D.W. Ansell¹, Dr. E.J. Hughes²

1, BAE Systems, UK, 2, Cranfield University, UK.

ABSTRACT

In this paper, a new and novel method for optimisation of subarray partitioning is presented that is inspired from a biological process. The process is optimised using a recent multi-objective genetic algorithm (MOGA) and demonstrated on a 15 x 15 element conformal array antenna. In installed arrays, element gain patterns are affected by mutual coupling and manufacturing tolerances and this optimisation technique takes these changes into account in order to optimise installed performance. Six objectives are used in the MOGA to optimise desired characteristics in the radiation pattern.

INTRODUCTION

Conformal array antennas are becoming increasingly important in the designs of future radar and communication systems, but do not enjoy the same coverage in the literature as planar array antennas.

The synthesis of conformal arrays is more complex than with planar arrays as the elements can all face in different directions. Therefore knowledge of the 'embedded' or 'active' element patterns must be considered when optimising operation and control variables. This is especially true in smaller arrays where the mutual coupling between elements is usually more significant. The mutual coupling coefficients can be estimated using a method of moments analysis, but it is better to use real measured patterns that can be stored and used in the optimisation process to improve accuracy of the results.

Once knowledge of the embedded patterns are known (or have been estimated), the complex excitations needed to steer the beam and reduce sidelobes can be optimised in order to give good installed performance. This is especially important in conformal arrays that generally exhibit higher sidelobes than planar arrays.

With a priori knowledge of the embedded patterns that include the affects of any EM coupling and radome distortion, it is possible to include them in an optimisation algorithm to improve the installed performance of an array. The problem is complex, with many hundreds of input variables (or thousands in large arrays) and multiple conflicting antenna performance objectives. The number of possible excitation sets is huge. One way to reduce the massive search space of possible excitation sets, is to partition the array into subarrays and apply a common excitation at the subarray level rather than at the element level. This raises the question of the best subarray partitions to use and the optimal excitation set to apply.

Genetic algorithms (GAs) are particularly well suited to complex problems of this type. This paper describes the application of Zitler's Strength Pareto Evolutionary Algorithm II (SPEA2) (1) to the optimisation of the complex excitations for a 225 element conformal array antenna (Fig. 1). A new and novel method for optimising the partitioning of conformal arrays into subarrays is also presented. The subarray partitioning is optimised simultaneously with the array excitations using SPEA2.

THE OPTIMISATION PROBLEM

In a standard or simple genetic algorithm (SGA), 'populations' of 'individuals' (solutions) are evolved in parallel over a number of 'generations' (iterations). An SGA samples the search space stochastically and is far less likely to converge on non-global optima than many of the classical optimisation techniques.

The SGA is generic and relies on a distinct 'fitness function' to calculate a measure of success for an individual during the optimisation process. In antenna optimisation, the fitness function may be monitoring sidelobe levels, beamwidth or gain. The fitness function is usually the most computationally expensive part of the algorithm as it involves synthesis and analysis of the antenna pattern. This is especially true when optimising large arrays.

When multiple objectives are to be optimised simultaneously, there is often more than one optimal answer. Solutions may be found that are good on one objective, but bad on another, forcing the designer to trade one objective for another. The set of optimal solutions is often called a trade-off surface, or more correctly, a Pareto optimal set.

SGA's converge to a point on the Pareto set and so provide a single optimised solution to a problem. This presents the system designer with little or no information on the shape of the Pareto trade-off surface unless multiple runs are of the optimiser are performed and the results are diverse (which is not usually the case). When multiple objectives are evident in a problem, they must be combined in some way in a SGA in order to form a single objective. This is usually achieved by forming a (weighted) sum of objectives. When maximising a function, summing objectives can cause a SGA to oscillate around two or more maxima on the cost surface and leave concave regions of the Pareto set undisclosed.

Multi-objective Genetic Algorithms (MOGAs) however, carry only a marginal increase in processor overhead compared with SGA's and evolve a set of solutions to describe a diverse Pareto optimal set in objective space. In the case of antenna optimisation, the optimised trade-off surface delivered by the MOGA presents the designer with a choice of optimised operating points for the system. In theory, unlike a weighted SGA, all points on the surface described by the Pareto set could be found with a MOGA.

