Array Failure Correction with a Genetic Algorithm

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***Abstract*— A flexible approach using the genetic algorithm (GA) is proposed for array failure correction in digital beamforming of arbitrary arrays. In this approach, beamforming weights of an array are represented directly by a vector of complex numbers. The decimal linear crossover is employed so that no binary coding and decoding is necessary. Three mating schemes, adjacent-fitness-paring (AFP), best-mate-worst (BMW), and emperor-selective (EMS), are proposed and their performances are studied. Near-solutions from other analytic or heuristic techniques may be injected into the initial population to speed up convergence. Numerical examples of single- and multiple-element failure correction are presented to show the effectiveness of the approach.**

***Index Terms*— Adaptive arrays, beamforming, genetic algorithms.**

I. INTRODUCTION

FOR an antenna array with traditional analog beamforming, if one or more elements are damaged by an unforeseen reason, the array may have to be pulled out from operation due to unacceptable pattern distortion, for example, a significant increase of sidelobe level (SLL). With digital beamforming, the defective elements of an antenna array need not to be replaced. Instead, the beamforming weights of the remaining elements can be recalculated to form a new pattern that is close to the original. The possibility of failure correction for digital beamforming arrays provides a cost-effective alternative to hardware replacement which might be too late or too time-consuming, especially for arrays performing critical operations, such as, for instance, in the battlefield. Other applications include satellite or extraterrestrial communications, where antenna element damage cannot be rectified easily by replacement. From the open literature, no analytic technique has been devised to yield a set of new beamforming weights that effectively corrects the deformed pattern. Since a failed array can be considered as a nonuniformly spaced array, analytic approaches are generally unable to tackle this kind of problem. In recent years, numerical algorithms have been proposed to correct the deformed patterns. However, due to the arbitrariness of the geometrical layout of the remaining functional array elements and of the desired beam shape, array failure correction even for numerical approaches is a very challenging problem. From literature review, only a few research results have been reported. Peters [1] proposed a method to reconfigure the amplitude and phase distribution of the remaining elements by minimizing the average sidelobe level, via a conjugate gradient method. Mailloux [2] used the method of replacing the signals from failed elements in a digital beamforming receiving array.

In this paper, an effective method based on the genetic algorithm (GA) [3] is proposed for array-failure correction of arbitrary digital beamforming arrays. GA's are stochastic optimization algorithms which have very wide applications [4], [5]. In recent years, genetic algorithms have also been applied to array beamforming. Haupt [6] applied GA to determine which element should be turned on, in thinned linear and planar arrays to obtain low sidelobes. Tennant *et al.* [7] demonstrated its use in null steering in a phased and adaptive array, while Yan and Lu [8] used a GA for array pattern synthesis, where the phase and magnitude are restricted to certain discretized values for easy implementation by commercially available digital phase shifters and attenuators, thereby greatly reducing the complexity and cost of array antennas. In this paper, an improved GA based on [8] is applied to array-failure corrections. As array-failure correction is a much more difficult task than simple sidelobe reduction of a uniformly spaced linear array, considerable improvement and new additional features have to be introduced. During the course of this study, various mating schemes; namely, adjacent-fitness-pairing (AFP), best-mate-worst (BMW), and emperor-selective (EMS); have been proposed and their performances are compared to determine the most effective. Numerical examples of single- and multiple-element failure corrections are presented to show the effectiveness of this approach.

II. PROBLEM FORMULATION

For array beamforming, one can employ amplitude-only, phase-only, or the amplitude-phase approach [9]. The amplitude-only approach cannot compensate for the degradation of a damaged array pattern, as the failed elements introduce an asymmetrical aperture distribution. On the other hand, phase-only synthesis with a constant amplitude [10] requires a large number of elements to yield low sidelobes. Consequently, beamforming using both amplitude and phase (arbitrary complex variables) is necessary for the redistribution of weights, in order to correct the damaged pattern.

For an arbitrary, the array factor (AF) can be generally given by

$$\mathrm{AF} = \boldsymbol{w}^T \boldsymbol{S}(\theta, \theta_{\boldsymbol{m}}) \tag{1}$$

where

$$\boldsymbol{w} = \{w_1, w_2, \cdots, w_N\}^T, \qquad w_n \in C^n \tag{2}$$

is the weighting vector, $\boldsymbol{S}$ is the steering vector, θ and θ_m are the direction variable and main beam direction, respectively. C^n is the set or a subset of all complex numbers.

