A QoS Multicast Routing Optimization Algorithm Based on Genetic Algorithm

Baolin Sun and Layuan Li

Abstract: **Most of the multimedia applications require strict quality of service (QoS) guarantee during the communication between a single source and multiple destinations. This gives rise to the need for an efficient QoS multicast routing strategy. Determination of such QoS-based optimal multicast routes basically leads to a multi-objective optimization problem, which is computationally intractable in polynomial time due to the uncertainty of resources in Internet. This paper describes a network model for researching the routing problem and proposes a new multicast tree selection algorithm based on genetic algorithms to simultaneously optimize multiple QoS parameters. The paper mainly presents a QoS multicast routing algorithm based on genetic algorithm (QMRGA). The QMRGA can also optimize the network resources such as bandwidth and delay, and can converge to the optimal or near-optimal solution within few iterations, even for the networks environment with uncertain parameters. The incremental rate of computational cost can close to polynomial and is less than exponential rate. The performance measures of the QMRGA are evaluated using simulations. The simulation results show that this approach has fast convergence speed and high reliability. It can meet the real-time requirement in multimedia communication networks.**

Index Terms: **Genetic algorithm, Internet, multicast routing, quality of service (QoS), uncertain parameters.**

I. INTRODUCTION

Multicast employs a tree structure in the network to efficiently deliver the same data stream to a group of receivers. Traditionally, research on Internet multicast has been centered on scalability and efficiency. The deployment of high-speed networks opens a new dimension of research, which is to provide quality of service (QoS) such as guaranteed throughput for audio/video streams. It is technically a challenging and complicated problem to deliver timely, smooth, synchronized multimedia information over a decentralized, shared network environment, especially one that was originally designed for best-effort traffic such as the Internet [1]–[8]. The provision of QoS guarantees is of utmost importance for the development of the multicast services. Multicast routing has continued to be a very important research issue in the areas of networks and distributed systems. It attracts the interests of many people.

QoS multicast routing relies on state parameters specifying resource availability at network nodes or links, and uses them to find paths with enough free resources [1]–[3], [7]–[12]. In turn, the successful routing of new flows together with the termination of existing ones, induce constant changes in the amount of resources available. These must then be communicated back to QoS multicast routing. Unfortunately, communicating such changes in a timely fashion is expensive and, at times, not even feasible [1]–[3], [7]–[12]. As a result, changes in resources availability are usually communicated either infrequently or uncertainly. There are two main components to the cost of timely distribution of changes in network state: The number of entities generating such updates and the frequency at which each entity generates updates. The goal of QoS based multicast routing is to search and construct a multicast tree that not only covers all the group members but also meets their QoS requirements.

To control the protocol overhead and to limit it to a tolerable level, large clamp-down timers are used to limit the rate of updates. The accuracy of network state is also affected by, for example, the scope of an update message and the types of value advertised (exact state values or quantized values). There is a fundamental trade-off between the certainty of state information and the protocol message overhead. Moreover, in large and dynamic networks, the growth in the state information makes it practically impossible to maintain accurate knowledge about all nodes and links. Instead, the state information is usually aggregated in a certain hierarchical manner, and the aggregation process inherently decreases the information accuracy and introduces imprecision. The uncertain state information kept at each node imposes difficulty in QoS provisioning. Guerin and Orda [7] investigated the problem of QoS routing when the state information is uncertain or inaccurate and expressed in some probabilistic manner. They then proposed a distributed ticket-based probing routing algorithm.

In recent years, some researchers have started using evolutionary algorithms to find near-optimal solutions for different Internet networking problems, like QoS routing [8]–[12]. More recently, researches in determining QoS based multicast routes clearly demonstrate the power of genetic algorithms to get a near-optimal solution satisfying the QoS requirements in computationally feasible time [9]–[11]. A little careful insight into these above optimization schemes reveals that all of them suffer from the same drawback: Multiple objectives are combined to form a scalar single-objective function, usually through a linear combination (weighted sum) of multiple attributes. In these cases, the solution not only becomes highly sensitive to the weight vector but also demands the user to have certain knowledge (e.g., priority of a particular objective, influence of a parameter over another, etc.) about the problem. Moreover, in case of multi-objective optimization, a unique solution that optimizes all the objectives simultaneously will rarely, if at all, exist in practice. Conventional genetic algorithms are clearly unable to

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B. Sun is with the School of Computer Science and Technology, Wuhan University of Technology, Wuhan 430063, P. R. China, and the Department of Mathematics and Physics, Wuhan University of Science and Engineering, Wuhan 430073, P. R. China, email: sun0163@163.com.

