A Genetic Algorithm for the Determination of Multiple Angles of Arrival in Linear Arrays of Antennas

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Abstract — *This work deals with the study of genetic algorithms in the determination of the directions of arrival of incident signals in linear arrays of antennas. For such, techniques of spectral esteem are used to define a spectral density function. To leave of this function the development of genetic algorithms becomes possible that will go to determine the values for which the function is maximized. Such values are the angles that indicate the directions of the incident signals.*

Key words **-** Genetic algorithms, angle of arrival, adaptive antennas

1. **Introduction**

The adaptive antennas have been widely applied in radars, sonar and mobile communications, where the objective is to magnify the directivity in the direction of the interest signal, canceling the action of interference signals. This is possible through the manipulation of the weights of the antennas by means of adaptive algorithms [1]. However, these algorithms need the knowledge of the Angle Of Arrival (AOA) of the signals. It is there that appear the methods of spectrum estimation as the method of Bartlett, Pisarenko, MUSIC, ESPRIT, MVDR and others [2-3].

These methods generate a specter for an array of sensors where the peaks of this specter are related with the angle of arrivals of the incident signals in the array. Generally, the values for which these peaks occur can be found through the method of Newton, the method of the steepest descent or some of the methods almost Newton [4]. The great problem of these methods is that they can converge to points of local maximum, instead of pointing with respect to the points of global maximum.

With intention to present a solution for this problem, we show in this work an algorithm that uses the spectral esteem by the MVDR method (Minimum-Variance Distortionless Response) associated to Genetic Algorithms (GA's).

The presence of the GA has as purpose to determine the points of global maximum generated by the MVDR. Its main advantage on the classic methods of optimization is that it converges of probabilistic form to the point of global maximum. Another very important feature is that, in contrast to the other methods of direct search, or either, making use only of the objective function, the GA's don't need to make all the sweepings of the specter, what reduces a lot the computation time.

In the next section of this work, the main concepts on Genetic Algorithms will be presented. In the following section we will argue the method of the MVDR. After that will be exposed the proposed method. In section V we show the gotten results and finally, the conclusions of this work will be present in section VI.

2. **Genetic Algorithms**

The Genetic Algorithms are random and evolutionary methods generally used in the solution of search problems and optimization. Its functioning is based on the genetics and in the Darwin's theory of the evolution of the species. The GA's search the best solution for one determined problem by means of the evolution of populations of solutions codified through artificial chromosomes. These are structures of data that represent one of the possible solutions to the problem. These structures are submitted to an evolution process that involves evaluation, selection, recombination (crossover) and mutation, until they reach the stop approaches.

The figure below shows the basic structure of a GA.

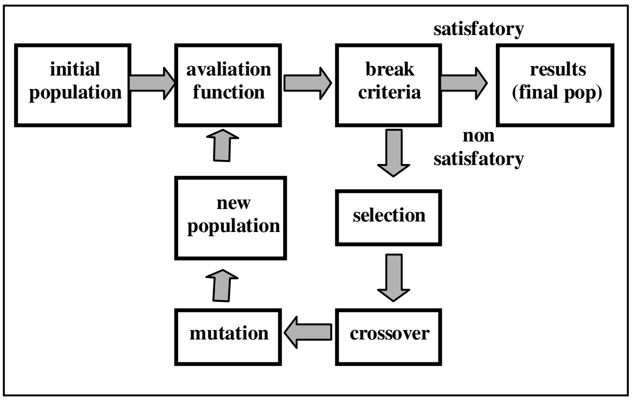

Figure 1: basic structure of a GA

Initially we create randomly, or of intuitively, a number of individuals that will form our first population. After that we submit these individuals to the function evaluation thus getting what we call initial generation. If the break criteria will not be satisfied then the creation of a new generation is initiated. Individuals are selected in accordance with its adaptations (smoothings) for production of descendants. The individuals parents are recombined for such production. All the descendants will suffer to mutations in accordance with certain probability. The evaluation of the descendants is computed. The descendants are inserted in the population substituting its parents, producing a new generation. This cycle is done until the break criteria be satisfied.

The Genetic Algorithms present significant differences when are compared to the more traditional methods of search and optimization. Such differences can be:

- GA' s searches a population of points in parallel, not of only point;
- GA' s does not require derived information or other auxiliary knowledge; but the objective function and the corresponding levels of smoothing influence the direction of research;
- GA' s uses rules of probabilistic transitions, no deterministic;
- GA' s is generally more directly to adaptation;
- GA' s can produce a number of potential solutions for a problem. The user makes the final choice.

