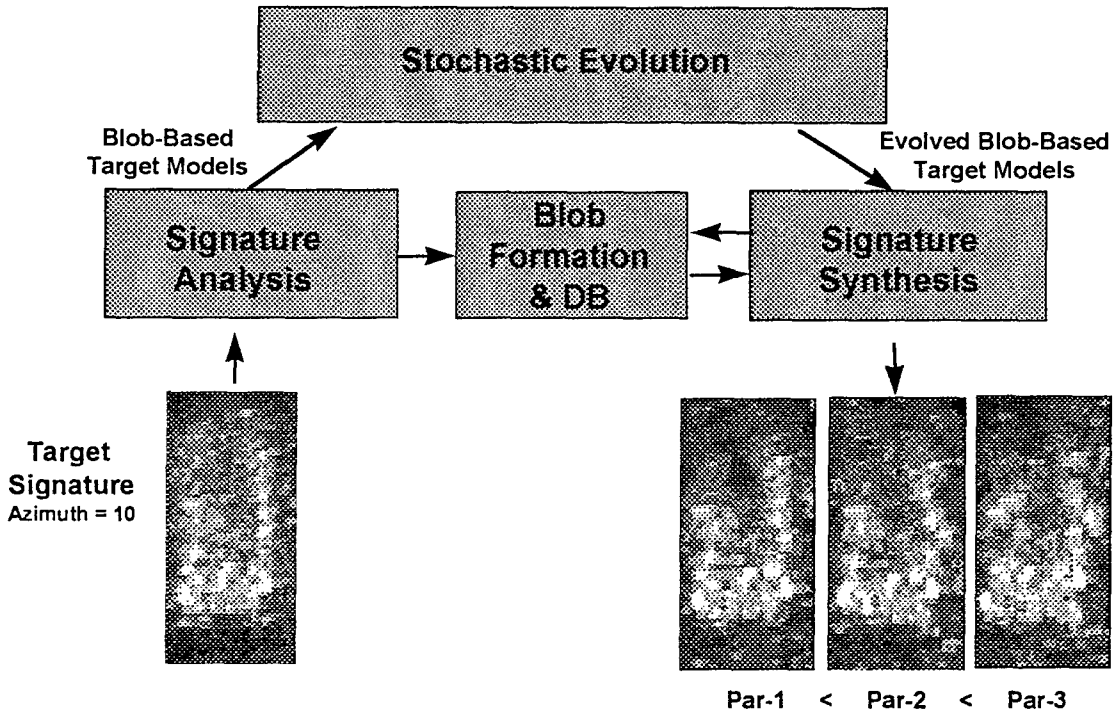


Figure 14. Results of Stochastic Evolution

4.4 Genetic Evolution

In the initial experiments the capabilities of the interpolation process was evaluated. Here, for a given a set of target signatures at a particular change of azimuth it is required to generate new target signatures for different changes in azimuth. For these experiments three sets of data were extracted: training, tuning, and testing. The selected genetic algorithm uses the training data as the initial input to the system. It then uses the tuning data to direct the search towards promising blob graphs. After new blob graphs are generated, the best graph variation is selected as the final result. The testing data is used to evaluate the fitness of the newly generated blob graph. To achieve our goal a suitable representation as well as an adequate evaluation function are required. In these experiments a graph of blobs is represented using a spiral coding. The coding approach and the evaluation function are presented in Sections 4.4.2 and 4.4.3. The next section describes basic ideas behind Genetic Algorithms (GAs) and explains how application of GAs to target signature interpolation are different from traditional GAs.

4.4.1 Genetic Algorithms

GA's are iterative procedures which maintain a "population" of candidate solutions to the objective function f(x):

$$P(t) = \langle x1(t), x2(t), \ldots, xN(t) \rangle$$

Each structure xi in population P is simply a binary string of length L. Generally, each xi represents a vector of parameters to the function f(x), but the semantics associated with the vector is unknown to the GA. During each iteration step, called a "generation", the current population is evaluated, and, on the basis of that evaluation, a new population of candidate solutions is formed.

The initial population P(0) is usually chosen at random. Alternately, the initial population may contain heuristically chosen initial points. In either case, the initial population should contain a wide variety of structures. Each structure in P(0) is then evaluated. For example, if we are trying to minimize a function f, evaluation might consist of computing and storing f(x1), ... , f(xN). The main idea of a Genetic Algorithm is depicted in Figure 15 (a flowchart) and a programming structure below:

```
t <- 0;
initialize P(t); -- P(t) is the population at time t
evaluate P(t);
        while (termination condition not satisfied) do
        begin
                t <- t+1;
                select P(t) from P(t-1);
                recombine P(t);
                evaluate P(t);
        end
```

The structures of the population P(t+1) are chosen from the population P(t) by a randomized "selection procedure" that ensures that the expected number of times a structure is chosen is proportional to that structure's performance, relative to the rest of the population. That is, if xj has twice the average performance of all the structures in P(t), then xj is expected to appear twice in population P(t+1). At the end of the

selection procedure, population P(t+1) contains exact duplicates of the selected structures in population P(t).

