

# Multiple constraints QoS multicast routing optimization algorithm based on Genetic Tabu Search Algorithm

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## Abstract

With the fast evolution of real time and multimedia applications, some quality of service (QoS) constraints need to be guaranteed in the underlying network. In this paper, we present a new method for least-cost QoS multicast routing problem based on genetic algorithm and tabu search. This problem has been proven to be NP-complete. The proposed genetic tabu search algorithm (GTS) combine Genetic Algorithm and Tabu Search adequately in order to improve the computing performance. In our method the chromosomes of the multicast tree represented by tree structure coding scheme. This coding scheme simplifies the coding operation and omits the coding and decoding process. A new population initialization method based on Prim's algorithm is proposed. This method ensures that every chromosome is a reasonable multicast tree without loops. The proposed algorithm is then compared with one of existing multicasting algorithms. The simulation results show that our method has high speed of convergence and effective in solving the considered problem.

**Keywords:** *Quality of Service (QoS), Genetic algorithm (GA), Tabu Search (TS), Multicast routing.*

## 1. Introduction

With the advances in networking, switching technology and rapid growth of the Internet, many new communication services, high-bandwidth real time and multimedia applications have been become reality. Some of these applications require the transformation of multiple copies from a source node to a set of destination nodes in a network with various quality of service (QoS) performance [1],[2]. This kind of communication is called multicasting and it must be supported by a network. Multicasting is defined as the ability of a communication network to accept a single message from an application and deliver copies of the message to many recipients at different locations. To carry large number of multicast sessions, a

network must minimizes the session's resource consumption, while meeting their QoS requirements [3],[4],[5]. QoS requirements are often versatile. For example, in video conference applications each link on the routing tree should guarantees a minimum available bandwidth (i.e., bandwidth constraint). In real-time applications, such as game applications and messages must be transmitted from the source node to their destinations within a certain amount of time. So, end-to-end delay can be considered as another important QoS parameter. The algorithms that construct multicast trees in the network are called multicast routing algorithms. An efficient QoS multicast algorithm should construct a multicast tree, by which the data can be transmitted from the source to a subset of destination nodes with guaranteed QoS [6],[7],[8],[9].

Several algorithms are proposed for solving the QoS multicast routing problem, these algorithms are based on separated metaheuristic methods such as genetic algorithm (GA), tabu search (TS) and simulated annealing (SA) [10],[11],[12]. But, few algorithms are proposed by combining two of these algorithms for solving this problem. A method based on genetic simulated annealing algorithm is proposed to solve this problem [5], in this method genetic algorithm or simulated annealing algorithm works respectively when the other algorithm can not be effective, which leads to a lower evolution speed.

Each of genetic algorithm, tabu search and simulated annealing have their characteristics and some shortages. For example the shortage of TS and SA is depending on initial value and lower convergence speed and the shortage of GA is the premature convergence.

Aiming to that shortage, the Genetic Tabu search algorithm (GTS) is proposed for QoS multicast routing. Our proposed algorithm combines GA and TS adequately to solve this problem. The character of TS is used to avoid the premature convergence of GA. And the character of GA is used to avoid the shortage of TS such as depending on initial value and the lower convergence speed. GA has the character of parallel processing and high convergence speed. TS has the capability of escaping from local optimum. The objective of the new hybrid algorithm (GTS) is keeping the advantages and avoiding the disadvantages of both search algorithms.

In the proposed algorithm GTS, the chromosomes of the multicast tree are represented by tree structure of Genetic Programming, to save the time of conversion between encoding space and solution space. A population initialization method is used to make sure that every chromosome in initial population is reasonable multicast tree without loops that satisfies the (link) bandwidth and (path) delay constraints. The crossover generates new chromosomes by exchanging partial chromosomes (i.e., sub-trees) without positional consistency of potential crossing site (crossover point) between two chromosomes. A new tabu search mutation operator is presented. Finally, a repair function treats infeasible chromosomes possibly generated after crossover.

