Issues Involved in Developing a Genetic Algorithm Methodology for Optimizing the Position of Ship Board Antennas

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ABSTRACT

While genetic algorithms are powerful optimization tools, they typically require many function space evaluations. This makes their utilization limited when the time per evaluation is significant. We discuss one such application, the optimization of antenna positioning on ship-board platforms. We present the issues involved and propose intelligent preprocessing and genetic algorithm modifications which reduce both function evaluation time and the extent and complexity of the function space. While these strategies were developed for this particular application, most would be suitable for other complex military optimization problems.

Keywords:, antenna positioning, antenna optimization, genetic algorithms, ship-board platforms

1. INTRODUCTION

The increasing use of higher bandwidth and multiple systems for communications and ISR (Intelligence, Surveillance, and Reconnaissance) functions creates an electromagnetic interference (EMI) environment which is fraught with numerous unintentional interactions, commonly referred to as cosite interference. Overlapping frequency bands and unintentional reflections can create system-to-system interference that may require adaptive filtering, system blanking or alternating system usage (shutting one system off while using the other). This scenario is complicated further by the interactions between the antennas and the physical platform itself, which is usually composed of EM reflecting material (i.e. metal).

While cosite interference can be mitigated by a wide physical separation of the various antenna systems, this cannot be easily achieved on a limited-size platform such as a naval vessel or an aircraft. Since the placement and orientation of antennas and arrays strongly affects the resulting electromagnetic coupling, it is prudent to consider these aspects in the design phase to determine the optimum arrangement of systems to produce the least amount of EMI.

This paper summarizes work conducted for Phase 1 of the US Navy STTR Topic #N08-T031, *Antenna Design by Genetic Algorithm*. The objective of this project was to develop a methodology for antenna optimization on a platform~~-~~. The specific area to be addressed in Phase I was to describe a genetic algorithm (GA) to place antenna elements on a platform, considering both the platform and the constraints in a typical scenario.

2. BACKGROUND

2.1 Cosite Interference Modeling and Mitigation Efforts

One of the earliest tools to study, analyze, and predict shipboard system degradation due to EMI was the COEDS (Communication Engineering Design System) tool, developed in the late 1980s by the University of Kansas under contract to the Naval Ocean Systems Center (NOSC) in San Diego, CA [1]. However, while COEDS was able to simulate and predict cosite interference, performance degradation, and resulting link performance based on each system's design specifications, there was no EM modeling of the antennas in-situ or the electromagnetic couplings due

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to the physical placements of multiple systems, and it was up to the user to modify these input specifications to design a workable set of system criteria that would offer an acceptable solution.

Cosite shipboard HF interference was also studied by AT&T Bell Laboratories in 1989 [2] as emerging naval requirements called for simultaneous transmissions of anti-jam and frequency hopping systems. However, this approach again considered mitigating this interference through hardware and transmission solutions, such as filtering and time-disciplined data transmission, and a study of antenna placement was not included.

The MITRE Corporation in 1990 [3] also reported their work on a Cosite Analysis Platform Simulation (CAPS) program to evaluate, through a discrete hop-by-hop simulation, a receiver's performance as a function of radio related parameters, such as receiver/transmitter characteristics, individual operator message statistics, hop rates, and frequency management techniques. ~~However, t~~They also included antenna-to-platform characteristics, such as antenna configuration, isolation, "rusty bolts" effects, and characteristics of supporting equipment. However, the study of multiple antennas and their relative placements on a platform to mitigate EMI was not a part of this study.

Modeling and simulating multiple antennas, their placement, and resulting cosite interference on-board a Navy ship was analyzed in 1996 by the Naval Command, Control, and Ocean Surveillance Center et. al. [4]. In order to determine the effects of adding the Army SINCGARS (Single Channel Ground and Airborne Radio System) to the shipboard environment, they needed to determine the interference that the SINCGARS frequency hopping (from 30-88MHz) would impose on existing collocated VHF receivers. Besides the cosite analysis interference modeling to determine undesirable received power from an interfering transmitter, a top-level study was also conducted to determine the antenna-to-antenna coupling loss or isolation. For this study, the antennas were modeled using a hybrid technique combining NEC method of moments simulations [5] and the geometric theory of diffraction (GTD) approach [6]. The ship under study (an LSD-41) was modeled first in NEC, using a wire-grid model gridded for the VHF frequencies under consideration, and then for Geometric Theory of Diffraction (GTD) analysis, using plates and cylinders to model the superstructure of the ship. In their hybrid analysis, the NEC code was used to determine the antenna input currents. These were then modeled in GTD as a "source" with those currents, and the coupling between various pairs of antennas identified. This computation was carried out for all combinations of antenna pairs and for three frequencies in each antenna's operating band to determine the isolation between that antenna pair for that potential placement.

A hybrid EM simulation technique combining full-wave techniques with circuit solvers was again proposed by the University of Michigan and US Army CECOM RDEC [7] for modeling cosite interference between multiple antenna systems on vehicular platforms. This hybrid time-domain analysis combined finite difference time domain (FDTD) and multi-resolution time domain (MRTD) methods with the TRANSIM object-oriented optimized SPICE-type circuit solvers, and a method of moments (MOM) code to simulate the cosite interference of a forest multi-path environment.

2.2 Genetic Algorithm Applications in Electromagnetics and Antenna Placement / Cosite Mitigation

Genetic algorithms have been successfully applied to optimizations in many different electromagnetics areas, including the design of Yagi antennas [8], loaded monopoles [9], electrically small antennas [10, 11], and ultra wide-band antennas [12] to list only a few. Some GA antenna optimizations have resulted in patentable designs, such as the genetically-improved transmit antenna for the Digital Ionospheric Sounding System (DISS) operated by the Air Force Weather Agency (AFWA) [13]. An excellent summary of efforts in this field can be found in *Genetic Algorithms in Electromagnetics* [14].