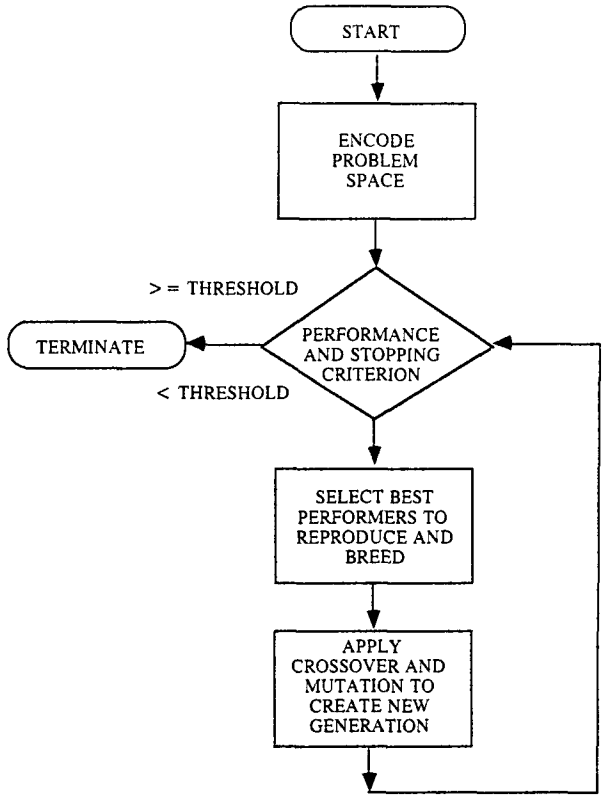


Figure 15. Genetic Algorithms

In order to search other points in the search space, some variation is introduced into the new population by means of idealized "genetic recombination operators." The most important recombination operator is called "crossover". Under the crossover operator, two structures in the new population exchange portions of their binary representation. This can be implemented by choosing a point at random, called the crossover point, and exchanging the segments to the right of this point. For example, let

x1 = 100:01010, and

x2 = 010:10100.

and suppose that the crossover point has been chosen as indicated. The resulting structures would be:

y1 = 100:10100 and

y2 = 010:01010.

Crossover serves two complementary search functions. First, it provides new points for further testing within the schemata already present in the population. In the above example, both x1 and y1 are representatives of the schema 100#####, where the # means "don't care". Thus, by evaluating y1, the GA gathers further information about this schema. Second, crossover introduces representatives of new schemata into the population. In the above example, y2 is a representative of the schema #1001###, which is not represented by either "parent". If this schema represents a high-performance area of the search space, the evaluation of y2 will lead to further exploration in this part of the search space.

Termination may be triggered by finding an acceptable approximate solution to f(x), by fixing the total number of evaluations, or some other application dependent criterion.

The basic concepts of GA's were developed by Holland 1975 [Holland, 1975] and his students [Bethke, 1981; DeJong, 1975; Frantz, 1972; Hollstien, 1971]. Theoretical considerations concerning the allocation of trials to schemata [DeJong, 1975; Holland, 1975] show that genetic techniques provide a near-optimal heuristic for information gathering in complex search spaces. A number of experimental studies [references] have shown that GA's exhibit impressive efficiency in practice. While classical gradient search techniques are more efficient for problems which satisfy tight constraints (e.g., continuity, low-dimensionality, unimodality, etc.), GA's consistently outperform both gradient techniques and various forms of random search on more difficult (and more common) problems, such as optimizations involving discontinuous, noisy, high-dimensional, and multimodal objective functions. GA's have been applied to various domains, including numerical function optimization [Bethke, 1981; Brindle, 1981], adaptive control system design [DeJong, 1980], and artificial intelligence task domains [Smith, 1983].

In this project GAs search approach is applied in a different way than in traditional GAs applications. Specifically, GAs search mechanism is not used to find the best individual by converging the fitness evaluation function. In addition, the initial population is not started randomly. In this project GAs search is used to shift initial population towards tuning set of individuals. For experiments with target signatures the initial population represents a set of targets with some aspect range. The tuning set represents another set of targets with different aspect range. The aspect distance between the closest targets in both sets defines range for the missing aspects. By genetically shifting the initial population from one set to another the bet performing target in the current population is traversing missing target aspects space. This different employment of GAs is illustrated in Figure 16.