2.1. **Solutions Representation**

The representation of the possible solutions in the search space of a problem defines the structure of the chromosome that goes to be manipulated by the algorithm. Each chromosome is represented by a vector of m positions, for example $p=\{x_1, x_2, x_3 \dots x_m\}$, where each component x_i represents a gene (or an variable of the solution).

These vectors (the chromosomes) generally are represented by binary numbers or whole numbers. However, the use of binary is more common for being of easy manipulation through the genetic operators, of easy hashing in whole number or real and in addition, for facilitating the demonstration of the theorems.

2.2. **Initial Population**

The initial population determines the process of creation of the individuals for the first cycle of the algorithm. Normally, are used for this end random procedures or heuristical algorithms, or either, the individuals of the first population, as already it was said, are created of random form.

2.3. **Evaluation Function**

The evaluation of the chromosome is carried through a function that represents of adequate form the problem and has as objective to manage a measure of aptitude of each individual in the current population. In optimization problems, it can simply represent the objective function of the treat problem.

2.4. **Selection**

In the selection process, individuals for the reproduction are chosen. This procedure is based on the aptitude of the individuals: more apt individuals have greater probability to be chosen for the reproduction.

Of this form, for a maximization problem, if f is the value of the evaluation function of individual i in the current population, the probability pi of being selected the individual i can be given by:

$$p_i = \frac{f_i}{\sum_{i=1}^{n} f_i} \qquad (1)$$

where n is the number of individuals in the population.

2.5. **Genetic Operators**

Without a doubt the genetic operators are the greater responsible for the variability of people in the nature. Perhaps without them, the men would not pass of an interminable reproduction in series. The same happens with the GA' s.

The genetic operators are methods of selection and reproduction that become possible the maximization or minimization of the number of solutions, as well as the advance of the best individuals for the following generations.

Two types of genetic operators exist: mutation and crossover. We can consider a third genetic operator when we allow the clone, or either, the perfect copy of a chromosome for the following generation.

a) **Mutation**

The mutation process consists in the realization of alterations (usually few) in the values of one or more genes of a chromosome. In a binary chromosome this operator consists of the random inversion in the bits of the genotype, as shows the figure below.

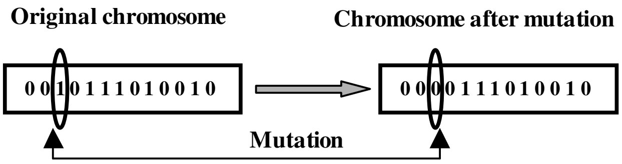

Figure 2: mutation

b) **Crossover**

The process of crossover or recombination consists of cuts that will be effected in the chromosomes parents who then will be changed according to a pre-defined rule. The cuts can be fixed for all the chromosomes or random.

Different types of crossover exist, where we can cite the following ones:

Crossover of a point: An only cut is made in the chromosomes parents and changing second part to it its descendants get themselves.

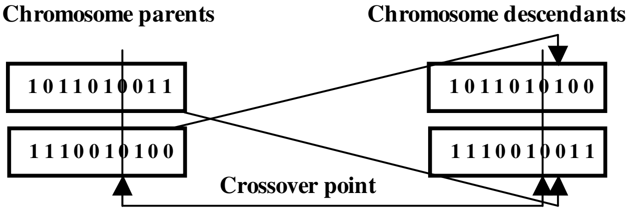

Figure 3: crossover of a point

Crossover of colon: In this process the chromosome is divided in three parts, being the extreme parts changed, generating two descendants.

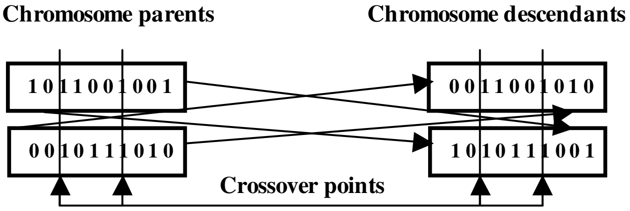

Figure 4: crossover of colon

Uniform Crossover: Each gene of the descendant is chosen randomly of the corresponding genes of the parents.

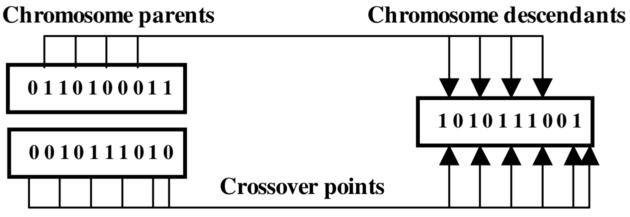

Figure 5: uniform crossover

The crossover operator is applied to the individual of a population with a constant probability p_c. In general $p_c \in [0.50; 0.80]$.

c) **Cloning**

The cloning process consists of perpetuating for the following generation some individuals of the current population. It is applied with a probability equal to 1 - p_c.

