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Multiobjectives GA-Based QOS Routing Protocol for Mobile Ad Hoc Network

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Abstract

Genetic Algorithm with Multiobjective formulations are realistic models for many complex engineering optimization problems such as QoS routing protocol for mobile ad hoc network. The paper presents QoS routing protocol for MANET with specialized encoding, initialization, crossovers, mutations, fitness selections and route search using genetic algorithm with multiple objectives. The aim is to find the best QoS route in order to optimize the design of MANET routing protocols. This NP-hard problem is often highly constrained such that random initialization and standard genetic operators usually generate infeasible networks. The performances of the protocol was done to indicate the feasible of the proposed multiobjectives formulation.

Keywords: *QoS Routing, Mobile ad-hoc networks, genetic algorithm, fitness function, performances*

1. Introduction

Future wireless mobile ad hoc networks ultimately will carry diverse multimedia applications such as voice, video and data. For quality delivery to delay sensitive applications it is imperative that mobile ad hoc networks (MANETs) [1] provide quality of service (QoS) routing support which manages bandwidth and delay [2] constraints. Various mechanism of routing protocols are available [5][8]. However, existing studies [3][4][6] showed that some protocols are more liable to suffer performance degradation than others. On-demand protocols, performed well compared to table oriented. Among the on-demand QoS routing protocols proposed [7][8][9], a CDMA/TDMA MAC layer is commonly used to eliminate the interference between different transmissions. A potentially promising approach is to establish multiple paths between source and destination. Then, we need to design algorithms that take advantage of multiple paths to improve the overall performance. For network design, Kumar *et al*. [8] uses genetic algorithm(GA) considering diameter, average distance, and computer network reliability. Coley *et al*. [10] outlines fields of engineering where GA had been applied, such as VLSI routing and communication networks. M. Gen *et al*.[11] produced detailed study of various GA-based industrial engineering applications as applied to scheduling, transportation and reliability. R. Elbaum *et al*. [12] used GA in designing LAN with an objective to minimise the network delay. S. Mao *et al*. used GA to solve the routing problem to multiple description video in MANET[13] . Researchers have applied GA to the shortest path routing problem [14], dynamic channel allocation problem [15] and routing problem[16]. Munetomo [17] proposed GA with variable-length chromosomes, whilst Inagaki [18] proposed GA employing fixed length chromosomes for networking problems. The rest of the paper is organized as follows. Section II outlined strategies facilitating QoS route selection, introduced MANET model and multiple objective formulations. In Section III, we dwelled on the implementation details of the GA-based QoS route algorithm. Lastly, Section IV concludes the paper.

2. QoS Route Selection Strategies

When using two additive or multiplicative metric, or one additive and one multiplicative metrics, MANET QoS routing is a NP-complete problem [19]. The QoS route selection algorithm must be addressed in order to produce QoS routing strategies that are efficient and scalable. The major heuristics for the solution to this problem typically are solved by the following techniques; (1) the ordering of QoS metrics[19]; (2) sequential filtering[20]; (3) scheduling discipline of QoS metrics[4]; (4) admission control techniques[4][21]; (5) control theory approach[9]. In this paper we proposed multiobjective QoS routing using genetic algorithm.

2.1 Problem Statement

MANET is modeled as a graph $G = \left(E, Q\left\{ nci,\ B_{AVA},\ D_{E2E},\ D_{MAC} \right\} \right)$ where E is a set of all mobile nodes in the network; and Q is a set of QoS routing constraints which set the limits on the performance of the network. Each mobile node $i \in E$ has a unique identity and moves arbitrarily. A circular plane, radius ***R*** defines a coverage area within which each node could communicate with each other directly. Neighbours of node ***i*** are defined as a set of nodes which are within radius ***R*** and reachable directly from the node ***i***. Every pair of neighbours can communicate with each other in both directions. Hence, there exists a connectivity between neighbours ***i*** and ***j*** with the index, *nci*[25]. If the pairs are moving towards each other or away from each other, the node pair connectivity index, ***nci*** should be a positive value which describes the quality of connectivity between any two adjacent nodes. The least ***nci*** value indicates a good quality connection, in which the node pair connectivity time is larger compared to high ***nci*** value. The node connectivity index, ***nci*** is defined as,

$$nci = \begin{cases} a - \left[\dfrac{10^5 \cdot b}{10^5.c - npem} \right]; & for\ P_2 < P_1 \\ \dfrac{10^5 \cdot b}{10^5.c + npcm}; & for\ P_2 < P_1 \\ 0\ ; & for\ P_2 = P_1 \end{cases} \tag{1}$$

where $npem = (1/(t_2 - t_1))\sqrt{((1/P_1) - (1/P_2))}$ and
$npcm = (1/(t_2 - t_1))((1/\sqrt{P_2}) - (1/\sqrt{P_1}))$.