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Take, for example, a linear array of N identical elements, its steering vector is

$$\boldsymbol{S} = \exp\left\{jkd\left(n - \frac{N-1}{2}\right) \cdot (\cos\theta - \cos\theta_m)\right\} \tag{3}$$

such that the same set of optimum weights for the main beam at broadside can be used for other directions, if the above $\boldsymbol{S}$ vector is recalculated for the new beam-pointing direction.

In the event of the mth-element failure, its weight w_m is assumed to be zero. Thereafter, the GA is applied to correct the SLL and the main beam shape of the pattern to prefailure specifications.

III. THE GENETIC ALGORITHM

Natural evolution is a search for the fittest in the species space. The success of life on earth demonstrates the effectiveness of this search process. Based on natural evolution [3], genetic algorithms capitalize on tools that work well in nature. It is considered a sophisticated search algorithm for complex, poorly understood mathematical search spaces. A mathematical treatment on GA's foundations is provided in [11], while numerous contemporary GA applications can be found in [5]. Living beings are encoded by chromosomes, with GA's one encodes the possible solutions in the form of data structures. Thus GA's are capable of arriving at an optimal solution without the benefit of explicit knowledge about the solution space.

A. Chromosome Structure

Most GA's use binary coding and binary genetic operations, [4]. The proposed approach, however, applies floating-point genetic operations on complex array weighting vectors. Hence, each chromosome is a vector of complex numbers and the dimension of the vector is equivalent to the number of array elements.

B. Initial Population

An initial population of at least 100 random chromosomes is generated. The weighting vectors $\boldsymbol{w}^{(D)}$ of the damaged array pattern and $\boldsymbol{w}^{(T)}$ of a Taylor (one-parameter) synthesized array with an identical beamwidth as the original pattern, are added to replace two of the weakest individuals among the initial population. Their insertion helps to improve the rate of convergence. In fact, it is observed that the best individual grown for mth-element failure correction should be inserted into the initial population of a double element failure, if one of the failed elements is in the mth position. In that case, the rate of convergence is increased significantly as compared to a GA run without any prior insertion.

C. Reproduction

Rank-based fitness assignment sorts the individuals in a descending order of fitness for the kth generation, G_k population of P individuals. Linear crossover is performed, where two parents produce two children. In [12], three selection methods, as shown in Fig. 1, are used concurrently. However, that has proven to be too computationally intensive. Out of the three methods, the dominant technique has been identified and singled out to improve the rate of convergence. Note the probability of crossover P_c is always one.

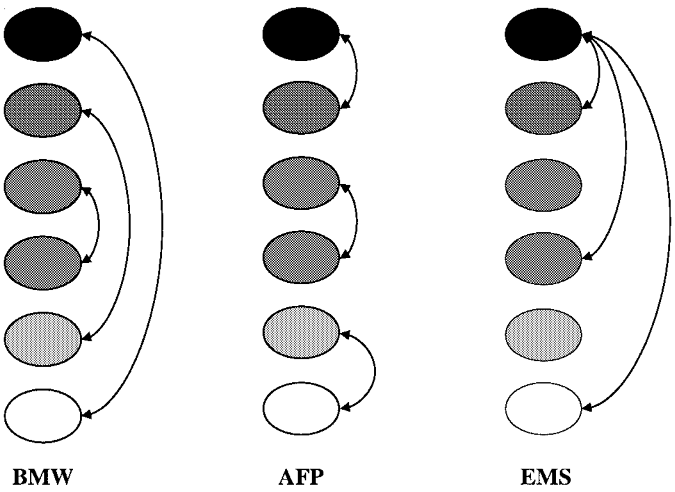


Fig. 1. The three different mating schemes. Darker shade represents higher fitness level.