L. Li is with the School of Computer Science and Technology, Wuhan University of Technology, Wuhan 430063, P. R. China, email: jwtu@public.wh.hb.cn.

provide this flexibility to the user [10]. However, the genetic algorithm (GA) can be readily modified to deal with multiple objectives by incorporating the concept of Pareto domination in its selection operation [13].

This paper focuses on determining multicast routes from a source to a set of destinations with strict end-to-end delay requirements and minimum bandwidth available. Though the path determination problem with a single optimization parameter can be solved in polynomial time, the uncertainty of precise values of multiple objective functions make the problem an NP-hard [1]–[7]. The goal of this paper is to develop an algorithm to find out QoS based multicast routes by simultaneously optimizing end-to-end delay, bandwidth provisioning for guaranteed QoS, and proper bandwidth utilization without combining them into a single scalar optimization function.

The rest of the paper is organized as follows. Section II describes a network model. Section III presents the QMRGA. Analysis of convergence and some simulation results are provided in Section IV. The paper concludes and future research in Section V.

II. NETWORK MODEL

A network is usually represented as a weighted digraph $G = (N, E)$, where N denotes the set of nodes and E denotes the set of communication links connecting the nodes. $|N|$ and $|E|$ denote the number of nodes and links in the network, respectively. Without loss of generality, only digraphs are considered in which there exists at most one link between a pair of ordered nodes [7]–[12]. We consider the multicast routing problem with bandwidth and delay constraints from one source node to multi-destination nodes. Let $M = \{u_0, u_1, u_2, \cdots, u_m\} \subseteq N$ be a set of form source to destination nodes of the multicast tree where n_0 is source node, and $U = \{u_1, u_2, \cdots, u_m\}$ be a set of destination nodes. Multicast tree $T = (N_T, E_T)$, where $N_T \subseteq N$, $E_T \subseteq E$, there exists the path $P_T(n_0, d)$ from source node n_0 to each destination node $d \in U$ in T [1]–[3], [11].

Definition 1: The cost of multicast tree T is

$$C(T) = \sum_{e \in E_T} C(e).$$

Definition 2: The bandwidth of multicast tree T is the minimum value of link bandwidth in the path from source node n_0 to each destination node $d \in U$, i.e.,

$$B(T) = \min(B(e), e \in E_T).$$

Definition 3: The delay of multicast tree T is the maximum value of delay in the path from source node n_0 to each destination node $d \in U$, i.e.,

$$D(T) = \max(\sum_{e \in P_T(n_0,d)} D(e), d \in U).$$

Definition 4: The delay-jitter of multicast tree T is the maximum value of delay-jitter in the path from source node n_0 to each destination node $j \in U$, i.e.,

$$J(T) = \max(\sum_{e \in P_T(n_0,j)} j(e), j \in U).$$

Definition 5: Assume the minimum bandwidth constraint of multicast tree is B, the maximum delay constraint is D, and the maximum delay-jitter constraint is J, given a multicast demand R, then, the problem of bandwidth-delay constrained multicast routing is to find a multicast tree T, satisfying

(1) bandwidth constraint: $B(T) \geq B$,
(2) delay constraint: $D(T) \leq D$,
(3) delay-jitter constraint: $J(T) \leq J$.

