

FINDING DEFECTIVE ELEMENTS IN PLANAR ARRAYS USING GENETIC ALGORITHMS

J. A. Rodríguez and F. Ares

Dpto. de Física Aplicada, Facultad de Física
Universidad de Santiago de Compostela
15706 Santiago de Compostela, Spain

H. Palacios

Dpto. de Sistemas Electrónicos y Comunicaciones
INTA, Ctra. Ajalvir, Km. 4, Torrejón de Ardoz, 28850 Madrid, Spain

J. Vassal'lo

CSIC, "Torres Quevedo", Instituto de Física Aplicada
Serrano 144, 28006 Madrid, Spain

Abstract—A technique that allows to locate defective elements in planar arrays by using some samples of the degraded far-field power pattern is described. This approach uses genetic algorithms to minimize the square of the difference between the far-field power pattern obtained for a given configuration of failed elements and the measured one. The method also allows to detect defective elements that don't fail completely

1. Introduction

2. The Method

3. Application of the Method

3.1 Array with Complete Failures

3.1.1 *Samples Spread Along the Main Beam Directions*

3.1.2 *Samples in the Pattern Maxima*

3.2 Array with Partial Failures

4. Conclusions

References

1. INTRODUCTION

In present years, active antennas are working in several systems as for example in SAR applications for earth observation, boarded on spatial platforms. The antenna, in such cases, has several hundreds of radiating elements or subarrays, and the possibility of failure of some of them increases due to the high number of elements. These element failures cause sharp variations in the field intensity across the array aperture, thus increasing both the sidelobe and ripple level of the power pattern. In aircraft antennas, this problem can be solved by replacing the defective elements each time the plane lands. But this is a critical problem in space platforms.

Active antennas have the advantage that the radiation pattern can be restored by changing their feeding distribution from base station [1]. In many cases, the excitations of the non-defective elements can be readjusted to produce a pattern with a minimal loss of quality with respect to the original one. In the literature, we found several approaches that perform this compensation by numerically finding a new set of excitations of the unfailed elements that optimizes some objective function [2–4]. Obviously, these techniques require to know the number and the location of the failed elements in the array.

To know which element or elements are damaged, active antennas include different calibration systems. These systems make an easy control of system components, but this control fails if the calibration is damaged too. Furthermore, it is very difficult to calibrate the behaviour of a radiating element without radiation disturbance, and then, failures due to a debris collision in radiators may not have an easy detection. On the other hand, in small platforms, calibration systems can be rejected because the inclusion of such a system in these cases means a critical increase in volume, weight and cost.

A smart solution to this problem consists on the location of the failing elements from external data: the initial radiation pattern and the measurement from base station of a small number of spatial directions of the damaged radiation pattern (it is assumed that it is not possible to know the whole damaged pattern). We can then obtain the radiators that must be failing to produce such damaged pattern by means of optimization algorithms. In this paper, we present a technique based on this procedure that allows to find the number and the location of the defective elements in planar arrays by means of genetic algorithms [5].

2. THE METHOD

Let us consider a planar array of N identical and equally oriented elements. Assuming that the elements are located over the xy -plane, the far field pattern, expressed in dB's, can be calculated using the following expression:

$$P(\theta, \phi) = 10 \cdot \log_{10} \left(fe(\theta, \phi) \cdot \sum_{n=1}^N I_n e^{jk \sin \theta (x_n \cos \phi + y_n \sin \phi)} \right)^2 \quad (1)$$

where I_n is the relative excitation of the n -element located at the position given by (x_n, y_n) , $fe(\theta, \phi)$ is the element pattern, and (θ, ϕ) gives the angular position of the field point.

As we have stated, the procedure of locating defective elements in a planar array begins with the measurement of several samples of the degraded pattern (emitted by the antenna presenting one or more failing elements). Hereafter, we will denote as $P_m(\theta_i, \phi_i)$ the i -th sample of this pattern expressed in dB's and measured at the angular direction specified by θ_i and ϕ_i .

