Effect of Maximum Node Velocity on GA-Based QOS Routing Protocol (QOSRGA) for Mobile Ad Hoc Network

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Abstract. 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 effect of maximum node velocity on the protocol performances is done conclusively shows that QOSRGA had a potential to be the protocol for MANET.

Keywords: QoS Routing, Mobile ad-hoc networks, genetic algorithm, fitness function, performances, maximum node velocity.

1 Introduction

Next generation of wireless communication would see a seamless connectivity and integration of various technology platform. It is anticipated that wireless mobile ad hoc network (MANET) would be an additional component in the upcoming LTE (Long Term Evolution) deployment. Ultimately, it would be carrying a diverse multimedia applications such as voice, video and data coupled with high security feature. For enhanced quality delivery of delay sensitive applications it would be imperative that MANET[1] provides QoS Routing support, in which it could manages bandwidth-delay [2] constraints and node-connectivity issues. Various mechanism of routing protocols are already available [5][8] at the research level. However, studies on those protocols[3][4][6] showed that some are more susceptible to performance degradation than others. Most on-demand protocols, performed better than the table oriented protocols. Among the on-demand QoS routing protocols proposed in [7][8][9], a CDMA/TDMA MAC layer is commonly used to eliminate the interference between different transmissions. A very promising approach is to establish multiple paths between source and destination. Hence, it would be wise to

T.-h. Kim et al. (Eds.): FGCN 2011, Part II, CCIS 266, pp. 301–311, 2011.

design the protocols which take advantages of multiple paths to improve the overall performance. In the design of computer network, Kumar *et al.* [8] uses genetic algorithm (GA), as the optimization technique. The authors considered diameter, average distance, and computer network reliability as the optimization parameters. 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 such as that 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 optimize the routing problem for multiple description video transmission 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. In Section 3, we dwelled on the implementation details of the GA-based The rest of the paper is organized as follows. Section 2 outlined strategies facilitating QoS route selection, introduced MANET model and multiple objective formulations QoS route algorithm. Lastly, Section 4 concludes the paper.

2 QoS Route Selection and Optimization

2.1 Route Selection Algorithm

MANET QoS routing algorithm is a NP-completer it considers two additive or multiplicative metric, or one additive and one multiplicative metrics19]. The QoS route selection algorithm should be efficient and scalable. Typically the heuristics for the solution to this problem would be 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 it proposed multiobjective QoS routing algorithm using genetic algorithm. MANET is modeled as a graph $G = \{E, Q(nci,\ B_{AVA},\ D_{E2E}\ ,\ D_{MaC})\}$ where E is a set of 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 $\boldsymbol{i} \in \boldsymbol{E}$ has a unique identity and moves arbitrarily. A circular plane, radius $\boldsymbol{R}$ defines a coverage area within which each node could communicate directly to each other. Neighbours of node $\boldsymbol{i}$ are defined as a set of nodes which are within radius $\boldsymbol{R}$ and directly reachable. Every pair of neighbours can communicate with each other in both directions. Hence, there exists a connectivity between neighbours $\boldsymbol{i}$ and $\boldsymbol{j}$ with an index of ***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 good quality connectivity, 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 ,

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

$$npcm = (1/(t_2 - t_1))((1/\sqrt{P_2}) - (1/\sqrt{P_1})) \cdot$$

The variable *npcm* and *npem* are positive quantities; *npcm* is due to the node moving toward another neighbour node; *npem* is due to the node moving away from that neighbour node. The values of *npcm* is high positive values and *npem* is low positive values. These two quantities must be integrated forming a single metric which indicate 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*. P_1 and P_2 is the power measured away from the each other's node. During operation, a route, R is created from source, s to destination, t as a sequence of intermediate nodes, such that $R(s, t) = \{s, \dots i, j, k, l, \dots t\}$ without loop. The node pair connectivity index, $nci_{(I,j)}$ associated with a node pair is specified by the matrix, C=[$nci_{(I,j)}$], 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 route reply, **RREP** packets from the destination after a time lapse due to route request packet, **RREQ**. The value of ***nci*** changes continually as the topology changes. A connectivity indicator $L_{i,j}$, provides the information on whether the link from node i to node j is included in the routing path. It is defined as follows,

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

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

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

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,

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

The sum of ***nci*** of the route ***R(s, t)*** constitutes the cost of the packet transmission process. In this approach, longer connectivity lifetime, indicate 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 solution 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 following constraints.

