

A Novel Pheromone-Based Evolutionary Algorithm for Solving Degree-Constrained Minimum Spanning Tree Problem

Xiao-ma Huang, Yue-jiao Gong (Corresponding Author) and Jun Zhang

Department of Computer Science, Sun Yat-sen University

Key Laboratory of Machine Intelligence and Sensor Networks, Ministry of Education

Key Laboratory of Software Technology, Education Department of Guangdong Province, P.R. China

gongyuejiao@gmail.com

ABSTRACT

The degree-constrained minimum spanning tree problem (dc-MSTP) is crucial in the design of networks and it is proved to be NP-hard. The recently developed evolutionary algorithm utilizing node-depth-degree representation (EANDDD) has successfully enabled the dc-MSTP solvable by generating new spanning trees in average time complexity $O(\sqrt{n})$, which is the fastest in the literature. However, as the generic operation of EANDDD is to change two edges that are randomly selected from the entire tree, the efficiency of EANDDD still has potential to be further improved. In this paper, we propose a novel pheromone-based tree modification method (PTMM) to improve the efficiency of EANDDD. For each edge, a pheromone value is defined based on the historical contribution of the edge to the fitness of the spanning tree. Then, PTMM considers the pheromone value on each edge as a desirability measure for selecting the edge to construct the spanning tree. In this way, the more promising edge is more likely to be selected and therefore the efficiency of the tree modification operation in EANDDD can be improved. The effectiveness and efficiency of PTMM is demonstrated on a set of benchmark instances in comparison with the original EANDDD.

Categories and Subject Descriptors

I.2.8 [Artificial Intelligence]: Problem Solving, Control Methods, and Search – *Heuristic methods*

Keywords

Degree-constrained minimum spanning tree; evolutionary algorithms; pheromone; tree modification; network design

1. INTRODUCTION

Given a weighted undirected graph G , a spanning tree T is a subgraph of G , which is connected, acyclic and contains all the vertices in G . The degree-constrained minimum spanning tree problem (dc-MSTP) is required to find a spanning tree, which has the minimum total cost of edges and satisfies the degree constraint, i.e., no node in the spanning tree has more than $d \geq 2$ incident edges.

Recently, a novel evolutionary algorithm utilizing node-depth-degree representation (EANDDD) [1] has been proposed. The node-depth-degree representation is an efficient data structure for

spanning trees. It requires time $O(\sqrt{n})$ to produce a new tree, which is the fastest reported in the literature for solving dc-MSTP. However, the convergence of EANDDD is slow since only two edges are changed for each evaluation. Moreover, it employs a random tree modification method (RTMM), i.e., selecting the edges to be changed at random, to modify a tree. This method is completely stochastic and makes no use of the historical information during the search. The efficiency of this method is relatively low. In this paper, we will propose a novel pheromone-based tree modification method (PTMM) to improve the efficiency of EANDDD.

2. THE PROPOSED PHEROMONE-BASED TREE MODIFICATION METHOD

The pheromone-based tree modification method (PTMM) is a method to generate feasible solutions. It introduces the concept of pheromone, which is borrowed from Ant Colony System [2][3], biasing the probabilities of the edges to be changed. Pheromone on an edge is a desirability measure for the edge to construct a spanning tree [4]. It is updated in the tree modification process. That is, when an edge is selected to be changed in a spanning tree, the pheromone on the edge will change as well. It will either increase or decrease according to the comparison of the fitness of the original tree and the newly-generated one. If a better tree with smaller total cost is generated, the pheromone on the new edge included in the newly-generated tree will increase by a certain value. Otherwise, it will decrease. In this way, the pheromone on the edges of the trees with better fitness will accumulate. With the ensemble of the pheromone on each edge, a superior structure in G is gradually formed, which in turn guides the search for better spanning trees and improve the efficiency of the algorithm.

2.1 Basic Tree Modification Operations

In EANDDD, two operations on trees are defined. Both operations are to transfer a subtree from one tree T_{from} to another tree T_{to} . The average running time they require is $O(\sqrt{n})$. For Operation 1,

there are two input nodes p and a . Node p is a prune node in T_{from} , that is, the root of the subtree to be transferred. Node a is in T_{to} and it is adjacent to p in G . Operation 2 is more general. It takes Operation 1 as a particular case. It has three input nodes p , a and r . Nodes p and a are similar to those in Operation 1. Node r is in the subtree to be connected to a in T_{to} . In Operation 2, the subtree pruned by p is reconstructed and r will be the new root of the subtree.

