An Efficient Genetic Algorithm Based Clonal Selection and Hill Climbing for Solving QoS Multicast Routing Problem

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Abstract

Quality of Service (QoS) multicast routing is essential for many network applications such as IPTV, Internet radio, multimedia broadcasting, and real-time telecommunication. Multicast routing involves transport of information from one single sender to multiple destinations. There are two requirements of multicast routing in many multimedia real time applications: one is optimized network cost and other is bandwidth, bounded delay constraints. In this paper an efficient genetic algorithm based on clonal selection and hill climbing is proposed to solve the least-cost multicast routing problem with bandwidth and end-to-end delay constraints. The performance and efficiency of the proposed algorithm have been evaluated by a comparison with other existing genetic algorithms. The simulation results show that the proposed algorithm has high speed convergence and effective in solving the considered problem.

Keywords: *QoS multicast routing, Genetic algorithm, Artificial immune system and Hill Climbing*

1. Introduction

Multicast communication has become a key requirement for many applications where one source transmits the same information simultaneously to many destinations. Various network applications, such as audio/video conferencing, IPTV, Internet radio, interactive distributed games and real time remote control systems, require satisfying some Quality of Service (QoS) constraints. Some of these constraints are bandwidth, end-to-end delay, delay jitter and packet-loss ratio [1], [5], [9], [11].
Multicast routing is to find the optimal multicast tree which is rooted from source node and contains all multicast destinations. There are several heuristics proposed by researchers to construct the multicast tree of lower cost [2], [4], [7], [8], [11]. Various researchers proposed the construction of a static least-cost multicast tree which satisfies either single or multiple constraints using the genetic algorithm (GA) [2], [10]. GA is a searching algorithm that emulates the evolution idea using natural selection and the survival of the fittest concept.

An artificial immune system (AIS) is a type of optimization algorithm inspired by the principles and processes of the vertebrate immune system. It can be defined as a computational system inspired by theoretical immunology, observed immune functions, principles and mechanisms in order to solve problems [3].

Hill climbing (HC) is an optimization technique which belongs to the family of local search. It is relatively simple to implement, making it a popular first choice.

This paper proposes an algorithm to solve the least cost multicast routing problem with bandwidth and end-to-end delay constraints. The proposed algorithm is based on Genetic Algorithm, Hill climbing and artificial immune system. The experimental results illustrates that the performance of the proposed algorithm is better than the well-known algorithm suggested by Sanghoun [10], in which he employed GA to solve the considered problem. This paper is organized as follows: Section 2 introduces the formulation of the constrained QoS multicast problem. The proposed algorithm for solving the considered problem is given in Section 3. The conducted experimental results is introduced in Section 4. Finally, Section 5 gives the conclusion of this work and the future work.

2. Problem formulation

A communication network is modeled as an undirected, connected weighted graph $G = (V, E)$, where V and E denote the set of both nodes and connected links respectively. Further, $/V/$ and $/E/$ denote the number of nodes and links in the network respectively. Each link e_{ij} connects two nodes i and j in V. It is characterized by an ordered triple (B_{ij}, D_{ij}, C_{ij}) representing capability of bandwidth, delay, and cost between nodes i and j. A multicast tree is defined by $T = (V_T, E_T)$, where $V_T \subseteq V$, $E_T \subseteq E$, and $T \subseteq G$, and there exists a path $P_T (s, M_k)$ from the source node s to each destination node $mk \in M = \{m_1, \ldots , m_n\}$ in T . Here, n is the number of destinations.

This paper considers two QoS constraints: the bandwidth constraint between adjacent nodes and end-to-end delay constraint from a source to each destination. Bandwidth is a basic requirement for transmitting information, and directly influences the balance of network load and the routing request success ratio for large-scale multicast sessions (i.e., video on demand). It is required that the minimum value of link bandwidth in the multicast tree T must be greater than the required bandwidth (Breq), along the path from a source node s to each destination node $d \in D$. That is,

$$B_T = \min_{\{i, j | e_{ij} \in E_T\}} B_{ij} \geq B_{req} \qquad (1)$$

The end-to-end delay constraint ensures that the maximum value of path delays from a source node to each destination is smaller than the required path delay (Dreq), i.e.,

$$D_T = \max_{\{k | k \in D\}} \left(\sum_{\{i, j | e_{ij} \in P_T (s, d_k)\}} D_{ij} \right) \leq D_{req} \qquad (2)$$