It is observed that *npcm* and *npem* are positive quantities; *npcm* is due to the node moves toward another neighbour node; *npem* is due to the node moves away from that neighbour node. The values of *npcm* is towards high positive values and *npem* is towards low positive values. These two quantities must be combined to form single metric indicating the quality of connectivity between the two adjacent mobile nodes. A node with *npcm* , indicated that its node pair connectivity time is longer than the node with *npem*. During operation, a route, ***R*** is created from source, ***s*** to destination, ***t*** as a sequence of intermediate nodes, such that ***R(s, t)*** = {***s,… I, j, k, l, …t***} without loop. The node pair connectivity index, $\boldsymbol{nci_{(I,j)}}$ associated with the node pair is specified by the matrix, *C*=[$\boldsymbol{nci_{(I,j)}}$], defined as follows,

$$C = \begin{bmatrix} nci_{0,0} & \cdots & nci_{o,k-1} \\ \vdots & \ddots & \vdots \\ nci_{k-1,0} & \cdots & nci_{k-1,k-1} \end{bmatrix} \tag{2}$$

The connectivity matrix is built at the source, upon receiving the RREP packets from the destination after a certain period of time after route request. The values continue to change as the topology changes. A connectivity indicator $\boldsymbol{L_{i,j}}$, provides the information on whether the link from node ***i*** to node ***j*** is included in the routing path. It is defined as follows,

$$L_{i,j} = \begin{cases} 1 & \text{if there exist connectivity } (i,j) \ . \\ 0 & \text{if otherwise.} \end{cases} \tag{3}$$

The diagonal elements of ***L*** must always be zero. Another formulation in describing the MANET topology is node sequence of the routes, such that,

$$N_k = \begin{cases} 1, & \text{if node } N_k \in \text{ route.} \\ 0, & \text{............ if otherwise.} \end{cases} \tag{4}$$

Using the above definitions, QoS routing can be formulated as a combinatorial optimization problem minimising the objective functions. The sum of ***nci*** of the selected route should be minimum, since this would be the most preferred route due to the higher probability of being connected longer with next hop neighbours. Then, the formulation statement is to minimise the sum of node connectivity index of the route,

$$C_{k\{SUM\ (S,T)\}} = \sum_{j=S}^{T} C_{k,j} . L_{k,j} \tag{5}$$

The sum of ***nci*** of the route ***R(S , T)*** constitutes the *cost* of the packet transmission process. In this approach, the longer the connectivity lifetime, the lower the *cost* of the route.

2.2 Multiple Objectives Optimization Formulation

In many real-life problems, objectives under consideration conflict with each other. Therefore, a perfect multiple objective solutions that simultaneously optimizes each objective function is almost impossible. The operation of GA will minimise the sum of node connectivity index of the route, $C_{sum(S,T)}$, subject to the various constraints.

There must be no looping

This constraint ensures that the computed result is indeed an existing path and without loop between a source, ***S*** and a designated destination, ***T*** such that,

$$\sum_{\substack{j=S \\ j\neq i}}^{T} L_{i,j} - \sum_{\substack{j=S \\ j\neq i}}^{T} L_{j,i} = \begin{cases} 1 & if \quad i = S \\ -1 & if \quad i = T \\ 0 & otherwise. \end{cases} \tag{6}$$

Available node bandwidth must be greater than the requested bandwidth
This constraint ensures that the node bandwidth can manage the request bandwidth such that, $B_{AVA,i} \geq B_{REQ}$, and for the whole route, $B_{REQ} \leq min\ (B_S,\ \ldots,\ B_i, B_j,\ \ldots B_T)$, where B_{REQ} is the bandwidth of the transmitted message. The node bandwidth must be greater than the demand bandwidth. Generally, for QoS operation to be effective, the bandwidth available for the node in question must be considered. Since the shared medium is being dealt with, CSMA/CA, as the link layer of the mobile ad hoc network, the problem of medium contention among the nodes within the transmission range must be taken into account. Hence, it is necessary to estimate the instantaneous $B_{AVA,i}$ and $B_{CON,i}$ for the node concerned.