Suppose $S(R)$ is the set and satisfies the conditions above, then, the multicast tree T which we find is

$$C(T) = \min(C(T_s), T_s \in S(R)).$$

III. QMRGA

Genetic algorithms are based on the mechanics of natural evolution. Throughout their artificial evolution, successive generations each consisting of a population of possible solutions, called individuals (or chromosomes, or vectors of genes), search for beneficial adaptations to solve the given problem. This search is carried out by applying the Darwinian principles of "reproduction and survival of the fittest" and the genetic operators of crossover and mutation which derive the new offspring population from the current population. Reproduction involves selecting, in proportion to its fitness level, an individual from the current population and allowing it to survive by copying it to the new population of individuals. The individual's fitness level is usually based on the cost function given by the problem (e.g., QoS multicast routing) under consideration. Then, crossover and mutation are carried on two randomly chosen individuals of the current population creating two new offspring individuals. Crossover involves swapping two randomly located sub-chromosomes (within the same boundaries) of the two mating chromosomes. Mutation is applied to randomly selected genes, where the values associated with such a gene is randomly changed to another value within an allowed range. The offspring population replaces the parent population, and the process is repeated for many generations. Typically, the best individual that appeared in any generation of the run (i.e., best-so-far individual) is designated as the result produced by the genetic algorithm.

A. Encoding Representation

In genetic algorithms, the critical problem is how to transform the solution of the problems to the chromosomes which represents with encoding. The chromosomes of genetic algorithms is composed of a series of integral queuing and the encoding method based on routing representation, which the most natural and simplest representing method. Given a source node n_0 and destination nodes set $U = \{u_1, u_2, \cdots, u_m\}$, a chromosome can be represented by a string of integers with length m. The chromosome of genetic algorithms is composed of a series of integral queuing with length m, and the gene of genetic algorithms is the path in path set $\{P_i^1, \cdots, P_i^j, \cdots, P_i^l\}$ [11] between n_0 and u_i, where P_i^j is the j-th path of destination node u_i, and l denotes the path number between n_0 and u_i. Each chromosome in population denotes a multicast tree. This coding method was first proposed in [11] for the point-to-point routing problem. Obviously, a chromosome represents a candidate solution for the multicast routing problem since it guarantees a path between the source node and any of the destination nodes. The major advantage of using the coding method of [11] is that given a chromosome, the links of the multicast tree can be easily identified and the path delay or bandwidth can be taken into consideration through the proper selection of routes in routing tables. Since there are so many paths between node n_0 and u_i, such that the encoding space of chromosomes possibly becomes larger, which decreases the convergence of solution. Now for each destination node $d \in U$, by the k-th the shortest route algorithm, the encoding space can be improved by finding out all routes that satisfy bandwidth constraint from source node n_0 to destination node $d \in U$ and composing routes set as candidate routes set of genetic algorithm encoding space. Assume that U_i is the set of destination node u_i which satisfies bandwidth constrained, then,

$$U_i = \{P_i^1, \cdots, P_i^j, \cdots, P_i^k\},\ k \leq l$$

where P_i^j denotes the j-th route which satisfies bandwidth constraint of destination node u_i. Choose arbitrarily a route from each route set U_i respectively, and compose the initial population of chromosomes. Obviously, the multicast tree covered all destination nodes, diminished bandwidth constraint in the algorithm and optimized the performace of networks, decreased searching space of the algorithm, diminished the probability which dissatisfied, bandwidth constraint link in algorithm selection, but satisfied the demand of bandwidth constraint.

Therefore, the chromosome of genetic algorithm can be made of a series of integral queuing, namely, the encoding method based on routing representation; this method decreased encoding space, also omitted decoding operation. The relationship among the chromosome, gene, and routing table is explained in Fig. 1.

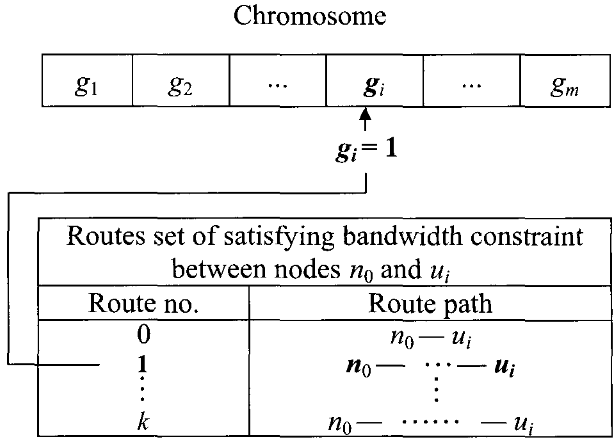

Fig. 1. Representation of chromosomes.

