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An Efficient Approach towards Network Routing using Genetic Algorithm

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Abstract

The network field has been very popular in recent times and has aroused much of the attention of researchers. The network must keep working with the varying infrastructure and must adapt to rapid topology changes. Graphical representation of the networks with a series of edges varying over time can help in analysis and study. This paper presents a novel adaptive and dynamic network routing algorithm based on a Regenerate Genetic Algorithm (RGA) with the analysis of network delays. With the help of RGA at least a very good path, if not the shortest one, can be found starting from the origin and leading to a destination. Many algorithms are devised to solve the shortest path (SP) problem for example Dijkstra algorithm which can solve polynomial SP problems. These are equally effective in wired as well as wireless networks with fixed infrastructure. But the same algorithms offer exponential computational complexity in dealing with the real-time communication for rapidly changing network topologies. The proposed genetic algorithm (GA) provides more efficient and dynamic solutions despite changes in network topology, network change, link or node deletion from the network, and the network volume (with numerous routes).

Keywords: RGA, Genetic Algorithm, Shortest Path, Network Field.

1 Introduction

In any network, such as the Internet, one of the main problems that significantly affect network performance is routing. Finding an optimal route to transmit data within a specific time frame must be a compulsory trait of any good routing algorithm and fulfill the need for a reliable and fast network [1]. With the change in network topologies, routing overheads appear to achieve the optimal performance while considering the parameters like packet delivery ratio, packet delays, packets dropped, and throughput [10]. Real-world networks employ algorithms based on random walks. A simple random walk's cover time may be exponential [11]. To guarantee that the time remains polynomial, the networks with no fixed infrastructure and the topology need to look for a strategy to avoid the adversary.

Genetic algorithm is a novel technique employed for network optimization. GA involves some defined operations [4], [5] which include conditions for encoding, initialization, evaluation, reproduction, crossover, mutation, and termination. Much work has already been done that involves GA to design and optimize the network [5]. GA involves time constraints as these algorithms take considerably longer times to generate a solution. A GA-based approach is presented to address the problems in the dynamic routing and coming up with an optimal solution. This approach suggests a new technique to fill the generation in a shorter time compared with different selection schemes. [3] Genetic algorithms prove very helpful to find effective yet quick solutions to complex problems. For this purpose, these algorithms involve genetic operators: crossover operators and mutation operators. On the other hand, heuristic search algorithms work fast but don't yield optimal solutions. Genetic algorithms have optimization algorithms adapting to changing requirements like the procedures of natural selection and genetics. Genetic algorithms owe their capability of providing optimal solutions to a blend of exploitation and exploration techniques [13]. The exploitation technique is applying prior knowledge for finding a better solution. While exploration refers to the investigation and finding of an unknown solution. Our exhaustive literature review identifies that the existing schemes such as link cost-based routing, delay-based routing, and throughput-based routing are static and can be drastically improved by evolutionary algorithms. An evolutionary algorithm or iterative algorithm such as a regenerative genetics algorithm randomly chooses the first population and finds the optimal route/ solution by reducing the solution space. Genetics algorithms have varied applications. For example, routing problems where the sequence of chromosomes (number) is used for encoding values of the different routes to finding an optimal one. Genetic algorithms have been applied to solve numerous problems, but for solving routing problems using the genetic algorithm, fewer studies have been done, which worked as an encouragement to put effort and research into this area. Following are a few reasons that drive us towards GA being the best solution for routing:

1. GA is highly customizable, which means if an improvement in throughput or jitter is needed, that metric can be added to a multi-objective optimization problem as a constraint. Thus, ensuring the best possible route considering the newly added condition. [12]

2. Implementation, configuration, and modification of GA do not incur additional complexity or delays to the network performance. [13]

3. GA is lightweight in terms of control overhead and information requirements. [15]

All of these reasons from existing literature and our study inspired us to develop an efficient routing scheme using a regenerative genetics algorithm. Our evaluations corroborate our claims that using GA drastically enhances the network performance with reduced delay and low complexity as compared to other schemes.