The application of genetic algorithm techniques specifically for the optimization of antenna placements has also been explored in recent years. A brief summary of three efforts, including an Air Force Institute of Technology thesis sponsored by Air Force Research Laboratory, array optimization research conducted by our collaboration partners at Southwest Research Institute, and a ARCON SBIR Phase I effort, are summarized here.

The use of a GA to determine the placement of multiple radiators on an aircraft to minimize coupling was studied by the Air Force Institute of Technology (AFIT) and the Air Force Research Laboratory (AFRL) in 2004 [15]. The goal of this research was to use a GA to determine the optimum arrangement of VHF antennas (150-300MHz) on a Boeing 747-200 aircraft platform which results in the lowest antenna-to-antenna coupling based solely on physical antenna positioning.

A secondary criterion was that this positioning must be accomplished without undue degradation of antenna performance, such as angular and polarization coverage. A hybrid EM computational solution was proposed for lower-fidelity fast electromagnetic solutions, which initially modeled the aircraft as a cylinder and considered only surface diffracted wave coupling mechanisms. Eventually a lofted Boeing 747 model was used for the computational platform and the placement of three movable antennas optimized. Long computational times led to the use of a seeded GA (rather than an initial random population) to speed up convergence.

SwRI has been optimizing the design of direction finding (DF) antenna arrays for shipboard, aircraft, land-based vehicles, and land-based sites for many years. While their research focus has been on DF arrays, they have also optimized communications antenna suites for large naval ships such as the Canadian Iroquois class ships and the TRUMP program. They have accomplished this work with the use of electromagnetic numerical models including NEC, WIPL-D, FEKO, and NEC-BSC and optimization algorithms including GA and PSO [16-21].

Antenna placement optimization via genetic algorithms was also studied in a 1997 SBIR conducted by ARCON Corporation for the US Air Force Radar Target Scatter Division (RATSCAT) at the White Sands Missile Range, Holloman AFB, NM. The RATSCAT test range required improved field taper incident on the target and reduced backscatter from clutter in order to measure targets with smaller radar cross sections (RCS). In this research, the ARCON team developed and delivered a genetically optimized placement of a three dish vertical X-band array for several target zones along the target support pylon [22].

In summary, while early efforts to mitigate cosite interference between multiple antennas on a platform focused on hardware techniques such as adaptive passive or active filtering, blanking, or simply turning systems off, advances in computational EM and global search algorithms, such as GAs, have led to the possibility of optimizing multiple antenna placements *a priori* to minimize EMI and antenna-to-antenna coupling. While optimal placement does not necessarily eliminate the need for hardware and filtering techniques, it provides a much better starting point for a compatible EM environment.

3. MODELING ENVIRONMENT

The selection of methods for modeling antenna systems *in situ* on the ship platform was a critical part of this initial research effort. The entire feasibility of using a genetic algorithm for antenna placements relied on rapid simulation of many antenna placement scenarios. Without this capability, GA optimization would not represent a viable technique for antenna placement optimization in any reasonable amount of design time. As such, each electromagnetic (EM) simulation needed to progress quickly, while still presenting results that reliably indicated which placement scenarios were better than others.

However, it was clear that each simulation did not need to accurately reflect the modeled EM environment with a great degrees of precision – it was only required that placement scenarios that would ultimately prove to be superior by a full and exact EM simulation, would also prove to be superior by a less-precise but more-rapid EM simulation. Thus, we searched for modeling “short cuts” that would allow for rapid evaluation of the members of the GA population while still accurately preserving features that could be used to compare modeling results and reliably select superior members.

3.1 Navy Ship Model

Our choices of modeling environment were further narrowed by the availability of valid EM ship models. With support from Southwest Research Institute (SwRI), we decided to model the DDG-51 Arleigh Burke Class destroyer, with Flight IIA antenna configurations using EM models supplied by SwRI. This new Flight-IIA configuration can be found on DDGs with hull numbers 79 and up, such as the USS WAYNE E. MEYER (DDG-108), recently christened in Bath, Maine on Oct 18, 2008. SwRI had numerically validated models of this ship and antenna configuration for several EM simulators, including NEC, FEKO, and WIPL-D. These electromagnetic models had been validated with extensive measured HF data from 0.25-30 MHz. The NEC model contained 7632 wires comprised of 7839 segments. The FEKO model has similar complexity, with 1706 triangles, 278 segments, and 2571 edges.

Within the valid frequency range for each model, we also had the potential to model up to five HF communications antennas on this platform, including:

- A twin fan transmit array from 2-9 MHz
- Twin 18’ whip antennas (configured as one antenna system) for transmit from 2-30 MHz
- A 35’ whip antenna for transmit from 9-30 MHz
- Two individual 14’ whip antennas for receive from 2–30 MHz

A NEC wiregrid model of this DDG-51 platform and antennas is shown in Figure 1. Antenna feed points are indicated by the red outlines.