B. Fitness Sharing Function

The fitness function interprets the chromosome in terms of physical representation and evaluates its fitness based on traits of being desired in the solution. But, the fitness function must accurately measure the quality of the chromosomes in the population. The definition of the fitness function, therefore, is very critical [9]–[11].

Fitness function should describe the performance of the selected individuals. The individual with good performance has high fitness level, and the individual with bad performance has low fitness level. Let links be service queues where packets to be transmitted get serviced. In most cases, this service can be assumed to follow Poisson distribution. The service time should follow an exponential distribution. Let the delay for link l be denoted by the variable d_l, which is a random variable following exponential distribution with parameter equal to λ. So, the delay over a path consisting of k links would be the sum of k independent random variables all having the same exponential distribution and so would follow an Erlang-K distribution. From the definition of Erlang-K distribution, we get that the probability that the delay d_p over a path P of length k is less than t is given by the following equation [10],

$$\Pr(d_p < t) = \frac{\lambda^k t^{k-1} e^{-\lambda t}}{(k-1)!}.$$

From the classical probability theory, we can say that the probability that the delay d of the selected multicast tree T will meet the specific delay constraint can be obtained by taking the product of delay over individual paths in that multicast tree [10],

$$\Pr(d_T < t) = \prod_{p \in T} \Pr(d_p < t).$$

To find an optimal path, our objective is to maximize this probability of satisfying delay requirements. The measure of the bandwidth guarantee can be obtained by assuming a similar model for the network links [10]. If the service rate or the transmission rate, which is basically a measure of link bandwidth, is assumed to follow a poisson distribution, the probability that a link $l \in E$ can provide a bandwidth of B is given by

$$\Pr_l(B) = \frac{\lambda^B e^{-\lambda}}{B!}.$$

We can now say that the probability with which the bandwidth guarantee of B is satisfied for an entire multicast tree T is given by

$$\Pr_T(B) = \prod_{l \in T} \Pr_l(B).$$

The normal conjecture is that the path which is capable of providing with greatest residual bandwidth is the best choice. The total residual bandwidth in the network after allocating bandwidth for a multicast $T(s, M)$ is given by $\sum_{l \in E}(c_l - b_l)$, where c_l is the capacity of a link $l \in E$ and b_l is the bandwidth allocated for all the paths in the multicast $T(s, M)$, along the link l. Obviously, b_l is 0 if $l \notin p$ where $p \in T$. The fraction of total bandwidth available as residual bandwidth is given as

$$R(T) = \frac{\sum_{l \in M}(c_l - b_l)}{\sum_{l \in M} c_l}.$$

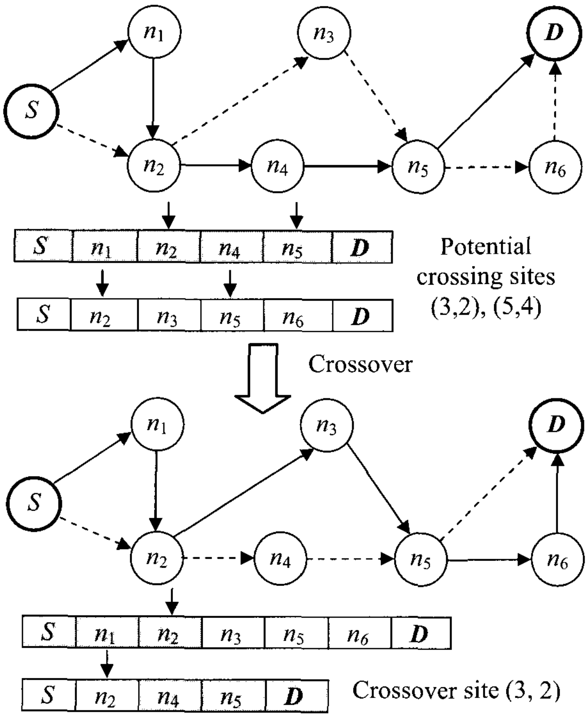

Fig. 2. Overall procedure of the crossover.