Total delay is a minimum
The constraints in terms of link delay and node delay must be considered.

$$D_w \geq \{ \sum_{i=1}^{m} \sum_{\substack{j=1 \\ j\neq 1}}^{|S\rightarrow T|} D_{i,j} \cdot L_{i,j} + \sum_{i=1}^{|S\rightarrow T|} D_j . N_j \} \tag{7}$$

If several routes exist, then the total delay for a route to be selected is the one that is the least.

3. The Genetic Algorithm Implementation

3.1 Encoding and Limited Population Initialization

The chromosome consists of sequences of positive integers, which represent the identity of nodes through which a route passes. Each locus of the chromosome represents an order or position of a node in a route. The gene of the first and the last locus is always reserved for the source node, ***S*** and destination node, ***T*** respectively. The length of the chromosome is variable, but it should not exceed the maximum length which is equal to the total number of nodes in the network. The information can be obtained and managed in real-time by MANET monitoring algorithm and non-disjoint multiple routes discovery protocols(NDMRD) [22]. Normally, the initial population was obtained by generating the chromosome randomly and then remove the invalid solutions before being fed to the GA module. Furthermore, the infeasible solutions can only be eliminated after the connectivity matrix is obtained by the multiple route discovery algorithms. Another approach is to produce an initial population by extracting the existing potential solutions from the result of NDMRD protocol [22]. Clearly, a set of useful solutions are extracted before being processed by the GA module.

3.2 Fitness of the Multiple Objectives Function

Fitness value of each route is based on various QoS parameters: bandwidth, node delay, end to end delay and the node connectivity index, *nci*. Clearly it can be classified as multiple-objectives optimization problem. According to M. Gen *et al*. [11] , each objective function is assigned a weight. These weighted objectives are combined into a single objective function.

Fitness function operates to minimise the weighted-sum ***F***, $F = \alpha.F_1 + \beta.F_2 + \gamma.F_3$ where F_1, F_2 and F_3 are the objective functions which describe ***nci***, delay and bandwidth respectively. F_1, F_2 and F_3 are defined as follows,

$$F_1 = \sum^{|s \to t|} C_{ij} \cdot L_{ij} \quad , \tag{8}$$

$$F_2 = \left(\sum_{j=1}^{|S \to t|} D_{ij} \cdot L_{ij} + \sum^{|s \to t|} d_j \cdot N_j \right) \tag{9}$$

$$F_3 = \begin{cases} 1/B_i & if \quad B_i - B_{QOS} > 0 \\ 1000 & if \quad B_i - B_{QOS} \leq 0 \end{cases} \quad . \tag{10}$$

The weights α , β and γ are interpreted as the relative emphasis of one objective as compared to the others. The values of α , β and γ are chosen to increase the selection pressure on any of the three objective functions. The fitness function ***F*** measures the quality and the performance of a specific node state. Having described these parameters, which are the bandwidth, *nci*, medium access delay and end to end delay, the next issue is how importance each parameter on QoS Routing protocol as a whole. The significance of each parameter is defined by setting appropriate weighting coefficients to α , β and γ in the fitness function that will be minimised by the GA operations. The values of these weighting coefficients were determined based on their equal importance towards the overall QoS Routing performance, hence α , β and γ are set to $\mathbf{10^{-3}}$, $\mathbf{10^{-4}}$ and $\mathbf{10^{-3}}$ respectively. The function which involved bandwidth, we need to find the minimum bandwidth among the nodes and compare this with the demand bandwidth, B_{QOS} . If the minimum bandwidth is less than the B_{QOS} , the fitness is set to a high value so that in the selection process it will be eliminated.

3.3 Mobile Nodes Crossover

In our scheme, the two chromosomes chosen for crossover should have at least one common gene, except for source and destination nodes. A set of pairs of nodes which are commonly included in the two chosen chromosomes but without positional consistency being first determined. Such pairs are called potential cross sites. Then, one pair (4,3) is randomly chosen and the locus of each node becomes a crossing site of each chromosome. It is possible that loops are formed during crossover. A simple restoration procedure was designed to eliminate the infeasible chromosomes.

The procedure for crossover operation is follows:

Step 1) Input a matrix which consists of a number of routes, as Eqn 11.

Step 2) Test for crossover rate. Initialise the random number generator and the new route array. The population size must be positive and even.