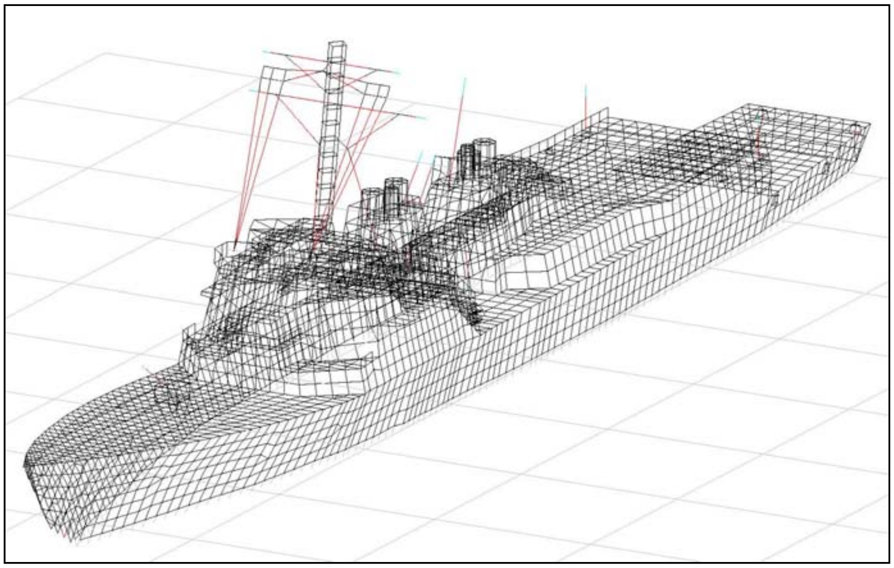

Figure 1. Wiregrid model of DDG-51 Arleigh Burke Class as rendered by EZNEC.

In Figure 2, we show the FEKO ship model of the DDG-51 with the calculated radiation pattern for the 14’ port aft whip antenna operated 5 MHz.

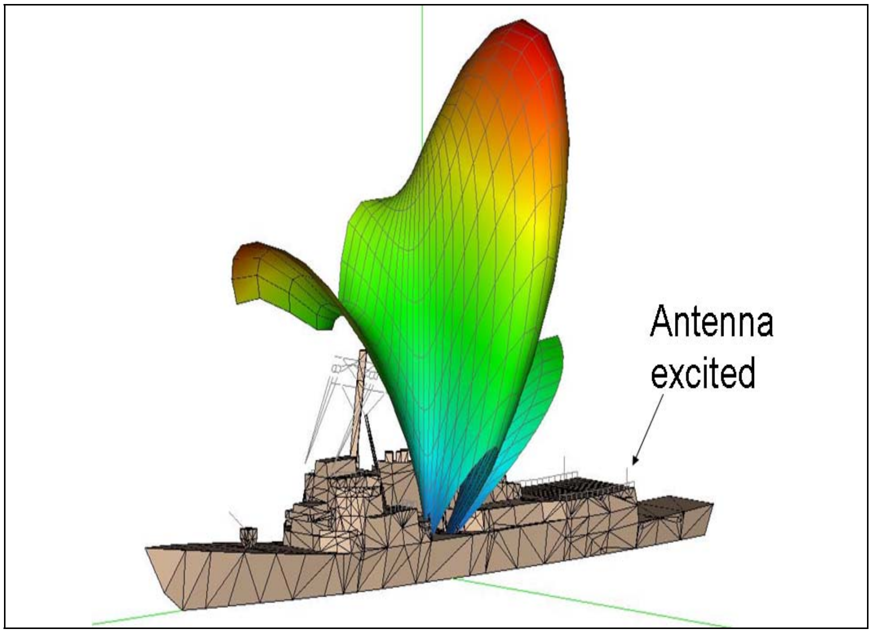

Figure 2. FEKO ship model with excited communications antenna

We explored modeling this ship platform with two different EM packages: the Numerical Electromagnetics Code (NEC 4.1), created by Lawrence Livermore National Laboratory (LLNL), and FEKO, a commercial code. As described in the following sections, we developed methodologies for both NEC and FEKO which de-embedded the antenna simulation from the ship platform simulation. Using these techniques, the large (and computationally-intensive) ship model could be simulated separately from the antenna models and the results stored. Note that this ship platform simulation needed to be accomplished for each frequency of interest. The antenna models were then combined with the ship simulation to obtain results for the composite EM structure, once again at a given frequency. ***As the antenna(s) were relocated by the genetic algorithm, only the new composite simulation needed to be performed, thus providing significant increases in computational speed.***

In the following sections, we describe the NEC and FEKO codes and our procedures for de-coupling, simulating, and then recombining antenna and ship simulations for each code.

3.2 NEC Modeling

The Numerical Electromagnetics Code (NEC) is an antenna modeling method for wire and surface antennas developed by Gerald Burke from Lawrence Livermore National Laboratory (LLNL) [5]. Originally written in FORTRAN in the 1970s, the code is based on the method of moments solution of the electric field integral equation for thin wires and the magnetic field integral equation for closed, conducting surfaces. The algorithm has no theoretical limit on the number of segments that can be simulated and can be applied to very large arrays or for detailed modeling of very small antenna systems. For this project, we primarily employed GNEC from Nittany-Scientific (www.nittany-scientific.com), as its multi-threaded option allowed NEC4 to be run across multiple processors and cores for decreased computational time.

The Numerical Green's Function (NGF) option in NEC proved to be crucial to this effort, as it allows a fixed structure and its environment to be modeled, and then the factored interaction matrix to be saved to a file. New parts may then be added to the model in subsequent computer runs, and the complete solution obtained without repeating calculations for the data on the file. Hence, the main purpose of the NGF is to avoid unnecessary repetition of calculations when part of a model (such as one or more antennas) in a complex environment, will be modified one or more times, while the environment remains fixed. This was exactly what was needed for this project.

With the NGF option, the self-interaction matrix for the fixed environment (in our case, the ship) is computed, factored for solution, and saved on a disk file as a `.WGF` file. When a new antenna position needs to be solved for, this simulation only requires the evaluation of the self-interaction matrix for the antenna, the mutual antenna-to-environment interactions and the matrix manipulations for the partitioned-matrix solution. When the previously written NGF file is used, the free-space Green's function the NEC formulation is, in effect, replaced by the Green's function for the environment.

The `.WGF` file ~~is~~ can be quite large – for the DDG-51 model, it was ~1.3 GB. Note also that this file is only valid for a single frequency, and must be created for each frequency of interest.