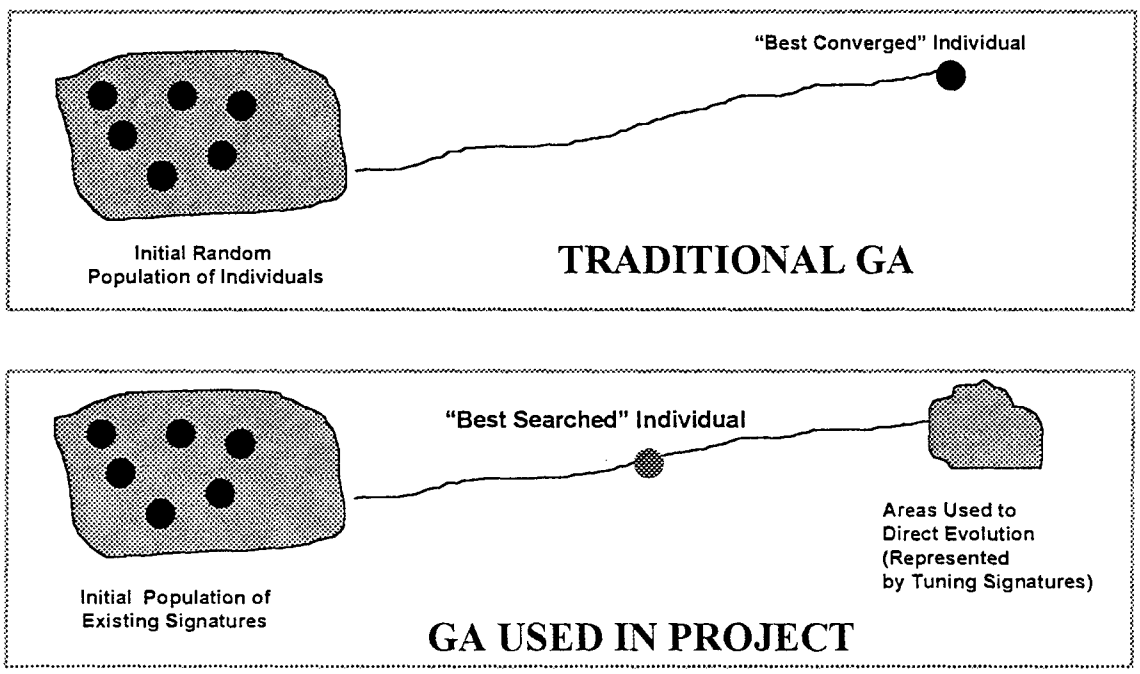


Figure 16. Genetic Algorithms Approach Used for Interpolation

The top level view of the genetic is depicted in Figure 17. The next sections describe the genetic encoding schema and the evaluation function.