2 Literature Review

GA has vast applications to solve real-life problems. Their nature allows the successor solutions to evolve from the previous ones. GA can rightly be termed as an adaptive heuristic method for finding optimal solutions [14]. Among its numerous applications, GA is applied to schedule ship routing optimally [12]. Genetic algorithm is put in this case to make sure that the ship reaches the destination port minimizing the distance traveled and avoiding repeating the visited ports. Many fields including navigation systems and transportation employ GA for solving optimal path problems. The vectors (chromosomes) between the source and the destination nodes may vary in length. The solution lies in finding a better crossover mechanism as the right method may outperform the others. [15] finds that the Same Adjacency (SA) crossover mechanism performs better than the Same Point (SP) method for variable-length chromosomes. E-learning with personalized yet efficient learning mechanisms is gaining significance. Curriculum sequencing or better termed as learning path matching with the learner's preferences with proper start and endpoints is defined [16]. Because of different learning preferences from different learners, the learning path cannot be of fixed length. Therefore, an effective learning path is recommended based on a variable-length genetic algorithm (VLGA) keeping in mind the learner's prior knowledge and style. To ensure error-free garment manufacturing and at the same time, for maintaining the product quality, paper [17] defines some rules as variable-length chromosomes to be followed and to ensure quality. The use of a novel GA called Slippery Genetic Algorithm (sGA) gives rise to diverse solutions and thus, better quality assurance is achieved. Genetic algorithm (GA) has its role in designing and implementation of intrusion detection systems. A GA-based approach is presented for intrusion detection with variable length chromosomes. The proposed approach is then found effective and efficient after being tested with Defense Advanced Research Project Agency (DARPA) 1998 data [19]. Genetic Algorithms have their significant application in optimizing search and routing problems. Optimizing routing involves taking into account the network traffic. Ensuring the internet reliability and performance, selecting an optimized path from source to destination, and finding alternate paths by using multipoint crossover and mutation are important considerations. The proposed method calculates the shortest yet efficient path using GA adapting itself to change in topology, node, and network volume [20].

Improvements in selection and mutation schemes have a significant impact on the performance of GA. These improvements enhance the GA in terms of both efficiency and diversity. Enhanced Selection and Log-scaled Mutation GA (ESALOGA) [18] is presented with an improved selection and mutation schemes and is compared with the standard GA and its variations. The comparison shows major improvements. The algorithm uses different length chromosomes to encode the problem. Crosses (dots) are loci (node positions in a lane), where the similar genes (nodes) on the two selected chromosomes (lanes) are in the same place [3]. Hence, this results in a state where only a few cross-sites yield feasible solutions. This means that the crossover is entirely position-dependent, and similar genes should be at the same place for crossover. An algorithm for fixed-length (deterministic) chromosomes is proposed. In the proposed algorithm, chromosomes are of the same (fixed) length and are represented as sets of integers and each gene corresponds to a node identifier. This note identifier is randomly selected from the set of nodes that are connected to the node related to its locus number [2]. In the crossover, one gene is chosen from parental chromosomes at the ID locus of the start node and placed on the same progeny locus. After that, one of the genes is randomly picked at the locus of the gene number already selected. The process is repeated until the destination node is touched. The algorithm does not explain the mutation details. Using a large population for the algorithm yields an optimal or high-quality solution due to an inconsistent crossing mechanism. Some offspring can produce new chromosomes that match the original chromosomes in fitness. This slows down the evolutionary process. A new algorithm is developed that works for both fixed-length and variable-length chromosomes. Although, this algorithm is proven efficient in comparison to the other algorithms, it is failed to obtain the optimal path in all cases [7]. Three hybrid algorithms based on GA are presented with a different local search technique which are then compared with bee (BEE) and differential evolution (DE-SK) algorithms. Sequential constructive crossover (SCX) is modified and it is compared with one-point crossover (OPX). SCX performed significantly better than the OPX. The GA was employed combining two local techniques: 3-exchange and constructive mutation algorithms. After the comparative study, the hybrid genetic algorithm with 3-exchange and constructive mutation (HGA3) is found to be the best in terms of computational time and solution quality [21]. To enhance the performance of GA, paper [22] proposes more than one crossover operator including collision crossover and two selection strategies i.e. selecting the best crossover operator and random selection of an operator. The evaluation of the proposed method such as collision crossover shows major improvement in the performance of genetic algorithms, especially in the case when more than one crossover operator is used. [23] suggests a novel GA approach keeping in view that different operators (selection, crossover, and mutation) are very crucial for the strength of the genetic algorithms. Paper introduced an improved crossover operator with variable length chromosomes that uses parents with high fitness levels to produce offspring with high fitness levels and parents with low fitness are also

