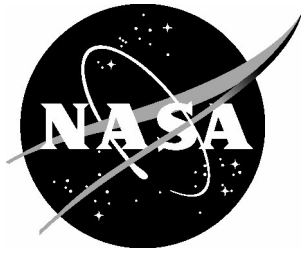NASA/CR-2004-212669

A Novel, Real-Valued Genetic Algorithm for Optimizing Radar Absorbing Materials

John Michael Hall
Lockheed Martin Space Operations, Hampton, Virginia

March 2004

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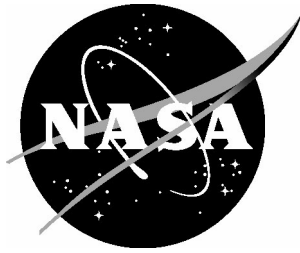
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Contents

Abstract

A novel, real-valued Genetic Algorithm (GA) was designed and implemented to minimize the reflectivity and/or transmissivity of an arbitrary number of homogeneous, lossy dielectric or magnetic layers of arbitrary thickness positioned at either the center of an infinitely long rectangular waveguide, or adjacent to the perfectly conducting backplate of a semi-infinite, shorted-out rectangular waveguide. Input is specified as the number of layers, their locations and thicknesses, the frequency band of interest, and the upper and lower bounds on the physioelectric constants to be obtained. Scattering is then minimized over the frequency band of interest using optimization strategies based upon principles of Artificial Intelligence (AI). Evolutionary processes extract the optimal physioelectric constants falling within specified constraints which minimize reflection and/or transmission over the frequency band of interest. Output in the form of the physiolectric constants of the layers and the scattering parameters of the entire stack is provided. This GA extracted the unphysical dielectric and magnetic constants of three layers of fictitious material placed adjacent to the conducting backplate of a shorted-out waveguide such that the reflectivity of the configuration was –55 dB or less over the entire X-band. This numeric Absorbing Boundary Condition (ABC) was validated by showing that the reflectivity of test cases backed with the ABC was identical to the reflectivity of those test cases backed by free space, to within 0.23% relative difference. This ABC could be used to numerically truncate open-region boundaries in Finite Element (FEM) waveguide problems, thereby eliminating the need to use the Method of Moments (MoM). Although this GA was specifically designed for creating "fictitious absorber" type ABCs to truncate FEM meshes, it can also be used to design real Radar Absorbing Materials (RAM). Examples of the optimization of realistic multi-layer absorbers will also be reported. Although typical Genetic Algorithms require populations of many thousands in order to function properly and obtain correct results, verified correct results were obtained for all test cases using this GA with a population of only four.

I. Introduction -

Artificial Intelligence (AI) is the study of computations which make it possible to perceive, reason, and act. Although the scientific goal of AI is to understand various sorts of natural intelligence, the engineering goal is to solve real-world problems. Since the inception of automated computation, conventional wisdom has held that computers can only do what they are told to do, and nothing more. However, contemporary applications of AI demonstrate that under certain circumstances, computers can acquire the ability to solve ambiguous problems which programmers generally have no clue how to solve, through the modeling of biological cognition and natural selection processes. The application of AI to real-world problems provides an ingenious avenue for technological advancement, which through its application sheds new light on questions traditionally asked by psychologists, linguists, and philosophers. The answers to these questions may help *us* become more intelligent, ourselves.

In his magnum opus, "The Origin of the Species" [1], Charles Darwin described the *principle of evolution through natural selection*, which after much heated debate, became generally accepted among scientists. Darwin's principle states that:

➢ Each individual tends to pass on its traits to its offspring.

➢ Nevertheless, nature produces individuals with differing traits.

➢ The fittest individuals – those with more favorable traits – tend to have more offspring than do those with unfavorable traits, thus driving the population as a whole toward favorable traits.

➢ Over long periods, variation can accumulate, producing entirely new species whose traits make them especially suited to particular ecological niches.

From a molecular-biological standpoint, Darwin's natural selection is enabled by variation in the species arising from *mutation*, which produces new genes previously unseen in the population, and *crossover*, which is the random recombination of genetic material that occurs during reproduction.

According to Darwin, successful evolutionary processes are neither purposeful nor directed. They require no foreknowledge of their final destination in order to eventually get there. For example, there is no scientific evidence to support the assertion that the purpose of evolution in nature is to produce Humankind. Instead, the success of the process seems to boil

down to a handful of simple principles operating in the context of individuals competing for resources in their environment. This unique capacity for improvement without foreknowledge of the eventual result offers a powerful way to solve ambiguous problems which may be otherwise insoluble using canonical formalism.

The Genetic Algorithm (GA), first introduced by John Holland in 1975 [2], is a model of machine learning which derives its behavior from a metaphor of evolution in Nature. Genetic Algorithms are used for a number of different applications, including multidimensional optimization problems where each chromosome in the population is a vector of numeric values which encodes the different parameters being optimized. The machine creates an initially random population of individuals represented by these chromosomes, and then subjects those individuals to selection pressure within an evolutionary simulation.

A GA is generally implemented using the following basic cycle of operations [3]:

➢ Evaluate the fitness of all individuals within the population.
➢ Individuals not meeting or exceeding the extinction criterion die; only the fittest survive. The empty spaces leave room for progeny.
➢ Create new progeny to replace extinguished individuals through fitness-proportionate reproduction (and subsequent genetic recombination) of the survivors.
➢ Account for the possibility of mutation (i.e., random environmental perturbations of chromosomal values) in the progeny who were just created.
➢ Repeat using the new population. Each iteration is known as a *generation*.

A more detailed flowchart illustrating the sequence of operations implemented in *this* GA is provided in the Appendix to this report, with each step explained sequentially in the text. Although simplistic from a biologist's viewpoint, these algorithms are sufficiently complex to provide robust and powerful mechanisms for adaptive search.

II. The Problem -

Consider a finite number of lossy magnetic and/or dielectric layers stacked at the center of an infinite rectangular waveguide, as shown in Fig. 1, or stacked against the metallic backplate of a shorted-out, semi-infinite waveguide, as shown in Fig. 2. Each layer is homogeneous, and will be characterized by its thickness, location, complex relative dielectric permittivity $\varepsilon_r = \varepsilon' - j \cdot \varepsilon''$, and complex relative magnetic permeability $\mu_r = \mu' - j \cdot \mu''$.
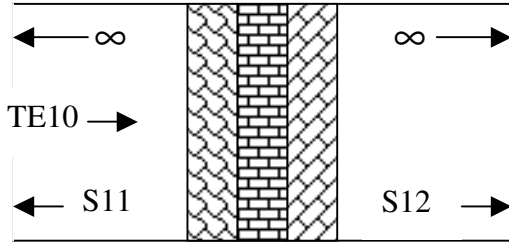
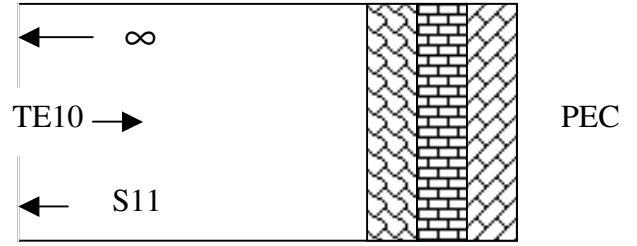Fig. 1. Problem geometry for the infinite rectangular waveguide.

Fig. 2. Problem geometry for the shorted-out waveguide.

Although any of a number of geometries could have been analyzed, the specific optimization task described in this report required extraction of the complex dielectric and magnetic constants for three layers of "fictitious" material placed adjacent to the metallic backplate of a semi-infinite, shorted-out waveguide such that the reflectivity would approach zero as closely as possible under the following condition:

➤ Each of the three layers should have a thickness of 1 mm.
➤ The waveguide should have a width of 2.29 cm and a height of 1.02 cm.
➤ Reflectivity should minimize over the entire X-band (from 8.2 to 12.4 Ghz).

These layers were intended for use as a numeric Absorbing Boundary Condition (ABC) for truncating Finite Element (FEM) meshes at open-region boundaries in waveguide problems, thereby providing an alternative to using the computationally expensive Method of Moments (MoM) for such truncation. The type of ABC sought here is referred to as "fictitious" because the complex physioelectric constants of the layers are allowed to take on unphysical values.

III. The Chromosomal Representation -

In a Genetic Algorithm, each individual within the population represents a test solution encoded as a vector of numeric values. Binary representations were used by Holland in the very first applications [1] and remain popular to this day; however, an important paper written by Jim Antonisse in 1989 [4] corrects the long-standing supposition that binary representations are the best. At the very least, there is no penalty incurred for using real values, and real-valued encoding is attractive because it eliminates the computational penalties incurred by translating test solutions into and out of binary format, therefore this GA was designed to use vectors of real values for encoding test solutions.

Extraction of the optimal dielectric and magnetic constants for multiple layers of material naturally requires that those quantities be allowed to vary during the optimization. Each complex constant is composed of a real part and an imaginary part, therefore there are two numeric variables for each complex constant, and four such variables for each material layer. In general, if there are N layers of material, there will be a total of 4N numeric values which must be encoded and optimized. In the evolutionary simulation, each of these 4N values is represented as a *gene*, or trait-determining factor. The concatenated numeric array of all genes composing a unique test solution constitutes a *chromosome*. The chromosome is a representation which determines the overall fitness of an individual, as evaluated by some sort of mechanism that uses the chromosome's genes as a blueprint. Strictly speaking, a chromosome is not associated with quality. A chromosome represents an *individual* (test solution) that is associated with quality. However, the characteristics of individuals are so tightly bound to their chromosomes that the two terms will be used interchangeably in this paper, even though it is really individuals that constitute the population.