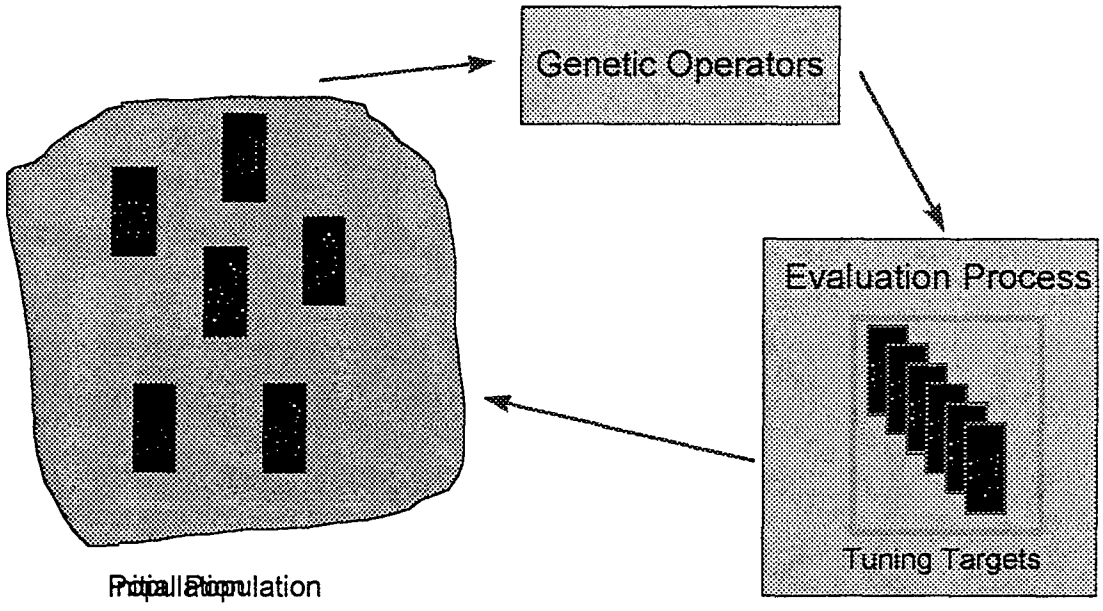
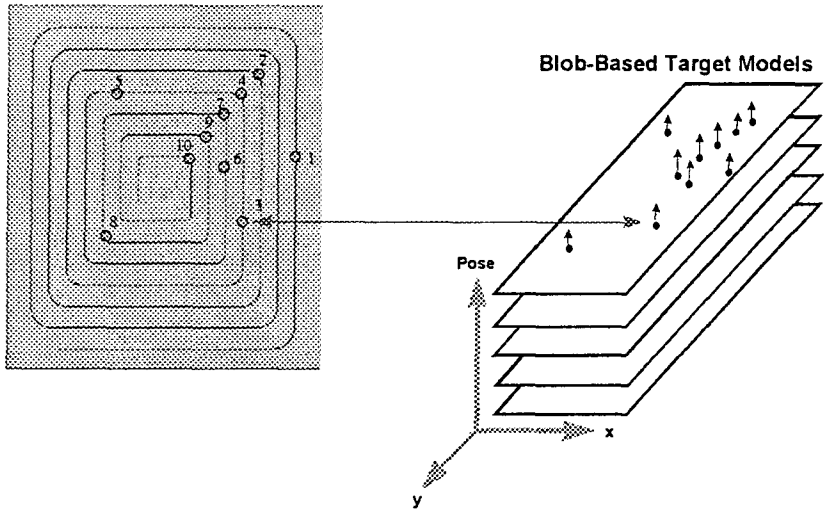


Figure 17. Genetic Evolution of Blob Representations

4.4.2 Genetic Encoding Technique

The target signature encoding/decoding used to represent targets consists of an ordered list of fields together with the look-up tables which indicate how bit strings are to be decoded to produce information about a given target. Figure 18 illustrates the encoding schema. Blobs are mapped to the string representation (i.e. a natural representation for GAs) through the spiral unwinding mechanism. The mechanism allows capturing the spatial distribution of blobs in the string representation. The one hand side of the string represents blobs closer to the center of the target, whereas other side represents blobs at the target peripherals. The spiral encoding is less disruptive for the crossover operation (Figure 19). Each blob encoding consists of fields that describe its x/y position, aspect of the signature that a given blob is part of, confidence, and presence or absence of blob. The presence/absence one bit field is used in order to maintain the constant string length for all target signatures being manipulated by GAs.