Using a cost function, the method compares the measured radiation pattern with that corresponding to the array with a given configuration of failed/unfailed elements. The configuration used in this comparison depends on the chromosome of the genetic algorithm. This chromosome contains a binary encoding of the array elements that describes the status of each array element. The encoding depends on the way of failing the defective elements:

- If we assume that defective elements fail completely, we just need N genes of 1-bit each in every chromosome, because there are two possibilities for the status of each array element (failed/unfailed). The chromosome encoding is as follows: a bit '1' denotes an unaltered element, whereas a bit '0' indicates that this element is failing. In this case, the relative excitation for the defective elements is zero.
- If some defective elements fail but irradiate some power (i.e., its effective excitation is a fraction of the original, but not zero), we need N genes of m -bits each, being 2^m the number of possible states of the elements that we want to encode. In this work we have assumed that partially defective elements fail in a 50%. This is equivalent to assume that their relative excitation is a half of the original one. Thus, there are 3 possibilities for each array element

status: completely failed/partially failed/unfailed. In this case, we need N genes of 2-bits each, assigning a ‘00’ to a gene if the corresponding element is completely failed, ‘01’ or ‘10’ if the element fails in a 50%, or ‘11’ if the element is unfailed. The method makes possible to generalize the study by introducing more different states for the partial failures, i.e., elements whose excitation is a 5% of the original one, 10%, 15%, and so on. However the changes in the pattern samples will be undistinguishable for these different states (or at least smaller than measurement errors) and the predicted results will not be good.

After encoding the configuration of defective elements in the chromosomes of the genetic algorithm, we define the following cost function:

$$\xi(chr) = c \cdot \sum_{i=1}^M [P_m(\theta_i, \phi_i) - P_{chr}(\theta_i, \phi_i)]^2 \quad (2)$$

where chr is a given chromosome, M is the number of samples used in the comparison, $P_{chr}(\theta_i, \phi_i)$ is the value of the pattern associated to that chromosome in the same direction, obtained by (1), and c is a normalization constant.

The minimization of this cost function by means of genetic algorithms allows us to calculate that chromosome generating the radiation pattern that is closer to the measured one (at least in the angular positions of the samples). This is equivalent to obtain the number and the location of the defective elements. In the case of partial failures, this chromosome also allows to know the grade of failure of the array elements.

Since we assume that an accurate measurement of samples of the degraded pattern is difficult to perform, it is important to assure that the algorithm achieves the right solution using a minimum number of samples. Therefore, we will study the influence of the number and the position of the samples in the algorithm convergence.

3. APPLICATION OF THE METHOD

As an example, we have considered a shaped beam pattern using a 8×8 element planar array in a rectangular grid with 0.7λ interelement spacing. The corresponding aperture distribution, obtained by application of the simulated annealing technique [6], yields a pattern with a side-lobe level of -15 dB and a ripple level in shaped region of ± 1.0 dB.

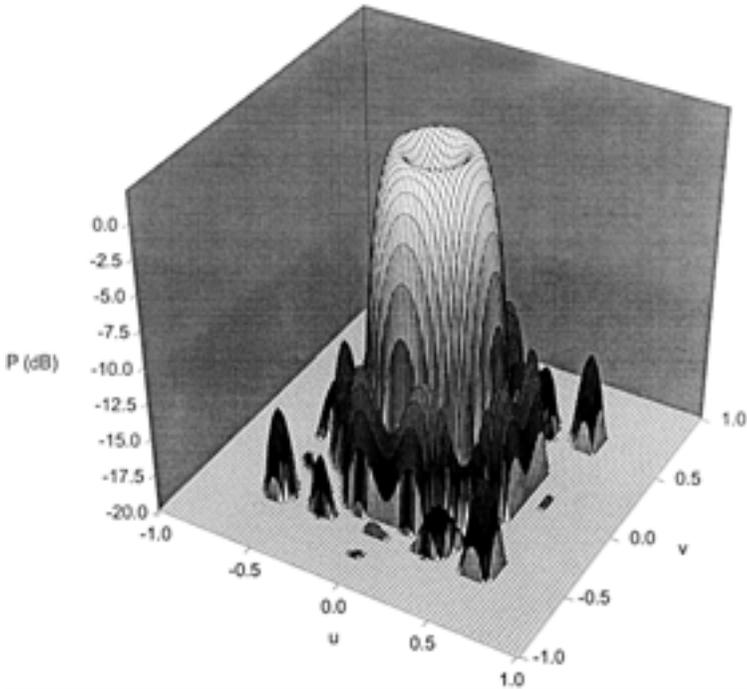


Figure 1. Simulated initial radiation pattern, corresponding to the array without defective elements.