To generate a new tree T_{child} , Operation 1 is first performed on a tree T_{father} selected from the population, transferring a subtree T_{sub}

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from T_{father} to an auxiliary tree T_{aux} . T_{aux} has only one node x not in G and x is connected to every node in G . T_{father} and T_{aux} after Operation 1 are denoted T'_{father} and T'_{aux} respectively. Then apply either Operation 1 or Operation 2 to transfer T_{sub} rooted at x back to T'_{father} , having $T_{from} = T'_{aux}$ and $T_{to} = T'_{father}$. In terms of the effect of the operations, the first step cuts an edge in T_{father} and gets T'_{father} and T_{sub} , the second step adds an edge between a node in T'_{father} and another in T_{sub} .

2.2 Selection of Input Nodes

In the PTMM, the input nodes for The new selection process includes the following steps:

Step 1: Select p randomly to get a subtree T_{sub} .

Step 2: Select a node in T_{sub} to be the new root r_{new} of the subtree T_{sub} . For Operation 1, $r_{new}=p$. For Operation 2, probe T_{sub} at random for r_{new} that is different from the root p and such that $degree(r_{new}) < d$.

Step 3: Create a set C of candidate nodes x which are in T'_{father} , adjacent to r_{new} and satisfy $degree(x) < d$.

Step 4: Pick a from C by the roulette wheel selection. Suppose there are k candidate nodes in C , the probability of node x_i to be selected is

$$p_i = \frac{\tau_{x_i, r_{new}}}{\sum_{j=1}^k \tau_{x_j, r_{new}}} \quad (1)$$

where $\tau_{x_i, r_{new}}$ is the pheromone value of the edge between x_i and r_{new} .

2.3 Update for Pheromone

After the input nodes selection process, a new solution T_{child} can be generated by the modification operations. The evaluation for the new solution is easy according to (3)

$$f(T_{child}) = f(T_{father}) - c(e_{cut}) + c(e_{add}) \quad (2)$$

where $c(e_{cut})$ is the cost of the edge cut off from T_{father} and $c(e_{add})$ is the cost of the edge added back.

Suppose e_{ij} is the edge selected to be added back, its pheromone is renewed by (4) and (5)

$$\tau_{i,j} = \tau_{i,j} + \Delta\tau_{i,j} \quad (3)$$

$$\Delta\tau_{i,j} = \lambda(f(T_{father}) - f(T_{child})) \quad (4)$$

where λ is a positive factor to adapt $\Delta\tau_{i,j}$ to a proper interval according to specific problems, called the update step factor.

3. EXPERIMENTS AND COMPARISONS

The effectiveness and efficiency of PTMM is verified on an instance set of twelve misleading graphs [5] with degree constraint $d=5$. Each case was executed independently 30 times to obtain an estimate of the best and mean solution values. In each execution, the evolution stops when it reaches 10000 function evaluations. Table 1 shows the experimental results in comparison with RTMM in the original EANDD and proves that PTMM outperforms RTMM.

Table 1. Best values and mean values of solutions of EANDD applying RTMM and PTMM

instance	n	RTMM		PTMM	
		best	avg	best	avg
m050n1	50	7.415	9.045	7.256	8.723
m050n2	50	6.555	8.437	6.543	7.957
m050n3	50	5.695	6.771	5.556	6.300
m100n1	100	15.217	18.410	11.893	14.438
m100n2	100	16.749	19.9472	13.596	15.760
m100n3	100	17.004	19.240	11.995	14.473
m200n1	200	43.239	46.427	23.375	26.481
m200n2	200	45.972	53.351	27.110	30.865
m200n3	200	39.156	41.558	19.938	22.253
m300n1	300	77.166	80.120	58.799	62.000
m400n1	400	129.817	134.762	100.238	104.811
m500n1	500	177.949	181.136	146.811	152.656

4. CONCLUSION

In this paper, we propose the pheromone-based tree modification method for evolutionary algorithm utilizing the node-depth-degree representation to solve degree-constrained minimum spanning tree problem. The proposed method uses the pheromone on the edges in the graph to help select the edges to construct new trees. Experiments are carried out to compare the new tree modification method with the original tree modification method which modifies a tree by changing a pair of edges randomly. The experimental results show that the proposed pheromone-based tree modification method makes a significant improvement on the performance of EANDD for solving dc-MSTP.

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