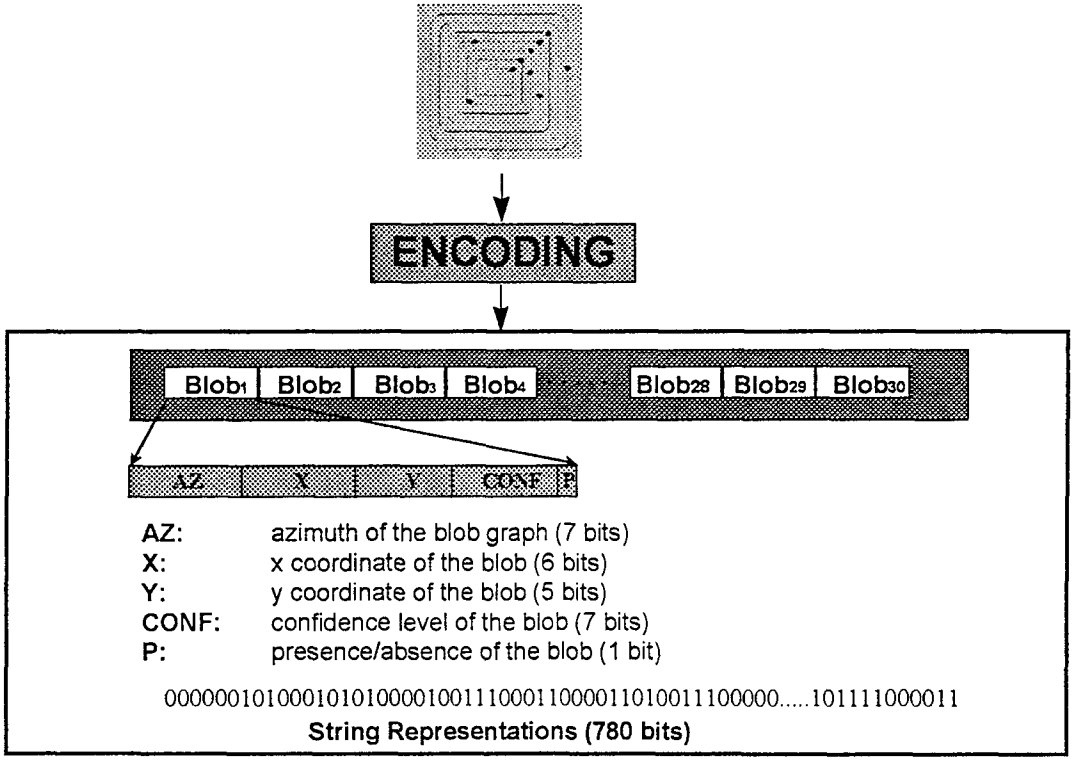


Figure 18. Encoding Schema

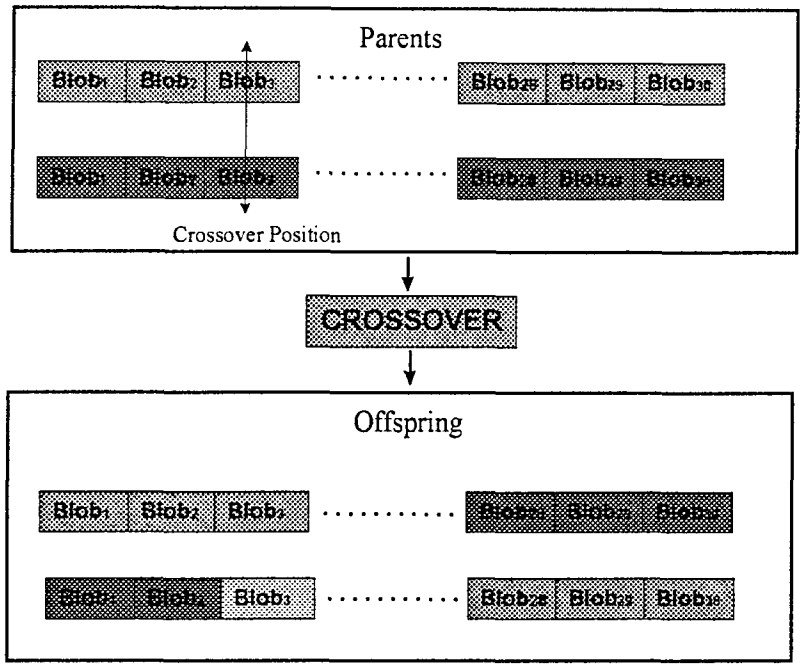


Figure 19. Crossover Operation

4.4.3 Evaluation Function

An evaluation function is used to determine fitness of each target signature in the population. Each individual in the current population is match to all tuning signatures. The best match is the value of the evaluation function. The match of the evaluated signature to the tuning signatures is expressed by three components illustrated in Figure 20. The following components are used:

i. Difference
ii. Misalignment
iii. Adjacency
iv. Consonance

These components are expressed as the integer values and the sum of these values is used as the match of the individual signature to the tuning signature. To compute fitness measure of the individual the match of this individual to all tuning signatures is computed. The smallest value, or the closest match, is used as the fitness measure.