The cloning allows that individuals considered better remain for some generations, until new more apt individuals be generated from them.

3. **The MVDR Method**

Consider a linear array of M+1 sensors equally spaced at distances *d*, and a plane wave incident on the array at a angle θ_1 with respect to the array normal, as shown below.

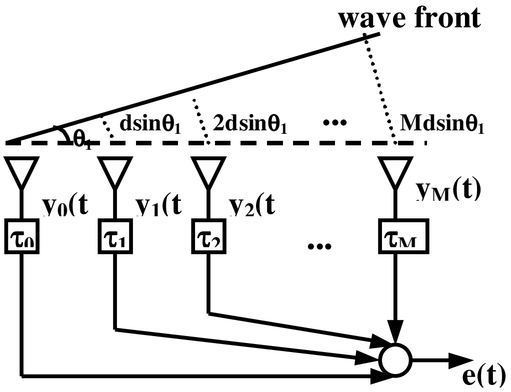

Figure 6: beamformer

The conventional beamformer introduces appropriate delays at the outputs of each sensor to compensate the propagation delays of the wavefront reaching the array. The output of the beamformer (the "beam") is the sum

$$e(t) = \sum_{m=0}^{M} y_m(t - \tau_m) \tag{2}$$

where $y_m(t)$; m=0, 1, 2...,M is the signal at the m-th sensor. To reach sensor 1, the wavefront must travel an extra distance d.sinθ_1; to reach sensor 2 it must travel distance 2.d.sinθ_1, and so on. The last sensor is reached with a delay of M.d.sinθ_1/c seconds. Thus, to time-align the first and the lest sensor, the output of the first sensor must be delayed by τ_0 = M.d.sinθ_1/c, and similarly, the mth sensor is time-aligned with the lest one, with a delay of

$$\tau_m = (M - m)d \sin\theta_1 / c \tag{3}$$

where c is the speed of propagation of the signal.

Applying the Fourier transform to the equation (2), we have, in the frequency domain

$$e(\varpi) = \sum_{m=0}^{M} y_m(\varpi) e^{-j\varpi\tau_m} \tag{4}$$

which can written of compactly as

$$e = \mathbf{a}^T \mathbf{y} \tag{5}$$

where **a** and **y** are the (M+1)-vectors of weights and sensor outputs

$$\mathbf{a} = \begin{bmatrix} e^{-j\varpi\tau_0} \\ e^{-j\varpi\tau_1} \\ \vdots \\ e^{-j\varpi\tau_M} \end{bmatrix}, \quad \mathbf{y} = \begin{bmatrix} y_0(\varpi) \\ y_1(\varpi) \\ \vdots \\ y_M(\varpi) \end{bmatrix} \tag{6}$$

We can also define the phase delay between the received signals for two consecutive sensors as being

$$\phi_m = \varpi.\tau_m \tag{7}$$

But we also know that v = 2π.f and c=λ.f. So we have

$$\varpi = 2\pi\, c / \lambda \qquad (8)$$

and finally

$$\phi_m = 2\pi \frac{d}{\lambda} \operatorname{sen} \theta_m \qquad (9)$$

This is the analog of the digital frequency. To avoid aliasing effects arising from the spatial sampling process, the spatial sampling frequency 1/d must be greater or equal to twice the spatial frequency the wave; namely, 1/λ. Thus, we must have $1/d \geq 2(1/\lambda)$, or $d \leq \lambda/2$. Since $\sin\theta_l$ has magnitude less than one, the sampling condition forces ϕ_m to lie within the Nyquist interval

$$-\pi \leq \phi_m \leq \pi \qquad (10)$$

Now we can define the signal in each sensor at the array as being

$$y_m(t) = A(t) e^{-jm\phi} + v_m(t) \qquad (11)$$

that gives us

$$\begin{bmatrix} y_0(t) \\ y_1(t) \\ \vdots \\ y_M(t) \end{bmatrix} = A(t) \begin{bmatrix} 1 \\ e^{-j\phi} \\ \vdots \\ e^{-M\,j\phi} \end{bmatrix} + \begin{bmatrix} v_0(t) \\ v_1(t) \\ \vdots \\ v_M(t) \end{bmatrix} \qquad (12)$$

or in the vectorial form

$$\mathbf{y} = A\mathbf{s}^* + \mathbf{v} \qquad (13)$$

where

$$\mathbf{s} = \begin{bmatrix} 1 \\ e^{j\phi} \\ e^{2j\phi} \\ \vdots \\ e^{M\,j\phi} \end{bmatrix} \qquad (14)$$

is the steering vector, while A(t) is the amplitude of the signal and $v_m(t)$ is the noise in each sensor.