The total cost of multicast tree must be minimized (while satisfying the above two QoS constraints):

$$\min \sum_{\{i, j | e_{ij} \in T\}} C_{ij} \qquad (3)$$

3. The proposed GACSHC for solving the QoS multicast routing problem

Genetic algorithms (GAs) were first introduced and investigated by Holland [12]. The process of a genetic algorithm usually begins with a randomly selected population of chromosomes. These chromosomes are representations of the solutions of the problem to be solved. GA utilizes the genetic operators, for example, crossover and mutation. It emulates the evolution idea using natural selection and the survival of the fittest concept. In each generation, a new population of solutions is created by

exchanging and combining the information obtained from the solutions through the previous generation. The main steps of the GA can be written as follows:

```
{
    Initialize population;
    Evaluate population;
    While termination criterion not reached
    {
        Select solutions for next population;
        Perform crossover and mutation;
        Evaluate population;
    }
}
```

Artificial Immune System (AIS) is a paradigm of soft computing which is motivated by the Biological Immune System (BIS) [3]. It is based on the principles of the human immune system, which defends the body against harmful diseases and infections. The human immune system is capable of recognizing virtually any foreign cell or molecule (antigen) and eliminating it from the body. To do this, it must perform pattern recognition tasks to distinguish molecules and cells of the body (self) from foreign ones (non self). The Clonal Selection (CS) principle, or theory, is the algorithm used by the immune system to describe the basic features of an immune response to an antigenic stimulus [4]. It establishes the idea that only those cells that recognize the antigens proliferate, thus being selected against those which do not. Generally, the basic steps of the clonal algorithm are as follows:

Input: S = set of patterns to be recognized, *n* the number of worst elements to select for removal

output: M = set of memory detectors capable of classifying unseen patterns

begin
    Create an initial random set of antibodies, *A*
    forall *patterns in S* do
        Determine the affinity with each antibody in *A*
        Generate clones of a subset of the antibodies in *A* with the highest affinity.
        The number of clones for an antibody is proportional to its affinity
        Mutate attributes of these clones to the set *A* , and place a copy of the highest affinity antibodies in *A* into the memory set, *M*
        Replace the *n* lowest affinity antibodies in *A* with new randomly generated antibodies
    end
end

Hill Climbing (HC) is an optimization technique which belongs to the family of local search. HC can be used to solve problems that have many solutions, some of which are better than others. It starts with a random (potentially poor) solution, and iteratively makes small changes to the solution, each time improving it. When the

algorithm cannot see any improvement anymore, it terminates. The main steps of HC can be written as follows [12]:

```
{
    T = 0;
    Repeat
        local = false
        select a current feasible solution Vc at random
        evaluate Vc
        repeat
            select a number n of new feasible solutions in the
            neighborhood of Vc
            select the solution Vn from the set of new
            feasible solutions with the best value of objective
            function
            if f(Vn) < f(Vc) then
            Vc = Vn
            else
            local = true
        until local
        t = t + 1
    until t = MAX
}
```

The following subsections present the implementation of the proposed Genetic Algorithm-Clonal Selection-Hill Climbing (GACSHC) for solving the considered problem.

3.1 Representation

Most of the proposed genetic algorithms for solving the considered problem use binary coding scheme, which makes the coding/decoding operations too complicated. In the proposed GACSHC, the tree structure coding scheme is chosen, in which a chromosome is a set of paths and each path is a set of positive integers (genes), which express IDs of nodes [10]. These paths are variable length and each locus (position) of the chromosome represents the node's order in the corresponding routing path. However, the length of a chromosome is not more than the total number of nodes. The procedure assembles a multicast tree while taking into account the connection between nodes. The gene of the first locus is always reserved for the source node. A chromosomes (i.e., a set of routing paths) encodes the IDs of the nodes from the source to each of destinations. Figures 2 and 3, show an example of the encoding methods in the context of the Figure 1. The first locus in each chromosome is assigned by the source node set to '1'. Each multicast tree extends the source s to the set of destinations D = {5, 7, 8}. The routing paths in the example are expressed as follows: the first path is (1 → 2 → 4 → 5), the second path is (1 → 7) and the last path is

(1 → 7 → 8), which represent feasible solution (chromosome).