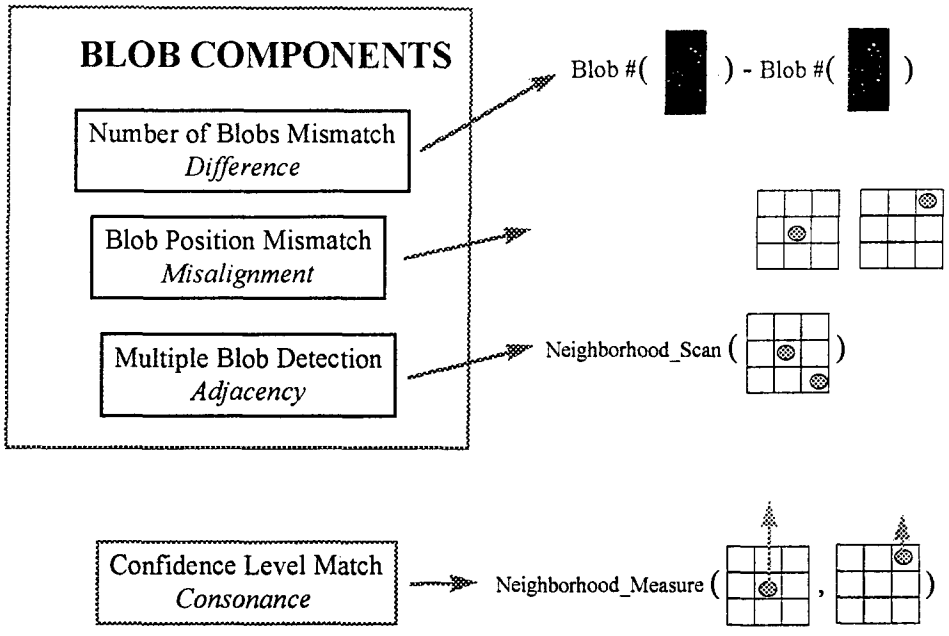


Figure 20. Fitness Measure Components

5.0 EXPERIMENTS

Two experimental studies have been performed. The objective of the first one was to interpolate missing aspects (represented by the green color lines in Figure 21a) among given interlacing aspects.

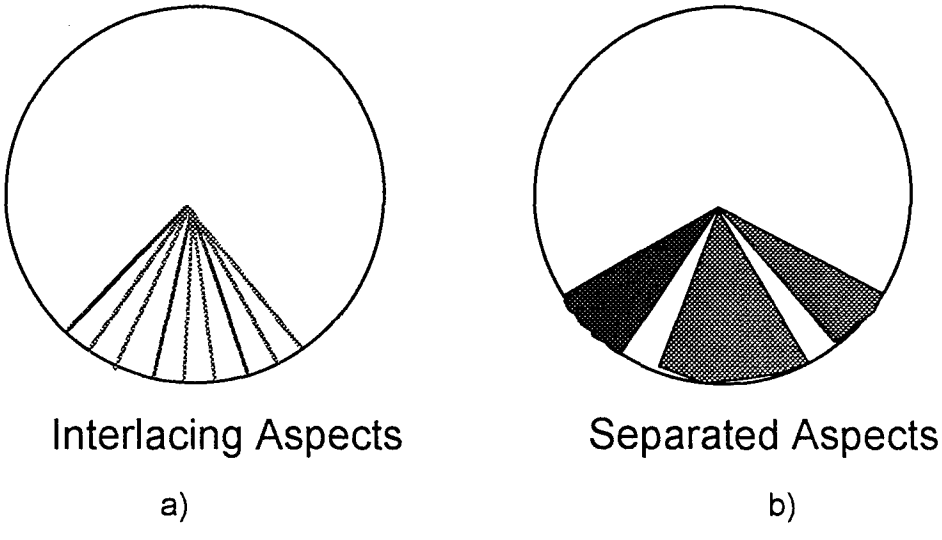


Figure 21. Experimental Setup For Target Aspect Data

The objective of the second experimental study was to interpolate missing aspects (represented by the green color lines in Figure 21b) between two separated aspect ranges (i.e. training aspects represented by blue color and tuning aspects represented by red color). Figure 22 illustrates the results of one experiment obtained during the first experimental study where couple of best matches have been evolved. The target signature with azimuth 27 degree was the best match when compared with testing aspect target signatures. The match value was computed using the evaluation function described in Section 4.3.2.