The rest of the paper is organized as follows. Section 2 describes a mathematical model for the representing multicast routing problem. The proposed GA is presented in Section 3. Section 4 shows experimental results. The paper is concluded in Section 5.

## 2. Problem Formulation

A communication network can be modeled as an undirected connected weighted graph  $G = (V, E)$ , with node set  $V$  and link set  $E$ .  $n = |V|$  is the number of nodes and  $l = |E|$  is the number of links in  $G$ . A link  $e \in E$  which connects  $v_1$  and  $v_2$  will be denoted by  $(v_1, v_2)$ . Each link is associated with link cost  $C(e)$ , bandwidth  $B(e)$  and delay  $D(e)$  respectively. A multicast tree is defined by  $T = (V_T, E_T)$ , where  $V_T \subseteq V$ ,  $E_T \subseteq E$  and  $T \subseteq G$ . There exists a path  $P_T(s, d_i)$  from the source node  $s$  to each destination node  $d_i \in M = \{d_1, \dots, d_k\}$  in  $T$ . Here, the index  $k$  is the number of destinations. The total delay of the path  $P_T(s, d_i)$  is simply the sum of the delay of all links along  $P_T(s, d_i)$  i.e.,

$$D(P_T(s, d_i)) = \sum_{e \in P_T(s, d_i)} D(e) \quad (1)$$

The bandwidth of the path  $P_T(s, d_i)$  is defined as the minimum available bandwidth at any link along the path i.e.,

$$B(P_T(s, d_i)) = \min \{B(e), e \in P_T(s, d_i)\} \quad (2)$$

The total cost of the multicast tree can be defined as the sum of the cost of all links in that tree i.e.,

$$C(T(s, M)) = \sum_{e \in T(s, M)} c(e) \quad (3)$$

Using the previous notations and definitions the considered problem can be stated as follows:

Given a source node  $s$ , a set of destination nodes  $M$ , a delay tolerance  $D_{bound}$  and a bandwidth tolerance  $B_{bound}$ .

Then finding a tree  $T (T \subseteq G)$  routed at  $s$  and spanning all of the nodes in  $M$  such that the total cost of the multicast tree given in Eq. 3 is minimized while satisfying the following QoS constraints.

$$D(P_T(s, d_i)) \leq D_{bound}, \quad \forall d_i \in M \quad (4)$$

$$B(P_T(s, d_i)) \geq B_{bound}, \quad \forall d_i \in M \quad (5)$$

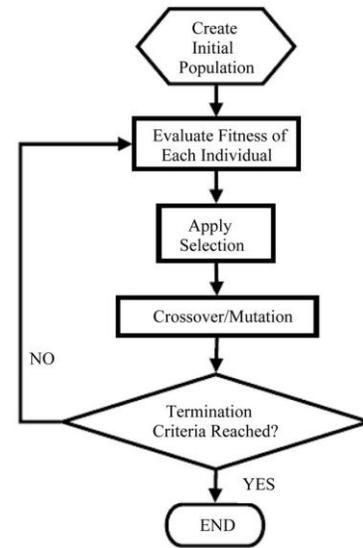


Fig. 1 Flowchart of genetic algorithm

## 3. The method for QoS multicast routing based on Genetic Tabu Search Algorithm (GTS)

In this section an efficient algorithm based on genetic tabu search algorithm (GTS) is proposed to solve the least-cost multicast tree with bandwidth and end-to-end delay constraints problem. The objective is determining a multicast routing tree (in the source based tree category),

from a designated source to a set of destinations with strict end-to-end delay requirements (in multicast group) and specified bandwidth (between adjacent nodes). The proposed algorithm replaces the standard mutation processes of GA by the TS operators. Fig. 1 shows the flow chart of heuristic genetic algorithm. Crossover and mutation operation is the two basic steps in GA that responsible for generation new solutions in order to find optimum solution. Our method will replace the mutation operation in GA by TS operations. The following subsections present the implementation of the proposed GTS for solving the considered problem.