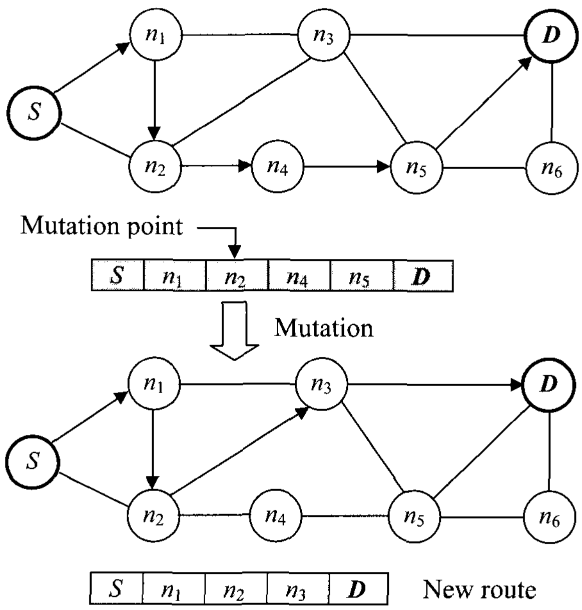

Fig. 3. Overall procedure of the mutation.

The fitness sharing function of QMRGA can be defined as follows.

$$f'(x_i) = \frac{f(x_i)}{m_i}.$$

To incorporate this idea of fitness sharing, we compute the value of niche count for every individual string present in the population as

$$m_i = \sum_{j=1}^{\text{popsize}} SH[d_{s1,s2}]$$

where $d_{s1,s2}$ is the distance between individuals $s1$ and $s2$ and $SH[d_{s1,s2}]$ is sharing function. For simplicity, triangular sharing function has been used

$$SH[d_{s1,s2}] = \begin{cases} 1 - \frac{d_{s1,s2}}{\sigma_{\text{share}}}, & d \leq \sigma_{\text{share}} \\ 0, & d > \sigma_{\text{share}} \end{cases}$$

where σ_{share} is the niche radius, and it is a good estimate of minimal separation expected between the goal of solutions. Individuals within σ_{share} distance of each other degrade each other's fitness, as they are in the same niche [10].

The phenotypic distance between two strings is nothing but the Eucledian distance between their different fitness values

$$d_{s1,s2} = \sqrt{(\sigma_{\text{delay}_{s1,s2}})^2 + (\sigma_{\text{bw}_{s1,s2}})^2 + (\sigma_{\text{bit}_{s1,s2}})^2}$$

where $\sigma_{\text{delay}_{s1,s2}} = \Pr(d_{s1} < t) - \Pr(d_{s2} < t)$, $\sigma_{\text{bw}_{s1,s2}} = \Pr_{s1}(B) - \Pr_{s2}(B)$, and $\sigma_{\text{bit}_{s1,s2}} = R(s1) - R(s2)$. Similarly, we compute the niche radius σ_{share} as some fraction of the maximum separation possible in the population [10], i.e.,

$$\sigma_{\text{share}} = \frac{\sqrt{(\sigma_{\text{delay}_{\max}})^2 + (\sigma_{\text{bw}_{\max}})^2 + (\sigma_{\text{bit}_{\max}})^2}}{4}$$

where $\sigma_{\text{delay}_{\max}} = \Pr_{\max}(d < t) - \Pr_{\min}(d < t)$, $\sigma_{\text{bw}_{\max}} = \Pr_{\max}(B) - \Pr_{\min}(B)$, and $\sigma_{\text{bit}_{\max}} = R_{\max} - R_{\min}$.

C. Crossover and Mutation Operations

As the algorithm executes, at every iteration we get a set of non-dominated strings whose fitness values represent the Pareto-optimal solutions for that iteration. The crossover and mutation operations are the same as normal genetic algorithms. But, it must be made sure that these operations must not produce any illegal paths. Crossover examines the current solutions in order to find better ones [9]–[11], [13]–[15]. Physically, crossover in the shortest path routing problem plays the role of exchanging each partial-route of two chosen chromosomes in such a manner that the offspring produced by the crossover represents only one route. The crossover between two dominant parents chosen by the selection gives higher probability of producing offspring having dominant traits. The population undergoes mutation by an actual change or flipping of one of the genes of the candidate chromosomes, which keeps away from local optima [9]–[11], [13]–[15]. Physically, it generates an alternative partial-route from the mutation node to the destination node in the proposed GA. Topological information database is utilized for the purpose. Of course, mutation may induce a subtle bias for reasons indicated earlier.