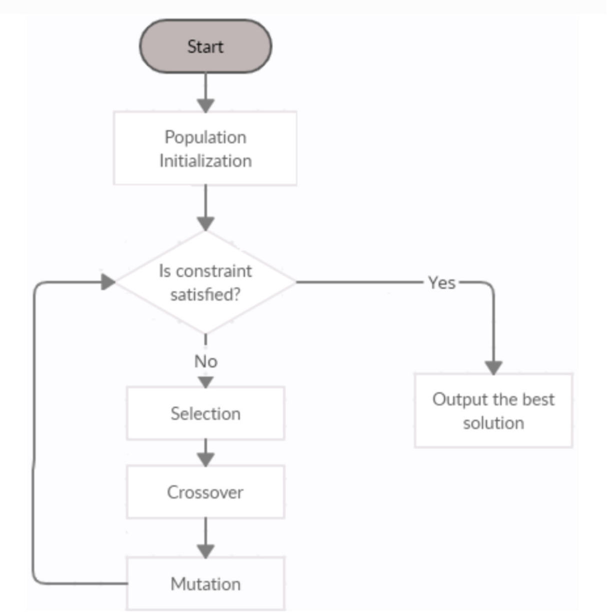


Figure 1: Methodology

used as well to introduce diversity in the resultant population. [24] introduces a new selection method in GA whose performance is evaluated in terms of individual and cumulative fitness. The selection method avoids the worst case where the selection pool may comprise of only poorly fitted chromosomes. The method gives them the chance to mate with successful and fit candidates as well. Candidates are arranged in descending order of the fitness levels. It is made sure that the candidate at nth best level mates with the candidate at the nth worst level. The proposed method performed better than the other selection methods and showed the potential to improve the overall strength of the GA.

The proposed approach (RGA) in this paper is based mainly on the fundamentals of the three operations of GA to do proper analysis and looking into the possibility of finding the optimal path in all cases.

3 The Proposed Methodology

Evolutionary and iterative algorithms such as GA and regenerative GA initialize the process with a population that is a set of solutions, randomly chosen from the solution space. A population is defined as candidate solutions for a particular problem, which in this case is efficient and low complexity routing. Generally, the selected population is not the optimal solution and requires further processing. The algorithm reproduces by selecting and performing a crossover operation (combining two or more solutions from the population), to mutate and create a refined population set. This repetitive process is evaluated on every iteration for constraints satisfaction to identify the optimal solution.

Representation mechanism: A coding mechanism with multiple parameters is used to configure the network [8]. A routing table is used to record entries for all pairs of node combinations. These entries correspond to the routes between a pair of nodes. Each route in the proposed algorithm is represented by a chain following the links of the routing table and thus configuration chains are constituted. GA encodes search space with a vector. These vectors are termed as chromosome. Each element of the chromosome denotes a gene. The collection of chromosomes results in a population. A fitness function is defined to estimate the strength of this population. Fitness function can also be used to estimate the strength is an individual chromosome. To start with GA, the initial population is created randomly. Then fitness is also evaluated for each chromosome. Then the following three steps are applied to produce the successor of the current generation:

- Reproduction – this phase works conforming to Darwin's theory of "Survival of the fittest". Only the population with the high fitness level is kept and moved to the next generation while the rest is eliminated.

- Crossover – from the population of high fitness, two parents are selected and a new offspring is produced. This process continues for the aforementioned number of times or until a certain condition is met to terminate the operation.
- Mutation – diversity is introduced with some new features in the offspring which make it quite different from its predecessors.

First of all, following a GA, the population is initialized (Figure 1). The selection of the routes is made from the routing table on a random basis. From the routing table, a route is selected between each pair of nodes to form a configuration chain (CS). The routing table is kept for all CSs that satisfy the given constraint. The routing table has a fixed size which is larger than the population size. With the generation of the new chains, older ones are discarded [9]. Fitness function is required to explain the physical representation and to assess the suitability of the chromosomes according to the characteristics required in the final solution. The role of the fitness function is very vital. So, fitness function must be defined carefully to precisely measure the fitness level of chromosomes in the population. Taking the shortest path routing problem into consideration, its fitness function is understandable as finding the SP is the same as discovering the cheapest route [10]. So the algorithm should use the topology database (a database that keeps track of the primary routes for all the network nodes) that would help to pick the initial generation randomly without any specific source and destination. A good selection of the successors is very crucial. Novel schemes are also proposed to generate population and carry out selection and crossover operations.

3.1 Genetic representation

A proposed RGA variable-length chromosome is composed of strings of integers or letters for the nodes' IDs representation that are traversed in a routing path. Each position on the chromosome depicts a node sequence (indicated by the gene for the locus) in a path. The first locus gene represents the source station (figure 2). As the chromosome varies in length, there is a limit on the maximum length and it should not go above the total number of nodes in the network.