### 3.1 Representation and initial population

Some of the proposed algorithms for solving multicast routing problem use binary coding scheme, which makes the coding/decoding operations too complicated. In the proposed GTS, the tree structure coding scheme is chosen [13], in which a chromosome is a set of paths and each path is a set of positive integers (genes), which express IDs of nodes. These paths are variable in length and each locus of the chromosome represents the node's order in the corresponding routing path. Fig. 3 shows an example of the encoding methods in the context of Fig. 2. Let node 1 be the source node and  $D = \{5, 7, 8\}$  be the destination nodes. The first locus in each chromosome is assigned by the source node. Each multicast tree (i.e., chromosome) extends the source node to the destination set. The routing paths in this example are  $\{(1 \rightarrow 2 \rightarrow 4 \rightarrow 5), (1 \rightarrow 7), (1 \rightarrow 7 \rightarrow 8)\}$ , which represent feasible solution.

The proposed GTS uses a new initial population method based on Prim's MST algorithm [14]. This method ensures that every chromosome in the initial population is a reasonable multicast tree without loops and satisfies each of bandwidth and end-to-end delay constraints. In the proposed method, for every chromosome in the initial population, a random binary string is generated. Each bit of the binary string ( $s$ ) corresponds to a different node in graph  $G(V, E)$ . Hence, the length of each string equals to  $n(n = |V|)$ . We use  $G'(V', E')$  to denote the subgraph corresponding to  $s$ .  $G'(V', E')$  is constructed as follows. Let the function  $\text{bit}(s, i)$  denote the  $i$ th bit of  $s$ . If  $\text{bit}(s, k) = 1$ , then  $v_k \in V'$ . If  $\text{bit}(s, k) = 0$ , then  $v_k \notin V'$ . If  $v_m \in V', v_n \in V'$ , and  $(v_m, v_n) = e_{mn} \in E$ , then  $e_{mn} \in E'$ .

Some strings may be bad, e.g., for group  $U = \{1, 5, 7, 8\}$ , the string  $s_i = 01011010$  is bad. Because each of bit  $(s_i, 1)$  and bit  $(s_i, 8)$  equal 0, the subgraph corresponding to  $s_i$  does not contain the two node 1 and 8. However, this case is undesired since nodes 1 and 8 are group nodes. To solve this problem, we generate a special chromosome  $s$ , such that if  $v_i \in U$ , then  $\text{bit}(s, i) = 1$ , otherwise,  $\text{bit}(s, i) = 0$ .

For group  $U$ , the special chromosome  $s = 10001011$ . Then any randomly generated  $s_i$  is Ored with  $s$ , i.e.,  $s_i \vee s \rightarrow s_i$ . Thus,  $s_i$  will contain all the group nodes.

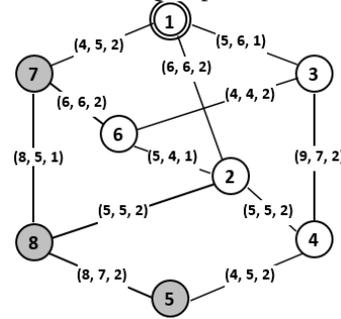


Fig. 2 An example of the network topology

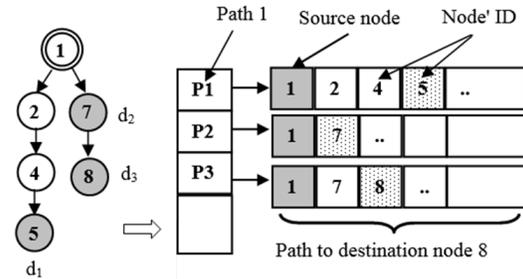


Fig. 3 Multicast with tree destination (5,7 and 8) and its corresponding chromosome representation

In our problem, string  $s_i$  needs to correspond to a multicast tree. We use  $T'_i(X'_i, F'_i)$  to denote the minimum spanning tree derived from  $G'_i(V'_i, E'_i)$ . The Prim's algorithm with Johnson's implementation is used to derive the spanning tree because it is known to be of less time complexity [12]. If there exist leaf nodes that do not belong to group  $U$  on  $T'_i$ , we prune it by deleting those nodes and their adjacent links. Denote the pruned tree as  $T_i$ , which is just the multicast tree (chromosome) represented by string  $s_i$ .