Antenna array excitation optimisation problems have very large search spaces due to the high numbers of elements and degrees (bits) of amplitude and phase control available. The use of subarrays reduces the number of the excitation values needed as a single excitation can be applied at the subarray rather than element level.

The method described below for finding optimal subarray partitions and excitation sets for good antenna array performance is one of effective genotypic representation in the evolutionary algorithm.

In a real array, in order to optimise beampattern performance to the highest possible degree, the subarray partitioning and excitations must be optimised simultaneously, taking into account the actual embedded gain patterns for each element. The method for performing this optimisation is described below and demonstrated on a conformal array antenna (Fig. 1).

LITERATURE

There are relatively few papers published concerning optimisation of subarrays using GA or EA techniques. Wang et al (2), proposed a GA method for the optimisation of seismic array subarray configuration. In their paper, the SNR performance of a 20 element array with inter-element spacing of 2.5km was optimised using a SGA. The algorithm formed simple subarrays by switching off certain elements in the array.

Haupt applied a GA to pre-defined subarrays and found optimum excitation tapers to apply to the subarrays with encouraging results (3). More recently, López et al (4) optimised linear array partitions and weights using a SGA.



Figure 1. Conformal Array Geometry. This is the testcase 225 (15 x 15) element array under optimisation. The lines projecting from the rear of the elements illustrate the pointing angle of each element. Array element spacing is 0.5λ in a 7 GHz system.

SUBARRAY PARTITIONING METHOD

The method presented in this work for partitioning the antenna array into subarrays was inspired by the biological process of cell division. Single celled organisms such as amoebas, divide into two new cells by a process known as binary fission. The cells have to grow before they can divide, and so the speed with which they grow, to some extent determines their division rate. If we place together N live cells (each with a different growth rate) and observe their numbers over time, the twodimensional area occupied by each cell type will grow and form a 'footprint' below each cell type. This footprint will be unique in shape and area. The shape of the footprint is determined by the initial starting location of each 'seed' cell, the growth rate (cell division) rate for each cell and the initial position of each new cell formed. It is this biological process that has been modelled to represent the division of array elements into subarrays.

To demonstrate this method, consider a simple $9 \ge 9$ element planar array. We initially form a $9 \ge 9$ grid which represents the possible element locations in the array. The first step is to temporarily divide this grid into the required number of subarray partitions.

We then choose nine divisions and randomly place four seed 'cells' in each of the partitions (Fig. 2). The number of cells need not be fixed at four and can be varied by the user or by the optimisation process. The partitions are then discarded.



Figure 2. Initial subarray seeds.

We then randomly create an array of growth rate variables R_{cell} , where $0 \le R_{cell} = <1$. A final array P_{cell} is created in memory that acts as the trigger for cell reproduction. Initially P is set to zero and each value in P refers to the corresponding element located on the grid.

The pseudo code to describe this process is given by:

```
While array is not full:

T = T + 1

For all existing cells

P_{cell} = P_{cell} + R_{cell}

If P_{cell} > 1

Form new cell of same type, placing

new cell at nearest available

orthogonal grid position.

End If

End For

End While
```

Each loop of the code represents one time period, T, during which the existing cells have time to 'grow'. Once they have reached a trigger size (as stored in P_{cell}) they divide. Each new cell formed occupies the first available grid position in a north, west, east and then south order.

Although the grid is planar, the grid positions can easily represent conformal array element locations and so is suitable for both classes of antenna.

MULTI-OBJECTIVE SUBARRAY AND RADIATION PATTERN OPTIMISATION

To generate an entire array excitation set for the 15×15 array, including the 15 subarray partitions, 270 variables need to be optimised by the MOGA. This are broken down as:

- 15 x amplitude variables,
- 15 x initial seed location variables,
- 225 (15 x 15) x growth-rate variables.

In order to apply the MOGA, we have to represent a solution to our problem using a genotypic representation of the variables (a chromosome encoding scheme).