The systems that work with adaptive antennas digitalize the outputs of the diverse elements to before realize the processing. The resultant vector of the digitalization, in a determined instant, from all the elements of the array, receives the name of snapshot. Thus, if we have L signals arriving on the array, to the n-th sample the signal in m-th sensory is given by:

$$y_m(n) = v_m(n) + \sum_{i=1}^{L} A_i(n) e^{-jm\phi_i} \qquad (15)$$

or still

$$\mathbf{y}(n) = \mathbf{v}(n) + \sum_{i=1}^{L} A_i(n)\mathbf{s}_i^* \qquad (16)$$

The beamformer must privilege the desired signal and minimize the effect of the interference signals. This problem can be compared to a bank of narrowband filters, each designed to allow a sinewave through at teh filter's center frequency and to attenuate all other frequency components. Thus, the vector of weights must satisfy the following condition [2-3]

$$\mathbf{s}^H \mathbf{a} = 1 \qquad (17)$$

while at the same time it is required to minimize the output power

$$\mathbf{a}^H \mathbf{R} \mathbf{a} = \min \qquad (18)$$

The solution of this minimization problem subject to above constraint is readily found to be

$$\mathbf{a} = \frac{\mathbf{R}^{-1}\mathbf{s}}{\mathbf{s}^H \mathbf{R}^{-1} \mathbf{s}} \qquad (19)$$

which gives for the minimized output power at this frequency

$$\mathbf{a}^H \mathbf{R} \mathbf{a} = \frac{1}{\mathbf{s}^H \mathbf{R}^{-1} \mathbf{s}} \qquad (20)$$

Thus, we have that the spectrum estimation by the MVDR method is given by the expression

$$S_{MVDR} = \frac{1}{\mathbf{s}^H \mathbf{R}^{-1} \mathbf{s}} \qquad (21)$$

The term **R** is the correlation matirx of vector y, given as

$$\mathbf{R} = E\left[\mathbf{y}(n)^* \mathbf{y}(n)^T\right] = \sigma_v^2 I + \sum_{i,j=1}^{L} \mathbf{s} P_{i,j} \mathbf{s}^H \qquad (22)$$

where σ_v^2 is the noise variance, I the identity matrix of order (M+1)x(M+1) and $P_{i,j}$ is amplitude correlation matrix, defined as

$$P_{i,j} = E\left[A_i(n)^* A_j(n)\right], \qquad 1 \leq i,j \leq L \qquad (23)$$

Normally, **R** is not known, therefore we need to estimate it. To the case of N samples, a solution is to use the expression:

$$\mathbf{R} = \frac{1}{N} \sum_{n=0}^{N-1} \mathbf{y}(n)^* \mathbf{y}(n)^T \qquad (24)$$

4. The Developed Method

The method presented in this work for the determination of the angles of arrival in a linear array of antennas consists of the development of a Genetic Algorithm whose function of evaluation is the expression for the specter of the MVDR.

The first step of the algorithm is to determine the matrix R for the incident sign, since this is necessary for the calculation of the MVDR. Done this, is generated an initial population where the individuals are written in binary code. The size of the population as well as the resolution of the individuals (chromosomes.) can be defined by the user.

Each individual of the population represents a θ. The individuals are decoded and by means of the equation (9) corresponding phase delay ϕ for each individual are found. After that the MVDR for each element of the population is calculated. By this way it is possible to do the evaluation of the individuals where the ones that had generated greater value in the MVDR will be chosen for the process of recombination and mutation to form a new population.

The new generated population will follow the same process that the initial population, thus closing a cycle that will stop only when a determined homogeneity degree between the individuals of the current population is reached. At this moment, the algorithm will present to the user the best found solution.

5. **Results**

We did diverse simulation for different signals and various values of SNR and antennas. Also diverse values for the size of the populations as well as for the resolution of the chromosomes had been used.

The figure 7 shows the specter estimated for an array of 4 antennas where happens a signal whose angle of arrival is 45° and possess an SNR equal to 10.