If the corresponding graph generated using the binary string is disconnected (i.e., the multicast group is not connected) then another string is generated randomly. The steps of initial population that satisfy each of bandwidth and end-to-end delay constraints based on Prim's MST algorithm can be summarized as follow.

Step 1: check the bandwidth constraint

- 1: From  $G(V, E)$ , delete all the links whose available bandwidth resources are less than requirement.
- 2: If the resulting graph is disconnected this means that this network don't satisfy the required QoS constraint (bandwidth constraint). Otherwise go to step 2.

- Step 2: Generation population of chromosomes
- 1: start ( $i = 0$ ). Generate the special string  $s$  that corresponds to the multicast group.
  - 2:  $i = i + 1$ .
  - 3: Generate string  $s_i$  randomly.
  - 4:  $s_i \vee s \rightarrow s_i$ .
  - 5: If the resulting subgraph  $G'_i$  corresponding to  $s_i$  is disconnected. Go to 3.
  - 6: Generate MST  $T'_i$  from  $G'_i$  by using prim's algorithm.
  - 7: Drive the multicast tree  $T_i$  from MST ( $T'_i$ ).
  - 8: Accept the multicast tree ( $T_i$ ) as a chromosome in initial population, if  $T_i$  satisfies the end-to-end delay constraint. Otherwise go to 3.
  - 9: Let  $k$  denote the population size. If  $i \leq k$  then go to 2 otherwise stop.
- Thus, the initial population  $\{T_1, T_2, T_3 \dots T_k\}$  is obtained.

### 3.2 Fitness function

The fitness should respond to the individual (chromosome) performance; the good individual has bigger fitness than the bad one. The QoS constraints in the proposed GA are directly incorporated in the course of constructing and assembling the trees. So, the proposed fitness function only involves network link costs.

The fitness value of each chromosome in the proposed GA is computed as follows: Let  $T_k$  be a multicast tree represented by the chromosome  $h_k$ , and  $C_{T_k}$  be the summation of the link costs of the tree  $T_k$ , the fitness value of this chromosome denoted as  $F(h_k)$ , is given by:

$$F(h_k) = [C_{T_k}]^{-1} = \left[ \sum_{i,j \forall e_{ij} \in T_k} C_{ij} \right]^{-1} \quad (6)$$

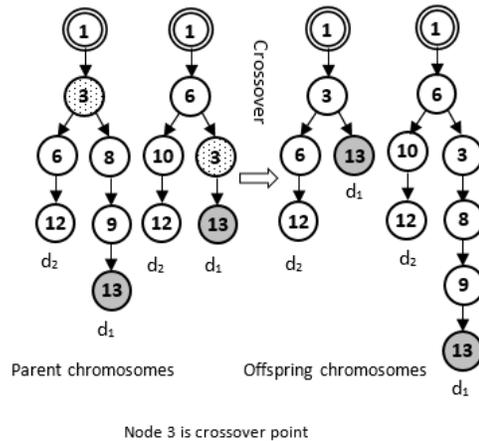
### 3.3 Selection

The proposed algorithm employs pair-wise tournament selection as the scheme to select the chromosomes [13]. The selected scheme randomly picks two different chromosomes and chooses the better one.