This pattern is plotted in Fig. 1, where $u = \sin \theta \cdot \cos \phi$ and $v = \sin \theta \cdot \sin \phi$. In the pattern calculation, we have assumed that the array elements are circular patches whose element pattern can be approximated by $fe(\theta, \phi) = 10^{(-\theta/82.16)}$, which falls to -22 dB at $\theta = 90^\circ$. Besides, some elements with nearly-null excitations were removed from the array because of their low influence in the radiation pattern so a total of 48 elements were excited.

To get optimal results, the genetic algorithm has been run several times for each search changing the number of chromosomes of the population as well as the seed of the random generator of the initial population. In each run, the number of chromosomes in the population was constant and a ranked replacement took place in each iteration if there was an improvement from parents to offspring. One point crossover was always applied and mutation happened every iteration, affecting one gene on every chromosome. The process ends when the best solution provided by the genetic algorithm does not change after three

runs.

To simplify the study, we have not made use of a real failing antenna, but we have simulated it. In the simulation process, some elements excitations of the initial array have been randomly cancelled (or divided by two to study partial failures). Afterwards, some pattern samples have been chosen in order to prove if the algorithm is able to find the right configuration. Two cases have been studied depending whether the array may have partially failed elements or not.

3.1 Array with Complete Failures

In the first study we consider that the array defective elements fail completely, which is equivalent to assume that their relative excitations are zero. Thus, the simulation begins cancelling the excitations of some array elements randomly chosen. In this case, each chromosome of the genetic algorithm has 48 bits.

In an ideal case, the genetic algorithm must find the failing elements configuration associated with a radiation pattern showing exactly the same samples than those calculated in the simulation process, which implies a cost function (2) equal to 0.

Unfortunately, in a real application a certain experimental error in pattern measurement is always present. The introduction of these errors affects to the algorithm convergence in several ways:

- In the ideal case the algorithm stops once the cost function is 0. But if we take into account measurement errors, the cost function will never reach the minimum value '0'. The cost function will have a minimum possible value, associated with the samples measurement error. Then, the algorithm does not stop by itself. The only thing to do is to run an adequate number of generations keeping the lower cost solution.
- If the measurements show an important error and/or the number of samples taken is very low, the algorithm may find a solution with a cost function lower than the right solution. In this case the problem has not solution, and it is necessary to use more samples and/or perform a more accurate measurement of them to find the right solution.
- Algorithm convergence is now strongly dependent on the pattern angular directions where the samples have been taken, because radiation pattern can be measured more accurately in the main beam

than in the secondary lobes directions, and because there are some areas more affected than others to the failure of some elements.

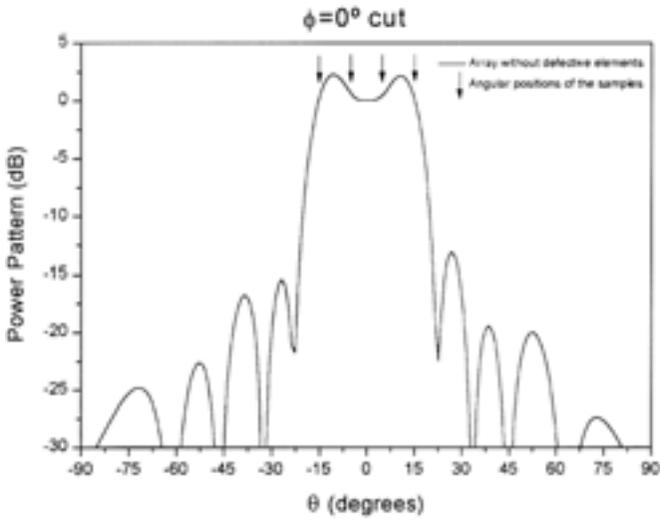
In the simulation, we have introduced certain errors to these samples in order to simulate the measurement errors. To study the influence of the samples position in algorithm convergence, two cases have been analyzed: in the first of them, the samples are spread over the beam directions, whereas in the second the samples are taken in the maxima of the radiation pattern. In both cases, we only take samples in the principal planes of the pattern ($\phi = 0^\circ, \phi = 90^\circ$) because they provide the algorithm with enough information to obtain good results and, at the same time, we minimize the number of samples required to be measured.