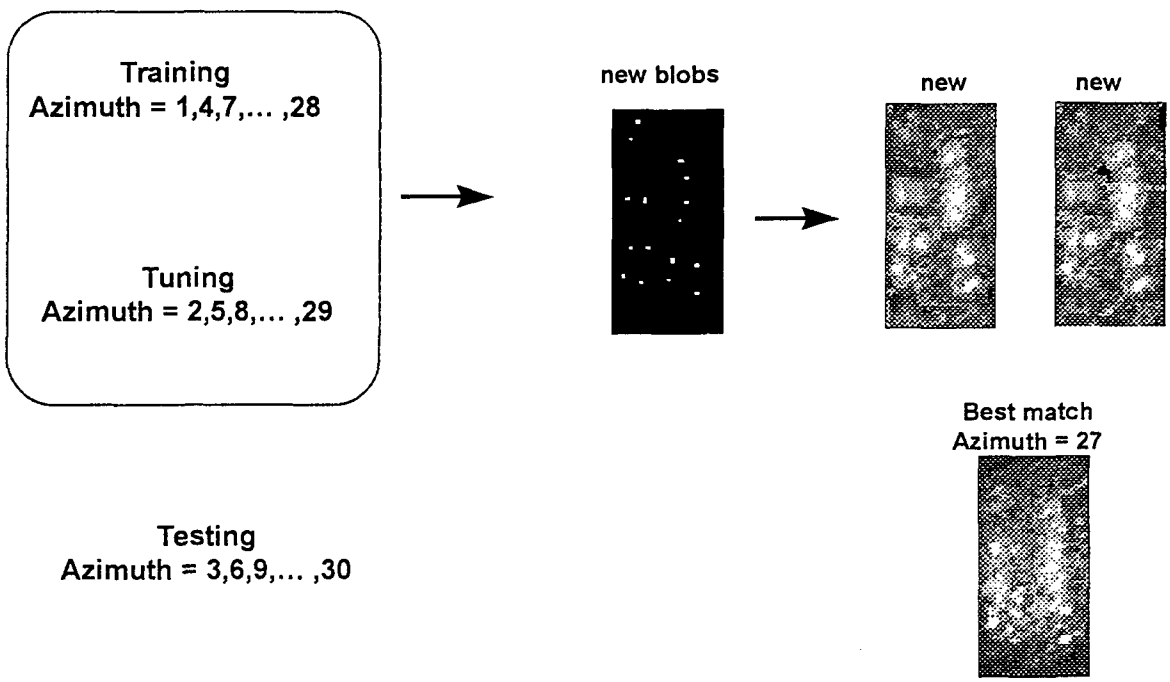


Figure 22. Result of Interlacing Aspects Experiment

Figure 23 illustrates results of one experiment obtained during the second experimental study. Similarly, as in the first experimental study, the match value was computed using the evaluation function described in Section 4.3.2. The target signature with azimuth 25 degrees was the best match when compared with testing aspect target signatures. When the newly generated target signature was compared with all training and tuning target signatures, it was verified that the best match is still the azimuth 25 degree target signature.

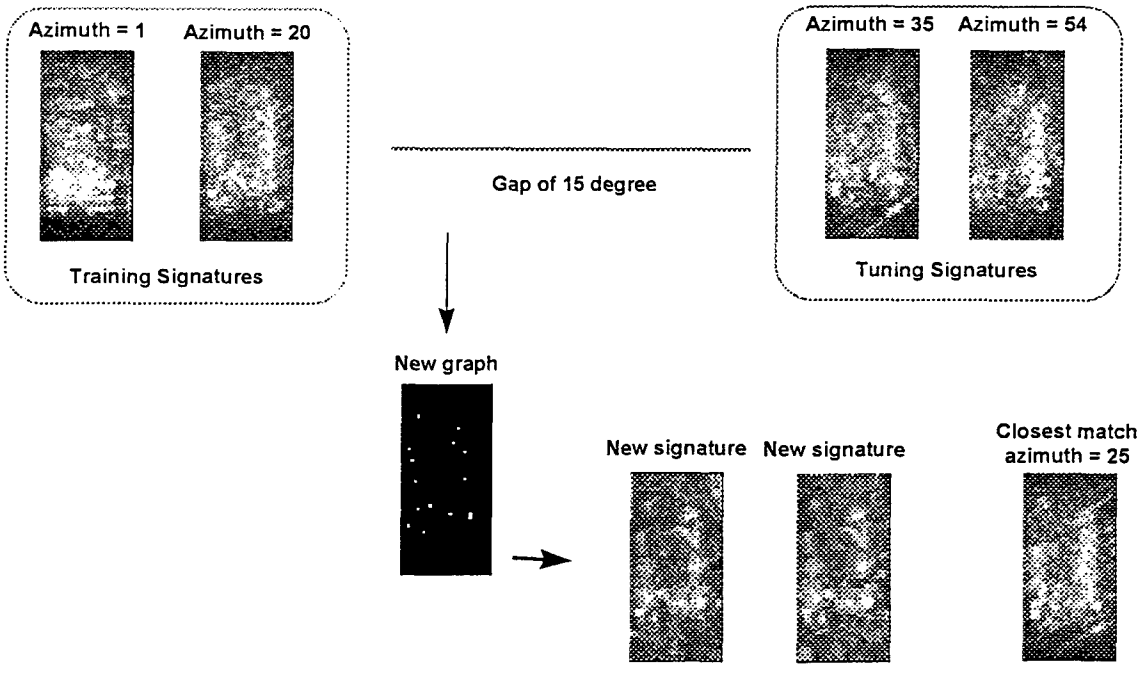


Figure 23. Results of Separated Aspects Experiment

6.0 CONCLUSIONS AND PHASE 2 OBJECTIVES

The following two main conclusions have been reached after the completion of Phase I:

i. Experimental results of the applicability of the Genetic Algorithms based SAR target signatures generation have been demonstrated to positively show feasibility of the approach on difficult problems involving interpolation of target aspects,

ii. For the future work it is necessary to develop a hybrid extrapolation technique which would work for wider interval of azimuth value.