### 3.4 Crossover scheme

The crossover performs an effective global search for discovering a multicast routing tree. In the proposed scheme, the crossover exchanges the partial paths (sub-tree) between intermediate node and destination, and this is dependent on the location of the crossing site. This dictates one-point crossover as a good candidate scheme for the proposed GTS. Two chromosomes chosen for crossover

should have at least one common gene (node), but there is no requirement that they be located at the same locus. That is to say, the crossover does not depend on the position of nodes in routing paths. If the crossover point satisfies probability of crossover  $p_c$ , the crossover will exchange the partial route path between two candidate chromosomes. Fig. 4 shows an example of the crossover procedure. As shown in this Figure, the selected gene number is '3' (crossover point) and the selected destination is '13'. The sub-trees for the first chromosome is  $(3 \rightarrow 8 \rightarrow 9 \rightarrow 13)$  and for the second chromosome is  $(3 \rightarrow 13)$ . The crossover swaps the two sub-trees if each end-to-end delay is less than path delay constraint.



Node 3 is crossover point

Fig. 4 Topology crossover

### 3.5 Tabu search mutation operation

The mutation operation in the proposed GTS algorithm is not the same as genetic algorithm but use tabu search technique. The mutation probability  $P_m$  is the key factor effecting on the mutation searching performance in mutation operation. In the proposed algorithm  $P_m$  will not be a specified value (i.e., constant value) it will differ from chromosome to another depending on the fitness of each chromosome and its generated neighbor solution. A neighbor solution (i.e., offspring) is created by parent and accepted with probability  $p_m$  which is created as the method of TS according to the procedure in Fig 5.

When the generated best neighbor solution is not tabu, then  $P_m$  will equal 1 and hence offspring individual will be copied into the population on next generation. Also when the generated best neighbor solution satisfies the aspiration level (its fitness value is greater than the best fitness obtained so far),  $P_m$  will equal 1 and also, the offspring individual will be copied into the next generation. But when the best neighbor solution is tabu and doesn't satisfy

the aspiration level, in this case it is not preferable to be copied into the population on next generation (disallowing the search to come back to solutions already visited), so in this case  $P_m$  equal 0.

```

X      : Current chromosome (current solution)
K      : Number of generated neighbors of X
X'     : Best neighbor solution
N(X)   : Neighborhood of solution X
TL     : Tabu list
AL     : Aspiration level
Fit    : Fitness for solution X
Fit'   : Fitness for solution X'
Begin
  Generate K neighbor solutions of N(X)
  X' = Find best solution in N(X)
  If (attributes of move X to X' are not in TL)
    Pm = 1;
  Else
    If (Fit' > AL)
      Pm = 1;
    Else
      Pm = 0;
    End If
  End If
End
    
```

Fig. 5 Procedure: Tabu search mutation operation

### 3.5.1 Backup-paths-set

Only a subset of the solutions of  $N(s)$  are evaluated for each chromosome not all neighbor solutions. So, backup-paths set is used to generate the neighbor solutions for each chromosome in the population. Thus, for each destination node  $d \in M$ , we compute least-cost paths from  $s$  to  $m$  by using  $K$ th shortest path algorithm [15] to construct a backup-paths-set,  $k$  is the number of generated least-cost paths from  $s$  to  $d$ . This means when  $k$  equals 7, it means that the number of generated neighbor solutions for each destination equal 7.

The following table shows backup-paths set of example network, where in the multicast tree the source node is (1) and destination set is {4,7},  $K=4$ .

Table 1: List of backup-paths set

Destination	Path(1)	Path(2)	Path(3)	Path(4)
4	1,2,4	1,5,4	1,3,5,4	1,6,8,4
7	1,5,6,7	1,2,4,11,7	1,2,3,7	1,8,4,7

### 3.5.2 Creating of neighboring solution

For generating neighbors, we choose a neighborhood structure based on paths switching operations. We randomly select a destination node  $d \in M$ , and delete the path from source  $s$  to  $d$  in current solution, then generate different neighbor solutions by selecting other paths from  $s$  to  $d$  in backup-paths set.