1) *Best-Mate-Worst (BMW)*: Adapted from [5] and [8], BMW effectively spreads the superior genetic material in G_k. It is maximally disruptive, but weaker individuals with any desirable traits do get a chance to produce offsprings with stronger partners. In BMW, the best gets to mate with the worst, and second-best with the second-worst individual. Thus it is inclined to reduce the difference in fitnesses between the best and the worst individuals, with a low bias for an elitist group.
2) *Adjacent-Fitness-Pairing (AFP)*: AFP mates two individuals with adjacent fitnesses. Thus the best pairs with the second-best, the third-best mates with the fourth-best and so forth. It is highly conservative of genetic information but may result in premature convergence. However, AFP ensures the union of strong individuals whose offsprings may prove to be fitter than their parents. In [5], a similar method, known as fit–fit selection, steps through the ordered list of individuals of a population that does not remain static for an entire cycle. Unlike [5], AFP does not allow any individual to breed twice. Moreover, the population G_k that it works on stays static throughout the mating process.
3) *Emperor-Selective (EMS)*: The best individual in G_k gets to mate with every other even sample in the population, as shown in Fig. 1. If one or more near-solutions are added to an initial population of random individuals, EMS usually yields the best chromosome among the three methods. It is the only method that allows the fittest individual to procreate freely with practically the rest of the population.

D. Survival Selection

EMS works on G_k to produce *cPop*, which is the child population after mating and crossover. Concurrently, a nonuni-

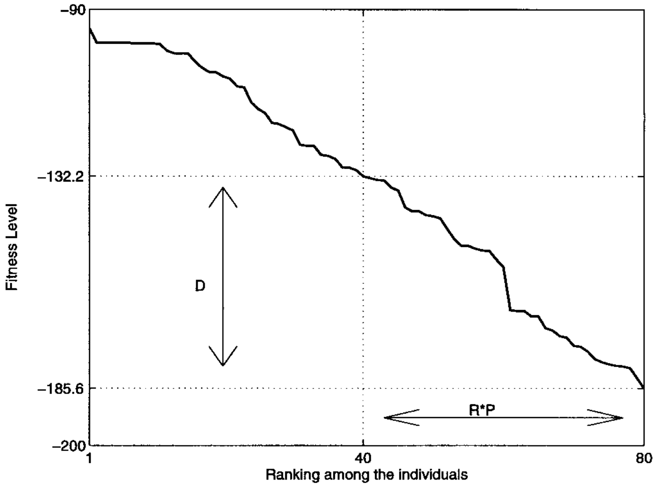


Fig. 2. Fitness ranking of the current population with Auto-Grooming On. D is the fitness difference, in this case, $D = -132.165 + 185.617 = 53.45$. While R refers to the rejuvenation ratio in percentage of the population size P.

form multimodal mutation operator is applied to a population $mPop1$ which comprises of $X (X \leq P)$ copies of the fittest individual prior to the mating operation above. The Gaussian distribution parameter S, which is inversely proportional to the size of mutational changes introduced, is adaptively increased once stagnated growth due to premature convergence is detected. The same mutation operator is performed across a copy of the original population G_k, giving $mPop2$, the mutated child population based on P_m, the mutation probability which is usually greater than 0.04.

Thus most of the fitter individuals from $mPop1$ and $mPop2$ may be the mutated versions of the current best sample. In a fixed-size population, too many of the above will increase the selective pressure in favor of the best individual or local maxima, resulting in a loss of diversity. Unlike [12], only the best $Y (Y \leq P)$ individuals from $mPop1$ and $mPop2$ are selected to produce $tPop$, the population of best individuals produced through unary transformation.

Finally, the new set of P individuals that forms the next generation G_{k+1} are those from the best of $cPop$ and $tPop$.

E. Auto-Grooming Mode

In order to ensure implicit parallelism, a portion of the population determined by the user-defined rejuvenation ratio R, in percentage, is earmarked for replacement by randomly generated individuals. This is carried out whenever the fitness difference D of the fittest and weakest individuals of the subpopulation, as shown Fig. 2, is below a user-specified trigger level, T, the minimum fitness difference.

The randomly generated subpopulation of $R * P$ individuals is seeded with the same solutions as the original population. In addition, it is allowed to grow or "be groomed" on its own for the next predefined Z number of generations before it can interact with the senior population. This technique has so far yielded better results than pure restarts of the GA. A good example is illustrated in Fig. 3.

