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Determination of Amplitude Distribution over a Large Parabolic Antenna from Its Power Radiation Pattern

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***Abstract*-A technique has been formulated to compute the unknown amplitude distribution over the surface of a large parabolic reflector from the radiation patterns measured in situ. The approach uses a novel Genetic Algorithm to determine the optimal illumination that produces best match with the measured patterns. The relevance of the work lies in the fact that in order to rectify the effects of surface irregularities developed during installation, the first step must be to accurately evaluate the aperture illumination.**

***Index Terms*- Parabolic reflector, phase error, amplitude distribution, radiation pattern, Genetic Algorithm.**

I. INTRODUCTION

Parabolic reflector antennas are used for very large gain applications. In actual situations, the antenna would have undergone transportation, storage and handling before it is installed and the radiation patterns are measured in situ. This results in irregularities on the surface of the reflector. These may be random or predictable as in the case of errors in the theodoliting done to align the panels. All such effects manifest themselves as phase errors on the aperture distribution of the field [1-6]. In order to correct such phase errors one needs to know the locations of these irregularities [7,8]. Although some efforts have been reported to compensate for these surface errors, without locating them properly the efforts continue to be of little practical relevance [9,10]. In order to perform the reverse engineering required, the unknown amplitude distribution must be determined at first. The aim of this paper is the estimation of the amplitude distribution over the surface of the antenna from the patterns measured in situ.

The radiation pattern of a reflector antenna which is essentially a circular aperture is related to the field distribution by the following equation

$$G(u,\phi') = \iint f(r,\phi')\, e^{jurCos\,(\phi-\phi')-g(r,\phi')}\, r\, dr\, d\phi' \qquad (1)$$

where $u = 2\pi a \sin(\theta)/\lambda$, $r = \rho/a$

a = radius of the aperture

$f(r,\phi')$ is the amplitude distribution on the surface of the antenna

and $g(r,\phi')$ is the phase error.

The various co-ordinates used in the above equation are shown in Figure 1.

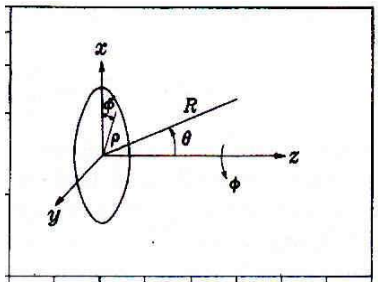


Figure 1

To achieve the enumeration of the amplitude distribution function $f(r,\phi')$, zero phase error (i.e. $g(r,\phi') = 0$) is assumed on the aperture as a first order approximation. With this simplification the problem considered in this paper may be proposed as an optimization problem which is given below.

Find the amplitude distribution function $f(r,\phi')$ to minimize

$$\sum_{n=1}^{points} [F(\theta_n - F_{computed}(\theta_n)]^2$$

where

$F(\theta_n)$ is the measured radiation pattern and

$$F_{computed}(\theta_n) = \iint f(r,\phi') e^{jurCos(\phi-\phi')} r\, dr\, d\phi' \quad (2)$$

at various values of θ_n

The above pattern measurements are both made on the same principal plane.

From the above discussion it is clear that the solution would involve an extremely large search space. We propose to use Genetic Algorithm (GA)[11] to combat this situation.

II. COMPUTATION METHOD

The function $f(r, \phi')$ is expressed as an array of values containing the amplitude distribution information. This representation defines a chromosome in the present application. Each individual allele is now a discrete point on the radial of the aperture and thus contains the amplitude at that point.

It was noted that the synthesized pattern had always extremely deep nulls. This is to be expected since phase error is assumed to be zero, but actual mechanical tolerances will tend to add to the phase error. Since the fitness function computes the absolute difference in computed and actual values at each point, this would prevent the search to converge on the solution. It is also to be noted that most modern day reflector antennas are modified paraboloids. The phase differences caused by these deviations are usually corrected by the corresponding phase reversal in the feed pattern.

To overcome the above practical problem, certain characteristics of the pattern were noted. Small phase errors generally manifest themselves in the following manner:

1) Nulls become shallower with higher phase errors
2) Sidelobe levels faraway from the main lobe are affected

Main lobe and the 1st sidelobe levels are principally unaffected to any significant extent by small phase errors. But these are significantly affected by minute changes in the amplitude distribution.