Fig. 3 shows the real-valued chromosomal representation for three layers of lossy magneto-dielectric material, and locations of the specific information encoded within that representation. The chromosomes used in this GA are *haploid*, because they do not exhibit the gene pairing which is observed in higher-order *(diploid)* biological organisms.

$$\varepsilon_{1r} = \varepsilon_1' - j \cdot \varepsilon_1'' \qquad \mu_{1r} = \mu_1' - j \cdot \mu_1''$$

$$\varepsilon_{2r} = \varepsilon_2' - j \cdot \varepsilon_2'' \qquad \mu_{2r} = \mu_2' - j \cdot \mu_2''$$

$$\varepsilon_{3r} = \varepsilon_3' - j \cdot \varepsilon_3'' \qquad \mu_{3r} = \mu_3' - j \cdot \mu_3''$$

$$\Downarrow$$

$$\boxed{\varepsilon_1' \mid \varepsilon_1'' \mid \mu_1' \mid \mu_1'' \mid \varepsilon_2' \mid \varepsilon_2'' \mid \mu_2' \mid \mu_2'' \mid \varepsilon_3' \mid \varepsilon_3'' \mid \mu_3' \mid \mu_3''}$$

Fig. 3. The complex dielectric and magnetic constants for three layers of material encoded into a real-based, haploid chromosome.

IV. The Genesis Population -

This GA operates using a fixed population size specified by keyboard input. If the population is too small, individuals will soon develop identical traits, and genetic recombination will become ineffectual. If the population is too large, computation time will be excessive. In most Genetic Algorithms, the population size is chosen to be quite large, sometimes requiring many thousands of individuals to prevent genetic stagnation. The conventional need to use such large populations to ensure proper functionality incurs an enormous penalty in increased computation time. As a pleasant surprise, this GA significantly relaxes the requirement that populations be very large, thereby increasing solution speed.

The genetic values of the first generation of individuals, or *genesis population*, are determined at random, subject to constraints specified by the input file. These constraints also extend to all chromosomes which come into being later in the simulation, thereby placing a hard upper and lower limit on genetic values which may be expressed in progeny as the result of mutation and/or genetic recombination. Fig. 4 shows the input file for the fictitious ABC optimization, which specifies that all chromosomes must have gene values falling between -10 and 10 at all times during the evolutionary simulation.

```
*************************************************************
A = 2.29              ! X-dimension of waveguide (in cm).
B = 1.02              ! Y-dimension of waveguide (in cm).
NLAYERS = 3           ! Number of layers.
FSTART = 8.2          ! Starting frequency (in Ghz).
FEND   = 12.4         ! Ending frequency (in Ghz).
FSTEP  = 0.1          ! Frequency step (in Ghz).
*************************************************************
EMIN'  = -10          ! Epsilon prime min (relative).
EMAX'  =  10          ! Epsilon prime max (relative).
EMIN'' = -10          ! Epsilon double prime min (relative).
EMAX'' =  10          ! Epsilon double prime max (relative).
MMIN'  = -10          ! Epsilon prime min (relative).
MMAX'  =  10          ! Epsilon prime max (relative).
MMIN'' = -10          ! Epsilon double prime min (relative).
MMAX'' =  10          ! Epsilon double prime max (relative).
*************************************************************
Z1 =  0.0             ! Reference plane 1 (along Z, in cm).
Z2 =  0.1             ! Reference plane 2 (along Z, in cm).
Z3 =  0.2             ! Reference plane 3 (along Z, in cm).
Z4 =  0.3             ! Reference plane 4 (along Z, in cm).
*************************************************************
```

Fig. 4. Sample input file for the fictitious ABC optimization.
Any desired values could have been chosen here.

V. **Pseudo-Random Number Generation -**

Generating the genesis population is the first "random" event that occurs during the course of a given evolutionary simulation but it will certainly not be the last, therefore the subject of random number generation should be addressed just briefly at this point.

It is important to emphasize that a Genetic Algorithm is *not* a random search for the solution to a problem. It is an evolutionary simulation which depends heavily upon certain random processes in order to function properly, but the results should be distinctly non-random (i.e., hopefully much *better* than random). Having said that, it is also fair to say that the overall quality of the evolutionary simulation, and consequently the rapidity of convergence, can only be as good as the randomness of the pseudo-random number generator (PRNG) used to simulate the random processes upon which the GA depends. Therefore it pays to use a strong PRNG. The pretext "pseudo" is used here because computers are deterministic by nature, therefore incapable of generating truly random numbers. There is some doubt as to the adequacy of the routines provided in the NAG library, therefore this GA uses a collection of FORTRAN functions and subroutines written by Richard Chandler and Paul Northrop [5], of Oxford University's Department of Statistics in the U.K., to produce pseudo-random numbers from a variety of distributions. The superiority of Chandler and Northrop's routines arises from their versatile implementation of a novel algorithm developed by Marsaglia and Zaman (1991) [6] which produces pseudo-random numbers uniformly distributed on the interval (0,1) using a "subtract with borrow" generator. This algorithm has a period of $2^{(1376)}$ compared to $2^{(57)}$ for the NAG generator, and is suitable for use whenever very long runs of data are required.

VI. **Determining Fitness by Mode Matching -**

Many Genetic Algorithms actually require *a priori* knowledge of the function to be optimized in order to function properly, which is merely a variation of the principle that it is always nice to know the answer before you work the problem. However, there is no such objective function for this GA, nor can there be any prior knowledge of the topology of the multidimensional space to be searched during optimization, because it is determined by the complex interdependence of Maxwell's Equations within the unique system being investigated. Instead, there is a small, fast fitness evaluation code which takes the place of an objective function, calculating the reflectivity and/or transmissivity of a given test solution, and using

those values as a metric for determining the relative fitness of individuals within the population. Ostensibly, any such fitness evaluator could be used with this GA for other applications.

The Fitness Evaluator for this GA derives from a program written by Dr. M. D. Deshpande of NASA Langley Research Center's Electromagnetic Research Branch which calculates the S-parameters (i.e., transmissivity and reflectivity) of a stack of N lossy dielectric layers placed at the center of an infinite rectangular waveguide using mode-matching techniques. With Dr. Deshpande's assistance, it was fairly straightforward to extend this program to handle lossy magnetic materials, as well as the geometry of N material layers stacked against the conducting backplate of a semi-infinite waveguide. Sample output generated by this fitness evaluator is given on the following pages for a single material layer of 1 cm thickness, with $\varepsilon_r = 5 - 0.05 \cdot j$ and $\mu_r = 5 - 0.05 \cdot j$. Figures 5 and 6 show results obtained for this layer placed at the center of an infinite rectangular waveguide. Figures 7 and 8 show results obtained for the layer placed adjacent to the conducting backplate of a semi-infinite waveguide. As expected, reflectivity is much greater in the latter case. In both cases, the waveguide has dimensions of 2.29 cm x 1.02 cm, operating in the X-band.

Fig. 5. Real and imaginary parts of the complex X-band reflectivity (S11) of a
single material layer placed at the center of an infinite rectangular waveguide.