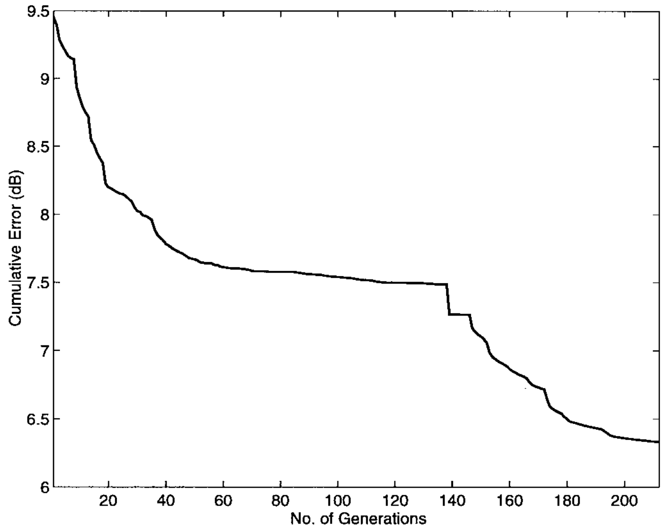


Fig. 3. Fitness progress curve with main beam directed broadside and secondnd-, fifth-, and sixth-element failures.

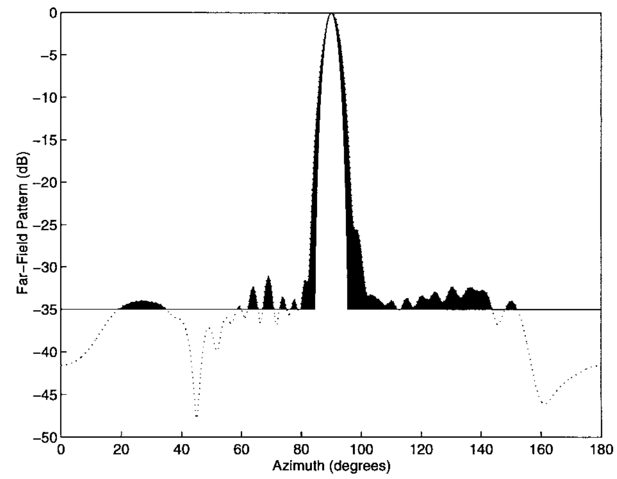


Fig. 4. Template cast over each decoded pattern to evaluate its fitness.

The rejuvenation ratio R must be set in proportion to the size of the initial population P. For instance, if $P = 100$, a reasonable R value may be no greater than 80%. So that the senior population of the top 20 individuals can continue to prosper, after their separation from the weaker crop of 80 individuals, for at least $Z = 2$ quarantine generations. The program may dynamically change the R and Z values as the GA progresses, by weighing the importance of greater diversity (higher R) against a smaller gene pool of top performing individuals. Usually, the maximum Z value should not be greater than 5, and it must be reduced for R higher than 60%.

F. Fitness Evaluation

A template, formed by the shape of the main lobe and the specified SLL, is cast over the array pattern produced by each candidate, as shown in Fig. 4, to compute their cumulative difference as a form of fitness measure in decibels. Thus the ideal array pattern is one that conforms to the original main beam shape with the specified SLL, as depicted in Fig. 4.

G. Termination Criteria

The maximum number of generations must be defined together with the desired fitness level. By satisfying either one of the above criteria, the GA will terminate. A log file of the GA progress in terms of the increasing fitness per generation, and the matrix containing the chromosomes of the current population are saved onto a hard disk. By reviewing the above data, it is possible to improve the performance of the GA through fine-tuning the Gaussian distribution of mutational changes or by introducing new heuristic marriage routines. The decreasing cumulative error of each generation can be extracted from the fitness log.

H. Convergence Observation

The best solution of each generation may be produced through linear crossover, after one of the selection methods, or from a mutated individual. Usually, the offsprings of fitter individuals from the previous generation show greater fitness, in the beginning of a GA run. However, when approaching convergence, the mutation operation may tend to produce better individuals.

A lower shape value S, which corresponds to larger mutational changes, will result in higher increments of the average fitness level at the start of a GA run, but ends up with premature convergence far from the desired fitness. Whereas, a high S value may yield a steady and continuous improvement in the fitness of future generations, but at a much slower convergence rate.

IV. Simulation Results

A classic Dolph–Chebyshev linear array design with an SLL of -35 dB is used as a reference. In simulation, the array consists of 32 identical dipoles, with a uniform spacing of half a wavelength. The steering vector $\boldsymbol{S}$ is (3).