The genotypic encoding schemes used to represent the above variables had to be resistant to the genetic operators of crossover and mutation; that means they must produce valid chromosomes after these operations have occurred.

Three real-valued chromosomes were used to represent a solution. The first ch1, was used to represent the amplitude values. The second ch2 encoded the initial seed locations and finally ch3 contained the growth-rate variables.

GENERATION OF UNIQUE ELEMENT GAIN PATTERNS

For this theoretical study, unique randomised element gain patterns were generated and stored in a look-up table for use in the optimisation process. The gain patterns were generated by starting with a theoretical cosine pattern and then distorting at different angles by randomly attenuating the gain. The randomised plots were then 'smoothed' by calculating a polynomial approximation to each one. The polynomial approximation curve served as the unique gain patterns. When optimising the installed performance of a real system, the gain patterns would first have to be measured or estimated for use in the optimisation process.

CONFORMAL ARRAY SYNTHESIS

In order to determine the success of a solution (defined by one set of chromosomes), it is necessary to model the far field pattern of the antenna. The far field radiation pattern of the conformal array was calculated using:

$$F(\theta,\phi) = \sum_{n=1}^{N} a_n \exp(j\alpha_n) \exp[jk(x_n \sin\theta\cos\phi + y_n \sin\theta\sin\phi + z_n \cos\theta)] FE_n(\theta_i,\phi_i)$$
(Eq. 1)

The steering phase required to steer the beam to $\theta_{\alpha}, \phi_{\alpha}$ was calculated using:

$$\alpha_n = -k[x_n \sin(\theta_o - \theta_n)\cos(\phi_o - \phi_n) + y_n \sin(\theta_o - \theta_n)\sin(\phi_o - \phi_n) + z_n \cos(\theta_o - \theta_n)]$$
(Eq. 2)

The multiple objectives used in the MOGA were chosen to characterise important defining features of the radiation pattern. The first fitness measure f1, measured mainlobe gain and was encoded for maximisation, while f2measured the maximum sidelobe level (minimisation). The third, f3, measured the maximum sidelobe level within $\pm 40^{\circ}$ of the mainlobe (minimisation). Both the azimuth and elevation beamwidths were measured and stored as f4 and f5 (both minimisation), with the magnitude of the difference between them being stored as another objective f6 (minimisation) - this encouraged solutions to form with equal az. and el. beamwidths.

SPEA2 was chosen for this task as it is not limited by the number of objectives or input variables and in trials on

this problem, has outperformed other recent MOGAs. A full explanation of SPEA2 is beyond the scope of this paper but in essence, SPEA2 uses the standard genetic algorithm operators of crossover and mutation to 'evolve' the input variables but maintains a fixed-size external archive of non-dominated solutions. It also includes measures to ensure the diversity in the non-dominated solutions found and maintained in the archive.

RESULTS

Several runs of SPEA2 were completed using 100 generations using the fitness measures defined above, population sizes of 100 individuals and a fixed external archive size of 35. Probability of crossover was 80 % and mutation 1 %. A single seed cell was used initially to grow each subarray. Once the maximum number of generations had been reached, the archive contained the best multiobjective solutions found during the run.



Figure 3. Azimuth cuts of optimised (solid line) solution and a full power uniformly excited array (dashed line). Plot is normalised to 43.99dB (EIRP).

Figures 3 and 4 show the az. and el. cuts of the radiation patterns of one such optimised solution contained in the archive set. Figure 5 shows the subarray partitions. Although the EIRP has dropped due to the tapering applied, the sidelobes have all been reduced in magnitude relative to the mainlobe, the az. and el. beamwidths are almost equal and the average sidelobe level is much lower than in full power transmission. With the exception of the far-out sidelobes, the sidelobe levels are relatively constant in the azimuth cut and low for an array of this size (15 x 15).

CONCLUSION

This work has demonstrated that state-of-the art multiobjective evolutionary algorithms can give good results when presented with difficult conformal antenna optimisation problems. In addition, a new and novel method for incorporating the subarray partitioning into the optimisation process has also been presented suitable for both planar and conformal antennas.







Figure 5. Optimised Subarray partitions

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