Our testing showed that the use of a Numerical Green's Function (`.WGF`) file greatly reduces the amount of CPU time required per genetic antenna chromosome evaluation. In Table 1, we compare the CPU times required for running the full DDG-51 NEC model to the CPU time required for using the Green's Function `.WGF` file of the ship with the antenna added at a new location. For these simulation runs, the 18' aft port whip was removed from the ship model (and hence not represented within the `.WGF` file), but rather added later in the composite run. For these simulations, all other antennas remained in the original DDG-51 configuration positions and were embedded within the `.WGF` file.

The simulations were performed on a Dell Latitude laptop with 2GHz dual-core processor, 2GB ram, and 150GB disk. Table 1 shows that the CPU time for antenna evaluations using the `.WGF` file was about 12% of the CPU required for the total "ship + antenna" NEC run. However, because we were writing and reading the `.WGF` file to and from the laptop disk (rather than using a RAM disk), the total runtime for the antenna evaluation using the `.WGF` file was greater than the individual NEC run (which did not require much disk activity). We were unable to test a RAM disk configuration on this machine, as the `.WGF` file was 1.3 GB in size (and we only had 2 GB physical RAM available). However, it is clear that the decrease in CPU time using this technique makes it a viable consideration for dramatically reducing the total amount of time per run. In the future we plan to test this technique and the resulting speed increase more thoroughly on a 64-bit workstation (with 16GB physical memory) so that a RAM disk may be created for the Green's file to obtain a better evaluation for the efficacy of this technique.

Table 1. Runtime and CPU usage comparisons with and without Green's Function creation and usage.

	CPU Time	Total Runtime
Entire ship and antenna NEC file	17:33 16:25	655 sec 576 sec
Creating ship Green's Function `.WGF` file	29:48 26:53	4981 sec 4632 sec
Using ship Green's Function `.WGF` file w/ antenna	02:01 01:48	2485 sec 1444 sec

Another technique suggested by SwRI was the simulation of multiple antenna positions per NEC run file. Since the possible antenna locations on ships is often very limited, it could prove to be more efficient to install an antenna at every possible location (provided the coupling is not great) and run all of them at once, picking the best one. This methodology should be investigated further in the future.

3.3 FEKO Modeling

FEKO is a set of commercialized, computational electromagnetic (CEM) software packages. Its comprehensive electromagnetic (EM) analysis can assist users to solve a wide range of electromagnetic problems (www.feko.info). FEKO is based on the accurate full-wave Method of Moments (MoM) which is fully hybridized with several other techniques including the Finite Element Method (FEM) and efficient high frequency approximation techniques such as Physical Optics (PO), Geometrical Optics (GO), and Uniform Theory of Diffraction (UTD). FEKO also offers the Multilevel Fast Multipole Method (MLFMM) in order to reduce the computational time

The combination of the MLFMM and the high frequency techniques, in particular, allow the efficient analysis of a wide range of EM problems in realistic operating environments. Those EM problems include the optimal antenna placement on large platforms like ships or aircraft, cable coupling (EMC) analysis of complex cable bundles in vehicles, and radiation hazard analysis for humans in close proximity to antennas that are mounted on large structures like mobile phone base stations. This particular ability distinguishes FEKO from the other popular EM codes.

The full ship model is reasonable to run at HF frequencies but becomes unfeasible at higher frequencies. For instance, consider the FEKO ship model in Figure 2. At 1 -- 10 MHz, the memory requirements are very reasonable and the model runs in just a few minutes on a PC (Table 1). At 100 MHz, the full ship model cannot be solved on a PC because of memory limitations. As a result, only the relevant portions of the ship can be included in the model with the antennas of interest. In order to accomplish this task, the FEKO model is reduced in size to include only relevant portions of the ship. The surfaces that will hold the antenna are separated out as well. This portion is gridded and stored in memory. Most of the ship does not have to be re-gridded each time the function is called, thus saving precious time. The antenna and surfaces that it will be placed on are developed and moved in PREFEKO. The antenna and antenna surfaces must have a new grid at each function call.

Table 2. Segment size and memory requirement for the ship model at 3 different frequencies.

frequency	wire segments	metallic triangles	memory
1 MHz	278	1706	70 MB
10 MHz	356	3283	230 MB
100 MHz	2096	157899	70 MB (using FMM)

Note that for the 100MHz frequency results in Table 2 we employ the fast multipole method (FMM). FMM accelerates the iterative solver in the method of moments by expanding the system Green's function using a multipole expansion that groups sources lying close together and treats them like a single source. By treating the interactions between far-away basis functions using the FMM, the corresponding matrix elements do not need to be explicitly stored, resulting in a significant memory requirement. The FMM can reduce the matrix-vector product in an iterative solver from $O\left(N^2\right)$ to $O\left(N \log N\right)$. If FMM were not used here, the memory requirement would have been 427 GB for the normal MoM instead of the 70 M .

3.4 When Do We (Really) Need EM Simulation?

As stated earlier, one of the major goals of this research project was to reduce the numbers and durations of EM simulations required during the genetic evolution. In a worst-case environment, it would be necessary, for each proposed antenna placement, to excite and simulate each antenna individually (and possibly in concert with other antennas) to determine the effect that the proposed placement has on each antenna. Realistically, however, there will be many placements and incremental changes in placement for an antenna which do not affect the behavior of some subset of the other antennas.

Our goal then was to determine the “comfort zones” for each antenna, i.e. those regions for which, if another antenna moved within, a re-simulation is necessary, but for which movement of other antennas outside of those regions would not require re-simulation. We determined that this should be a distance of about 1/2 - 1 λ, which would be straightforward to define and verify using a simple series of numerical model runs. A further realization was that the “comfort zones” (for *Antenna A)* may vary for *Antennas B, C,* etc, and that the placement of some antennas may not affect *A* at all, while the placements of other antennas may induce more coupling and interference.