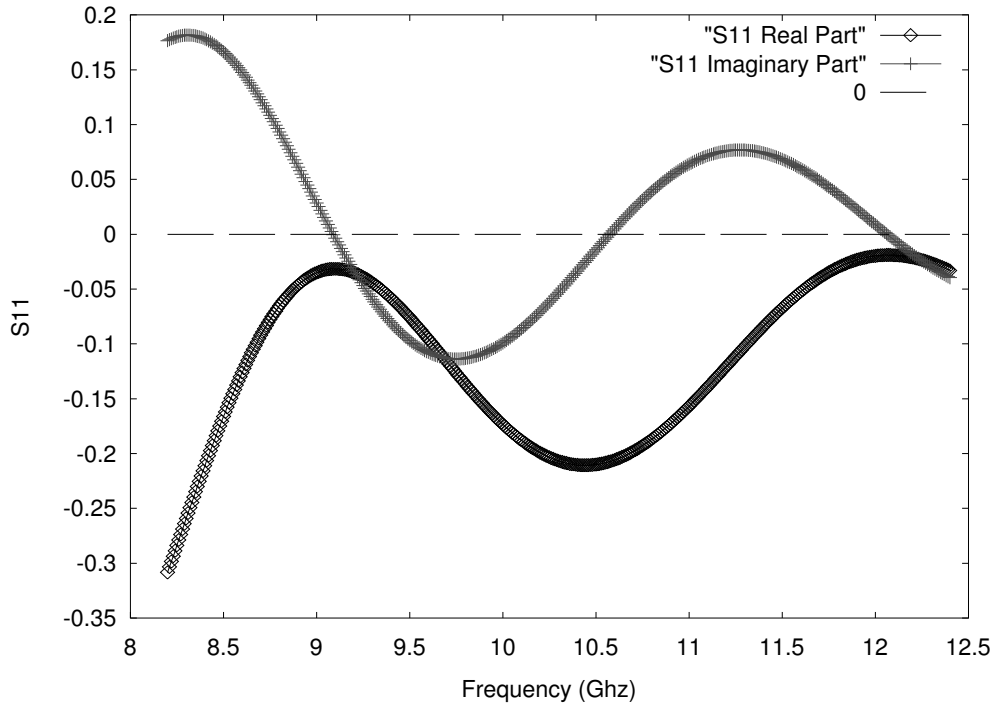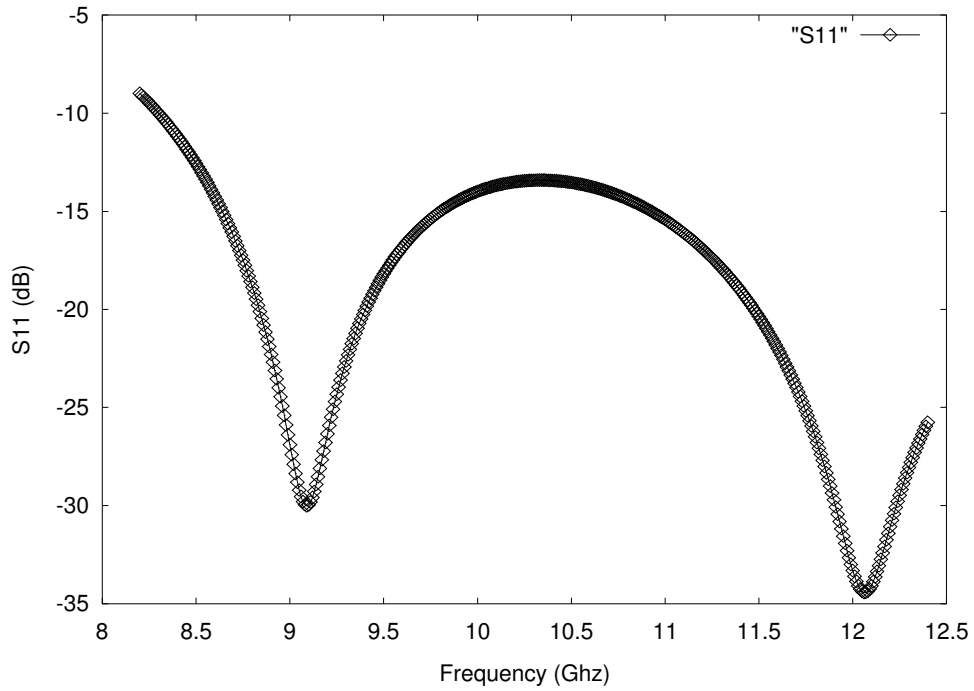Fig. 6. Magnitude of the complex X-band reflectivity (in dB) of a single
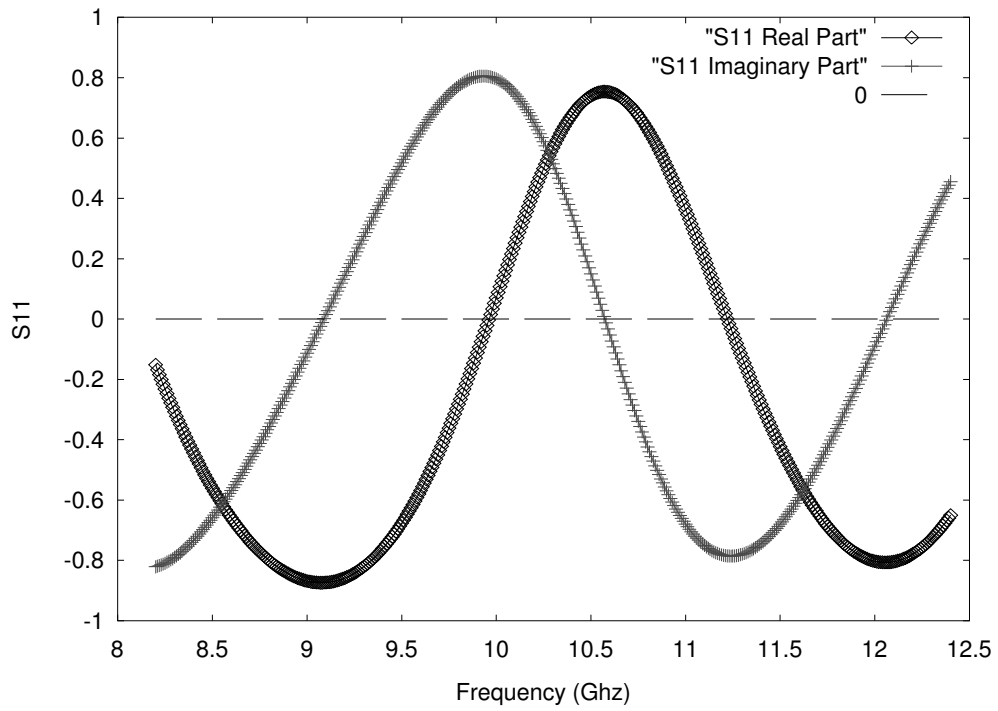material layer placed at the center of an infinite rectangular waveguide.

Fig. 7. Real and imaginary parts of the complex X-band reflectivity (S11) of a single material
layer placed adjacent to the conducting backplate of a semi-infinite, shorted-out waveguide.
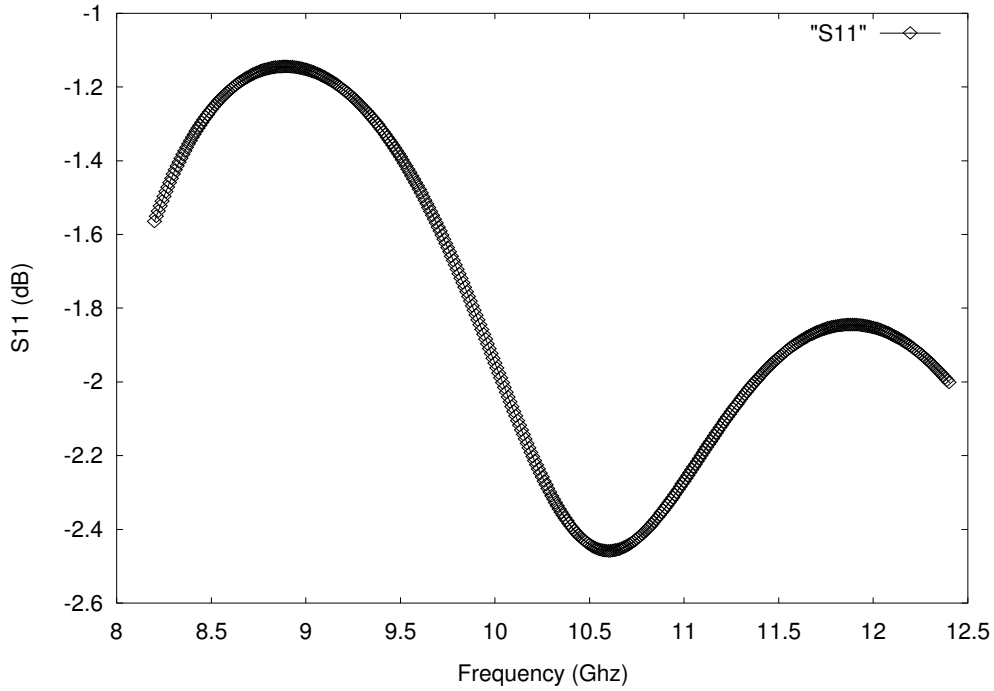
Fig. 8. Magnitude of the complex X-band reflectivity (in dB) of a single material layer placed adjacent to the conducting backplate of a semi-infinite, shorted-out waveguide.

Reflectivity must be minimized over a relatively broad frequency band, therefore fitness evaluation will generate many data points for each test solution. The GA will examine every data point generated for a given test solution and, with minimization in mind, define the *fitness metric* of the corresponding chromosome to be the magnitude of the *maximum* reflectivity (in dB) observed over the entire frequency band of interest. This way, when the final "solution chromosome" is obtained and decoded into graphical results, the entire reflectivity graph of the solution will be guaranteed to fall below the value specified by its chromosomal fitness metric.

Fig. 9 shows a sample genesis population (i.e. first generation population) of ten chromosomes, after being evaluated for fitness. The most fit chromosome is designated *Alpha Chromosome*, which for this population is chromosome number eight. Alpha is assigned a fitness score of unity, and the rest are assigned

N	FIT	FITSCORE
1	−8.62384094	0.9
2	−4.37511789	0.7
3	−2.18397387	0.5
4	4.11816322	0.2
5	0.03295778	0.3
6	−3.65058913	0.6
7	−4.92421662	0.8
8	−16.98639790	1.
9	6.35784406	0.1
10	−1.22262877	0.4

Fig. 9. Sample genesis population of ten chromosomes ranked by fitness.

fitness scores normalized relative to unity according to their relative fitness *rank*, as opposed to their fitness *metric*. This prevents whatever scale is used for the fitness metric from impacting the process of natural selection in any way.

It is interesting to note that there is gain associated with some of the chromosomes in the sample population of Fig. 9. This is a spurious effect arising solely from the fact that the complex dielectric and magnetic constants of the materials were allowed to take on unphysical values for the purpose of obtaining the "fictitious absorber" type ABCs.

VII. <u>Survival of the Most Diverse</u> -

Judging quality by fitness alone completely ignores the issue of *diversity*, which is defined as the degree to which chromosomes in a population exhibit different genes. Sometimes in Nature, very unfit-looking individuals and species survive quite well in ecological niches which lie outside the view of other, more fit-looking individuals and species. The *diversity principle* states that it can be just as good to be different as it is to be fit [3]. Equating quality with fitness alone encourages instances where extremely diverse individuals, which might be able to contribute greatly to the gene pool, can be completely eliminated just because they have a fitness metric slightly lower than other individuals who look very much like the rest of the population. Such termination of unique individuals results in genetic uniformity, thereby impeding the evolutionary process.

This GA implements a unique method for preserving diversity in populations. Once a population has been ranked by fitness and the Alpha Chromosome has been identified, the GA calculates the multidimensional genetic "distance" between each of the remaining chromosomes and Alpha. This genetic distance is calculated in exactly the same way as one might calculate the distance between two points in Euclidean three-space, except there are as many dimensions in the diversity calculation as there are genes in each chromosome (i.e., 4N for N layers). This quantity then becomes the *diversity metric* for each chromosome. Alpha is assigned a diversity score of unity, since it is the standard against which all others are judged, and the rest of the chromosomes are assigned diversity scores normalized relative to unity according to their diversity *rank* as opposed to their diversity *metric*, to prevent arbitrary scale issues from impacting the process of natural selection, as before. Fig. 10 shows the sample population from Fig. 9 after being evaluated and ranked by fitness *and* diversity.

N	FIT	FITSCORE	DIV	DIVSCORE
1	−8.62384094	0.9	21.8770694	0.5
2	−4.37511789	0.7	21.4814842	0.4
3	−2.18397387	0.5	19.539844	0.2
4	4.11816322	0.2	25.7370131	0.8
5	0.03295778	0.3	22.2742858	0.7
6	−3.65058913	0.6	25.7379826	0.9
7	−4.92421662	0.8	19.4708345	0.1
8	−16.98639790	1.	1.e+100	1.
9	6.35784406	0.1	19.6973937	0.3
10	−1.22262877	0.4	22.2196678	0.6

Fig. 10. Sample population of ten chromosomes ranked by fitness and diversity.