But the mechanism of the crossover is not the same as that of the conventional one-point crossover. In the proposed scheme, 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. Fig. 2 shows an example of the crossover procedure [15]. As shown in Fig. 2, a set of pairs of nodes which are commonly included in the two (chosen) chromosomes without positional consistency are formed (i.e., (3,2) and (5,4)). Such pairs are also called "potential crossing sites." Then, one pair (i.e., (3,2)) is randomly chosen and the locus of each node becomes a crossing site of each chromosome. The crossing points of two chromosomes may be different from each other.

Fig. 3 shows the overall procedure of the mutation operation [15]. As can be seen from Fig. 3, in order to perform a mutation, a gene (i.e., node n_2) is randomly selected from the chosen chromosome (mutation point). One of the nodes, connected directly to the mutation point, is chosen randomly as the first node of the alternative partial-route.

Both the crossover and mutation operations can only be performed at the end of an existing path. To give an equal probability to all such possible crossover and mutation points, we randomly select one such point. The crossover operation is performed by swapping the portion of the two consecutive chromosomes after the particular selected point. In case of mutation, we just replace the part of the chromosome after the mutation point by a corresponding part of any other valid chromosome. To combine the good strings and simultaneously preserve the effective ones we have taken the probability of cross over as 0.4 and that of mutation as 0.02 [11], [13], [14].

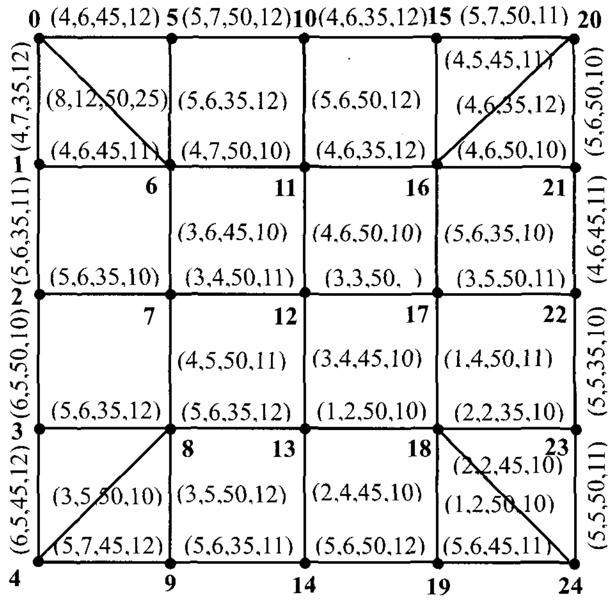

Fig. 4. Network topology structure.

IV. ANALYSIS OF CONVERGENCE AND SIMULATIONS EXPERIMENTS

A. Analysis of Convergence

Theorem 1: The genetic algorithm proposed in this paper converges to the global optimal solution.

Proof: The genetic algorithm has following merits: (1) Changeable length chromosome encoding method based on routing expression is used; (2) crossover probability between (0,1); (3) mutation probability between (0,1), randomly choosing some individuals from the population with championship selection method; (4) the individuals which has higher fitness level in the population, caused these individuals to reproduce rapidly in population, easily produce convergence and the random selection which maybe tend to purity in evolution process, and make it difficult to find the global optimal solution problem. According to the merits about championship selection, changeable length chromosomes, crossover and mutation operations, etc. in literature [11], [13], [14], the genetic algorithm can converge to the global optimal solution. □