Step 3) Consider a pair of variable length chromosomes denoted as parents, V_1 and V_2 , starting from the last chromosome within the population.

Step 4) Locate the potential pair of crossing sites.

Step 5) If more than one pair of crossing sites exist, apply a random number to establish only one particular pair of crossing sites.

Step 6) Do the crossover of V_1 and V_2. Two offsprings, V_1**'** and V_2**'** are produced.

$$ROUTE\_ARRAY = \begin{bmatrix} n_{0,0} & n_{0,1} & n_{0,2} & \cdots & n_{0,k-1} \\ n_{1,0} & \cdots & \cdots & \cdots & \cdots \\ n_{2,0} & \cdots & \cdots & \cdots & \cdots \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ n_{m-1,0} & \cdots & \cdots & \cdots & n_{m-1,k-1} \end{bmatrix} \quad (11)$$

3.4 Route Mutation

Mutation is used to change randomly the value of a number of the genes within the candidate chromosomes. It generates an alternative chromosome from a selected chromosome. The procedure for the mutation process is outlined below:

Step 1) Input two matrices, population matrix(Eqn. 12) and connectivity matrix (Eqn. 13).

Step 2) Select randomly a parent chromosome ***V,*** from the *POP_MATRIX*. It is selected with the probability P_m.

Step 3) Randomly select a mutation node i from ***V,*** .

Step 4) Generate the first subroute r_1 from source node, ***S*** to node i by deleting a set of nodes in the upline nodes after the mutation node.

POP_MATRIX

$$\begin{bmatrix} n_{0,0} & n_{0,1} & n_{0,2} & \cdots & n_{0,k-1} \\ n_{1,0} & \cdots & \cdots & \cdots & \cdots \\ n_{2,0} & \cdots & \cdots & \cdots & \cdots \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ n_{m-1,0} & \cdots & \cdots & \cdots & n_{m-1,k-1} \end{bmatrix} \quad (12)$$

CONNECTIVITY MATRIX,

$$L_{i,j} = \begin{bmatrix} l_{1,1} & l_{1,2} & l_{1,3} & \cdots & l_{1,n} \\ l_{2,1} & \cdots & \cdots & \cdots & \cdots \\ l_{3,1} & \cdots & \cdots & \cdots & \cdots \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ l_{n,1} & \cdots & \cdots & \cdots & l_{n,n} \end{bmatrix} \quad (13)$$

Step 5) Generate a second subroute r_2 from i to the destination node ***T***. It is done as follows.

Step 5-1) Determine node degrees of ***I*** , deg(***i***), neighbours of ***i***. If deg(***i***)=1 and { deg(***i***) } = ***T*** , then terminate the search, since the second subroute consist of ***T*** . If deg(***i***) =1 and { deg(***i***) } # ***T*** , then terminate the mutation process. If deg(***i***) > 1 go to **Step 5-2**.

Step 5-2) Select node {1, 2, 3, … deg(***i***) }. If deg(1)=1 and {deg(1)}=***T*** then second subroute is generated. Proceed with 2 and so on. If deg(1)=1 and {deg(1)}#***T***, proceed with 2 and so on. If deg(1)>1 go to **Step 5-3**.

Step 5-3) Select node { 1, 2, 3, … deg(1) }. If deg(1)=1 and {deg(1)}=***T*** then second subroute is generated. Proceed with 2 and so on. If deg(1)=1 and {deg(1)}#***T***, proceed with 2 and so on. If deg(1)>1 terminate. We search for the second subroute up to two stages so that the effort will not take much processing time.

Step 5-4) If the number of second subroute generated is more than one, then choose the least hop.

Step 6) Combine the first subroute and second subroute forming a new route. Add to the *POP_MATRIX.*

Step 7) If any duplication of nodes exists between r_1 and r_2, discard the routes and do not perform mutation. Otherwise, connect the routes to make up a mutated chromosome.