VIII. Total Score and Extinction -

The initial approach to modeling natural selection was to define each individual's *total score,* which is the score used for natural selection purposes, as the average of its normalized fitness and diversity scores, ostensibly incorporating the influence of both criteria when exerting selection pressure. However, instead of incorporating the influence of the additional selection criterion (i.e., diversity), empirical investigation demonstrated that the averaging operation effectively diluted the influence of *both* selection criteria, slowing down the evolutionary process, as a whole. Computing total scores as the average of fitness and diversity scores produced worse convergence than using fitness alone, therefore, another approach was developed to more robustly incorporate the influence of both.

After much trial-and-error, the best convergence was obtained when each generation was randomly evaluated for extinction using *either* fitness *or* diversity as a selection criterion, but not both. A "digital coin toss" for each generation uniquely determines with equal probability whether fitness or diversity will be used as the selection criterion for that generation's population. Once the determination is made, each individual's total score is set equal to either its fitness score or its diversity score. Then, all individuals having total scores which do not meet or exceed the *extinction criterion,* which is the minimum total score necessary for survival, are extinguished. The effects of both selection criteria are preserved, and much swifter convergence is obtained compared to that obtained by repetitively using either criterion alone or both criteria simultaneously, generation after generation.

The *extinction criterion* is defined as the average total score of all individuals composing a full population, prior to extinction. This way, only "below-average" individuals will be extinguished, by definition. This method was developed with non-normalized total scores in mind, however, it functions just as effectively in populations using normalized total scores. In such populations, about half of each generation will be extinguished. The Alpha Chromosome always remains on top no matter which selection criterion is used, guaranteeing that there will never be any retrograde motion in the best solution, as generations evolve.

Fig. 11 shows our sample population before and after an extinction event. Depending upon the random FLAG, the total SCORE will be set equal to either FITSCORE or DIVSCORE. In this case FLAG=1, so total SCORE is set to FITSCORE, and all individuals with total SCORE not meeting or exceeding MINSCORE (the extinction criterion) are extinguished. Only the fittest survive, and Alpha remains on top. In the case of selection by diversity, the total SCORE would be set to DIVSCORE, and only the most diverse individuals in the population would survive, with Alpha remaining on top. Periodic extinction by diversity ensures that the population does not become "genetically frozen", i.e. dominated by a single phenotype which may not be optimally fit. The empty spaces in the population leave room for progeny.

```
Before Extinction:                    After Extinction:

FLAG = 1                              MINSCORE = 0.55

  N        FIT        SCORE            N        FIT        SCORE

  1    -16.98639790    1.              1    -16.98639790    1.
  2     -8.62384094    0.9             2     -8.62384094    0.9
  3     -4.92421662    0.8             3     -4.92421662    0.8
  4     -4.37511789    0.7             4     -4.37511789    0.7
  5     -3.65058913    0.6             5     -3.65058913    0.6
  6     -2.18397387    0.5             6      0.             0.
  7     -1.22262877    0.4             7      0.             0.
  8      0.03295778    0.3             8      0.             0.
  9      4.11816322    0.2             9      0.             0.
 10      6.35784406    0.1            10      0.             0.
```

Fig. 11. Sample population before and after extinction. The nature of the total score is determined by a random flag, which in this case indicates extinction by fitness. The fitness score is copied into the total score, individuals are sorted by total score, and all individuals having total scores which do not meet or exceed the extinction criterion are extinguished.

IX. **Propagation of the Species -**

The process of extinction leaves vacancies in the population which must be filled. These vacancies are filled using numerical analogues of reproduction, providing mechanisms for genetic recombination whereby new individuals (i.e. "children") are created that have a chance to be more fit than their parents. Since total scores are normalized, half of the population will be killed off during each extinction, requiring creation of exactly as many replacements as there are individuals left in the population after each extinction. This uniquely symmetric result *guarantees* every survivor a chance to produce a child for the next generation, therefore every survivor reproduces at least once, in this GA. Reproduction may be asexual or sexual, and if reproduction is sexual, then the survivor's mate is chosen randomly from the other survivors, with probability of selection weighted by total score. Reproduction can occur in any of four possible ways, with equal probability:

> ➢ Mitosis -

Mitosis is an asexual cell division process in which the nucleus divides, normally resulting in two new cells, each of which contains a complete copy of the parental chromosomes. Essentially, the individual selected for mitosis creates a clone of itself in the population. The clone will be subject to the possibility of mutation during the next phase of the evolutionary process, but the parent will not.
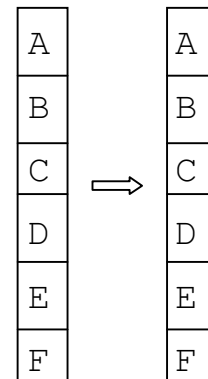

Fig. 12. Mitosis.

> ➢ Mitosis with Chain Reversal -

An asexual cell division process similar to mitosis, with one major difference. *Chain reversal* is a chromosomal aberration which occurs during replication when a subdomain of the original chromosome detaches, reverses polarity, and reattaches at opposite ends, forming a new chromosome.
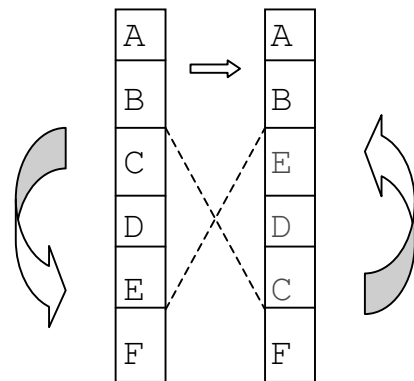

Fig. 13. Mitosis with chain reversal.

Chain reversal can occur on a chromosomal subdomain as small as a single pair of genes or as large as the entire chromosome, and it always produces a child which is uniquely different from the parent. Like the mitotic clone before, this child will also be subject to the possibility of mutation during the next phase of the evolutionary process, but its parent will not.

➢ N-Point Crossing Over -

Crossing over is genetic recombination arising from the sexual reproduction of two parents. When parent chromosomes come together during the process of reproduction, genetic material is exchanged between them in the vicinity of one or more points of contact. One such point, known as the *centromere*, is that place where the midpoints of two parent haploid chromosomes join so that the pair looks like the letter "X". There may also be other points of contact along the chromosomal chain known as *chiasma*. In this GA, the minimum number of crossover points is one (always at the centromere), and the maximum number of crossover points cannot exceed one-half the total number of genes in each chromosome. Chiasma may be located anywhere along the chromosomal chain, and the locations of these points in conjunction with the centromere are used to define distinct chromosomal subdomains, on which genetic information is exchanged between parents to form the blueprint of a new individual.
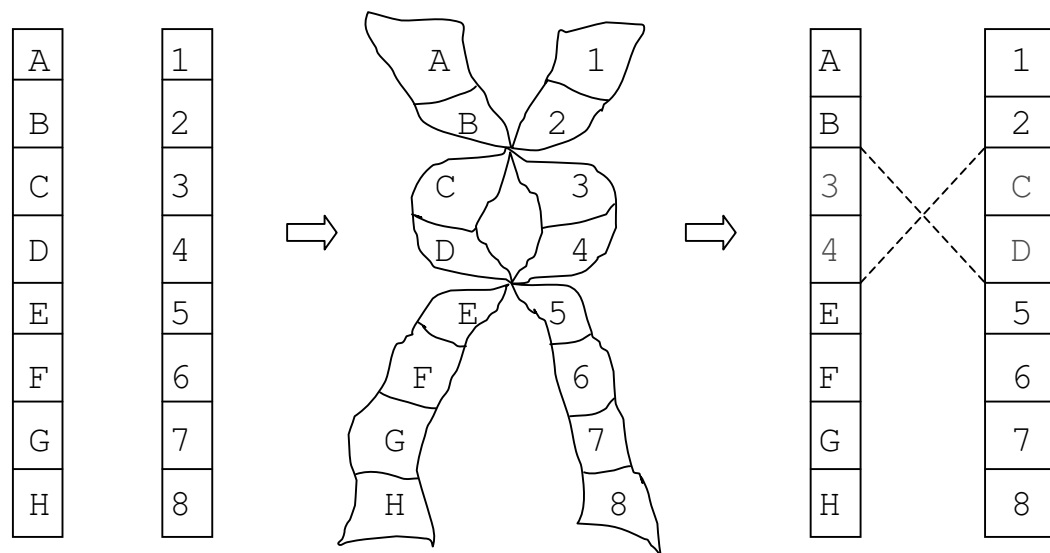

Fig. 14. 2-Point crossing over involving the centromere and one chiasm.
Genes within one subdomain are exchanged between parents.

The source of genetic material alternates on each subdomain, with Parent 1 contributing to all odd subdomains and Parent 2 contributing to all even subdomains. Although two children could be created using this method, in this GA only one child is created and propagated to the next generation. The question of which child to propagate is arbitrary, depending solely upon which chromosomes are defined as Parent 1 and Parent 2.