2.2.1 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,

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

2.2.2 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 $\boldsymbol{B_{REQ}}$ 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 bandwidth available, $B_{AVA,i}$ and bandwidth consumed, $B_{CON,i}$ for the node concerned. Part of the cooperative protocols that are developed, is the Node State Monitoring protocol (NSM), where a method of monitoring bandwidth available and bandwidth consumed is established.

2.2.3 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 QOSRGA 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 the Node State Monitoring(NSM) protocol and the non-disjoint multiple routes discovery protocols(NDMRD)[22]. The the initial population was obtained by extracting the existing potential solutions from the result of NDMRD protocol [22].

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***. 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,

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

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

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

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, $\boldsymbol{B}_{\mathbf{QOS}}$. If the minimum bandwidth is less than the $\boldsymbol{B}_{\mathbf{QOS}}$, 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 pair of nodes which are commonly included in the two chosen chromosomes but without positional consistency is first determined, the potential crosspoint. Then, one pair is randomly chosen and the locus of each node becomes a crossing point of each chromosome. It may be 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. If the generated crossover rate is more than the given crossover rate, then skip the step. If not proceed. 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, $\boldsymbol{V_1}$ and $\boldsymbol{V_2}$, 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 $\boldsymbol{V_1}$ and $\boldsymbol{V_2}$. Two offsprings, $\boldsymbol{V_1'}$ and $\boldsymbol{V_2'}$ 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 $\boldsymbol{P_m}$.

Step 3) Randomly select a mutation node $\boldsymbol{i}$ from $\boldsymbol{V}$, .
Step 4) Generate the first subroute $\boldsymbol{r_1}$ from source node, $\boldsymbol{S}$ to node $\boldsymbol{i}$ by deleting a set of nodes in the upline nodes after the mutation node.

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

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

Step 5) Generate a second subroute $\boldsymbol{r_2}$ from $\boldsymbol{i}$ to the destination node $\boldsymbol{T}$. It is done as follows.

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

Step 5-2) Select node {1, 2, 3, … deg($\boldsymbol{i}$) }. If deg(1)=1 and {deg(1)}=$\boldsymbol{T}$ then second subroute is generated. Proceed with 2 and so on. If deg(1)=1 and {deg(1)}#$\boldsymbol{T}$, 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)}=$\boldsymbol{T}$ then second subroute is generated. Proceed with 2 and so on. If deg(1)=1 and {deg(1)}#$\boldsymbol{T}$, 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 $\boldsymbol{r_1}$ and $\boldsymbol{r_2}$, 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 technique. Next, the parameters $\boldsymbol{P}_c$, $\boldsymbol{P}_m$ and population size are considered.

3.5.1 Determination of Population Size by Finding Average Minimum Cost, C_{AMC}

The effect of population was investigated by fixing the mutation rate ($\boldsymbol{P}_{\mathrm{m}} = 0.01$) and changing the population size and recording the average minimum cost. The simulation was run for 2000 generations. 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.

3.5.2 Crossover and Mutation Probability

Another very important parameters for GA implementation are the crossover probability $\boldsymbol{P}_{\mathrm{c}}$ and the mutation probability $\boldsymbol{P}_{\mathrm{m}}$. 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 $\boldsymbol{P}_{\mathrm{c}}$ and $\boldsymbol{P}_{\mathrm{m}}$ 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, that is the maximum number of generations to 20. Simulation experiments were run by setting MANET scenario running the protocol, with 20 nodes placed within an area of 1000 meter x 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. The investigation concluded that the crossover probability and mutation probability could be taken as 0.7 and 0.1 respectively.

4 Effect of Maximum Velocity on QOSRGA Performances

Node mobility generally influences the overall performance of the network. The influenced of velocity on the APDR, AETED and ARLR was investigated. The number of CBR sources was set to five. The simulation was ran by varying uniform velocity distribution with mean outcome of V_{max} as 1, 2, 5, 10, 15, 20 and 25 m/s. For stationary nodes, the RWP parameter setting was removed altogether. The source data rates used were 40 kbps and 200 kbps. The aimed of the simulation experiment was to relate the mobility of nodes and its effect on the overall performance of QOSRGA. The results were shown in Figure 1 to Figure 4.