A. Two-Element Failure Correction

Fig. 5 depicts the fitness progress curves, obtained over an average of 20 runs, for three different main beam directions. Notice that convergence is observed for all the above cases before 200 generations. The cumulative error after 200 generations is the highest for the corrected main beam at broadside. Since its beam shape is narrower than the others, its corrected SLL is observed to be comparatively higher.

Shown in Fig. 6(a)–(c) are the corrected array patterns for the secondnd- and fifth-element failure, with the main beam pointing at broadside, 52°, and 138°, respectively. All corrected patterns have a SLL of at most -34.78 dB. The half-power beamwidths of the original patterns are Fig. 6(a) 3.89°, Fig. 6(b) 5.27°, and Fig. 6(c) 6.21°, respectively, whereas the corrected main beams have half-power beamwidths of Fig. 6(a) 4.77°, Fig. 6(b) 6.06°, and Fig. 6(c) 7.17°.

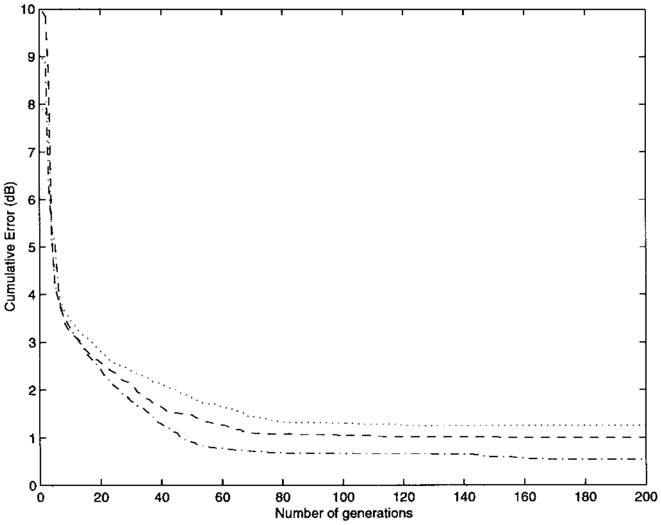
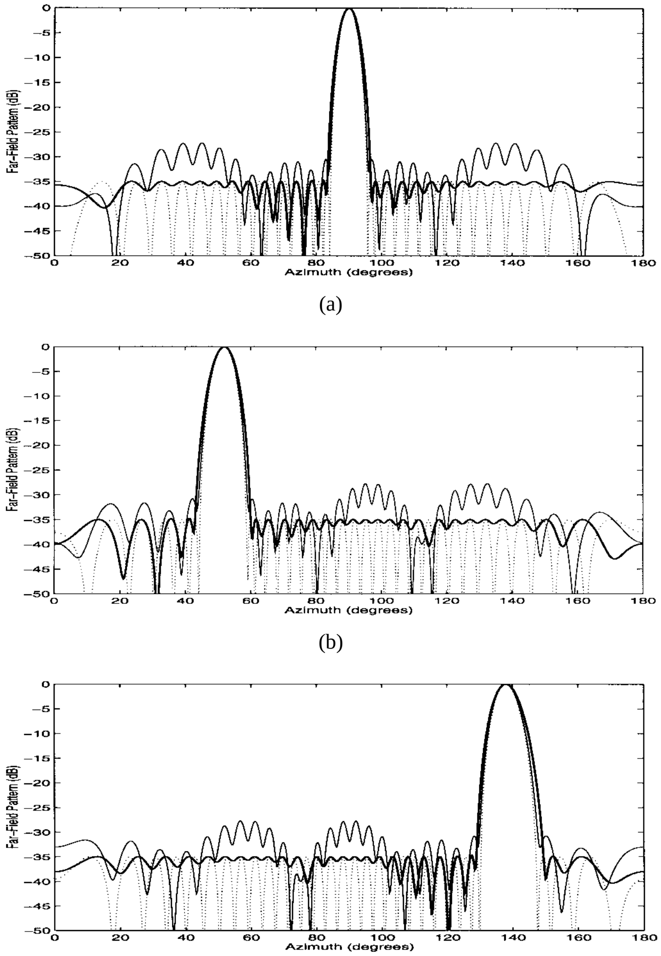


Fig. 5. Fitness progress curves, obtained from an average of 20 runs, with main beam directed at i) broadside (dotted line), ii) 52° (dot-dashed line), and iii) 138° (dashed line).