➢ "Channeled" Crossing Over -

Channeled crossover is also the result of sexual reproduction between two parents. This recombination strategy exploits the specific chromosomal encoding pattern unique to this application. Examination of section III. above shows that the primed and double-primed values of all variables encoded within each chromosome alternate regularly along the chromosomal chain. The process of "channeled" crossover randomly selects two breakpoints on the chromosomal chain and exchanges every other gene along this subdomain between parents, to beget progeny. It is reasonable to assume that real problems may impose very different constraints upon primed and unprimed quantities. This type of crossover offers a unique opportunity for individuals doing well in the primed dimensions to unite with individuals doing well in the unprimed dimensions. As before, only one child is created and propagated to the next generation. The question of which child to propagate is completely arbitrary, depending on the definition of parents.
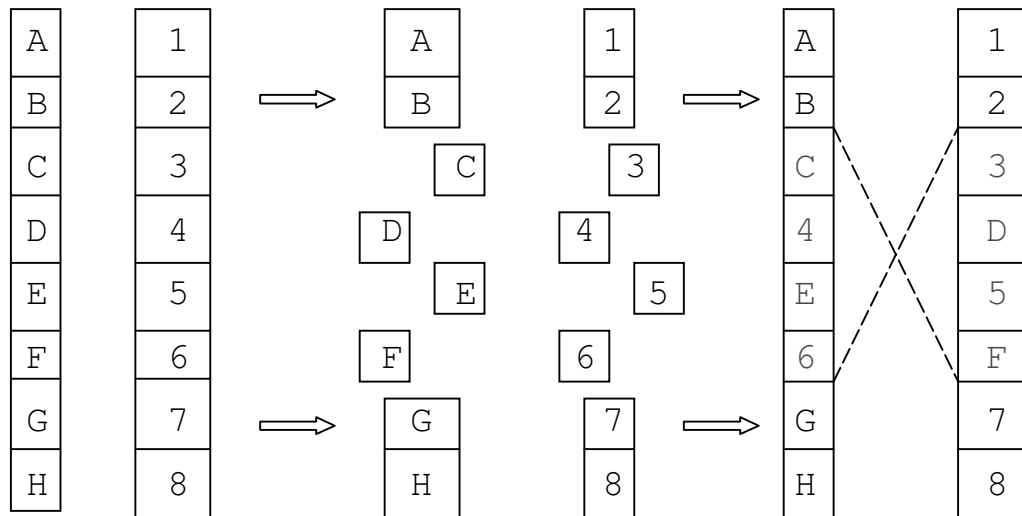

Fig. 15. Channeled crossover between two parents
on a chromosomal subdomain of length four.

X. <u>Hybridization</u> -

Once the population has been replenished through reproduction, there exists the possibility that one or more offspring may contain gene values lying outside constraints specified by the input file. One particular reproduction operation that could produce this effect is mitosis with chain-reversal. Such genetic defects are relatively infrequent in this GA, occurring in only eight percent of genes expressed in offspring, on average. Nevertheless, that is frequent enough to necessitate that some method be implemented to correct these defects within progeny after reproduction, once they have already been written into the population.

After all children are born, this GA examines each child for genetic defects (i.e. gene values which lie outside specified constraints). If one is found, the GA will excise that gene from the chromosome in question and artificially replace it with the corresponding gene from the current Alpha Chromosome, creating a transgenic *hybrid*. This process, which is analogous to recombinant genetic engineering (as might be implemented within a biological laboratory), ensures that all genes in the new population fall within constraints specified by the input file before being propagated to the next generation for fitness evaluation. The rationale underlying this operation is that Alpha should always donate the very best gene available, because it is the fittest individual in the population. Although it would seem reasonable that this practice might promote crippling uniformity in the population, the consistent inclusion of diversity as a selection criterion, as well as the infrequent necessity of such artificial recombinations seems to successfully offset any tendency toward uniformity.

It should be noted that other potential strategies for handling this situation include *random* generation of a new gene whenever an outlier is found, or simply omitting reproductive processes which give rise to such defects in the first place. However, correction by hybridization using genetic material donated by Alpha consistently produced significantly faster convergence.

XI. <u>Mutation</u> -

Mutation is the random environmental perturbation of one or more genes within the chromosomal chain of an individual which may alter its phenotype, thereby giving it a greater or lesser advantage in the process of natural selection. The vast majority of mutations are unfavorable, however, the occasional mutant may actually be more fit than the species from whence it arose, enabling its propagation and subsequent introduction of new genetic material

into the population. This process drives variation of the species in nature. In an evolutionary simulation, *mutation operators* provide analogous numerical mechanisms for introducing new "genetic material" into the population, thereby enabling full exploration of the search space.

Naturally, it is a good idea to protect the fittest individuals (i.e. solutions) in the population from the damaging effects of mutation, therefore mutation isn't allowed to affect the parents of a given generation; it can only affect their children. Once children are checked for mutations, the newly-created population becomes a new generation of its own, starting another iteration of the evolutionary process beginning with fitness evaluation.

The *mutation probability* determines the frequency with which gene values will be changed. If the mutation rate is too low, then new traits will appear too slowly in the population to obtain convergence in any reasonable number of generations. Conversely, if the mutation rate is too high, then each generation of children will bear little or no resemblance to their parents, and the entire algorithm will degenerate into a crude random search. In this GA, the mutation probability is calculated as unity minus the average total score of all individuals surviving extinction (i.e., the parents *only*). This way, if the average fitness of survivors is high, then mutation rate will be low, and if the average fitness of survivors is low, then the mutation rate will be high. This tends to stimulate variation in the species when necessary, and tends to suppress the potentially damaging effects of mutation on the children of a very fit group of survivors. Although this formula for the mutation probability was originally developed with *non-normalized* total scores in mind, it functions properly when total scores are normalized, as well.

Once children have been created and the mutation probability has been calculated, the GA will check all children on an individual gene-by-gene basis to see whether or not each gene will be mutated. If a gene is selected for mutation, then its numerical value is randomly changed. Traditional real-based mutation operators usually take the form $gene = gene \pm \delta$ [3], where delta is a random number determined from the normal probability distribution having a mean of zero and arbitrary standard deviation sigma.
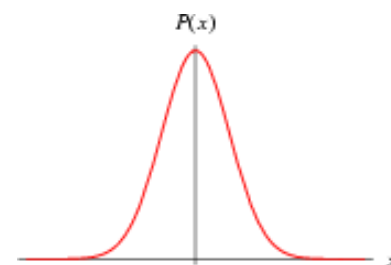

Fig. 16. A normal probability distribution with a mean of zero and arbitrary standard deviation sigma.

This particular algorithm foregoes the additive mutation operator in favor of two other mutation operators, each having a unique mathematical form and method of determining sigma. A proper choice of *sigma*, the standard deviation of the normal distribution, is critical for successful mutation. Sigma determines the width of the normal distribution, thereby constraining the most likely order of magnitude of the random numbers generated. In theory, sigma should be large at the start of the algorithm and then decrease as the algorithm converges, so variability will be favored during the early stages of evolution but the damaging effects of mutation on nearly optimal solutions will be mitigated. Certainly, different choices of sigma produce radically different evolutionary behaviors, and fine-tuning sigma to adapt properly to the progress of the evolutionary simulation can be extremely difficult. When this GA determines that a gene must be mutated, it will randomly select one of the following operators, with equal probability of each. If a mutation would carry a gene outside specified constraints, the mutation is ignored as if it never happened:

➤ Mutiplicative Operator -

This mutation operator has the form $gene = gene * \delta$ where delta is a random multiplier determined from the normal probability distribution having a mean of 1.0, and sigma determined as: $\sigma = 1. - $ (*Current Best Fitness*) / (*Target Fitness*). This way, delta will randomly fluctuate around unity, presenting mutated genes with an equal probability of increasing or decreasing, on average. The magnitude of that increase or decrease will be determined by a value of sigma which adapts to the progress of the algorithm. Sigma begins as unity at the first generation and then decreases linearly, approaching zero as the "current best fitness" (i.e., the fitness metric of the current Alpha Chromosome) approaches the desired target fitness. Since the target fitness is specified by keyboard input, it is easy to change the slope of linear decrease in sigma by simply specifying a different target fitness.

➤ Perturbative Operator -

This operator perturbs genetic values by replacing the original gene with a slightly different value, determined from the normal probability distribution having a mean equal to the *original gene value*, and an adaptive value of sigma. The distribution now randomly fluctuates around the original gene value relatively tightly, and the influence of sigma is more absolute. The adaptive value of sigma is determined as follows:

Whenever a newer, fitter Alpha Chromosome replaces an older, less fit one, an integer counter (call it β…) is set equal the current generation number. As the generation number increases, the value of each generation is successively added to β, and sigma is calculated as the current generation number divided by β.

To see how this works, consider two generations with no improvement in the solution. On generation 1, β = 1, and therefore σ = 1. On generation 2, β = (1+2), and σ = 2/(1+2), or 0.67. Now, on generation 3, let a new Alpha Chromosome be found. As a consequence, β is set equal to three, and σ = 3/3, or 1. On generation 4, there is no change, therefore β = (3+4), and σ = 4/(3+4), or 0.57. This method of calculating sigma insures that it always begins as unity whenever a new Alpha Chromosome is found, and asymptotically decreases to zero more and more quickly after each replacement of the Alpha Chromosome.

Essentially, the algorithm attempts progressively smaller perturbations of the genetic values selected for mutation as generations progress, until one is found (almost by "brute force") which yields a better solution. As generations increase, the asymptotic dropoff becomes steeper and steeper, so that less effort is expended using larger values of sigma in the late stages of evolution without having to abandon the use of large values entirely. Sigma now determines an absolute magnitude of perturbation, and it may be scaled to a range appropriate for each specific application by using a multiplier, if desired. Fig. 17 shows the progression of sigma over 20 generations using this method (without scaling), assuming that a new Alpha Chromosome is discovered at the tenth generation.
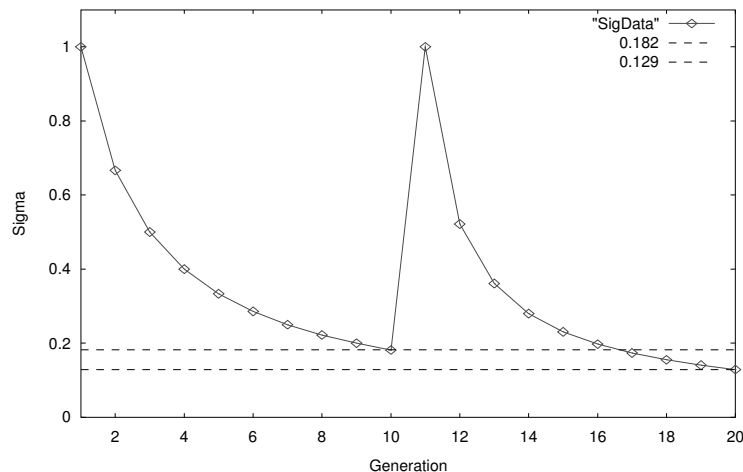

Fig. 17. Standard Deviation of the Perturbative Mutator.