For future research in this area, we anticipate using both user input and automatically acquired experience (i.e. learning) to define these comfort zones. The user could initially define a physical area around an antenna *A* for which, movement of another antenna *B* within that region triggers a subsequent re-simulation of *A.* However, it was expected that these areas may be unknown or uncertain. Hence, we also plan on employing a learning system (either an expert system or neural network) which would train *in situ* to determine when re-simulations are required. Initially, many re-simulations might be necessary, as the system learned where interactions occur or do not occur by observing how the pattern of antenna *A* is affected by various placements of *B.* However, after training via observation, we expect this system to eliminate re-simulations of antennas which are outside of the comfort zone of an antenna and which have been shown by previous simulations to not to be affected by movements of that antenna outside that zone.

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Note however, that any final solutions require re-simulation of all antennas to verify their performance in the final configuration. Additionally, some spot-checking of the “comfort zone” definer is warranted to verify that its predictions regarding non-interference conditions are valid.

4. GENETIC ALGORITHM METHODOLOGY

There were three areas of concern in developing the methodology for this genetic antenna: selection of the GA and chromosome representation, generation of the antenna subspaces, and development of the cost function. In the following sections, we briefly discuss each of these areas.

4.1 Overview of Genetic Algorithm Design

The design of a GA begins with the design of the chromosome and the cost function. The chromosome is a method to encode potential problem solutions. While the very first simple GAs used binary encoded chromosomes, there are now mechanisms for real-valued and mixed-valued (both real and integer value) chromosome representations [23]. When the variables are naturally quantized, the traditional binary GA, which encodes the values associated with the variables into a binary number, is a good choice of algorithm. However, when the variables are continuous, it is more logical to represent them by real numbers.

The cost function is used to compare different solutions against each other to determine which are better. The cost function evaluates the combination of input parameters (a proposed solution) represented by the chromosome to determine by more figures of merit how well this solution meets the desired optimization goals.

After the chromosome representation and the cost function are established, the GA begins with an initial population. This initial population is random but may be seeded with good solutions developed outside the GA (by experimentation, rules of thumb, etc.). The solutions represented by each member of the population are then evaluated and ranked using the cost function and the figures of merit to determine which are better. For problems which require more than one figure of merit, a weighted aggregate combination is used in a simple GA. There are also multi-objective GAs which optimize for multiple goals independently.

Good parents are selected and then used in recombination to create children. Various methods of selection have been proposed and utilized; the general idea is to favor picking better parents (i.e. those with higher figures of merit) over those with lower figures of merit, while maintaining sufficient diversity within the population to allow for global exploration. There are a variety of possible recombination methods. For binary-encoded chromosomes, uniform or multi-point crossover is common, where portions of the parent chromosomes are swapped to exchange genetic information. For real-valued chromosomes, averages or weighted “mixings” of the input parameters or polynomial fits, for three or more parents, are often used.

After new chromosomes are created by recombination of the parent chromosomes, these children undergo possible mutation which introduces new genetic material into the population. Binary chromosomes can be mutated by inducing the probability of random bit changes; for real-valued chromosomes, parameters may be randomly offset or replaced with an entirely new random value. After mutation, this new population is evaluated and ranked, and the next generation is created. The process continues until an acceptable solution is found, convergence occurs (solutions do not continue to improve), or a predetermined maximum number of iterations is reached.

The methods for selection, recombination, and mutation, along with population sizes and mechanisms to preserve numbers of parents into the next generation (elitism) constitute internal variations of the simple GA [24,25]. Common GA tailoring techniques include: changing the mutation rate as the algorithm proceeds, changing cross-over boundaries (intra-parameter vs. along parameter boundaries), and awarding higher figures of merit for diverse chromosomes (i.e. those who are generally dissimilar in parameter space from the majority of the population).

The simple operations of selection, recombination, and mutation act to combine pieces of salient information (called schema) from multiple superior solutions together [26]. The general theory is that chromosomes with some of these good schema should perform better than other chromosomes without them and therefore be selected as parents. Through recombination, good schema representing different parts of a superior solution have the chance of occurring simultaneously within the same chromosome to create an even more-superior solution. Mutations allow for small changes to occur in the schema and new genetic material to be introduced which may not be present in the initial population.

Over many iterations, we want the GA to generate a chromosome which contains all the best schema and which represents the best possible solution to the problem. In a simple GA, that sometimes happens. Other times, especially in multi-modal problems, the GA converges prematurely to a non-optimal solution which represents a local minimum. Depending on the problem, the solution represented by one of these local minima might still be quite acceptable as a solution to the problem; however, one should be careful about declaring this to be an optimal solution.

4.2 Antenna Placement Chromosome Representation

The basic chromosome proposed for this antenna placement GA consisted of a number of sub-chromosomes containing placement and orientation information for a particular antenna or antenna system, as shown in Figure 3. There was no requirement for these sub-chromosomes to be identical, as some antennas may have more placement variables than others. It is also conceivable that the user may wish some optimization within the antenna design itself, and this is a viable addition to the chromosome representation.