(a)

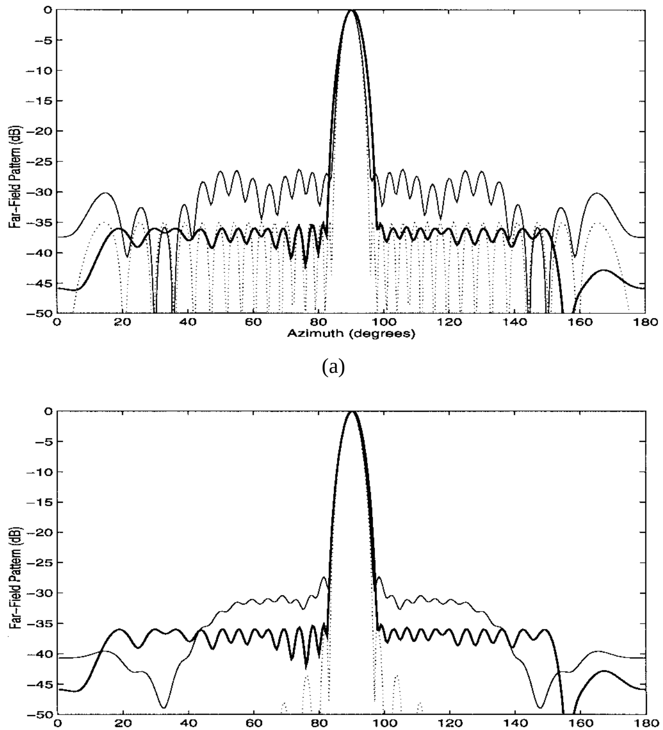
(b)

(c)

Fig. 6. Corrected pattern with main beam pointing at (a) broadside, (b) 52°, and (c) 138°. Thick solid line: the corrected pattern; thin solid line: the damaged array pattern; and dotted line: the original array pattern.

B. Three-Element Failure Correction

Now, if a sixth-element failure follows, the fitness progress curve, obtained over an average of 20 runs, is illustrated in Fig. 3. Auto-Grooming usually kicks in somewhere between the 100th and 115th generation, discarding the bottom 50% of the population to accommodate the new individuals. The



(a)

(b)

Fig. 7. Corrected beam pattern for second-, fifth-, and sixth-element failures using references (a) Dolph–Chebyshev and (b) Taylor Line-Source (one-parameter). Thick solid line: the corrected array pattern; thin solid line: the damaged array pattern; and dotted linr: the original array pattern.

operation ensures implicit parallelism, while retaining the fitter individuals produced so far for further breeding. Similarly, convergence is observed at around 200 generations, even though three elements have failed. This is made possible by the insertion of the solution for the above second- and fifth-element failure correction, else more generations will be required before the GA yields a solution of satisfactory fitness level.

The corrected far-field pattern for second-, fifth-, and sixth-element failures with a half-power beamwidth of 5.36° is shown in Fig. 7(a), where the reference pattern is of Dolph–Chebyshev design with a half-power beamwidth of 4.14°. If a Taylor Line-Source (one-parameter) [9] with a half-power beamwidth of 4.76° is used, Fig. 7(b) depicts a corrected beam shape that is closer to the original reference. Hence it is much more difficult to recover the beam shape or half-power beam width of a Dolph–Chebyshev design as compared to a Taylor pattern for the same SLL.

In this case, the highest SLL of the above is -35.2 dB. The corrected patterns for other main beam directions are not shown, since they are essentially similar.

The normalized excitation coefficients of the double- and triple-element failures are listed in Table I. By using (3), only one set of normalized weights is required for different main beam directions, but different $\boldsymbol{S}$ vectors are generated each time.

Usually, the number of generations required to obtain a satisfactory fitness value increases with the number of failed elements. However, the increase in the number of generations is largely dependent on the position or weighting of the failed element(s). This applies even if the solution for a single-element failure correction is planted in the initial population for a double-element failure correction, and so forth.