XII. <u>Results</u> - *The Fictitious ABC.*

Once the GA executes 1000 iterations with no change in the Alpha Chromosome, it decodes the Alpha Chromosome and delivers the optimal physioelectric constants, along with the reflection (and/or transmission) data over the frequency range of interest. This iteration limit is purely arbitrary, and can easily be changed. Other strategies could conceivably be implemented to try to deal with this kind of asymptotic approach, such as conditional inclusion of more chaotic social dynamics, or the modeling of periodic global catastrophes, however none of these strategies have proven to be reliable and/or effective enough to merit permanent inclusion into the algorithm (yet).

Fig. 18 shows the convergence and asymptotic approach of the fitness metric of the Alpha Chromosome toward the solution obtained for the fictitious ABC. Fig. 19 shows the output file generated for the fictitious ABC, and Fig. 20 shows the reflectivity of the ABC over the X-band. Although the target fitness was specified as –100 dB, the GA encountered asymptotic approach at a best fitness of approximately –55 dB. Because this represents the fitness metric of the final Alpha Chromosome, the entire reflectivity graph of the solution encoded by Alpha falls below this value, as desired. Unfortunately it is impossible, due to the non-deterministic nature of the GA, to ascertain whether or not this, or any solution obtained through asymptotic approach, is in fact the hard physical limit. This optimization was completed in less than one CPU minute using a population of only four.
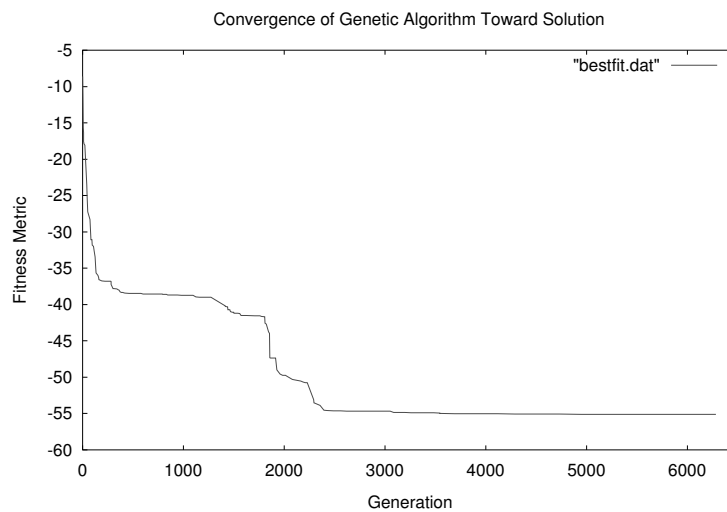

Fig. 18. Convergence and asymptotic approach of the GA
toward the solution for the fictitious ABC optimization.

```
******** PARAMETERS **********          ****************************
A =  2.29
B =  1.02                               Population = 4
NLAYERS = 3                             Generations = 7284
FSTART =  8.2                           Bestfit =  -55.1051287
FEND =  12.4                            CPU Time =  0.891666667 minutes.
FSTEP =  0.1
********* LAYER 1 ************           ********* LAYER 3************
Z    =  0.                              Z    =  0.2
E'   = -5.81435204                      E'   =  1.24189401
E''  =  7.9716177                       E''  =  1.19435549
M'   = -8.3258419                       M'   =  8.84083939
M''  =  9.08495998                      M''  =  2.78866553
********* LAYER 2************            ********* LAYER 4************
Z    =  0.1                             Z    =  0.3
E'   =  7.82274437                       E'   =  0.
E''  = -8.25729847                      E''  =  0.
M'   =  3.17915225                       M'   =  0.
M''  = -3.83381701                      M''  =  0.
****************************             ****************************
```

Fig. 19. Output file for the fictitious 3-layer ABC. Physioelectric constants take the form of (primed value) – j * (double primed value). For example, epsilon for layer 2 is (7.82 + j * 8.26). It is interesting to note that the first layer is composed of a double-negative, or *meta*-material.
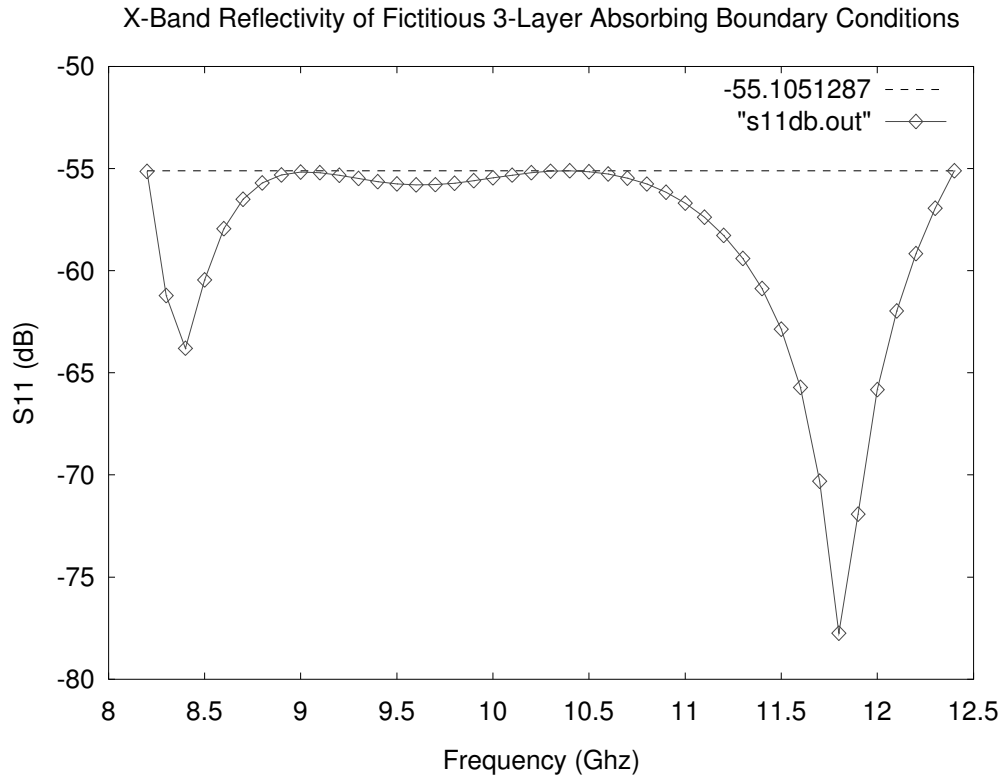

Fig. 20. Magnitude of the X-band reflectivity (in dB) of the fictitious 3-layer ABC.

The fictitious 3-layer ABC was validated using multiple test cases. As an example, Fig. 21 shows the performance of the fictitious ABC used in conjunction with the single magneto-dielectric slab of 1 cm thickness having $\varepsilon_r = 5 - 0.05 \cdot j$ and $\mu_r = 5 - 0.05 \cdot j$, which was analyzed in section VI. The performance of the fictitious ABC used in conjunction with this dielectric slab is compared to the reflectivity of the slab backed by free space. The "Slab Open" case, indicated by the solid black line, shows the reflectivity of the dielectric slab placed at the center of an infinitely long waveguide, as shown in Fig. 6. The "Slab Shorted" case, indicated by the dashed line, shows the reflectivity of the same slab placed against the perfectly conducting backplate of a semi-infinite, shorted-out waveguide, as shown in Fig. 8. As expected, reflectivity is much higher in this case. The "Slab Shorted With ABC" case, indicated by large diamonds, shows the reflectivity of the slab backed by the fictitious 3-layer absorber, clearly demonstrating that backing the slab with the 3-layer ABC is numerically equivalent to backing it with free space, even though the ABC includes a PEC enclosure. The average error produced by backing the test case with the ABC relative to backing the test case with free space was 0.23%.
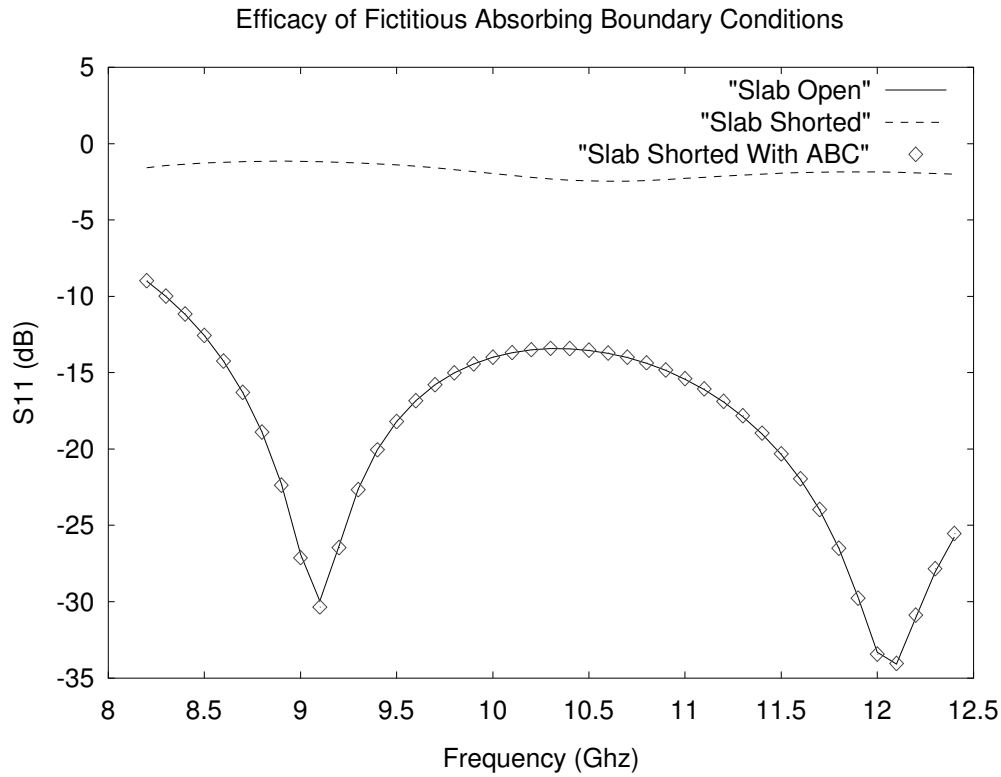