Figure 1 shows the APDR against maximum velocity for 40 kbps and 200 kbps. With the increase in velocity, the 40 kbps remained constant at approximately 82%. The performance of the 200 kbps traffic shows a decreasing trend as the velocity

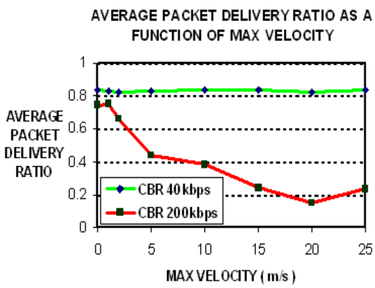

Fig. 1. Average Packet Delivery Ratio as a Function of Max Velocity

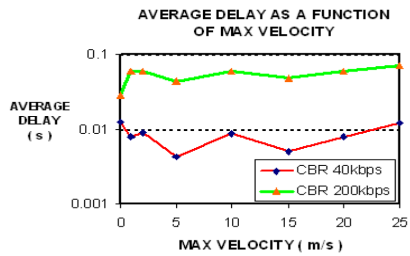

Fig. 2. Average Packet Delay as a Function of Max Velocity

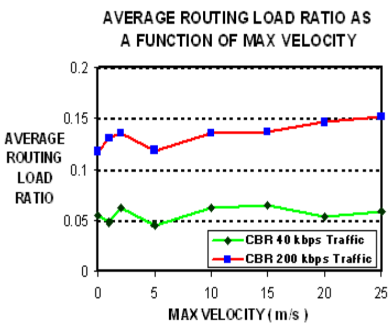

Fig. 3. Average Routing Load as a Function of Max Velocity

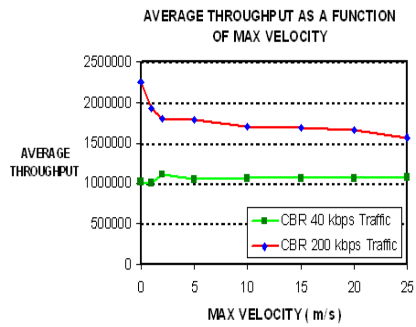

Fig. 4. Average Throughput as a Function of Max Velocity

increased. It dropped substantially from 78% to 42% at 5 m/s, then to 19% at 20 m/s and improved a little to 22 % at 25 m/s. QOSRGA performed effectively with low source data rate throughout the range of velocities but not with high source data rate. With higher data rate and faster node movement, more packets are dropped due to short node pair connectivity time, that is, high ***nci*** value. Figure 2 shows the average delay against maximum velocity. With 40 kbps source, the average delay was much less than that with a source of 200 kbps. The 200 kbps source generated more packets and resulted in higher congestion, and hence produced a greater delay. Nevertheless, it was still below the 100 ms, which was the maximum delay allowed for most multimedia services. The reading also shows a constant trend and not an increasing trend. It was due to the delay reading, which was based on all the packets that actually arrived at the destinations, thus not considering the dropped packets. Figure 3 shows the variation of average routing load ratio (ARLR) against maximum velocity. The routing traffic for 200kbps is 100% more than that of 40kbps. Also, as the velocity increases, the ARLR for the 200kbps source shows an incremental trend. The 40kbps source on the other hand remains constant at approximately 0.06%. As the velocity increased, the higher source needs more overhead packet for every successful packet reception at the destination. Figure 4 shows the variations of throughput. Once again the CBR 40 kbps source produced a constant throughput for all velocities. The throughput for CBR 200 kbps showed an immediate decline, after which the decline was gradual. At higher velocity, the node pair connectivity time was less, the packet dropped tend to increase, and hence the bit rate transfer to the destination was reduced considerably.

5 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 performance study was done to study the effect of maximum node velocity on the average throughput, average packet delivery ratio, average delay and average routing load. The performances indicated that the protocol is feasible for a reasonable node velocity.

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