3.1.1 Samples Spread Along the Main Beam Directions

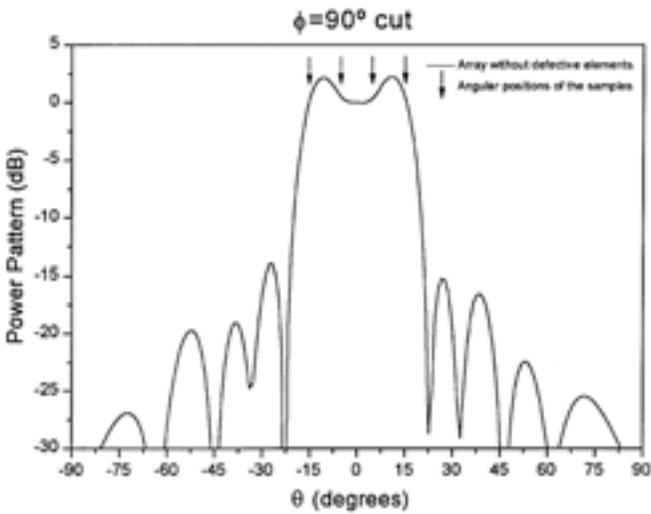
In this case, the samples are equally spaced along main beam area in the principal planes ($\theta \in [-15^\circ, 15^\circ]$, $\phi = 0^\circ$ and $\phi = 90^\circ$ cuts). The distance between the samples depends on the number of samples (M) that we are introducing in the algorithm. Fig. 2 shows the radiation pattern cuts corresponding to the array without defective elements as well as the position of the samples for $M = 8$ (4 in each main plane).

Although we have tested the algorithm using a different number of failed elements, we only present results considering 2 defective elements in the array. To study the algorithm convergence, we start with 10 configurations of 2 failed elements randomly chosen, and we change M . In the evaluation of these samples, we have assumed a maximum experimental error of $\Delta = \pm 0.2$ dB. This is equivalent to add/subtract to the exact value of each simulated sample, obtained by (1), a random value calculated between 0 and Δ . Since the results are dependent on these values, we run the algorithm 10 times for every configuration, just as if for each run we were repeating the measurement of these samples. The results are listed in Table 1, in which $t(s)$ is the average time used in seconds to find the right solution (measured on a Pentium-II processor running at 350 Mhz); and *Found* indicates how many times of the total runs the algorithm was able to find the right solution.

Note that using 8 samples with a maximum error of ± 0.20 dB the algorithm provided a wrong solution in 78 of a total of 100 runs. This behaviour is due to the fact that, in these cases, it exists a given chromosome with a cost value lower than the corresponding to the chromosome associated to the right solution, so the algorithm is unable



(a)



(b)

Figure 2. Power pattern ϕ -cuts corresponding to the array without defective elements. Angular positions of the 8 samples used in the simulation are also shown.

Table 1. Simulation results using 10 random configurations of 2 defective elements completely failed. The samples for the genetic algorithm have been taken over the main beam region.

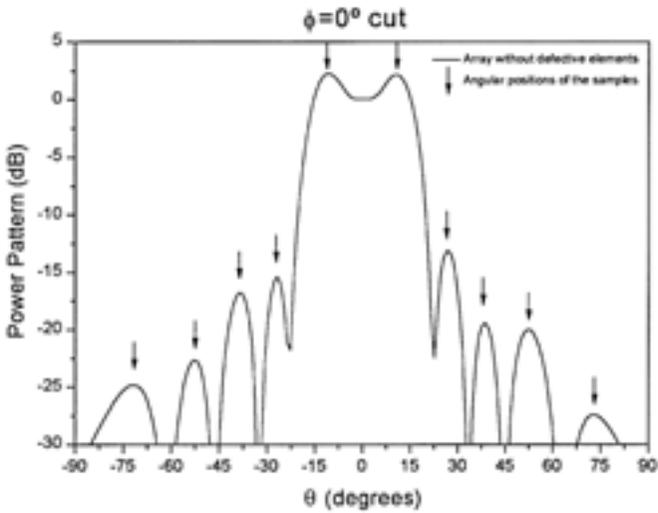
2 defective elements, $\Delta = \pm 0.20$ dB						
8 samples		20 samples		28 samples		Failing elements positions
$t(s.)$	Found	$t(s.)$	Found	$t(s.)$	Found	
31	2/10	63	6/10	85	6/10	1,32
31	2/10	63	4/10	85	6/10	17,46
36	3/10	63	5/10	85	8/10	34,48
31	1/10	63	7/10	85	7/10	6,45
31	2/10	63	8/10	85	8/10	46,48
31	2/10	63	5/10	85	6/10	5,18
31	3/10	63	6/10	85	7/10	15,32
31	2/10	63	6/10	85	8/10	27,42
31	2/10	63	5/10	85	7/10	7,36
31	3/10	63	6/10	85	5/10	10,31
32	22/100	63	58/100	85	68/100	← Average