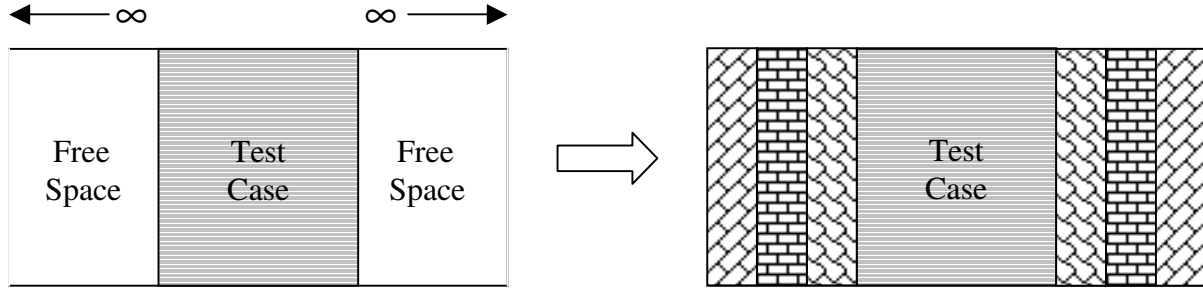Fig. 21. Efficacy of fictitious ABCs obtained using the GA.

Fig. 22. Using fictitious ABCs within a complete PEC enclosure could be useful for terminating open-region FEM meshes. This conjecture has not yet been tested using FEM.

XIII. <u>Results</u> - *Real Absorbers.*

Satisfactory performance of Radar Absorbing Materials (RAM) requires getting the maximum amount of radiofrequency energy into the RAM as possible, and then providing a sufficient amount of loss to absorb that energy within the allowed thickness. Unfortunately, very lossy materials usually have impedances that are very different than free space, producing high reflection at the free space boundary. This issue complicates deterministic RAM design.

Although intended for development of fictitious absorbers, this GA can also be used to design real Radar Absorbing Materials by specifying realistic constraints corresponding to whatever materials will be used to fabricate the multilayered structure. The problem then reduces to minimization of the reflectivity of an arbitrary number of homogeneous, lossy dielectric or magnetic layers of arbitrary thickness positioned adjacent to the perfectly conducting backplate of a semi-infinite, shorted-out rectangular waveguide.

The performance of this GA was analyzed over a broad range of realistic absorber design problems. The initial study attempted to minimize reflection using up to ten layers of 1mm-thick non-magnetic dielectric material, with each layer subject to the following constraints: $1 \le \varepsilon_r' \le 10$ and $0 \le \varepsilon_r'' \le 10$. Fig. 23 shows the *maximum* X-band reflectivity as a function of the number of layers used. The X-band reflectivity curve for a given stack will fall entirely *below* the value indicated in Fig. 23. Asymptotic behavior is clearly observed. Fig. 24 extends this analysis to permit the dielectric materials to become magnetic as well, subject to the same dielectric constraints as above, plus: $1 \le \mu_r' \le 10$, and $0 \le \mu_r'' \le 10$. A quasi-odd-even effect is observed.

Figures 25 and 26 show results obtained for 2-layer MagRAM on PEC consisting of two layers of custom material bonded to metal, having a total thickness of two millimeters and providing a minimum X-band RCSR of approximately 36 "dB down" within the waveguide.
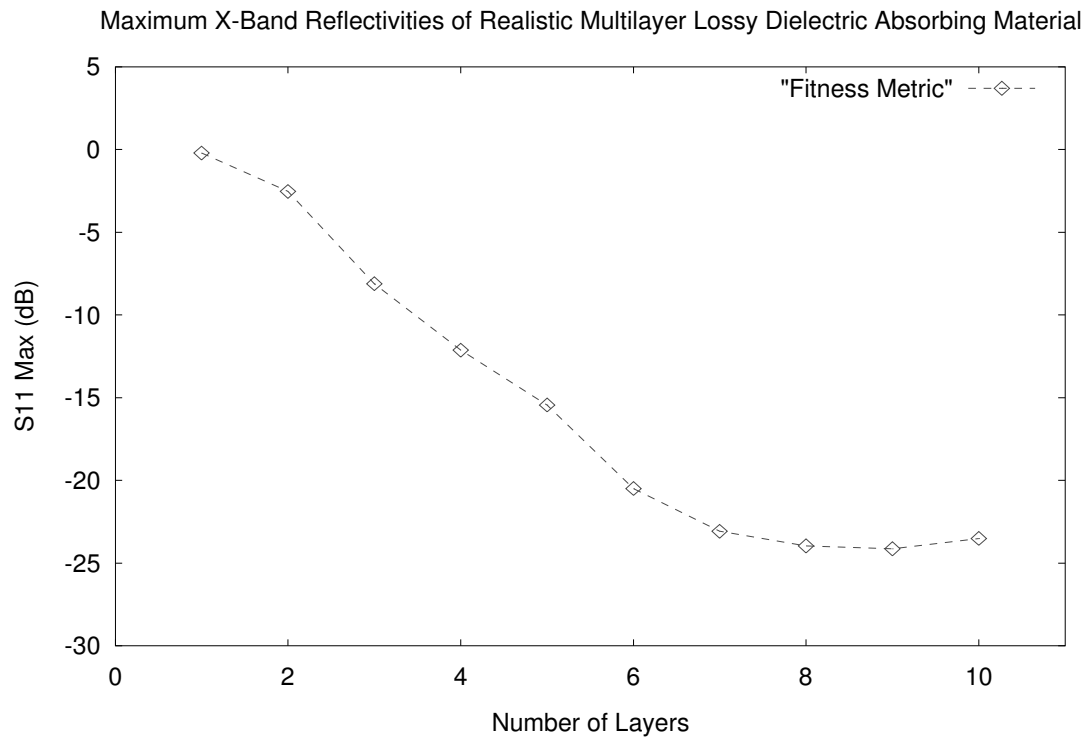
Maximum X-Band Reflectivities of Realistic Multilayer Lossy Dielectric Absorbing Material

Fig. 23. Maximum X-band reflectivities of realistic multilayer dielectric absorbers.

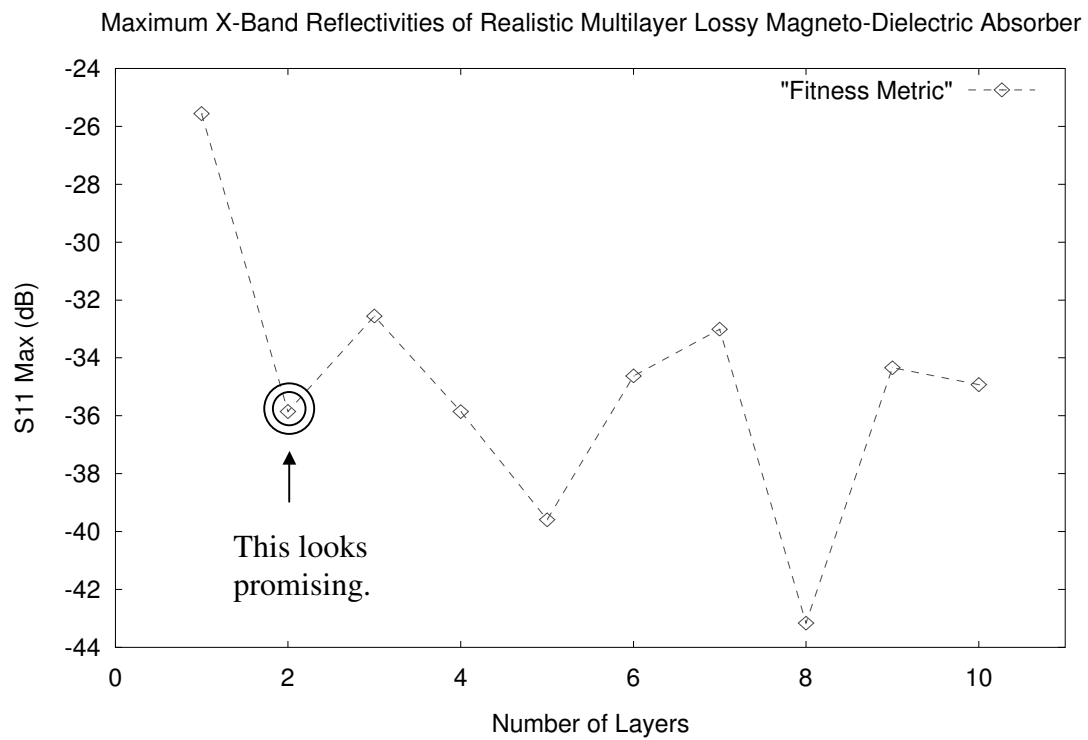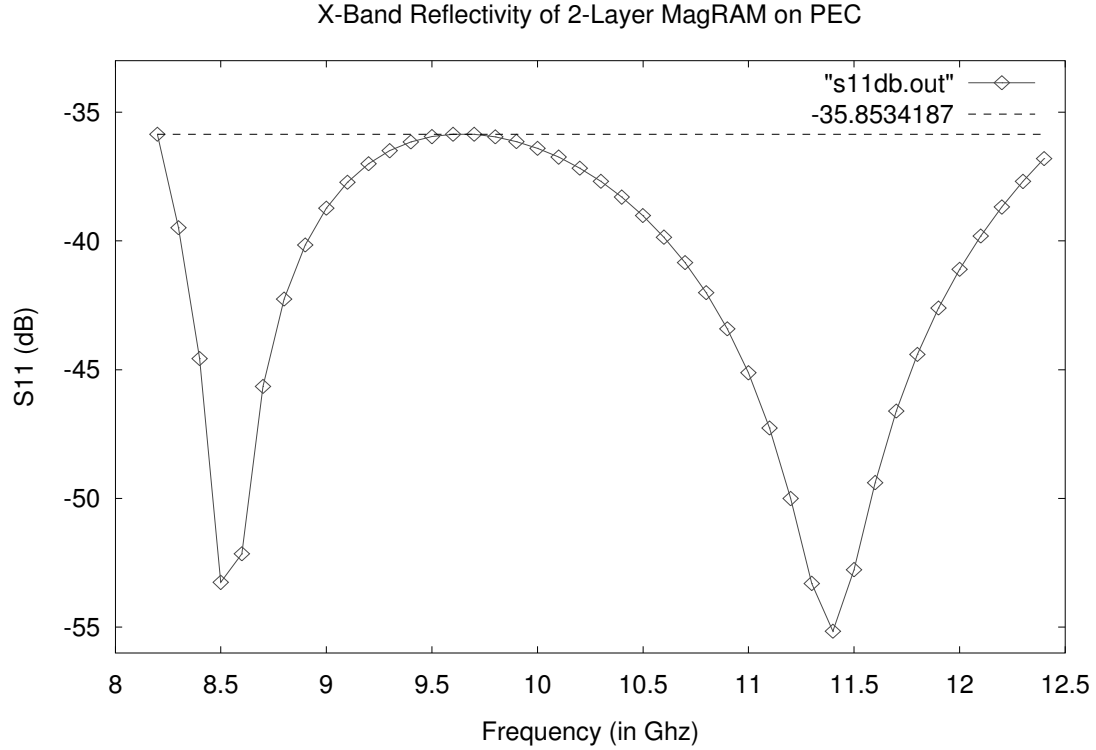Maximum X-Band Reflectivities of Realistic Multilayer Lossy Magneto-Dielectric Absorber