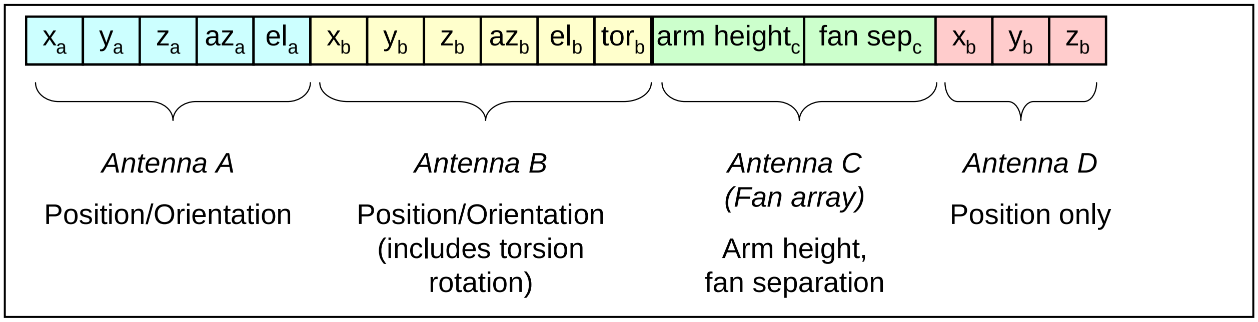


Figure 3. Chromosome layout depicting four potential sub-chromosome types for antennas A thru D.

Within each sub-chromosome, the physical position of the antenna would be encoded using Cartesian coordinates. Orientation information, such as azimuth and elevation pointing angles, would be encoded in either polar or spherical coordinates as required by that system. For example, a whip antenna could require only position information, if a vertical orientation is specified, or require both azimuth and elevation angles if an orientation other than vertical is used. Other antennas, such as reflectors or arrays would similarly have both azimuth and elevation angles. One could also conceive of antennas that may require a third degree of orientation information, although this would be the exception rather than the norm.

It is also possible that the user may require optimization of an antenna configuration itself *in situ*, without any required repositioning of the basic antennas structure. For example, on the DDG-51 destroyer model we studied, it would be impractical to move the entire fan array as the attachment points are well-specified. However, variations in this array's performance can be achieved by repositioning the horizontal attachment arm of the array or the separation between the fans for better excitation of the ship. Since there was no requirement for the sub-chromosomes to be identical, optimizations of antenna parameters within the fan (or other antenna designs) could be conducted as part of this overall genetic placement optimization.

4.3 Antenna Placement Genetic Algorithm

A continuous parameter genetic algorithm [24] such as presented in *Practical Genetic Algorithms* proves a good initial choice for the genetic algorithm for this antenna placement optimization. Shown in Figure 4, this GA is similar to a binary GA with the primary difference being that the variables are not represented by bits of zeros and ones, but instead by real numbers over whatever range is deemed appropriate. All variables in the continuous GA are normalized to have values between 0 and 1, and later unnormalized in the cost function.

The GA begins with an initial population of N_{pop} chromosomes with values created by a uniform random number generator. A matrix represents the population with each row in the matrix being a $1\times N_{var}$ array (chromosome) of continuous values. Given an initial population of N_{pop} chromosomes, the full population matrix contains $N_{pop}\times N_{var}$ random values. Each chromosome is evaluated by the cost function, so it has an associated cost. Next, natural selection allows only the best chromosomes to breed, while the rest are discarded. The mating and mutation processes create new chromosomes that need to be evaluated by the cost function. This iteration continues until a satisfactory solution is found. Tournament selection is used to pick a group of chromosomes for potential mating. A small subset of chromosomes (two or three) is randomly selected from the mating pool, and the chromosome with the lowest cost in this subset becomes a parent. The tournament repeats for every parent needed.

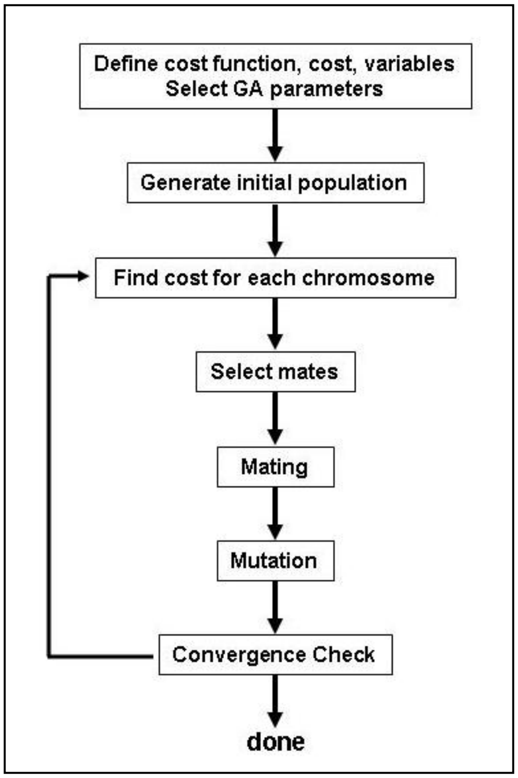


Figure 4. Flow chart of a continuous GA

The mating approach used here randomly selects a variable in the first pair of parents to be the crossover point

$$\alpha = \textbf{roundup}\{\textbf{random} * N_{var}\} \tag{1}$$

The selected variables are in same position in the two parents.

$$\begin{aligned} parent_1 &= [\,p_{m1}p_{m2}\cdots p_{m\alpha}\cdots p_{mN_{var}}\,] \\ parent_2 &= [\,p_{d1}p_{d2}\cdots p_{d\alpha}\cdots p_{dN_{var}}\,] \end{aligned} \tag{2}$$

where the *m* and *d* subscripts discriminate between the two parents. Selected variables are combined to form new variables that will appear in the children:

$$\begin{aligned} p_{new1} &= p_{m\alpha} - \beta[p_{m\alpha} - p_{d\alpha}] \\ p_{new2} &= p_{d\alpha} + \beta[p_{m\alpha} - p_{d\alpha}] \end{aligned} \tag{3}$$

where β is also a random value between 0 and 1. The final step is to complete the crossover with the rest of the chromosome as before:

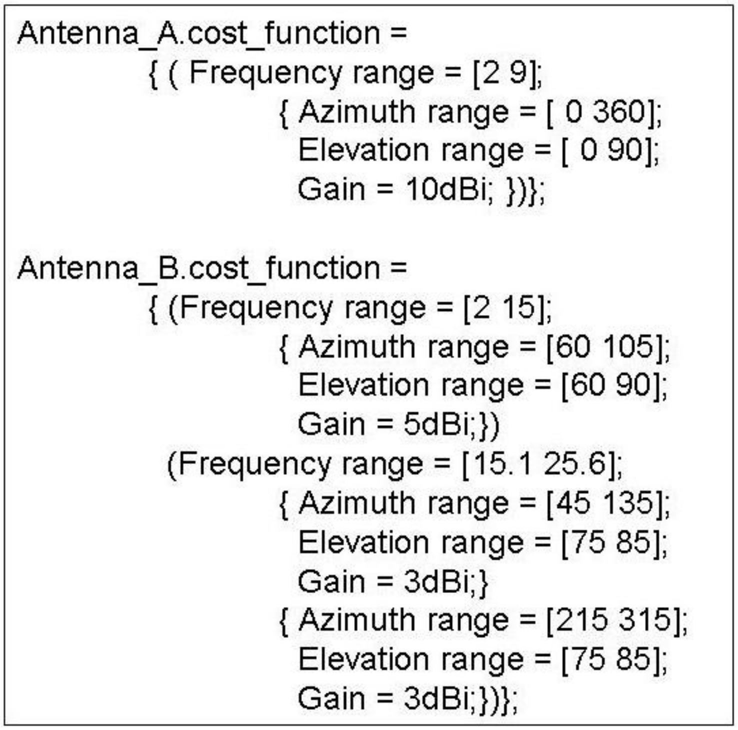
$$\begin{aligned} offspring_1 &= [p_{m1} p_{m2} \cdots p_{new1} \cdots p_{dN_{var}}] \\ offspring_2 &= [p_{d1} p_{d2} \cdots p_{new2} \cdots p_{mN_{var}}] \end{aligned} \tag{4}$$

Random mutations alter a certain percentage of the variables in the population other than the lowest cost chromosome which remains unaltered.

As the parameters are represented by continuous numbers, there is no need for the user to predetermine the accuracy of final solution or to translate placement and orientation parameters into a binary representation and back. Extensions to this basic algorithm, such as decreasing or cyclic mutation rates and transitioning mutation type from random to offset (with a variable standard deviation) will be explored. Additionally, we will need to ensure population diversity by never allowing duplicate chromosomes within the population, which would represent duplication solutions and wasted simulation time. A minimum solution granularity (i.e. the point at which two very close positions are declared identical) is also warranted in this problem to ensure that antenna placement is not specified to sub-millimeter precision.

4.4 Cost Function

The figures of merit that were considered during the initial phase of this research included directionality, omni-regularity, and spectrum utilization efficiency. For each proposed positioning of an antenna or antenna system to be optimized (***Antenna A)***, we wanted to examine not only the effect of this new position on that antenna's radiation pattern, but how this positioning affected other antennas ***(Antennas B, C, … N)*** within the same frequency band. In our cost function, we consider the radiation patterns of multiple antennas, across the azimuth and elevation regions of concern. These regions and desired radiation pattern performance would be defined by the user as part of the GA initial setup.



```
Antenna_A.cost_function =
          { ( Frequency range = [2 9];
                    { Azimuth range = [ 0 360];
                      Elevation range = [ 0 90];
                      Gain = 10dBi; })};

Antenna_B.cost_function =
          { (Frequency range = [2 15];
                    { Azimuth range = [60 105];
                      Elevation range = [60 90];
                      Gain = 5dBi;})
            (Frequency range = [15.1 25.6];
                    { Azimuth range = [45 135];
                      Elevation range = [75 85];
                      Gain = 3dBi;}
                    { Azimuth range = [215 315];
                      Elevation range = [75 85];
                      Gain = 3dBi;})};
```

Figure 5. One potential syntax for describing desired radiation pattern attributes for each antenna. The composite cost function would consist of a weighted combination of individual antenna scores. Additional characteristics, e.g. polarization or minimum gain may be added as necessary.

While the exact syntax of the cost function definition files will be determined in future research, the basic concept entails defining two-dimensional angular regions within the operational radiation hemisphere and the minimum acceptable radiation required for each region. We allow for the possibility that there may be a frequency dependence on these criteria, i.e. the minimum acceptable radiation and/or angular regions may differ depending on the operational frequency, and there may be requirements for polarization characteristics as well. The maximum allowable radiation within an angular region could also be a desired optimization goal for the antenna radiation pattern, to address RADHAZ concerns, and our approach allows that to be added to the cost function definition.

Therefore, the construction of the overall multi-antenna cost function consisted of a weighted expression considering the fitness of each antenna as compared to a user-defined desired set of criteria. These criteria may range from a simple expression requesting, for example, 10dB omni-directional gain from 2-9MHz, to a more complex expression detailing angular regions and frequencies and the desired minimum (and/or maximum) radiation within those regions at those frequencies. A sample of one potential syntax definition for two antennas is shown in Figure 5.

4.5 Methodology to Find and Use Antenna Subspaces

Our initial investigations in this area indicated that the placement of many of the antennas would be constrained by the user. This was advantageous, as it limited the function space representing possible placements, which will speed up the optimization. If these areas proved to be very restricted, they could also be used to define and refine the "comfort zones" defined earlier in Section 3.4. Certainly, if the placement of two disparate antennas was constrained so that each was physically isolated from the other, then the physical distance would make it easy to rule out some forms of interference.