At the end of Phase II a full scale simulation software package for the MSTAR ATR community will be developed. The software will be an integral part of the KHOROS environment and will use software procedures developed by the other groups working

under the MSTAR Program. The following are requirements for the Phase II research and software system:

i. Generate synthetic signatures with an estimated one degree resolution in azimuth from the user provided real data of six degree resolution in azimuth for several target classes,

ii. Develop quality evaluation methodology and software in order to validate synthetic signatures,

iii. Develop a theoretical approach to validate applied interpolation techniques and to estimate the error introduced by interpolation techniques,

iv. Apply principles of electromagnetic phenomenology to model scatters over the interpolation space,

v. Investigate and integrate different approaches to signature synthesis such as linear and polynomial interpolations, use of a geometric model for interpolation, stochastic property sharing, and genetic operators for property and data inheritance,

vi. Estimate and validate the pose for each generated synthetic signature,

vii. Estimate a base-line quality reference which can serve for the interpretation and validation of the results,

viii. Investigate the extension of the initial six degree resolution for the initial data base toward lower resolutions,

ix. Investigate how far the interpolation potential can be extended (i.e. interpolation break-point determination),

x. Investigate the applicability of the developed approach for target signature extrapolation,

xi. Compare results against current interpolation approaches, and

xii. Determine the ability of the algorithm to handle resolution cell migration.

Experimenting with different types of signature evolution, we recognize that an extrapolation of a signature towards another signature and over a larger interval of azimuth must be associated with geometric modeling of a target. We propose an approach which will exploit geometric elements of a target by aligning blobs extracted from the signature to geometric elements of the target. This concept is briefly illustrated in Figure 24 where blob data grouped into target geometric/functional elements is then a subject of evolution. It means that the evolution is localized rather than global as in the Phase I experiments. This will further improve the quality of synthetic signature.

A proposed hybrid approach to the interpolation and extrapolation will be presented in the Phase II proposal. It will involve an integration of blob extraction, blob modeling, interpolation of blob electromagnetic characteristics, interpolation of blob positioning, interpolation techniques, geometric and functional modeling.

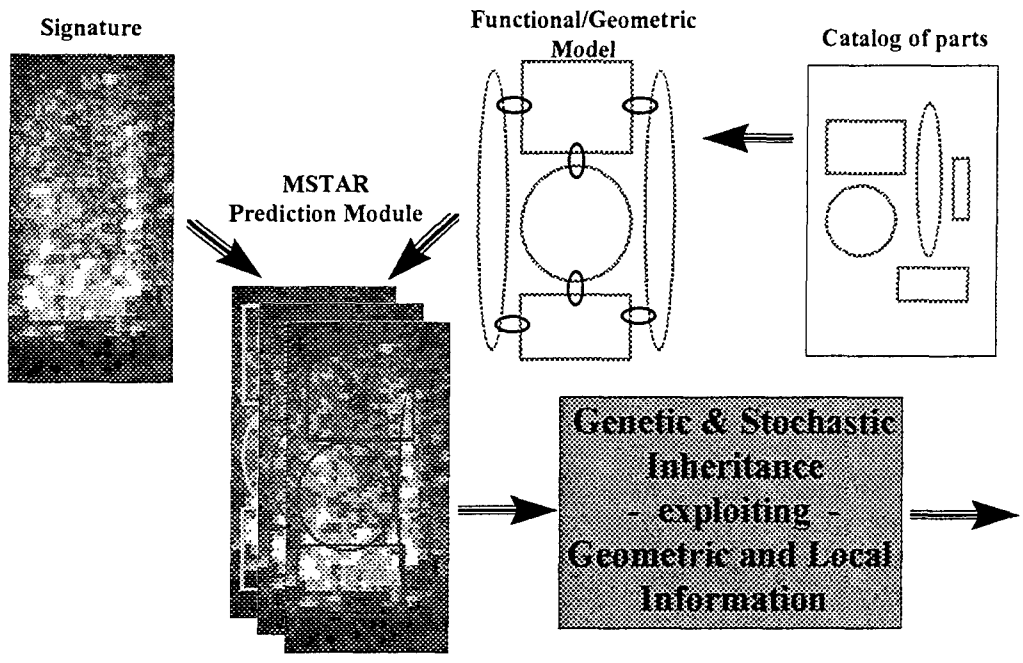


Figure 24. Hybrid Approach

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