

An Improved Multiobjective Evolutionary Algorithm Based on Dominating Tree

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Abstract. There has emerged a surge of research activity on multiobjective optimization using evolutionary computation in recent years and a number of well performing algorithms have been published. The quick and highly efficient multiobjective evolutionary algorithm based on dominating tree has been criticized mainly for its restricted elite archive and absence of density estimation. This paper improves the algorithm in these two aspects. The nearest distance between the node and other nodes in the same sibling chain is used as its density estimation; the population growing and declining strategies are proposed to avoid the retreating and shrinking phenomenon caused by the restricted elite archive. The simulation results show that the improved algorithm is able to maintain a better spread of solutions and converge better in the obtained nondominated front compared with NSGA-II, SPEA2 and the original algorithm for most test functions.

1 Introduction

Multiobjective optimization problems (MOPs) are those problems that involve simultaneous optimization of more than two objectives (often competing) and usually there is no single optimal solution [1]. It is usually difficult or even impossible to assign priorities as in single objective optimization problems (SOPs). This makes an algorithm returning a set of promising solutions preferable to an algorithm returning only one solution based on some weighting of the objectives. For this reason, there has been an increasing interest in applying evolutionary algorithm (EA) to MOPs in the past ten years.

Over the past decade, a number of multiobjective evolutionary algorithms (MOEAs) have been suggested [2-5]. These MOEAs use Pareto dominance to guide the search, and return a set of nondominated solutions as result. Unlike in single objective optimization, there are two goals in a multiobjective optimization: 1) convergence to the Pareto optimal set and 2) maintenance of diversity in solutions of the Pareto optimal set [4]. Many strategies and methods are introduced to overcome these two difficulties existing in MOPs [7]. These algorithms perform well in some benchmark problems. However, there are some disadvantages existing in current MOEAs. Many MOEAs are

intricate. To achieve better solutions, many methods and strategies are used and many parameters need to be adjusted according to experiences and prior knowledge of the given problems. On the other hand, many MOEAs have high computation complexity. So designing a simple, yet efficient, MOEA is desirable.

We have proposed a simple and highly efficient multiobjective evolutionary algorithm [6]. This algorithm uses a novel fitness assignment: tree structure, which is a binary tree with the dominating information of individuals. The tree structure is called dominating tree in this paper. Moreover, the algorithm is called the multiobjective evolutionary algorithm based on dominating tree (DTEA). The experiment shows that DTEA can converge to the Pareto front, maintains the diversity of the population and cost less time. However, the algorithm has a restricted elite archive, which can cause oscillating/retreating phenomenon in the Pareto front; and it is also criticized that there are no density estimation. In this paper, we improve DTEA in these two aspects. The simulation experiment shows that the improved algorithm can obtain better solutions and the active elite archive can improve the performance of algorithms indeed.

The rest of the paper is organized as follows: in the following section, we review the related work. Section 3 explains the improvement of DTEA in detail; and then the simulation results are given in the section 4; at last, the section 5 makes a conclusion.

2 Related Work

There are some new developments of MOEAs in recent years. NSGA-II [4] is advanced from its origin, NSGA [2]. In NSGA-II, a nondominated sorting approach is used for each individual to create a Pareto rank, and a crowding distance assignment method is applied to implement density estimation. Similar to NSGA-II, SPEA2 [5] is an enhanced version of SPEA [3]. In SPEA2, each individual in both the main population and the elitist archive is assigned a strength value, which incorporates both dominance and density information. Meanwhile, a k th nearest neighbor density estimation method is applied to obtain the density value of each individual.

Recent research clearly shows that the elitism can speed up the performance of MOEAs significantly, and it helps to prevent the loss of good solutions once they have been found [8]. Fieldsend points out a consequence of restricting the number of solutions in the elite front can be shrinking and oscillating/retreating estimated Pareto front [9]. A remedy to this situation is simply to retain all the nondominated solutions found (as an active input to the continuing search process) [9].

Shi has introduced a simple and highly efficient multiobjective evolutionary algorithm [6]. Ref [6] has pointed out that there are many redundant comparisons in the former fitness assignments that is the main time-consuming part in MOEAs, and then proposed a novel tree structure (dominating tree) to preserves the necessary dominating relationships among individuals. As shown in Fig.1, the dominating tree maintains the necessary relationships among individuals; however, it uses fewer comparisons. The dominating tree is a binary tree; its child point links to its left subtree whose root is dominated by that node; and its lsibling and rsibling point link to its right subtree whose root is nondominated with that node (lsibling and rsibling point constitute a bidirection list actually). The tree's sibling chain refers to the chain constituted by the root and the root nodes of its right subtrees. Taking the right figure of Fig.1 for example, N1 and N4