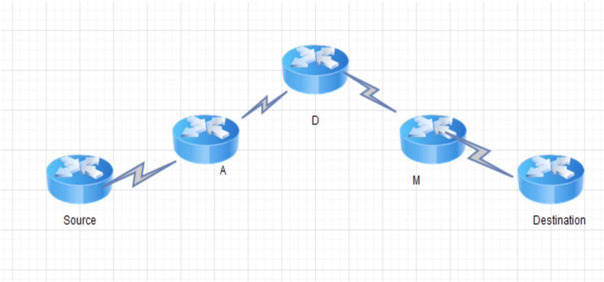


Figure 2: Gene Representation

3.2 Produce the first generation (select G0)

- Heuristic generation- Previously, this phase is not yet studied and analyzed deeply. But in this proposed approach, it is tried to have the initial generation cover all the aspects of the solution.
- Topological database – A database keeping track of the primary paths of all network nodes used in algorithms. It aids in randomly picking the first generation, without any specific or fixed source and destination.

This paper used a different approach to pick first-generation paths. This technique takes into account the origin and destination nodes. When the first routes are created, the 1st generation (G0) must include all the network nodes.

- All links (AB, AD, DM, AM...) that are available in the networks at any time must be in the database.

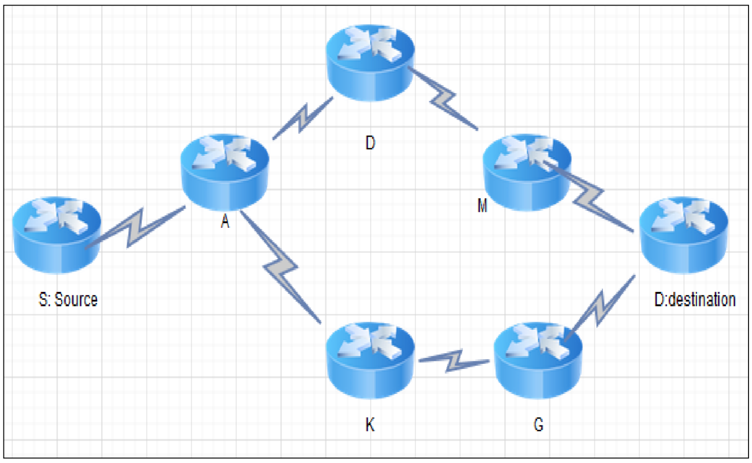


Figure 3: Mutation

- Start with all the links existing in the database and create the initial paths where the start node depicts the source and the end node represents the destination.
- A link should not show up twice in every path (infinite loop problem).
- All the connections present in the network have to be taken.

3.3 Crossover between chromosomes

Crossover finds better solutions based on the current solutions. Talking about the crossover operation in the shortest path routing problem, each partial pathway of two selected chromosomes is exchanged in a way that the resultant offspring represents only one pathway. This suggests the use of a one-point intersection for the proposed RGA. Partial paths connect the source node to the middle node and then the middle node to the destination node.

- One-point crossover: From the first chromosome, one locus is picked. This locus serves as the location to perform the crossover. Then the position for the other chromosome is the same. However, there is a chance that the crossover result thus produced may be invalid as it may suggest routes that are not present in the topological database of the network. For example: Consider the routes taken from the suggested network (Figure 2), and location 2 is the position where the crossover is performed between them: ADM, KGD. The resultant paths produced after the crossover are: (AGD, KDM) which don't exist in the topological database of the network. This kind of crossover is hard to produce consistent results.
- Two-point crossover: In this kind of crossover, for the crossover position, one location is chosen randomly in the first chromosome. Then the position for the other chromosome is taking the same gene name, but it does not have the same location. For example: Consider the routes taken from the suggested network (Figure 3), and location 3 is the position where the crossover is performed between them then the location in the second path is 2: AEBD, ABF. The resultant paths produced after the crossover are: (AEBF, ABD) which exist in the topological database of the network. This kind of crossover may face the looping path problem (this means that two similar genes exist in the same chromosome).

3.4 Mutation

In the mutation process, the selection of a gene is made randomly from a selected chromosome which is termed as "mutation site". To select the first node of the alternative partial-route, a node directly connected to the mutation point is picked randomly. For example- Examine paths (Source $\rightarrow A \rightarrow D \rightarrow M \rightarrow$ Destination). Location 2 is the position to make the mutation. The resultant path is (Source → $A \to K \to$ Destination). This path may be evaluated to be more efficient than the first path.