to find the right solution. As we have stated, this problem can be alleviated (or even avoided) by increasing the number of samples used in the comparison of the pattern and/or by reducing their measurement errors. It has been found that in an ideal case with $\Delta = \pm 0.0$ dB (i.e., we assume no experimental errors), the algorithm was able to find the right solution in all cases using 8 samples only.

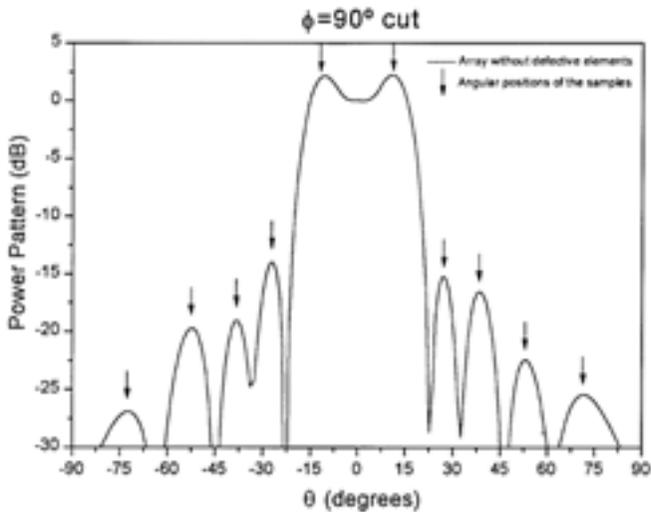
3.1.2 Samples in the Pattern Maxima

Since the maxima of radiation patterns are very sensitive to the failure of elements of the array, it is a good idea to characterize these points as samples in the optimization algorithm. The positions of the samples used in the algorithm are taken in the directions of the maxima of the initial pattern in the principal planes (it is likely that we would obtain better results if we take these samples in the maxima of the degraded pattern, but we assume that we don't want to measure the whole pattern but a small number of samples only). Fig. 3 shows the radiation pattern cuts corresponding to the array without defective elements as well as the position of the samples for $M = 20$ (10 samples in each main plane). The maximum experimental error assumed for these samples is of $\Delta = \pm 0.75$ dB.

To compare the results, we tested the same 10 random configura-



(a)



(b)

Figure 3. Power pattern ϕ -cuts corresponding to the array without defective elements. Angular positions of the 20 samples used in the simulation are also shown.

tions of 2 defective elements as before, varying the number of samples from 12 to 20 (in the cases $M = 12$ and $M = 16$, some of the samples at extreme angles of Fig. 3 are not used). The results are shown in the Table 2. We found that, for this case, the success percentage is better than before because the samples used now are more sensitive to the failure of the array elements.

Table 2. Simulation results using 10 random configurations of 2 defective elements completely failed. The samples for the genetic algorithm have been taken in the maxima of the initial pattern.

2 defective elements, $\Delta = \pm 0.75$ dB						
12 samples		16 samples		20 samples		Failing elements positions
$t(s.)$	Found	$t(s.)$	Found	$t(s.)$	Found	
38	5/10	50	5/10	63	9/10	1,32
38	6/10	50	7/10	63	9/10	17,46
38	6/10	50	8/10	63	9/10	34,48
38	6/10	50	5/10	63	9/10	6,45
38	4/10	50	8/10	63	10/10	46,48
38	3/10	50	8/10	63	9/10	5,18
38	6/10	50	7/10	63	10/10	15,32
38	3/10	50	6/10	63	10/10	27,42
38	7/10	50	8/10	63	8/10	7,36
38	5/10	50	7/10	63	9/10	10,31
38	51/100	50	69/100	63	92/100	← Average

One more time, it is clear that the decrease of the samples number implies the decrease of the probability of finding the right solution, being necessary at least 20 samples to assure a good result.