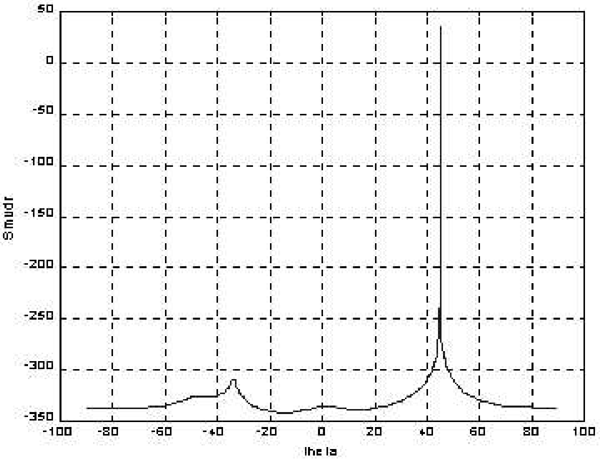

Figure 7: signal with $\theta = 45^o$, SNR = 10

For a population of 30 individuals with resolution of 16 bits, the algorithm after 3 generations presented as solution an angle of arrival equal to 44,98°. We notice that the algorithm converged of extremely fast form to the peak of the specter as well as presented a very small error to the angle of arrival.

In the following figure, it is presented the specter for an incident signal in an array of 7 antennas with an angle of -60,20° and relation signal-noise equal to 10. For this problem, the simulation was did for populations of 25 individuals with resolution of 16 bits. Again the algorithm converged in little interactions, taking only 7 generations to present as reply an angle of arrival equal to -60,17°. The specter generated for such situation is seen in figure 8.

Also simulations for multiple signals had been done. In the figure 9, we can see the resultant specter for three incident signals with angles of 45°, 20° and 60° with SNR = 10 and 5 antennas. The results of the algorithm for this case were 44,97° in 11 generations, 19.98° in 13 generations and 60° in 51 generations.

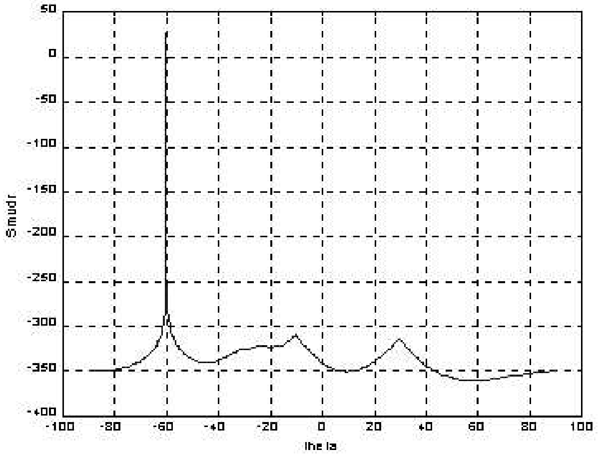

Figure 8: signal with $\theta = -60{,}20^o$, SNR = 10

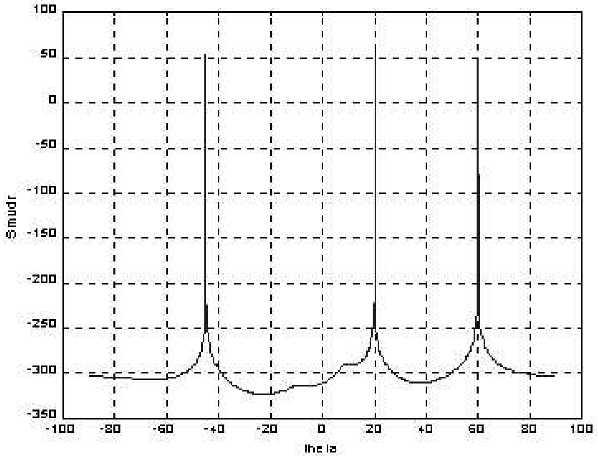

Figure 9: signal with $\theta_1 = -45^o$, $\theta_2 = 20^o$, $\theta_3 = 60^o$, SNR = 10

After various simulations, noticed that a good choice for the size of the populations would be of 30 individuals. We also perceived that, as waited, how much bigger the resolution of the chromosomes, minor the error of the reply, however the computation time also magnified. The resolution that presented the best relation between the computation time and the error was of 16 bits. However, in cases that demands a lesser severity in the error of the reply for the angle of arrival, it is possible the use of a resolution of 8 bits.

6. Conclusion

Was presented an algorithm as solution for the determination of the angles of arrival in linear arrays of antennas based in the conjugated use of Genetic Algorithms and spectral esteem by the MVDR method.

The algorithm revealed fully capable to determine the angle of arrival with low computational cost and presenting an small error, never bigger than 0.05, between the solution supplied and the exactly value.

By this way, the Genetic Algorithms were presented as a computational tool of great interest in the branch of the Adaptive Antennas.

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