Taking this into consideration, the fitness function was modified to compare the difference of the peaks of the synthesized and the actual measured pattern. For this process to be successful, a proper Peak Search Algorithm was needed which would take into account the factors of periodicity of sidelobes in a radiation pattern. In addition to the peaks of the sidelobes, the shapes of the Main lobe and the 1st sidelobe were also taken into account for the fitness function. The total number of peaks to be compared was user defined. But a value of 5 peaks with shape correction for the main lobe was found sufficient for approximation of the amplitude distribution.

The next step was to suitably encode the chromosome so that a linear array of values corresponds to points along the radius of the aperture. The encoding process was made a

function of the number of integration points along the *r* axis. The user is first required to give an input of the number of points on the *r* axis. This allows the program to compute the distance between a pair of points along the *r* axis. The program then uses this value to compute the optimal number of integration points along the ϕ' axis as a function of *r*. The various points of *r* are obtained as discrete points with a spacing determined by the number of integration points along the *r* axis. Thus the chromosome is mapped for each discrete *r* point.

In attempting to encode the chromosome a deviation from conventional GA techniques was required. Conventional GA requires the alleles of the chromosome to be binary – i.e. it can take values of only 0 and 1. But the requirement of the allele to represent the amplitude at a discrete point on the surface implied a real value for the allele. Thus, the allele was made a floating point value instead of a binary value and the changes in its value were made continuous (within the 0.0 to 1.0 range) rather than discrete as dictated by conventional GA. This deviation removed the requirement of a computationally complex binary to real string encoding function. It reduced the size of the chromosome to manageable levels for the required computational accuracy. This also helped in improving the overall speed since this function would have been called for every allele when the fitness of the chromosome needed to be computed.

The above deviation can be easily explained with an example. The following are initial assumptions.

Chromosome Size = 5 alleles
Population = 2 Chromosomes
Probability of Mutation = 0.5 (50%)
Probability of Crossover = 0.6 (60%)
Maximum deviation = 0.125

Initial random values are chosen for the chromosomes as

[0.8, -0.5, 0.1, 0.2, -0.3]
[-0.6, 0.1, 0.8, 0.2, -0.1]

Imposing the maximum deviation restriction the chromosome values become

[0.1, -0.0625, 0.0125, 0.0250, 0.0375] 1
[-0.0750, 0.0125, 0.1000, 0.0250, -0.0125] 2

A mutation is highly likely in the 2nd generation. So is a crossover. Mutation can occur at any location inside the chromosome. Assuming the following values, Mutation location = 3, Chromosome # 1, Random Value (between 0 and 1) = 0.3, the new chromosome becomes [0.1, -0.0625, **0.0500**, 0.0250, 0.0375]. The allele in reverse color indicates the mutated allele.

The computation of the mutated allele goes as below:

Allele Value = Existing Allele Value + (Sign of Existing Allele Value × Random Value × Maximum Deviation)

If |Allele Value| > 1 then Allele Value = Maximum Deviation × New Random Value (between -1 and 1)

The other chromosome remains the same i.e. there is no mutation. After this the crossover occurs. Again crossover can occur at a random location inside the chromosome. Assuming a random crossover location of 4, the new chromosomes formed are as follows:

[0.1, -0.0625, 0.0500, **0.0250, -0.0125**] 3
[-0.0750, 0.0125, 0.1000, **0.0250, 0.0375**] 4

The crossover location is given by the allele in reverse color. There are now 4 chromosomes. But the population size is fixed to two. Thus only the 2 chromosomes with the highest fitness values go over to the next generation.

The chromosome with the above characteristics has a tendency to have widely varying alleles (value wise). While this is to be expected in a phase distribution (phase errors), amplitude distribution requires a slow variance in successive alleles of the chromosome. This necessitated the processing of allele data prior to its use for computing the fitness function. Various processing methods were tried – e.g. Moving point average, Exponential moving point average, Cubic splines. The moving point average and the cubic spline method both produced acceptable results.

The initial values of the chromosome at the start of the program are randomly generated. The program may also load in biased chromosome values from previous computation runs.

The total number of chromosomes is the population. Optimal values of population will vary from problem to problem. For the problem at hand, the optimal value of the population was found to be 32. Corresponding probability of mutation which is the inverse of the size of the population is 0.03125. Or there is approximately 3 % chance of a mutation in any chromosome involved in a generation crossover. Too high a probability of mutation will result in divergence (as experienced in real life – too many mutations in the parental genes lead to the death of the progeny)

Each allele in the chromosome is randomly mutated. Chromosomes are mated with other chromosomes of the population depending on the fitness. Mating involves crossing of alleles from one chromosome to the other at a random selected crossover point. Crossover probability is set at 0.6 or 60%. This prevents chromosomes from becoming too alike at the end of the computation run.