3.5 Fitness function

F_i is the fitness value of the i^{th} chromosome, that represents each solution from the population:

$$F_i = \frac{1}{\sum_{j=1}^{I_i=1} Cg_i(j), g_i(j=1)}, \tag{1}$$

where l_i is the length of the i^th chromosome, gi (j) is the gene (node) of the j^th locus in the i^th chromosome, and (C) is the link cost between nodes.

Example explaining the proposed approach:

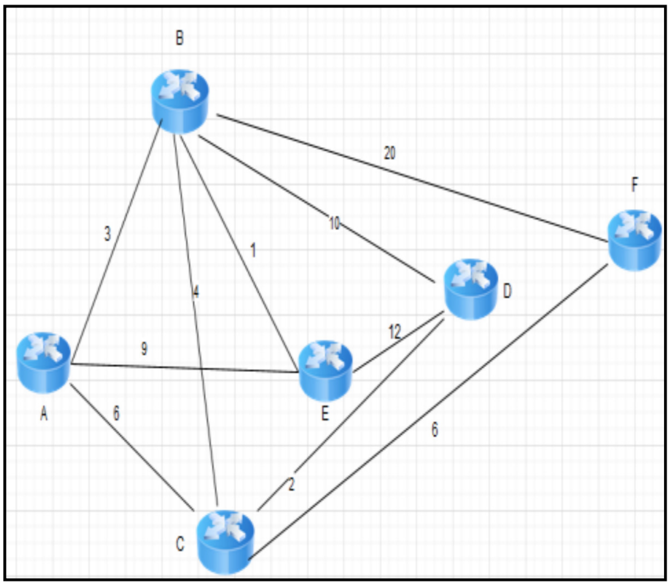


Figure 4: Network with the link cost

Let's consider network illustrated in Figure 4, to demonstrate the working example of the proposed scheme. Node A is assumed to be the source of the transmission, where as node D is destination. The process of the proposed regenerative GA includes:

Initial paths: $A \to B \to D = 13, A \to C \to B \to D = 20, A \to E \to D = 21, A \to B \to E \to D = 16, A \to B \to F \to C \to D \to = 31$. All links are taken.

Crossover: $A \to B \to D, A \to C \to B \to D \Rightarrow A \to C \to B \to D = 20$ and $ABD = 13\ldots$The same paths $A \to C \to B \to D, A \to B \to E \to D \Rightarrow A \to C \to B \to E \to D = 23 and A \to B \to D = 13\ldots.$ Not taken because the first path has more cost than the initial and the second path that already exists.

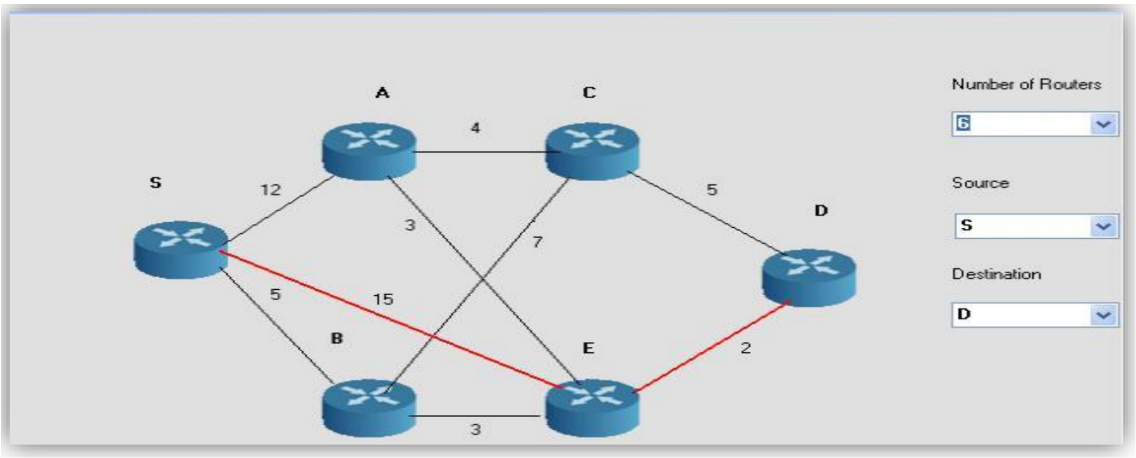
$A \to B \to F \to C \to D, A \to C \to\to B \to D \Rightarrow A \to B \to F \to C \to B \to D$ (loop in B), $A \to C \to D = 8$

The first path is not taken, but the second is taken for the reason that its cost is less than the other paths. Network's analysis clearly shows that no path less than $A \to C \to$ D can be produced which makes it an optimal path. The cost of the path is 10 which makes it an optimal path using RGA approach as in (Figure 6). Whereas using RIP approach, path cost is 17 which makes it not an optimal solution (Figure 5).