3.2 Array with Partial Failures

In this case we consider that some of the array defective elements may not be completely failed. As we stated, we assume that the excitations of the partially failed elements are a half of the original ones, having 3 different states for each array element status. Therefore each chromosome of the genetic algorithm will have 96 bits.

The procedure begins modifying the original excitations of some array elements to simulate a given grade of failure. The position as well as the grade of failure of these elements are randomly chosen.

To study the behaviour of our algorithm to this problem, we have se-

lected 10 random configurations of 3 complete/partial failures each. In the searching process, we have used 20 samples located in the maxima of the initial pattern as Fig. 3. shows. In order to study the influence of the maximum measurement error in the process, we have modified this value in the samples evaluation. The final results for each configuration are shown in Table 3, where the values between parenthesis denote the percentage of failure of each element.

Table 3. Simulation results considering 10 random configurations of 3 defective elements completely and partially failed. A total of 20 samples located in the maxima of the initial pattern were used in the algorithm.

3 defective elements, 20 samples, partial failures						
$\Delta = \pm 0.00$ dB		$\Delta = \pm 0.50$ dB		$\Delta = \pm 0.75$ dB		Failing elements positions
$t(s.)$	Found	$t(s.)$	Found	$t(s.)$	Found	
263	1/1	261	7/10	240	5/10	5(100%), 19(100%), 29(50%)
66	1/1	66	4/10	66	1/10	2(50%), 14(50%), 17(50%)
66	1/1	66	4/10	66	3/10	18(100%), 23(50%), 43(50%)
66	1/1	85	7/10	88	3/10	13(100%), 31(50%), 42(50%)
66	1/1	102	5/10	148	1/10	2(50%), 18(50%), 25(100%)
66	1/1	66	8/10	66	5/10	8(50%), 26(50%), 47(50%)
99	1/1	219	8/10	181	3/10	9(100%), 36(100%), 27(50%)
66	1/1	66	6/10	66	1/10	13(50%), 17(50%), 31(100%)
66	1/1	66	4/10	66	1/10	13(50%), 28(100%), 42(50%)
99	1/1	305	2/10	247	3/10	41(100%), 29(100%), 35(50%)
93	10/10	130	55/100	123	26/100	← Average

In this case, the algorithm not only need to know the location of defective elements, but also its grade of failure. It is remarkable that with an experimental error of ± 0.75 dB, we have obtained a success percentage equal to 26%. If this maximum error is reduced to ± 0.50 dB this percentage is increased to 55%, whereas if no errors are considered the right solution is achieved in all cases.

4. CONCLUSIONS

We have introduced a method of locating defective elements in planar arrays by using samples of their far-field patterns. It has been found that the probability of finding the right solution increases as the number of samples increases. Besides, it is extremely important to

accomplish a very accurate measurement of the samples. This method is specially useful for those applications in which the near-field pattern is not accessible, such as systems boarded on space platforms.

ACKNOWLEDGMENT

This work has been supported by the Synthetic Aperture Radar (S.A.R.) program of I.N.T.A. (National Aerospace Techniques Institute).

REFERENCES

1. Mailloux, R. J., *Phased Array Antennas Handbook*, Artech House, Inc., Norwood, MA, 1994.
2. Peters, T. J., "Conjugate gradient-based algorithm to minimize the sidelobe level of planar arrays with element failures," *IEEE Trans. Antennas Propagat.*, Vol. 39, 1497–1504, 1991.
3. Rodríguez, J. A. and F. Ares, "Optimization of the performance of arrays with failed elements using the simulated annealing technique," *J. Electromagn. Waves Appl.*, Vol. 12, 1625–1637, 1998.
4. Yeo, B. and Y. Lu, "Array failure correction with a genetic algorithm," *IEEE Trans. Antennas Propagat.*, Vol. 47, 823–828, 1999.
5. Rahmat-Samii, Y. and E. Michielssen, Eds. *Electromagnetic Optimization by Genetic Algorithms*, John Wiley & Sons, Inc., New York, USA, 1999.
6. Rodríguez, J. A. and F. Ares, "Síntesis de diagramas de radiación de una antena para GNSS," CASA Space Division, Madrid, Spain, Tech. Rep. USC/GNSS/RPT/001, March 1999.