TABLE I
NORMALIZED EXCITATION COEFFICIENTS FOR CORRECTED POWER PATTERNS BY THE GA

Element Position	Original / Undamaged Tschebyscheff Weights	Corrected Weights	
		Double Element Failure	Triple Element Failure
1.	0.44388	0.05154031 -0.01497736j	-0.01032058 -0.03439333j
2.	0.24331	0.00000000	0.00000000
3.	0.30354	0.12233283 -0.00771323j	0.01307182 -0.04754893j
4.	0.36838	0.17110660 +0.00158334j	0.06741992 -0.03870225j
5.	0.43670	0.00000000	0.00000000
6.	0.50723	0.28477727 -0.02154652j	0.00000000
7.	0.57851	0.35062150 -0.03180481j	0.22110788 -0.05947521j
8.	0.64897	0.47318948 -0.02422230j	0.22049067 -0.07215443j
9.	0.71699	0.49495041 -0.02796476j	0.34545619 -0.04855551j
10.	0.78094	0.59820219 -0.01922468j	0.40620057 -0.06571700j
11.	0.83923	0.65812510 -0.02042224j	0.49593857 -0.04161112j
12.	0.89036	0.74010398 -0.01792784j	0.59766384 -0.02776258j
13.	0.93301	0.79391671 -0.02261699j	0.66609431 -0.02814328j
14.	0.96604	0.85219414 -0.02424158j	0.74400625 -0.01047802j
15.	0.98858	0.88666918 -0.02359771j	0.80096395 -0.00209044j
16.	1.00000	0.91229164 -0.02095085j	0.84791367 +0.00681141j
17.	1.00000	0.91895081 -0.01467082j	0.87554310 +0.03153805j
18.	0.98858	0.91147812 -0.01211285j	0.87598020 +0.03350884j
19.	0.96604	0.88486647 -0.00492927j	0.86463867 +0.05852919j
20.	0.93301	0.84312000 -0.00426408j	0.82582626 +0.05856186j
21.	0.89036	0.78781560 +0.00141028j	0.77977006 +0.06860908j
22.	0.83923	0.72080771 -0.00232503j	0.70366526 +0.07151124j
23.	0.78094	0.64170296 +0.00249546j	0.63166452 +0.07005025j
24.	0.71699	0.55892723 -0.00069730j	0.54702039 +0.06632380j
25.	0.64897	0.47334602 +0.00663294j	0.46193190 +0.05876960j
26.	0.57851	0.39666461 +0.00087765j	0.37978203 +0.05548133j
27.	0.50723	0.31623428 +0.00737544j	0.29183811 +0.04165807j
28.	0.43670	0.25404895 +0.00311330j	0.23143702 +0.04062947j
29.	0.36838	0.19345241 +0.01158597j	0.16635663 +0.02310862j
30.	0.30354	0.16025616 -0.00320436j	0.12054244 +0.02034418j
31.	0.24331	0.10543200 -0.01017618j	0.07016293 +0.00487534j
32.	0.44388	0.05718009 -0.01637797j	0.05418648 +0.00018126j

V. CONCLUSIONS

A genetic algorithm is proposed for the (linear 32-element) array failure correction of single-, double-, and triple-element failures. For a triple-element failure, the solution for a double-element failure can be included in the initial population for the correction of the former, if two out of the three failed elements are identical to those involved in the latter, and so forth. The decrease in the corrected SLL comes at the price of a slightly broader main beam. All corrected main beams have a half-power beamwidth of less than one degree broader than the original.

The success of correcting a damaged pattern depends heavily on i) the original weighting of the failed element(s) and ii) the number of failures. In this instance, if the 15th or 16th element fails resulting in a blockage, it would be impossible to correct or yield any improvement using this GA.

Incidentally, for the same number of element failures, it is easier to recover those cases where all failures occur on the same side (with respect to the central element) as compared to those with failed elements on each side. Since a higher SLL is observed in the latter.

The genetic algorithm demonstrates the possibility of its application for nonlinear array synthesis, since damaged linear arrays are essentially nonlinear in nature. Though the rate of convergence may be too slow for real-time applications, the results for different combinations of element failure for a digital beamforming array may be stored in the memory of a digital beamformer. Notice that the number of possible combinations will not be too large, since not all failures are correctable. Too many failed elements will ultimately render the array unusable. Therefore, the aperture distribution can be dynamically reassigned in real time only if a correctable array failure scenario arises.

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