3.5 Selection Schemes, GA Parametric Evaluations and Preferences

Choosing genetic algorithm parameters such as selection schemes, population size, mutation rate and crossover rate is a very difficult task. Each combination of parameters may produce a variety of outcomes. Haupt *et al* [23] outlined a general procedure for evaluating these parameters. In our case, four selection methods were considered, namely the roulette wheel selection (RWS), tournament selection (TS), stochastic universal selection (SUS) and elitism (ET) technique. Next, the parameters $\boldsymbol{P}_c$, $\boldsymbol{P}_m$ and population size were considered. It is necessary to examine the performance of each and select according to preferences. Matlab was used to design a GA-based routing algorithm without QoS functionality. The cost for each path was randomly generated. The main objective was to examine all the GA parameters that are useful for protocol design and utilise them in the QoS routing algorithm. Hence, mobile network considered, consists of 20 nodes, randomly distributed within a perimeter of 1000 metres by 1000 metres. Each node had a transmission range of 250 metres. For each reading taken, 10 simulation runs were done and averaged.

Determination of population size by finding average minimum cost, C_{AMC}

The effect of population was investigated by fixing the mutation rate ($\boldsymbol{P}_m = 0.01$) and changing the population size and recording the average minimum cost. The simulation was run for 2000 generations. Figure 1 plots $\boldsymbol{C_{AMC}}$ for the four different selection methods (with $\mu = 0.05$ for Elitism). It shows that in RWS, a population size in excess of 700 produces a significantly low cost. The minimum cost in each generation was recorded and the average minimum cost $\boldsymbol{C_{AMC}}$ was evaluated over the range from 0 until the 2000th generation. The most significant results were shown by the tournament selection and elitism. With a population size of approximately 10, it produces very low $\boldsymbol{C_{AMC}}$. The graph is re-plotted as in Figure 2, focussing on population size below 200. The results reinforced the view that population size below 100 is appropriate for both the Elitism and Tournament selection. In fact, a population of 20 could be used and still produce good fitness. Hence, tournament selection was chosen. It also meant that the population as low as 20, in MANET, will produce a reasonably good results.

Crossover and Mutation Probability

Another very important parameters for GA implementation are the crossover probability $\boldsymbol{P}_c$ and the mutation probability $\boldsymbol{P}_m$. These probabilities determine how many times crossovers and mutations occurred within a transmission period. The occurrence of crossover and mutation increases the convergence rate. De Jong [10], tested various combinations of GA parameters and concluded that mutation was necessary to restore lost genes, but should be kept at low rate, avoiding random search phenomenon. Further study by Schaffer *et al*. [24], suggested that the parameters should have these recommended ranges: population size of 20 ~ 30, mutation rate of 0.005 ~ 0.1 and crossover rate of 0.75 ~ 0.95. Another study by Haupt *et al* [23] concluded that the best mutation rate lies between 5% and 20% while the population size should be less than 16. In this paper, where GA operation is done in real time, the value of $\boldsymbol{P}_c$ and $\boldsymbol{P}_m$ is taken to be between 0.4 and 0.9 and between 0.05 and 0.2 respectively. The population size is limited up to the number of routes discovered. The limit is also imposed on the number of generations. We designed the algorithm so that it stops when the next value of the route does not change and restricted the maximum number of generations to 20.

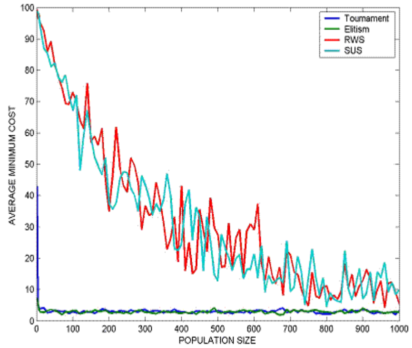

Figure 1 Plot Of Average Min Cost for Various Selection Methods

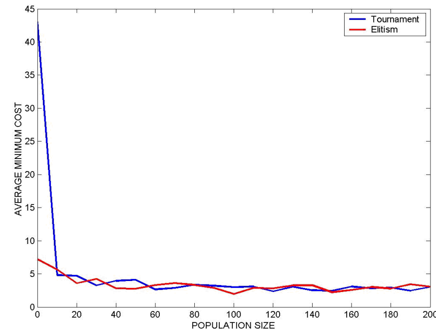

Figure 2 Plot of C_{AMC} as a Function of Population Size – Tournament and Elitism