4 RESEARCH QUESTIONS

In this research, several questions can arise. The questions at the moment are as follows:

- What is the best way for the network path to be represented?

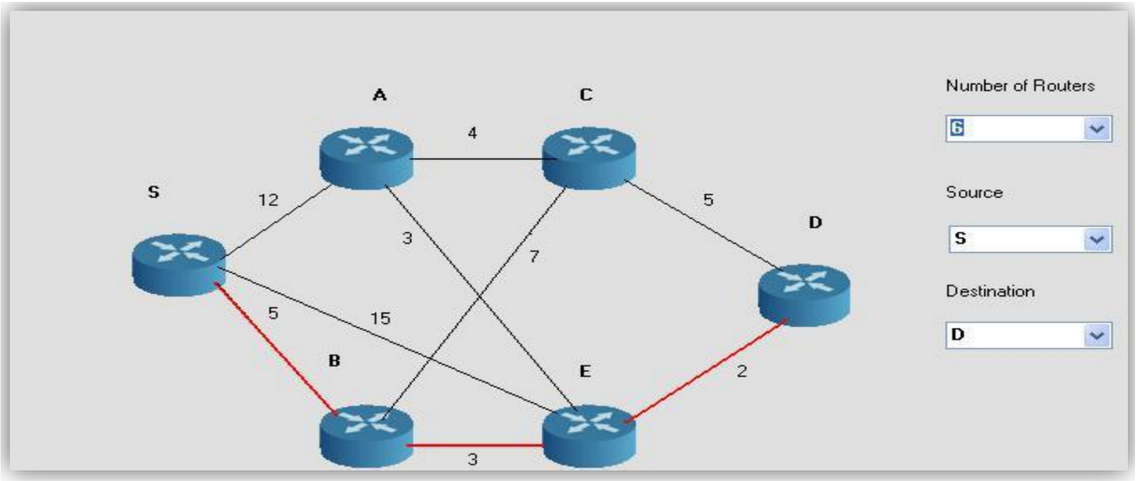


Number of Routers 6

Source S

Destination D

Figure 5: Finding Path using RIP



Number of Routers 6

Source S

Destination D

Figure 6: Finding Path using RGA

- How are new modifications proposed to produce good generations in the operations of the genetic algorithm?
- How can a good fitness function be established to assess the consistency (various route variables) of the generations (paths)?

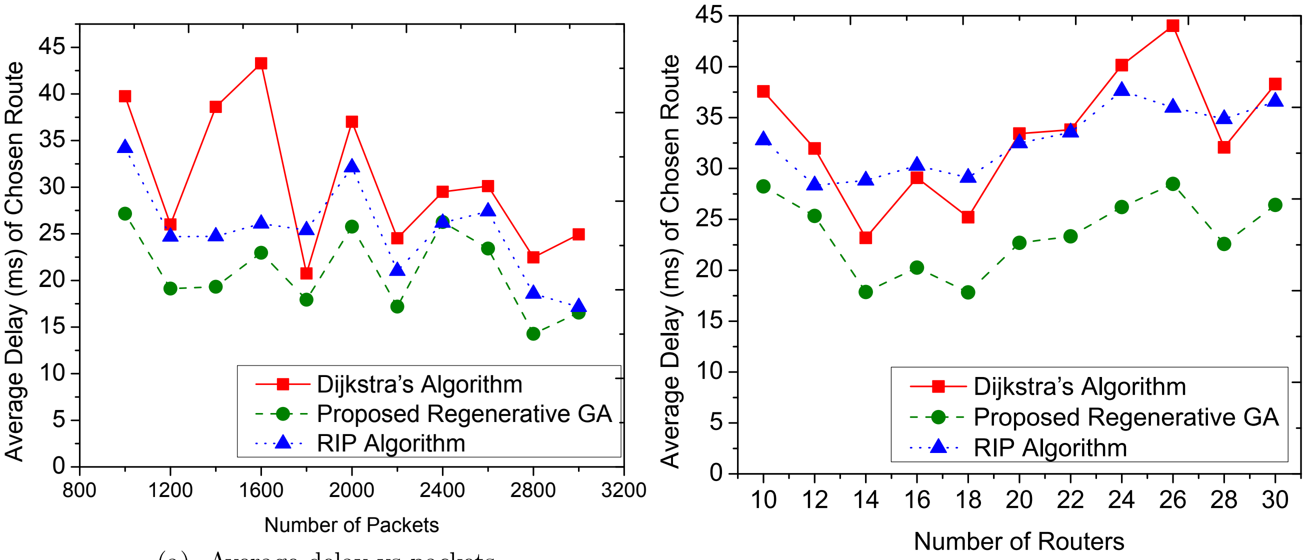
5 CLAIMED CONTRIBUTIONS

This research will prove beneficial to:

- Develop software to visualize the networks to implement the suggested algorithm.
- Compare the proposed algorithm with other routing protocols, such as RIP.
- Use genetic algorithms to build a new routing approach: always finding the optimum route in any network. The findings of this research are not limited. Rather, they will surpass the local aspects. Taking into account the distributed aspect, this research will play a vital role. The wide and genetic applications of the generic algorithms enhance its effectiveness.

6 Performance Evaluation

To comparatively evaluate the proposed regenerative GA solution for routing, we have developed a discrete-event custom-built python simulator. The simulation incorporates a various number of



(a) Average delay vs packets

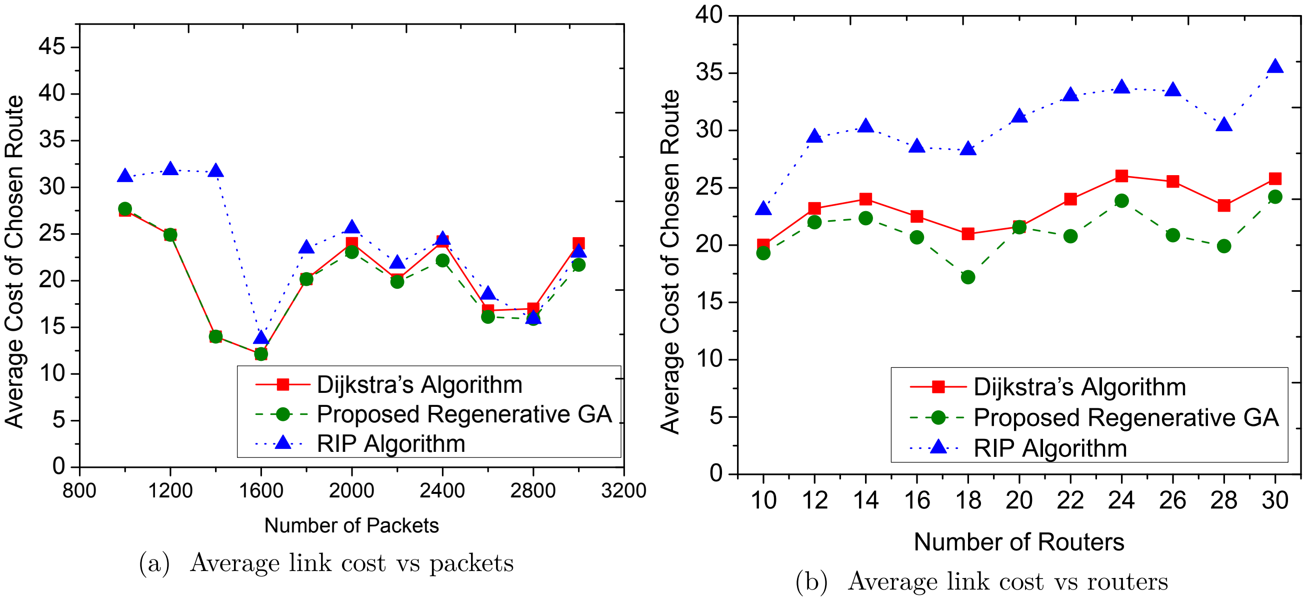
(b) Average delay vs routers

Figure 7: Link delay with packets and routers

routers from 10 to 30 with a step of 2 routers. Each router is assigned a link with other neighboring devices, where a link is represented by multiple parameters such as id, link cost (0 ∼ 50), link delay (0 ∼ 50 ms), and link connection speed (10 Mbps), etc. Moreover, we designed a separate class of packets where each packet has an id, source address, destination address, best path using RIP, best path using Dijkstra's, and best path using the proposed regenerative GA. Considering multiple routers in the system, for each packet, a random source and destination are chosen. A total of 1,000 ∼ 3,000 packets are generated for each evaluation, which sums up to an exhaustive amount of more than 50,000 packets. Nevertheless, our simulation performs an extensive search and finds all possible routes between source and destination without loops.