In the course of constructing the multicast tree, the nodes that are already included in the current sub-tree are excluded, thereby avoiding reentry of the same node. Moreover, chromosomes are encoded under the (link) bandwidth and (path) delay constraints. In case they are violated, the encoding process is

usually repeated in part so as to satisfy the requirements. Thus, it effectively constructs a multicast routing tree whose root is the source node and whose terminal nodes are a specified set of destinations with bandwidth constraint (B_{req}) and end-to-end delay constraint (D_{req}).
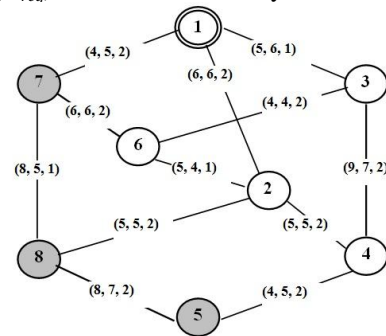

Fig. 1 An example of the network topology. Each link is characterized by an ordered triple (B_{ij}, D_{ij}, C_{ij}) representing capability of bandwidth, cost and delay between nodes i and j.
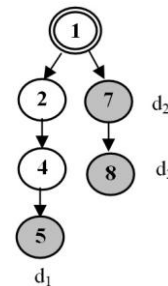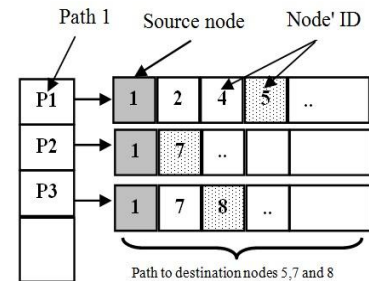

Fig. 2 A tree structure

Fig. 3 A Chromosome of source node 1 and destinations set (5. 7. 8)

3.2 Fitness function

This function must accurately evaluate the quality of the solution encoded by its chromosome in the population. The good individual has better fitness than the bad one. The QoS constraints (bandwidth and delay) in the proposed GAHC and GACSHC algorithms are directly incorporated in the course of constructing and assembling the trees. So, the proposed fitness function only involves network link costs. Given an initial population $H = \{h_1, h_2, \ldots, h_N\}$, the fitness value of each chromosome is computed as follows. Let T_k be a multicast tree represented by the chromosome h_k, and C_{Tk} be the sum of the link costs of the tree T_k. The

proposed GACSHC algorithm employs AIS clonal selection method to select chromosomes. The fitness value of each chromosome will be used to determine the affinity value. We used the average of the fitness function for each chromosome as the affinity value. In our implementation the chromosome with fitness value that exceed the affinity value is selected in the new generation. The fitness value of the chromosome h_k, denoted as $F(h_k)$, is given by:

$$F(h_k) = \left[C_{T_k} \right]^{-1} = \left[\sum_{\{i,j|e_{ij} \in T_k\}} C_{ij} \right]^{-1} \qquad (4)$$

3.3 Selection

Selection (i.e., reproduction) plays an important role in improving the average quality of the population. In our implementation the clonal selection is used to select the chromosomes for the new generation. The generated chromosomes are considered antibodies. As mentioned above, the fitness value of each chromosome is used to determine the affinity value. All chromosomes with fitness value exceeding the affinity value are inserted into clone (A) and selected for the new generation. Otherwise, the chromosomes that have fitness value less than the affinity value are inserted into other clone (B). The size of the clone A must equal the population size. To complete the population set new chromosomes are generated at random. The fitness value of these chromosomes are evaluated and compared with the affinity value. All chromosomes having fitness values exceeding the affinity value are inserted into clone A. The number of generated chromosomes is equal to the number of chromosomes existing in the clone B.