Simulation experiments were run by setting MANET scenario running the protocol, with 20 nodes placed within an area of 1000 meter by 1000 meter. Each node has a radio propagation range of 250 meters and channel capacity of 2 Mbps. Up to 10 sources were initiated transmitting CBR with a data payload of 512 bytes. For each point, 10 simulations run were carried out and for each run it executed for 200 seconds. Two sets of simulation experiments were conducted, one for calculation of crossover probability and the other for mutation probability. The experiments were conducted using the source traffic rate of 40 kbps, 100 kbps and 900 kbps. The aim of the first set is to identify the possible values of P_c which would give the best results. The metric is the transmission efficiency, defined as the ratio of average throughput of all nodes to the average load of all the nodes in the network. We varied P_c but set P_m constant as 0.1. The results are shown in Figure 3. For P_c with values from 0.4 to 0.8 the transmission efficiency is more than 80%. For 100 kbps CBR source, the maximum efficiency occurred when P_c is approximately 0.65 and for 40 kbps CBR source it is 0.4. The 900 kbps CBR source, the efficiency does not deviate very much. Hence, the value of 0.7 was chosen for P_c in all future simulation experiments. For mutation probability, similar simulation was run, this time the crossover probability was fixed at 0.7 and the mutation probability varies from 0.04 to 0.8. Figure 4 shows the result of mutation probability. Mutation probability produces the highest transmission efficiency when it is 0.1, which is more than 80 % for all three different traffic rates. Hence it is concluded that the crossover probability and mutation probability could be taken as 0.7 and 0.1 respectively.

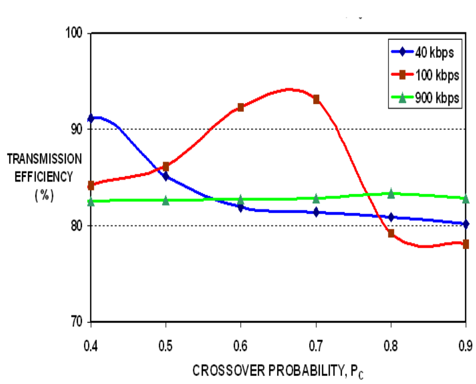

Figure 3 Transmission Efficiency as a Function of Crossover Probability

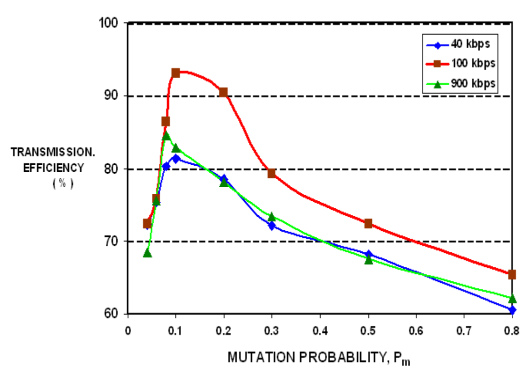

Figure 4 Transmission Efficiency as a Function of Mutation Probability

3.6 Qos Routing Performances

In this section, an extensive performance evaluation is presented through simulations for one important objective, that is to determine the behaviour of GA based QOS routing algorithm(or QOSRGA) as CBR sources are varied. The performance is influenced by the number of routes, number of CBR sources and the respective data rate. The source data rate controls the amount of packets being transmitted from a node. Multiple routes are generated as a result of NDMRD protocol [22]. Subsequently multiple CBR sources could also generate traffic congestion within the network. The metrics measured are the Average Packet Delivery Ratio (APDR) and Average Packet Delay (AETED). APDR is defined as the ratio between the average total traffic received and average total traffic sent. AETED is defined as the average end to end packet delay for the whole network.

Simulation Parameters

Simulations were conducted using Opnet Modeler that includes the wireless module. Network of 20 mobile nodes, was setup in a field configuration of 1,000 m x 1,000 m area with nodes movement according to random waypoint model(RWP). It is configured into our model through the mobility profile definition. The pause time was kept constant at 1 second for all simulation experiments. It maintained the consistency in the nodes' movement for all the scenarios. Start time was set to zero until the end of simulation. The only variation on the RWP model that was made is the maximum velocity. The velocity was configured according to uniform distribution between zero and $V_{\max}$. Traffic sources with 512 bytes data packets were the CBR type and the packet sizes were configured to vary according to exponential distribution. Each reading is a result of averaging 10 simulation runs using different seed value.

Effect of the Number of CBR Sources on Performances

The performance of QOSRGA was analysed when the network was congested. The performance metrics were measured for one, three, four and five CBR sources during the simulation period showing the effect of congestion. The results of Average Packet Delivery Ratio (APDR) and Average Packet Delay are shown in Figure 5 and 6 respectively. There will be an increase in probability of control packets that were broadcasted and collided with the unicast packets from each of the destination nodes. Data packets will be dropped and thus limits the data packet received. The Average Packet Delivery Ratio (APDR) was shown in Figure 5, and the highest APDR was a single-source scenario, and the least is the five-sources scenario. Furthermore, the delay of data packets was higher when the network was highly congested, as shown in Figure 6.