As the search progresses, there is a tendency of the search to diverge if the probability of mutation is too high. There is also a tendency to diverge if the deviation of each allele is too high. High mutation probabilities and deviations are required at the beginning of the search to quickly converge on the approximate solution. Once, the search is on the correct track, the number of mutations and the amount of deviations need not be high. The program automatically detects any divergent tendencies and automatically reduces the mutation probabilities and the maximum deviation allowed for each mutation in an inverse proportion to the average fitness of the population. Thus, the closer the search gets to its target, the lesser the deviation for each mutation. The number of mutations is also decreased the closer the search gets to its target. An analog equivalent of this process would be “negative feedback” in any control loop. Conventional GA techniques do not have any comparable processes or methods for implementation of “negative feedback”.

For each chromosome in the population, the program has to compute the fitness of each chromosome. Fitness of a chromosome is a value, which determines its quality, and how greatly it is beneficial to the population. A chromosome with a high fitness value has a better chance at surviving a few generations than a chromosome with a low fitness value. Thus the fitness function – the function that actually computes the fitness of the chromosome must reflect accurately the needs of the search algorithm.

For the case in hand, the search is for that combination of alleles which will gives a computed pattern closest to the reference pattern (the measured pattern).

This specification leads to the basic fitness function

$$Fitness(m)= \sum_{n=1}^{points} \frac{1}{[F(\theta_n) - F_{Computed}(\theta_n)_m]^2} \quad (3)$$

where $F(\theta_n)$ is the reference/measured antenna radiation pattern and $F_{Computed}(\theta_n)_m$ is the pattern computed using chromosome #*m* at the angle θ_n, where *n* corresponds to the number of comparison points on the pattern, and *m* corresponds to the chromosome number in the population.

Maximizing fitness will provide a chromosome which is the optimal (may not necessarily be the best) solution to the given problem. For better convergence fitness function is slightly modified. The modified function becomes

$$Fitness(m) = \frac{1}{\sum_{n=1}^{points} T_{nm}}$$

Where

$$T_{nm} = \left[F(\theta_n) - F_{Computed}(\theta_n)_m\right]^2 \quad \text{if } \left\|F(\theta_n) - F_{Computed}(\theta_n)\right\| > \text{error range} \quad (4)$$
$$= 0 \qquad \text{otherwise}$$

Thus, when the fitness is being computed, the function compares the error value with the error range, and if the value lies within the error range, it is assumed to be zero error. This allows the algorithm to concentrate more on first doing a coarse search for those chromosomes which are the closest to the reference pattern. The algorithm then fine-tunes these chromosomes by reducing the error range and thus matching the computed pattern as closely as applicable to the reference pattern.

The above modified fitness function can run into the "divide by zero" error especially for high values for the error range. This special case is handled by the program by detecting a zero in the denominator and replacing it with an abnormally low value (~10^{-308}). This results in a high fitness value, which should be greater than the target fitness allowing the algorithm to continue. Note that the above assumes that the target fitness is less than ~10^{308}. The program therefore restricts target fitness values to less than 100 for 64 point comparison which gives a maximum error value of approximately 0.002 dB per point which is less than the uncertainties of the measurement. Actual target values are set much more realistically (error ranges to the tune of 0.1 dB per point) so as to complete the search in reasonable time.

The computation comes to an end when the average fitness of the population reaches a user set target value – usually around 0.1 dB / point. Further accuracy is meaningless due to the fundamental uncertainties involved in the measurement – Spectrum Analyzer uncertainty (usually 0.5 dB), position accuracy (usually $\frac{360}{2^{14}}$ degrees) etc.

It should be noted that when the error range is high, the above average fitness can be reached quite easily. Thus quite a few iterations are needed before the final end to the computation – wherein the error range is successively decreased until it reaches a value whereby the fitness error is less than the uncertainties and other inaccuracies due to measurements. The program automatically reduces the error range and continues with the iterations until the target error range (usually the inverse of the number of points compared) is reached.

III. RESULTS

Fig. 2 indicates the success of this method. The measured pattern of a 9.3m diameter antenna has been used but with one constraint that zero phase error has been assumed. The actual distribution of amplitude on the aperture is reconstructed successfully after a conic spline based smoothening procedure [12] is applied, as shown herein.

