Multi-criteria design methodology of a dielectric resonator antenna with jumping genes evolutionary algorithm

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Abstract

A novel evolutionary computing algorithm, jumping genes evolutionary algorithm (JGEA) is used for designing a dielectric resonator antenna with multiple parasitic strips. This scheme provides an effective methodology for the antenna design, searching for the necessary parameters to achieve the optimal performance. The obtained non-dominated solutions for the antenna configurations have been used to select and determine the appropriate impedance bandwidth and radiation pattern. In the LP DRA optimization, the impedance bandwidth of 21% has been achieved. In the CP DRA optimization, the antenna can be designed to achieve the operation frequency ranged from 3 to 4.2 GHz. The results show enhancement of impedance bandwidth and the CP operation frequency range comparing with the original designs.
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1. Introduction

Dielectric resonator antenna (DRA) is one of the popular choices for millimeter wave application nowadays, as it has several advantages such as low-loss, small size and lightweight. The use of DRA has been widely accepted since the original paper on the cylindrical DRA [1]. Thereafter a number of DRA configurations have been developed to satisfy a wide range of wireless applications [2–4]. The shapes of the developed designs also differ a lot, including the cylindrical, hemispherical and rectangular DRA designs. Hence, the polarization of DRA can be linear, circular or elliptical, depending also on the design. As the main body of the DRA is not made of metal, the metallic loss would be greatly reduced when compared with some antenna designs consisting of mainly metallic structure, such as the patch antennas.

Thus, only small dielectric leakage would the main source of the loss in DRA. Due to this reason, the use of DRA is practical when the energy consumption is an important issue of the wireless equipment design. For instance, the saving of energy in the equipment will result in the downsizing of the battery, and hence the downsizing of the overall equipment size.

Even with the advantage of its low loss structure, a main drawback of the DRA application is its narrow impedance bandwidth. For adapting DRA into some wireless applications with a wider bandwidth requirement, a parasitic conducting patch has been recently employed to increase the impedance bandwidth, with the DRA fed by a probe or a conformal strip [5,6]. They show the fact that the degenerated mode of the parasitic patch combines with the DR fundamental mode as a result of bandwidth enhancement. Then, the use of multiple parasitic strips in frequency tuning of the linearly and circularly polarized DRA have been demonstrated in [7]. However, this antenna configuration consist a large number of tunable parameters in order to fulfills a

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several design criteria, such as the impedance matching and the radiation pattern. These antenna parameters include the length, the width, the angular position and the number of parasitic strips. These are not easily to be determined by any trial-and-error design method, and therefore a powerful optimization method should be applied to reach the desirable design solutions in a huge search space.

Since there are more than one design criteria, a multi-objective optimization algorithm should be used in the optimization process. The multi-objective evolutionary algorithm (MOEA) [8–12] can be applied in which it mimics the evolutionary principles in nature for driving its search towards the Pareto-optimal solutions.

This paper proposes a design method to determine a desirable set of DRA parameters using the MOEA approach. To achieve better genetic diversity in the evolutionary optimization process, the algorithm includes a newly developed genetic operator, namely Jumping Genes Transposition [13–16]. It is a methodology to enable genes mobility within the same chromosome or even to the neighboring chromosomes [13], and hence increase the chance of merging various genes combination that can direct the search towards the Pareto-optimal solutions. With the adaptation of Jumping Genes Operators in the use MOEA, this algorithm is named as jumping genes evolutionary algorithm (JGEA) [14–16].

The basic formulation of the objective functions and some simulation results were presented in an IEEE AP-S symposium held at July 2006 [17] in New Mexico, USA. However, the multi-objective methodology in the symposium paper is not in detail and the experimental results were not included for verification. Moreover, the radiation patterns of the antennas have not been shown for both simulation and experimental results. In this paper, the detailed methodology of the design will be given and both the simulation and experimental results for both the return loss and radiation pattern will be included for verification.

The paper is organized as follows: Section 2 will show the JGEA, including the operational mechanisms for the jumping gene and the use of Pareto-optimal in the multi-objective ranking. The design methodology and results of the DRA with multiple parasitic strips will be presented in Section 3. Finally, a conclusion will be given in Section 4.

2. Jumping genes evolutionary algorithm

2.1. The algorithm JGEA

JGEA is a newly developed evolutionary algorithm specially designated for multi-objective optimization. It introduces a new genetic operator based on a horizontal gene transmission mechanism, i.e. jumping genes transposition. The advantage of using JGEA is its ability for obtaining a set of non-dominated solutions that is close to Pareto-optimal front. It has the capacity for achieving better performance in convergence and diversity over the other MOEA [14–16].
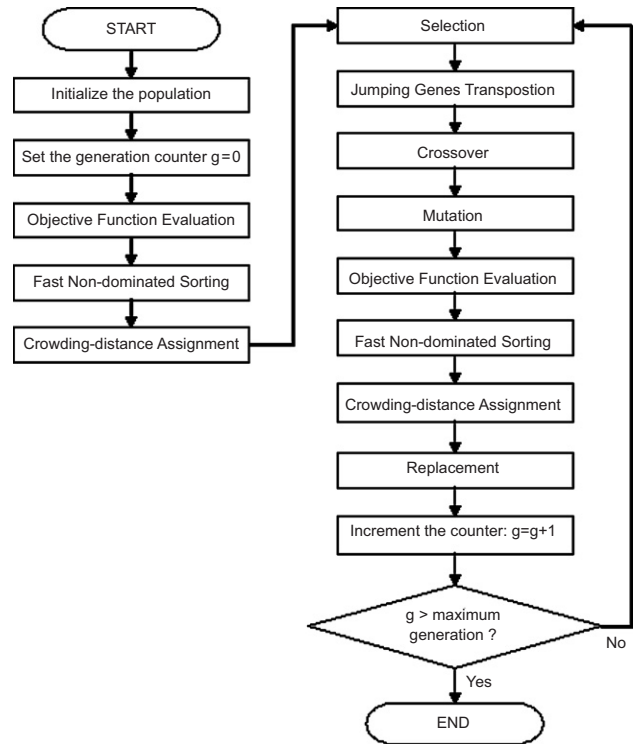

Fig. 1. Flowchart of jumping gene evolutionary algorithm.

A flowchart of JGEA operation is shown in Fig. 1. The fast non-dominated sorting [10] for multi-objective ranking and crowding distance assignment [10] can be incorporated together to enhance the diversity preservation.

Within the JGEA, there exist two basic JG transposition operations. These are cut-and-paste transposition and copy-and-paste transpositions. Fig. 2 shows the cut-and-paste transpositions among same and different chromosomes. It is an action that the element in the chromosome is cut from an original position and then pasted into a new position of its own or another chromosome. Fig. 3 shows the copy-and-paste transposition among same and different chromosomes. In this transposition, the element will replicate itself and be inserted into a new position of the chromosome while keeping the original position unchanged. The JG operations enhance the possibility of merging the various types of genes together that eventually benefit the phenotypic shaping of chromosome.

The flowchart of the jumping genes transposition is shown in Fig. 4. The operation of cut-and-paste or copy-and-paste transposition is determined by a certain probability, namely the jumping rate. As described in the figure, every transposon jumps with a probability equal to the jumping rate. There is no preferred selection advantage for using either the cut-and-paste or the copy-and-paste scheme for jumping. Therefore, this is randomly selected. Since each transposition selection is opportunistic, the jumping process is neither streamlined nor planned in advance, then, the jumping process is similar