B. Simulation Experiments

Simulation experiments are performed over a network of 25 nodes, consider a link from i to j that has a QoS descriptor denoted as (d, j, b, c), where d is delay, j is delay jitter, b is bandwidth, and c is link cost. In these simulation experiments, the source node is node 0, and the number of multicast destination nodes being $\{4, 9, 14, 19, 24\}$. When delay constraint $D = 30$, delay jitter constraint $J = 40$, and bandwidth constraint $B = 50$, Fig. 5(a) shows the multicast tree found by the algorithm for the indicated from source to destination set. When delay constraint $D = 20$, delay jitter constraint $J = 30$, and bandwidth constraint $B = 40$, Fig. 5(b) shows the multicast tree found by the algorithm for the indicated from source to destination set. The multicast QoS routing protocol designed by us tries to maximize the probabilities of meeting end-to-end delay, bandwidth requirement, and bandwidth utilization within a few generations by building the Pareto optimal fronts. For simplicity, we assume that QoS constraints of all leave nodes (end nodes) are the same. Fig. 6 shows the varied curves of cost, delay, and delay jitter of the multicast tree with the increasing genetic algebra. From Fig. 6, we can see that QMRGA can quickly break away from local optimal solution, and achieve global optimal solution by using the above instructional mutation operations. The reason is that it can maintain the solution's variety better, stronger capacity to globally search optimal solution and convergence speed with niche genetic algorithms.

By repeating the simulation with increasing number of network nodes, the efficiency of our algorithm can be observed. As the network becomes highly condensed, our algorithm exhibits a more linear and stable pattern than existing scalar optimization algorithm. Fig. 7 shows the comparison of multicast tree cost brought out by the three different algorithms of multicast nodes of 5 with constraint delay of 50 ms. The figure indicates the cost of the proposed algorithm to the optimal or near-optimal multicast tree with in few iterations, the convergence speed are better than that of [9], [11]. Fig. 8 details the cost compare of multicast with nodes variety from 5 to 50, and delay constraints of 50 ms. We can see that the algorithms proposed in this paper is superior to that at [9], [11]. Fig. 9 shows the convergence of the proposed algorithm with nodes from 5 to 50 and delay constraint of 50 ms is also superior to that of [9], [11] due to the niche count technique applied to improve the searching speed of global optimal solutions.

V. CONCLUSIONS AND FUTURE WORK

Multicast applications involving real-time audio and/or video transmissions require strict QoS constraints (end-to-end delay bound, delay jitter, and bandwidth availability) to be met by the

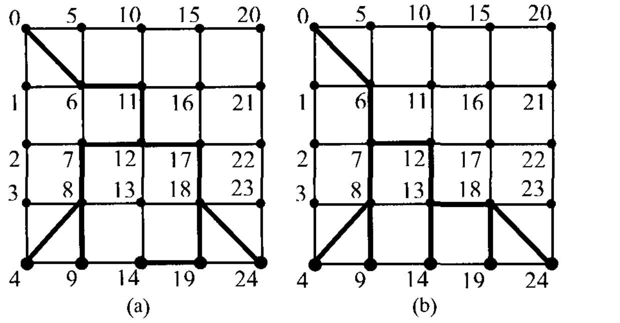

Fig. 5. Genetic algorithm generate multicast tree: (a) $D = 30,\ J = 40$, and $B = 50$, (b) $D = 20,\ J = 30$, and $B = 40$.

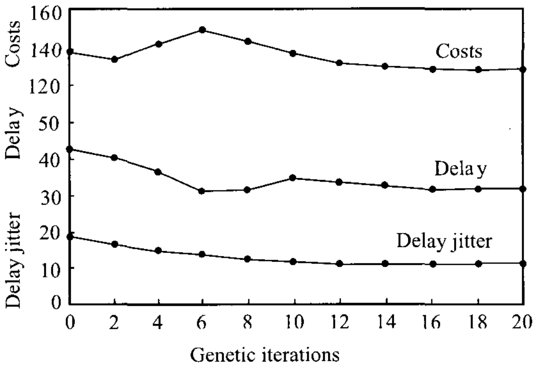

Fig. 6. Network costs, delay, and delay jitter vs. genetic iterations.

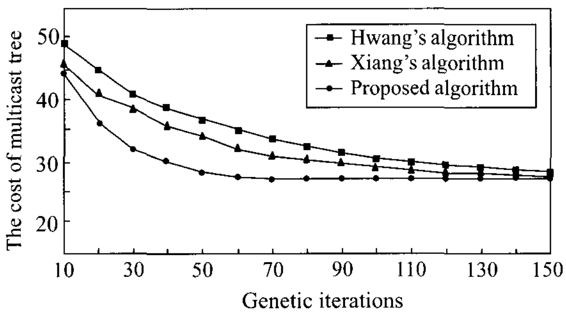

Fig. 7. Genetic iterations and cost.