3.4 Crossover

Crossover processes the current solutions so as to find better ones[2], [6]. The crossover in the proposed algorithm consists of choosing a random common intermediate node in each parent and exchanging the sub trees beneath those nodes to produce new two offspring. Figure [4] shows an example of the crossover procedure. As shown in this Figure, the selected node 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 and bandwidth are less than path delay and bandwidth constraints.

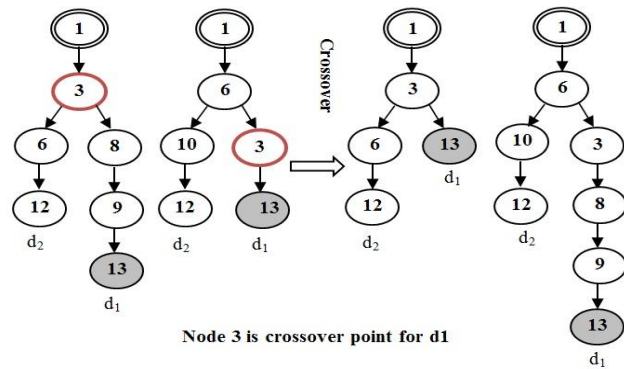
Node 3 is crossover point for d1

Fig. 4 Crossover process

3.5 Mutation

In the proposed algorithm, the mutation procedure employs Hill Climbing algorithm (HC) as the scheme to generates an alternative partial route from the mutation node to the destination. For each chromosome Vc in the population set, the mutation node is selected according to the mutation probability. In our implementation of HC algorithm we generate all the possible partial routes in the neighborhood of the mutation node to the destination. The fitness value of each generated route is evaluated and compared with the fitness value of the chromosome Vc to choose the best one.

4. Experimental Results :

In this section, we present a comparison between the performance of the algorithm suggested by Sanghoun's [10] and the proposed approaches: Hybrid Genetic-Hill Climbing (GAHC) algorithm, and Hybrid Genetic-Clonal Selection-Hill Climbing (GACSHC) algorithm for solving the QoS multicast routing problem. Sanghoun used GA that employs tournament selection to solve the considered problem. All of the experiments were carried out using Pentium Core i5 ® 2.30 GHz. All the three algorithms were implemented in C++. A random generator is used to create a different connected network sizes (20, 40, 60, 80 and 100 nodes) with different multicast group size. 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 in different network scale is shown in Figures 5 and 6. Each of the three algorithms is executed 100 times. The average of tree cost is shown in Figure 6, this figure shows that the average of tree cost obtained by the proposed GACSHC and GAHC algorithms are better than Sanghoun algorithms. As can be seen Figure 5 The performance of GACSHC is better than GAHC algorithm.
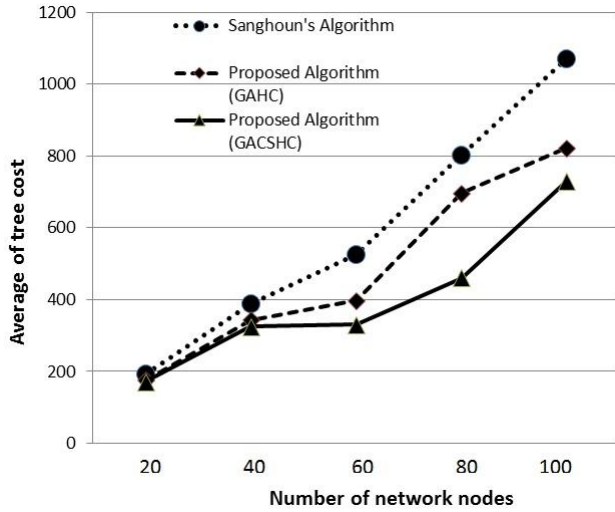
Fig. 5 Average tree cost versus number of network nodes