We have implemented the RIP algorithm that prefers shorter distance paths where the number of hops is minimal. Dijkstra's algorithm considers the minimum cost of the link as a routing metric. However, the proposed regenerative GA solution calculates the fitness function for each link/ route that relies on not only the cost of the link but also considers other parameters. First, the proposed scheme randomly selects an initial population from available solutions (that is routes between source and destinations). The solution set is mutated towards the Pareto front (set of possible optimal solutions) and with mutation (offspring of previous solutions) repetitively evaluates a set of constraints. If constraints are satisfied, the optimal route is provided as a solution for communication between the source and the destination. Once each routing scheme identifies its preferred route from the list of possible paths, the performance evaluation module calculates the delay and cost for each methodology. We have considered two metrics of average cost and average delay of 10,000 packets, for each scheme.

Figure 7 (a) shows the average delay of chosen route for three routing strategies (RIP, Dijkstra's, and the proposed scheme), with respect to the number of packets in the network. The proposed GA routing outperforms existing solutions due to the fact that it considers fitness function and optimizes with an iterative process. A random solution space is chosen at first, but with each iteration, the solution space reduces to the most optimal solution (which in this case is the optimal path). On the other hand, RIP chooses shorter paths which is also a way to reduce delay in packet transmission. However, Dijkstra's algorithm performs poorly because it considers only the cost metric that negatively impacts the communication delay. Figure 7 (b), corroborates our claims that with the increase in the number of routers which leads to more possible routes for iterative solutions, the proposed scheme performs better and reduces the delay as compared to existing schemes. The optimization of population and solution space removes the routes between source and destination which are against the GA algorithm's objectives. A minimization optimization problem in regenerative choose routes as best that have minimal cost and delay. Thus, the proposed scheme outperforms RIP and Dijkstra's algorithm. Figure 8 (a) illustrates interesting observations that the proposed scheme performs slightly better than



(a) Average link cost vs packets

(b) Average link cost vs routers

Figure 8: Link cost with packets and routers

Dijkstra's algorithm. Our GA routing selects the best routes with minimal link cost, however, it should also be noted that Dijkstra's algorithm also chooses routes with the lowest link cost. Nevertheless, the proposed scheme with an increase in the number of packets performs well ahead of the RIP and Dijkstra's algorithm. Figure 8 (b) highlights the relation of the number of routers in the network with the performance of routing schemes. It is quite obvious that the RIP performs worst than all because it considers the shortest distance, disregarding any other metric. The proposed regenerative GA selects routes that show optimal cost over than other two schemes. Over and all, our iterative solution finds the best possible path from a source to destination while reducing the delay and cost of communications. Moreover, the proposed GA demonstrates the lowest complexity of existing schemes.

7 Conclusion

In this article, we proposed to utilize regenerative GA to efficiently choose optimal routes that satisfy multiple constraints including reducing complexity, delay, and link cost. State-of-the-art evolutionary algorithms such as regenerative GA have myriads of applications in choosing optimal solutions, including autonomous vehicular networks, packet routing, decisions related to sorting and manufacturing in industry 4.0, and such. Our exhaustive evaluation includes two parts of performance evaluation and complexity analysis. For comparative evaluation, we simulated RIP, Dijkstra's algorithm, and the proposed scheme and identified that the proposed scheme reduces communication delay by 10 $\sim$ 15 ms. Moreover, with a variable number of packets and an increase in the number of routers, the proposed regenerative GA still outperforms existing solutions. Moreover, the proposed genetic algorithm has been compared with other routing algorithms such as Bellman Ford's Algorithm, Dijkstra's Algorithm, and Floyd Warshall's Algorithm. Bellman Ford's Algorithm depends on the concept that it has at most (n-1) edges and thus the path does not have a loop. This algorithm also suffers from time complexity O(V.E) in case E = V 2, O(V 3). The time complexity of Dijkstra's Algorithm is O(V 2). It reduces to O(V + ElogV) for the min-priority queue. Warshall's Algorithm calculates with O(V 3) for all the shortest distances between two vertices. The proposed algorithm overcomes all these time complexities efficiently.

We believe that the proposed scheme is the pivotal step towards improvement in the routing process using state-of-the-art evolutionary algorithms. Regenerative GA itself is a solution to traditional GA's problem of local optimal solution. However, there are still some limitations that needs to be addressed such as control overhead of information sharing. Almost all algorithms require information related to possible paths before making the routing decision, that incurs additional cost of message sharing. We believe that with advancements in the predictive methods, regenerative GA can be coupled with a learning scheme to overcome aforementioned limitation.

Conflict of interest

The authors declare no conflict of interest.

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