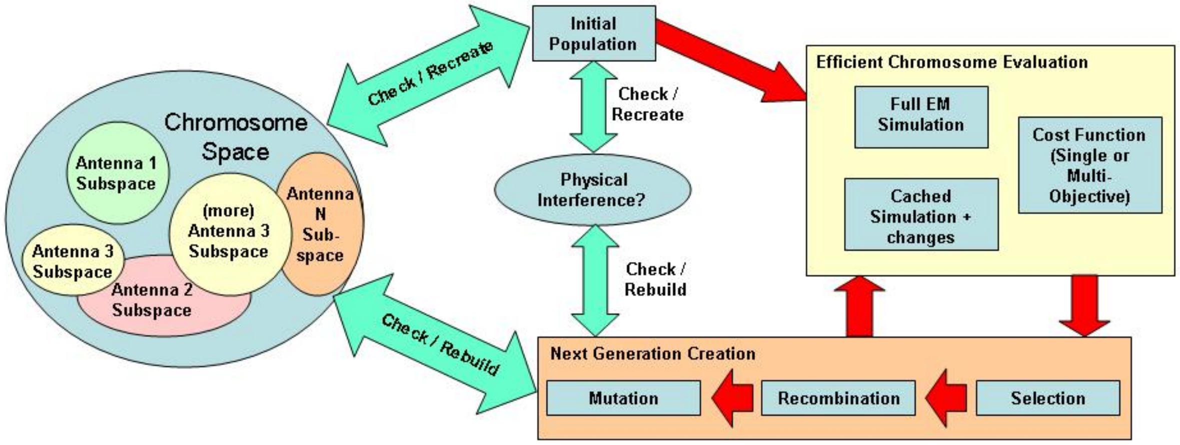
We anticipated at least three possible scenarios regarding antenna subspaces. First, the antenna may already be located on a platform area, and optimization choices may be limited to moving the antenna within the constraints of that physical platform and adjusting the antenna azimuth and elevation orientation. A second option may be where there are more degrees of freedom, for example both the antenna on the platform, and the platform on the ship may be allowed to move within some restricted area. This is somewhat more difficult to model. Finally, there is the case where an extended area of positionings are allowed, for example "anywhere along the rail", or "up on the mast".

Depending on the genetic representation of the chromosome, it is likely that there would be potential solutions emerging from the genetic recombination and mutation which locate antennas in unacceptable positions. While one could envision a chromosome encoding for which all possible gene values (for *Antenna A)* are "mapped" into valid antenna placements for *Antenna A* (etc.), an elegant encoding method such as this seems unlikely outside of some very simple placement areas (for example, a rectangle). Much more likely, is the fact that valid antenna placements will occur within the bounds of restricted, irregularly shaped (and possible discontinuous) areas. As such, the random mechanisms of recombination and mutation will produce chromosomes with antenna placement genes which are sometimes invalid.

There are several obvious methods for dealing with invalid antenna placement and orientation genes that lie outside the known workable subspace, including: 1) discarding (or severely penalizing) the entire chromosome; 2) repairing the bad antenna gene by moving it to the closest position within the known good subspace; or 3) replacing it with a random gene from within the known good subspace.

A fourth method conceptualized during our research involved checking the validity of the antenna placement genes during the actual recombination and mutation operations within the GA. As these operations typically involved random mixing of parameters between two parents, this operation could be repeated multiple times until a gene representing a valid placement and/or orientation was obtained. Similar "early intervention" and correction could also be applied in the subsequent mutation phase.

This method was preferable for several reasons. Discarding the entire chromosome throws away many genes which may represent valid and useful placements for the other antennas under consideration. Severely penalizing the chromosome makes it likely that it will be discarded subsequently and causes that EM simulation to essentially be wasted time. Repairing the bad gene by moving it to the closest position within the subspace introduces statistical biases towards the edges of the function space which could impair convergence towards a global optimum solution. Replacing with a random gene presents a reasonable choice; however it eliminates potentially good inheritance that could have been achieved by blending those two parent genes and therefore biases the genetic algorithm away from schema-based building blocks and towards more random searching.



- **Within all possible antenna placements (x,y,z,θ,φ), subspaces are created for each antenna indicating valid physical placement and reasonable electromagnetic performance**
- **Antenna genes are selected randomly from antenna subspaces to create initial population**
- **Potential solutions are filtered for physical interference, recreated if necessary**
- **Population is simulated and ranked with cost function. Cached simulation results used if available**
- **Next generation chromosomes are created from high-ranking parents and are checked for physical interference and location within good antenna subspaces. Only viable antenna placement candidate solutions are created within the next generation population**

Figure 6. Conceptual use of antenna placement subspaces to create or verify initial population and to verify or genetically correct next generation chromosomes.

Therefore, our methodology developed a filtering system within the GA itself (shown in Figure 6) to validate potential antenna placements against a set of user constrains while the child chromosomes are being created. Iterative recombination and/or mutation is performed until valid positions are obtained for each antenna. No child is created with damaged, unviable positioning or orientation genes; all chromosomes created by the genetic process represent viable candidates (within the tolerances and intelligence of our sub-chromosome gene screening algorithms).

5. CONCLUSIONS

In this paper, we described the methodology for a genetic algorithm designed to optimize the positioning of multiple antennas on a ship-board platform. This is a difficult application to apply genetic optimization to, given the extensive time required for complex electromagnetic simulations. In developing this methodology, we concentrated on two major areas: 1) reducing the amount of time required to simulate an antenna placement scenario in order to make a judgment as to the relative superiority of a chromosome compared to its peers, 2) reducing the number of full simulations that need to be performed by learning where correlations do and do not exist between antenna placements, and 3) reducing the number of chromosomes that require the time-intensive EM simulation by preprocessing chromosomes to repair or eliminate unviable candidates before any simulations are performed. While these strategies were developed for this particular application, most would be suitable for other complex military optimization problems in which the time required to evaluate a chromosome is extensive and prohibitive to the use of a simple genetic algorithm.

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