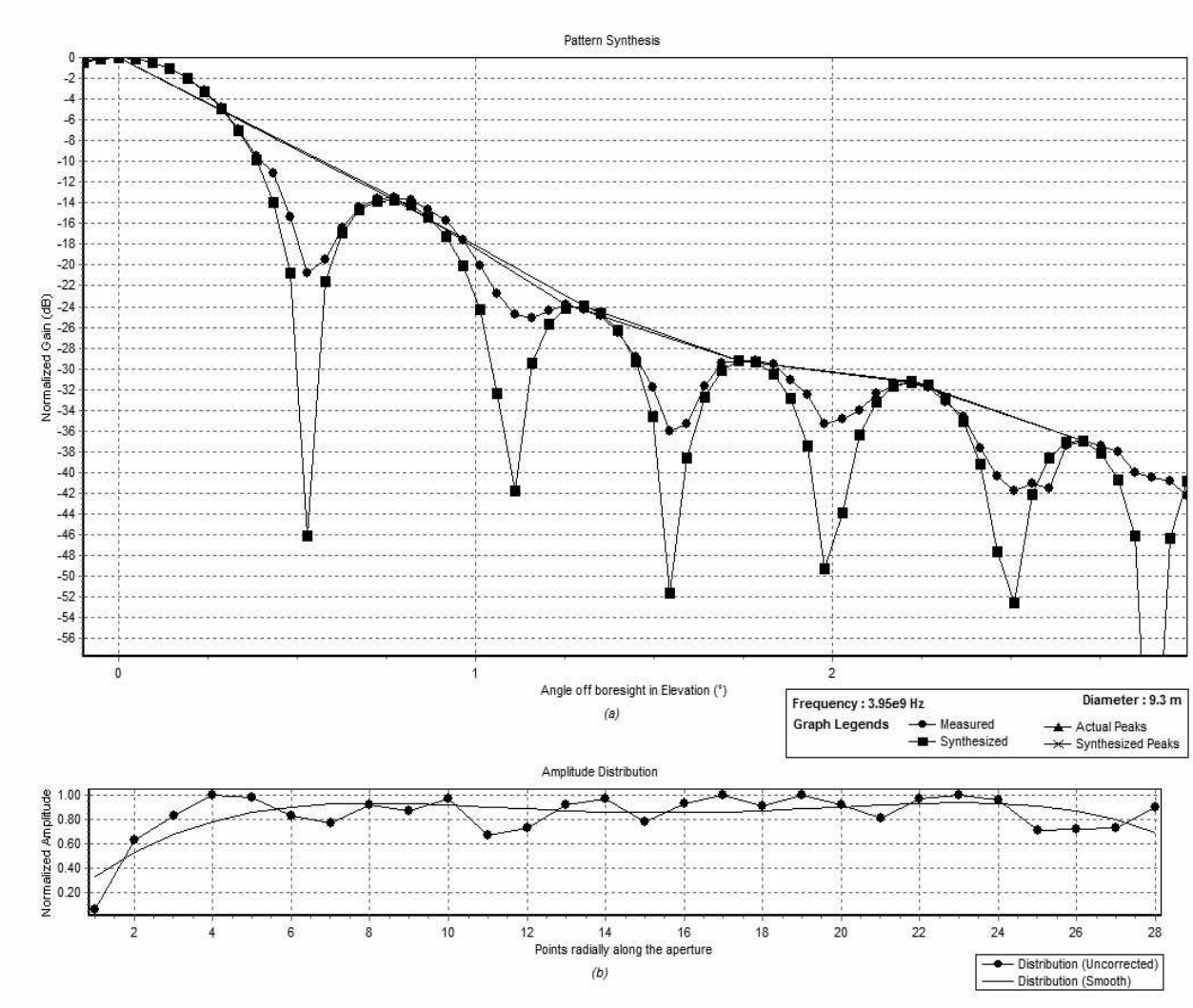


Figure 2

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IV. CONCLUSION

The unknown amplitude distribution over the aperture is determined successfully considering the problem as an optimization one and applying a modified Genetic Algorithm to solve it. However, the phase distribution still remains to be determined and the phase faults reconstructed there from. Only then the locations of the irregularities formed on the surface during transportation and handling can be accurately obtained and necessary corrections can be made. Further work in this regard is presently being pursued and will be reported shortly.

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