The least- cost of multicast tree is shown in Figure 6. It can be seen that the proposed GACSHC also is better than both the proposed GAHC and Sanghoun algorithms for least-cost multicast tree.
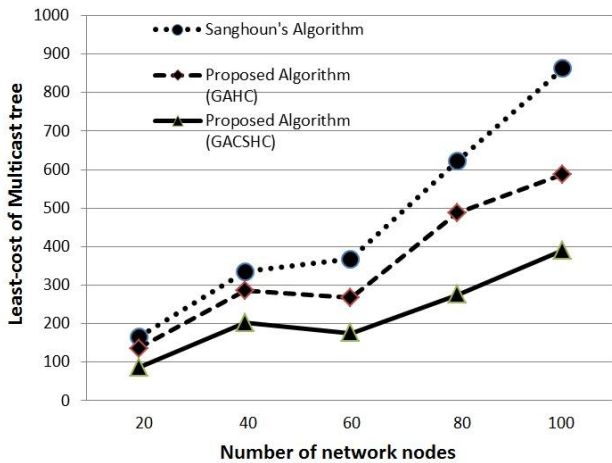

Fig. 6 Least-cost versus number of network nodes

Figure 7, shows the cost of multicast tree with different group sizes for a 100-node network. The curves in the figure indicate that at the initial stage of multicast groups (5 destination nodes), the three algorithms are similar, but with increasing of multicast groups the speed of cost increase is smoother in the proposed algorithm. The result shows that both GACSHC and GAHC algorithms have good performance on different group sizes, with lower cost than Sanghoun algorithm.
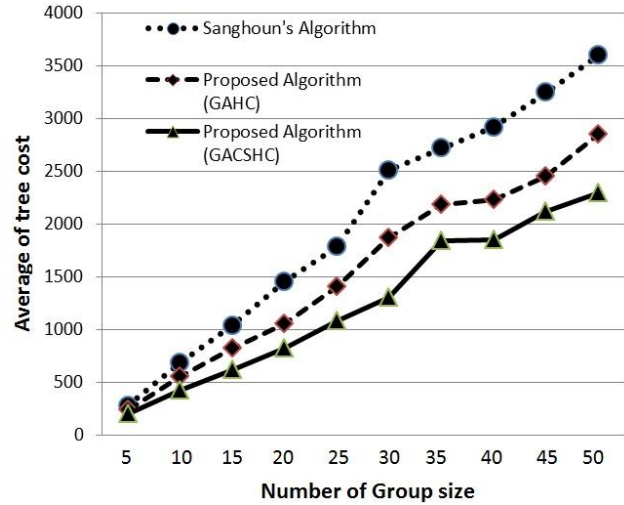

Fig.7 Average cost versus number of group size

The least- cost of multicast tree is shown in Figure 8. It can be seen that the proposed GACSHC also is better than both the proposed GAHC and Sanghoun algorithms for least-cost multicast tree.
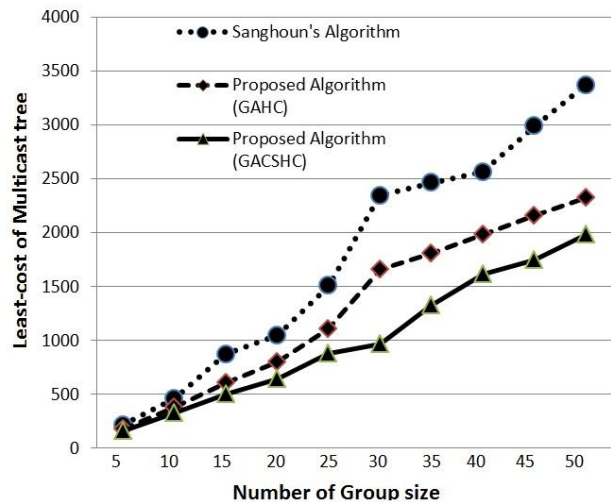