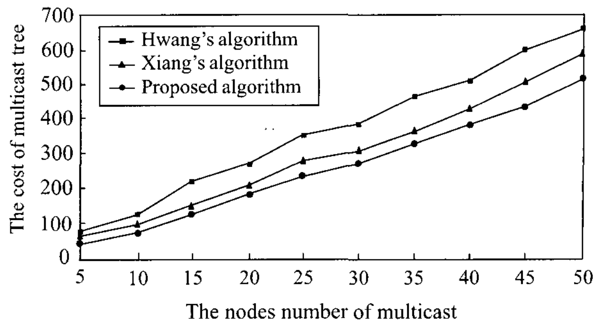

Fig. 8. The nodes number of multicast the cost of multicast with variable multicast nodes.

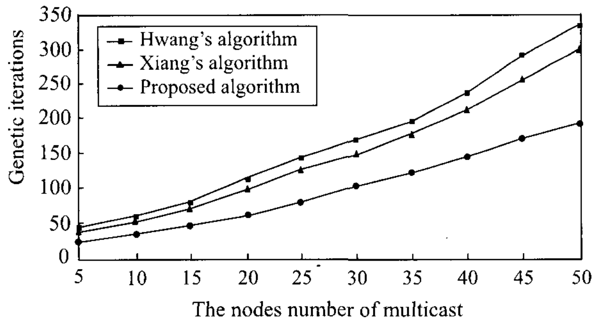

Fig. 9. The nodes number of multicast the genetic iterations with variable multicast nodes.

network. To guarantee real-time delivery of multimedia packets, a multicast channel needs to be established in advance by using a path selection policy that takes into account the QoS constraints. Among numerous advances in high-performance networking technology, the multicast routing with QoS constraints has continued to be a very important research area. This paper has discussed the multicast routing problem with multiple QoS constraints in the networks environment with uncertain parameters. On-demand multicasting with guaranteed QoS is currently an active area of research. Researches in the QoS routings are mostly done to optimize these QoS parameters by combining their different, conflicting characteristics into a single scalar function with the real intuition and logic behind the combinations being often fuzzy. The QMRGA can both optimize the network resources such as bandwidth and delay and converge to the optimal on near-optimal solution within few iteration, even for the networks environment with uncertain parameters. The incremental rate of computational cost can close to polynomial and is less than exponential rate. Simulation results delineate the efficiency, performance, and scalability of the protocol. Our future interest is to mathematically model this protocol to analyze its performance and complexity. Finally, we think our work will be helpful in solving some new problems in the domain of QoS routing.

In a word, the deep research of QoS constraint multicast routing will increase the technology of high performance network routing system, and it will be widely applied in video, multimedia broadcasting, and distance education fields, etc.

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Baolin Sun was born in 1963, Hubei, P. R. China. He is currently an associate professor of Wuhan University of Science and Engineering and Ph.D. candidate in computer science of the Wuhan University of Technology. He is a paper reviewer of Journal of Computer Applications and FSKD. His research interests include QoS multicast routing, distributed computing, network optimization, ad-hoc networks, and protocol engineering. He has published over fifty technical papers.

Layuan Li was born in 1946, Hubei, P. R. China. He received the B.E. degree in Communication Engineering from Harbin Institute of Military Engineering, China in 1970 and the M.E. degree in Communication and Electrical Systems from Huazhong University of Science and Technology, China in 1982. He academically visited Massachusetts Institute of Technology (MIT), USA in 1985 and 1999, respectively. Since 1982, he has been with the Wuhan University of Technology (WUT), China, where he is currently a professor and Ph.D. tutor of Computer Science, and Editor in Chief of the Journal of WUT. He is also the Director of International Society of High-Technol and paper reviewer of IEEE INFOCOM, ICCC, and ISRSDC. His research interests include high-speed computer networks, protocol engineering, and image processing. Professor Li has published over one hundred and eighty technical papers and ten books. He was also awarded the National Special Prize by the Chinese Government in 1993.