For example, by conceding the current solution in Fig. 6, we assume that destination node 7 is selected and path from source node 1 to 7 is deleted, then we select other paths from table 1 to construct new neighbors. If the number of generated neighbor solutions for each chromosome is 2. In this case we select the first two shortest paths for the table 1. The two neighbors of current chromosome are shown in Fig. 6. We observe that the second neighbor solution represents illegal solution where the node number 11 is repeated. In this case the repair function presented in Section 3.6 is used to solve this problem.

Thus every chromosome in initial population is reasonable multicast tree that satisfies (path) delay constraints and the paths-switching fails to consider delay constraint, so it might happen some of the trees violate delay constraint. So the modified  $K$ th shortest path algorithm is presented, it is used to generate a backup-paths-set that satisfies the delay constraint.

### 3.5.3 Tabu list and tabu length

To avoid local minimum, a tabu list is constructed, where forbidden moves are listed. It is maintained to prevent returning to previously visited solutions. This list contains information that to some extent forbids the search from returning to a previously visited solution. In the proposed algorithm, any solution has been generated will be tabu for a specified number. This number is called tabu tenure ( $tt$ ). In the proposed algorithm the value of tabu tenure ( $tt$ ) equals 5.

### 3.5.4 Aspiration criterion

While central to TS, tabus are sometimes too powerful: they may prohibit attractive moves, even when there is no danger of cycling or they may lead to an overall stagnation of the searching process. So, it is necessary to use algorithmic devices that will allow one to revoke (cancel) tabus. These are called aspiration criteria.

The proposed GTS algorithm used aspiration criterion which consists in allowing a move, even if it is tabu, if it results in a solution with fitness value better than that of

the current best-known solution (since the new solution has obviously not been previously visited).

### 3.6 Repair function

Often, variation operator (i.e. crossover and mutation) yields illegal offspring. It contains lethal genes that possibly form a loop. It means that the tree condition is violated, and thus it needs to be fixed. Then repairing procedure is needed to resolve the illegitimacy of offspring. The proposed method is exhibited in Fig. 7. It shows that node 5 is duplicated, and then there are two possible routes to the destination node 15 (i.e., (1 →2 →4 →5 →15) and (1 →5 →15)), so this offspring is illegal. The first and second branches lead to (1 →5 →11 →13 →20) and (1 →5 →15), respectively.

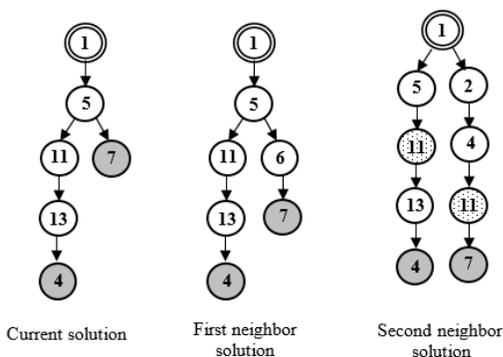


Fig. 6 Topology mutation

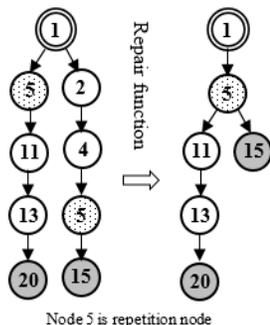


Fig. 7 Topology repair

## 4. Experimental Results

In order to evaluate the performance of the proposed GTS, networks with 20,40,60,80 and 100 nodes with different multicast group size were considered. The algorithms were programmed in the C++ language. In this section we compared the proposed GTS with Sanghoun's algorithm

[13]. In all experiments, crossover and mutation probabilities are set to 0.75 and 0.15, respectively. Bandwidth constraint is set to 10 Mb/s and delay constraint is set to 10 ms.