Fig. 8 Least-cost versus number of group size

Finally, Figure 9 shows the tree cost for varying iteration number, for a 100-node network and multicast group size of 10 nodes. The result shows that the proposed GACSHC algorithm has good convergence performance and fined minimum cost tree compared with both GAHC and Sanghoun algorithms.
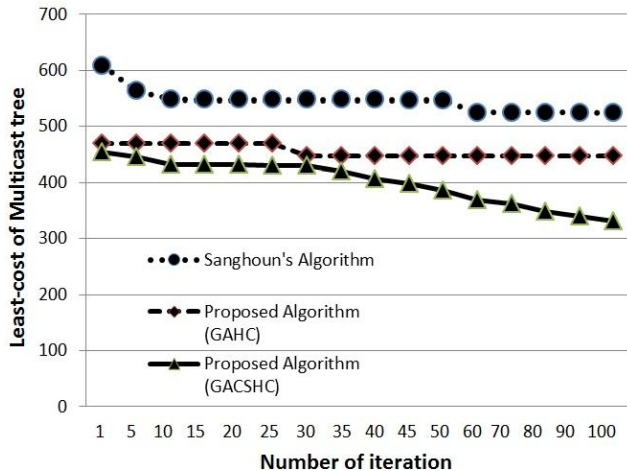
Fig. 9 Least-cost versus number of iteration

5- Conclusion and Future Work

In this paper we have presented hybrid GA based clonal selection and hill climbing for solving the least cost multicast routing problem considering end to end delay and bandwidth constraints. In our implementation the clonal selection is used to select the chromosomes for the new generation instead of the classical selection methods such as tournament selection. Hill Climbing algorithm is used to generate an alternative partial route from the mutation node to the destination node in the mutation step of the genetic algorithm. Experimental results demonstrated that the performance of the proposed hybrid genetic hill climbing algorithm and the proposed hybrid genetic-clonal selection-hill climbing compared with Sanghoun's algorithm are better. Further, it satisfies the QoS (i.e., bandwidth and end-to-end delay) constraints for different networks and multicast group sizes. In future elaboration of using the proposed algorithm to solve the multicast routing algorithm with different QoS constraints is considered. Also this work can be extended by considering other metaheuristic algorithms such as ant colony, swarm intelligence and simulated annealing algorithms.

References

[1] C. Hua and S. Baolin, "Multicast routing optimization algorithm with bandwidth and delay constraints based on GA", Journal of Communication and Computer, Vol. 2, No. 5, 2005, pp. 63-67.

[2] C. Wook, and R. Ramakrishna, "A Genetic Algorithm for Shortest Path Routing Problem and the Sizing of Populations", IEEE Transactions on Evolutionary Computation, Vol. 6, No. 6, 2002.

[3] J. Greensmith, A. Whitbrook, and U. Aickelin, Artificial Immune Systems, Handbook of Metaheuristics, 2nd edition, Springer, 2010.

[4] K. Vijayalakshmi and S. Radhakrishnan, "Artificial immune based hybrid GA for QoS based multicast routing in large scale networks (AISMR)", Computer Communications, Vol. 31, 2008, pp. 3984–3994.

[5] L. Layuan and L. Chunlin, "Multicast Routing Protocol with QoS Constraints", Vol. 15, No. 2, 2004, pp. 286-291.

[6] L. Sanna and L. Atzori, "A Genetic Algorithm Based Approach for Group Multicast Routing", Journal of Networks, Vol. 1(4), 2006.

[7] L. Zhang, C. Lian, L. Meng and F. Wang, "A method for least-cost QoS multicast routing based on genetic simulated annealing algorithm", Computer Communications, Vol. 32, No. 1, 2009, pp. 105-110.

[8] M. Kima. ,C. Mutkac, M,Limd, and H, Park, "On QoS multicast routing algorithms using k-minimum Steiner trees", Information Sciences, Vol. 238, 2013, pp. 190–204.

[9] M. Shankar, S. Radhakrishnan, and C. Sekharan. "Multicast Routing with Delay and Delay Variation Constraints for Collaborative Applications on Overlay Networks", IEEE Transactions on Parallel and Distributed Systems, Vol. 18 , Issue 3, 2007, pp. 421-431.

[10] S. Oh, C. Ahn, and R. Ramakrishna, "A genetic-inspired multicast routing optimization algorithm with bandwidth and end-to-end delay constraints", Proceeding 13th International Conference on Neural Information Processing, Hong Kong, China, 2006, pp. 807-816.

[11] Y. Xu, R, Qu, "GRASP Approach for the delay-constrained multicast routing problem", In Proceedings of the multi displinary international scheduling conference; 2009, pp. 93–104.

[12] Z. Michalewicz, Genetic algorithms + Data structures = Evolution Programs, Springer Verlag Berlin Heidelberg, 1996.