Fig. 24. Maximum X-band reflectivities of realistic multilayer magneto-dielectric absorbers.

X-Band Reflectivity of 2-Layer MagRAM on PEC

Fig. 25. X-band reflectivity of 2-Layer MagRAM on PEC.

```
******** PARAMETERS **********
A =  2.29
B =  1.02                          Population = 4
NLAYERS = 2                        Generations = 15856
FSTART =  8.2                      Bestfit =  -35.8534187
FEND =  12.4                       CPU Time =  1.30182292 minutes.
FSTEP =  0.1
********* LAYER 1 ************
Z   = 0.
E'  = 5.40971899
E'' = 2.51661348
M'  = 8.34440517
M'' = 1.03202021
********* LAYER 2 ***********
Z   = 0.1
E'  = 2.51000571
E'' = 6.66792727
M'  = 6.0845685
M'' = 2.59887004
********* LAYER 3 ***********
Z   = 0.2
E'  = 0.                          Total Thickness = 2mm
E'' = 0.
M'  = 0.
```

$$\varepsilon_{1r} = 5.40971899 - j \cdot 2.51661348$$
$$\mu_{1r} = 8.34440517 - j \cdot 1.03202021$$

$$\varepsilon_{2r} = 2.51000571 - j \cdot 6.66792727$$
$$\mu_{2r} = 6.0845685 - j \cdot 2.59887004$$

Fig. 26. Material parameters and text output for 2-Layer MagRAM on PEC.

XIV. <u>Conclusion</u> -

Traditionally, successful RAM design requires familiarity with the types of materials available, good engineering judgment, and thorough knowledge of RAM performance. In this work, elements of Darwin's Theory of Evolution were modeled algorithmically to implement a novel, real-based Genetic Algorithm for the non-deterministic optimization and design of Radar Absorbing Materials. Although typical Genetic Algorithms require populations of many thousands in order to function properly and obtain correct results, verified correct results were obtained within a reasonable time interval using this GA with a population of only four.

Although the algorithm described herein was designed optimize, it is by no means optimal. Obtaining the most favorable combination of operators and their associated probabilities requires extensive trial-and-error, which is an extremely time-consuming process. This work merely represents the current best draft obtainable within the time allocated for its development and is still a work in progress, not unlike any given generation of the organisms it models. This GA could probably be vastly improved and even better results obtained if the work were extended. In conclusion, it is, perhaps, most important to point out that although this report describes one particular application of the GA, any fitness evaluator could be used with this GA for different applications.
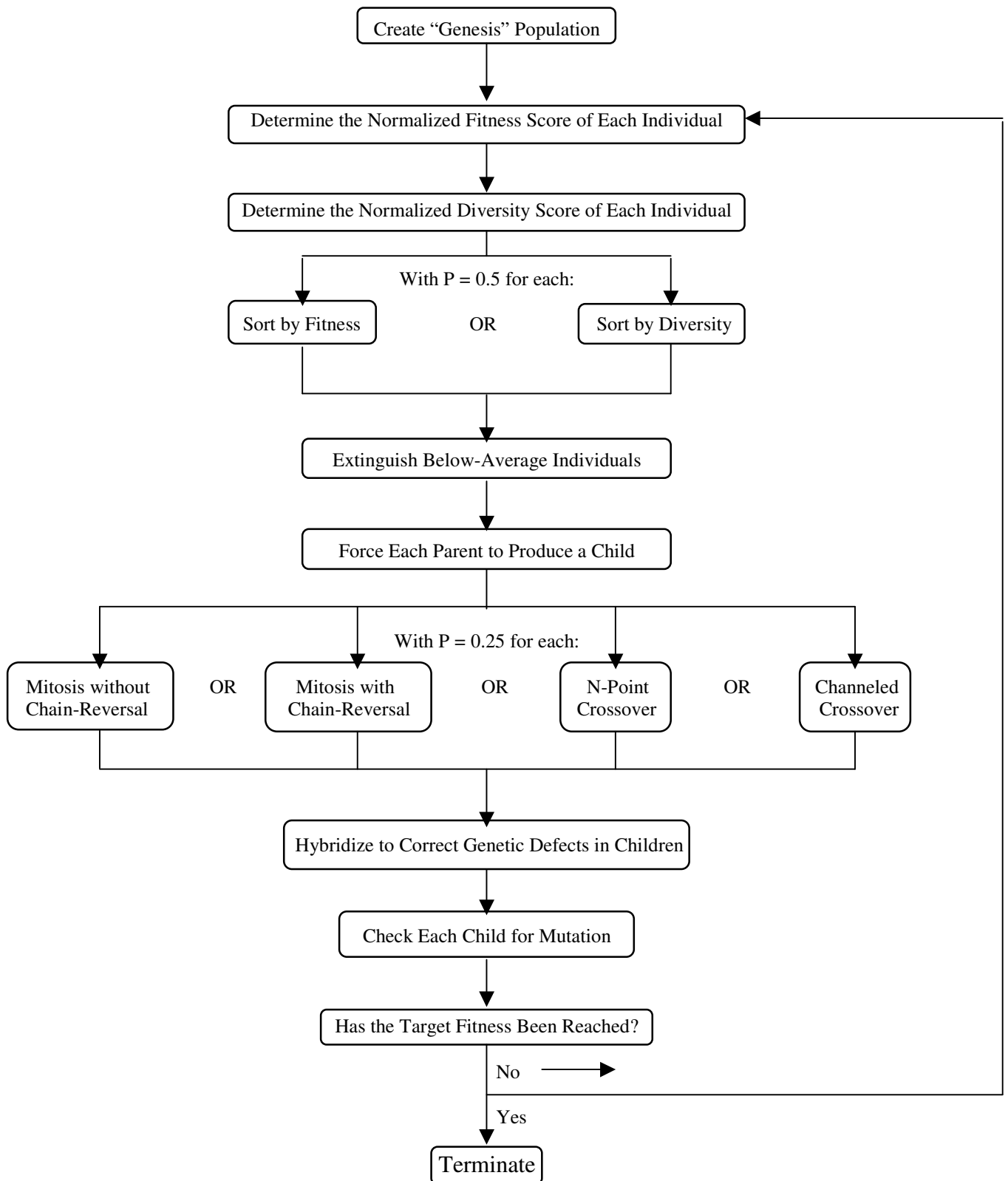
XVI. <u>References</u> -

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XVII. <u>Appendix</u> – *Genetic Algorithm Flowchart.*

Create "Genesis" Population

Determine the Normalized Fitness Score of Each Individual

Determine the Normalized Diversity Score of Each Individual

With P = 0.5 for each:

Sort by Fitness　　　OR　　　Sort by Diversity

Extinguish Below-Average Individuals

Force Each Parent to Produce a Child

With P = 0.25 for each:

Mitosis without Chain-Reversal　　OR　　Mitosis with Chain-Reversal　　OR　　N-Point Crossover　　OR　　Channeled Crossover

Hybridize to Correct Genetic Defects in Children

Check Each Child for Mutation

Has the Target Fitness Been Reached?

No

Yes

Terminate

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14. ABSTRACT
A novel, real-valued Genetic Algorithm (GA) was designed and implemented to minimize the reflectivity and/or transmissivity of an arbitrary number of homogeneous, lossy dielectric or magnetic layers of arbitrary thickness positioned at either the center of an infinitely long rectangular waveguide, or adjacent to the perfectly conducting backplate of a semi-infinite, shorted-out rectangular waveguide. Evolutionary processes extract the optimal physioelectric constants falling within specified constraints which minimize reflection and/or transmission over the frequency band of interest. This GA extracted the unphysical dielectric and magnetic constants of three layers of fictitious material placed adjacent to the conducting backplate of a shorted-out waveguide such that the reflectivity of the configuration was –55 dB or less over the entire X-band. Examples of the optimization of realistic multi-layer absorbers are also presented. Although typical Genetic Algorithms require populations of many thousands in order to function properly and obtain correct results, verified correct results were obtained for all test cases using this GA with a population of only four.

15. SUBJECT TERMS
Artificial Intelligence, Genetic Algorithms, Radar Abosrbing Materials

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