The comparison of cost performance is shown in Fig. 8 and 9. Each of the two algorithms is executed 100 times. Fig. 8 shows tree cost with varying iteration numbers. We considered 80-nodes network and multicast group size of 6 nodes. It is seen that the proposed algorithm has a higher rate of convergence than that of Sanghoun's algorithm.

Fig. 9 illustrates the average of tree cost. As can be seen in this figure the performance of the proposed algorithm is better than Sanghoun's algorithm. It concluded that the proposed GTS is superior to Sanghoun's algorithm in respect of total tree cost. There are two reasons for this result. First, the new tabu search mutation operation provides higher exploratory power and a fair measure of genetic diversity. Second, the repair function cures all the infeasible trees by simply removing lethal (sub-) paths forming a loop in each tree.

We still work in comparing the bandwidth saving performance between the two algorithm and running time for each algorithm. Which algorithm can deliver the multicast packets in short delay time? Also will presented in the future work.

## 5. Conclusions

This paper presented an efficient algorithm GTS based on genetic algorithm and tabu search to solve the least-cost multicast routing problem with bandwidth and end-to-end delay constraints. It combines GA and TS adequately to solve this problem. The chromosomes of the multicast tree representing by tree structure coding scheme. This coding scheme simplifies the coding operation and omits the coding and decoding process. A new population initialization method based on Prim's algorithm is proposed. This method ensures that every chromosome is a reasonable multicast tree without loops and satisfies each of bandwidth and end-to-end delay constraints.

In the proposed GTS algorithm the character of TS is used to avoid the premature convergence of GA and the character of GA is used to avoid the shortage of TS. We have used the simulation results to compare the performance of two proposed algorithms with other existing GA-based algorithms. Simulation results showed that the proposed GTS algorithm is better, because the new mutation operation in the proposed algorithm provides higher exploratory power and a fair measure of genetic diversity.

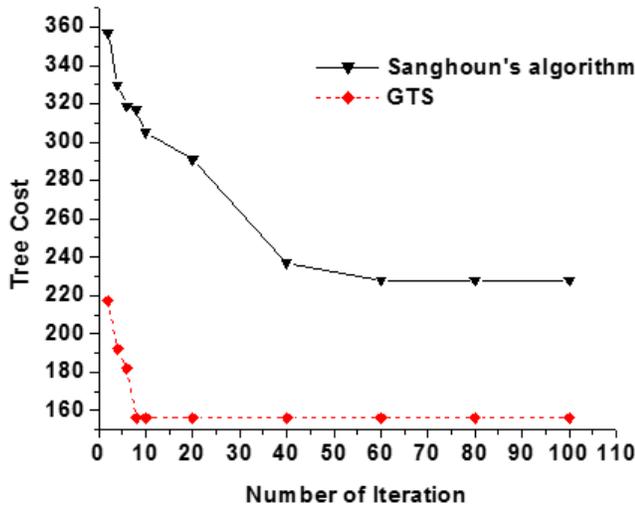


Fig. 8 Comparison of cost performance (Least-cost of multicast tree)

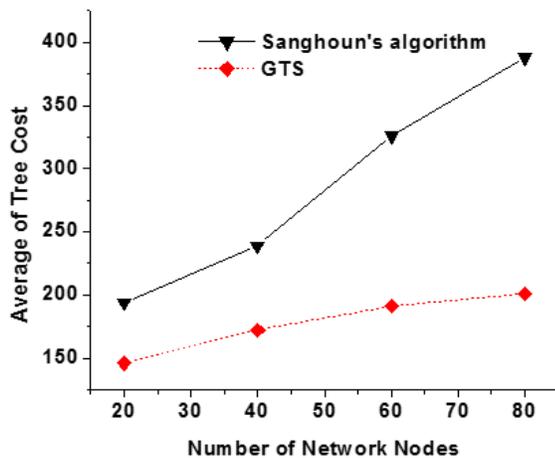


Fig. 9 Comparison of cost performance (Average tree cost)

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