4. Conclusions

A scheme has been presented for multiple objectives QoS routing protocol for MANET based on Genetic Algorithm. In the proposed scheme of QoS routing, selection of a route was based on node bandwidth availability, short end to end delay and the longest node pair connectivity time indicated by node connectivity index (***nci***). The route selection algorithm was outlined and implemented. The variable length chromosomes represented the routes and genes represented the nodes. The algorithmic process was initialised by introducing a limited population, accumulated during the route discovery by the Node non-Disjoint Multiple Route Discovery (NDMRD) protocol. The fitness calculation was done using the weighted sum approached, combining the entire objective functions into a single objective. The performances indicated that the protocol is feasible.

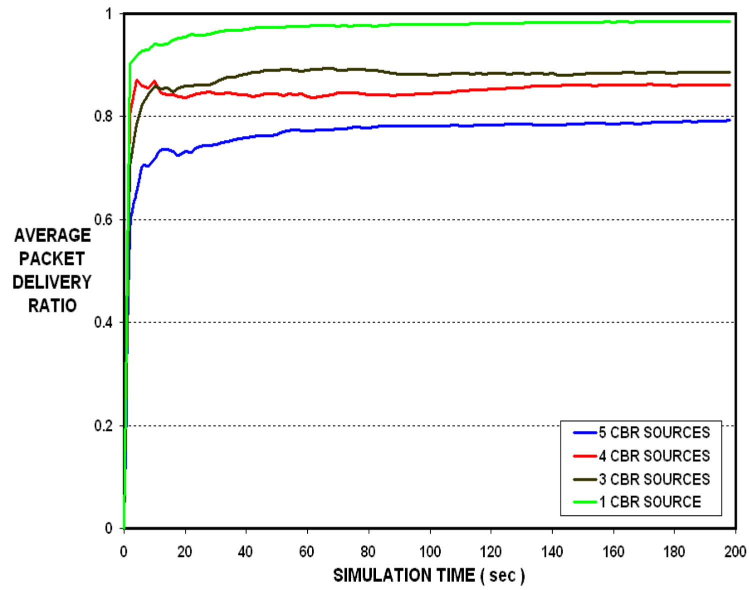

Figure 5 Average Packet Delivery Ratio as a function of simulation time with different congestion level

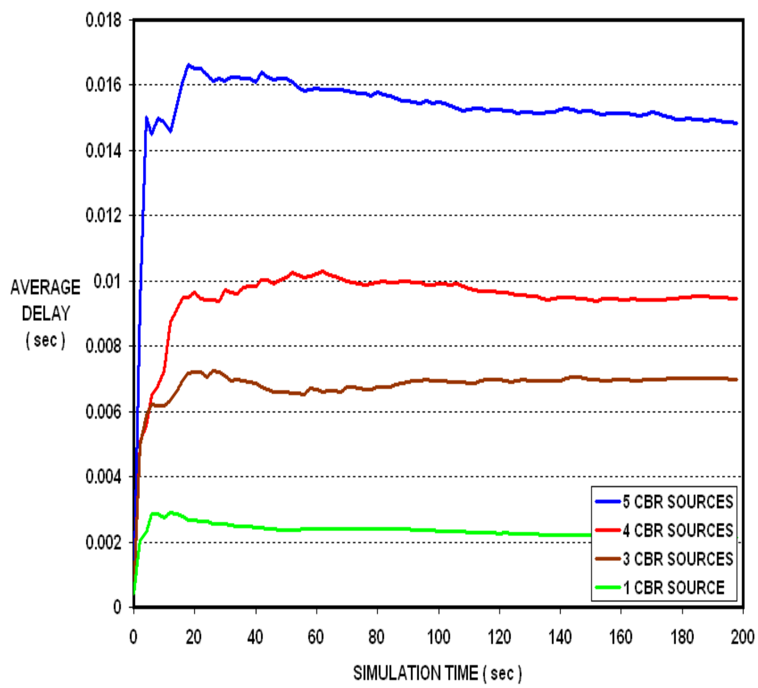

Figure 6 Average Packet Delay as a function of simulation time with different congestion level

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