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Research paper

Comparative study of prim and genetic algorithms in minimum spanning tree and travelling salesman problem

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Abstract

Optimization is the essential thing in an algorithm. It can save the operational cost of an activity. At the Minimum Spanning Tree, the goal to be achieved is how all nodes are connected with the smallest weights. Several algorithms can calculate the use of weights in this graph. Genetic and Primary algorithms are two very popular algorithms for optimization. Prim calculates the weights based on the shortest distance from a graph. This algorithm eliminates the connected loop to minimize circuit. The nature of this algorithm is to trace all nodes to the smallest weights on a given graph. The genetic algorithm works by determining the random value as first initialization. This algorithm will perform selection, crossover, and mutation by the number of rounds specified. It is possible that this algorithm can not achieve the maximum value. The nature of the genetic algorithm is to work with probability. The results obtained are the most optimal results according to this algorithm. The results of this study indicate that the Prim is better than Genetics in determining the weights at the minimum spanning tree while Genetic algorithm is better for travelling salesman problem. Genetics will have maximum results when using large numbers of rotations and populations.

Keywords: *Prim; Genetic Algorithm; Minimum Spanning Tree; Artificial Intelligent.*

1. Introduction

Electricity is a significant resource [1]–[4] in the use of electronic devces. Speed and security are the essential things in the delivery of digital information [5]–[11]. Minimum spanning tree is a tree that connects between nodes of the result of minimizing the weights present in a complete graph. A graph is a mathematical representation of a fact that is related to distance [12]–[14]. This tree can be defined with a weighted graph. Directed graphs and non-directional graphs are subgraphs that each node is connected to one another. A graph can produce multiple ranges that have different weights [15]–[17] The smallest weights are the minimum spanning tree. The more branching in the tree, the more the different ranges. Weighting is done by choosing the smallest weights on each edge [18]–[20]. Each weight will be compared with the other weights that lead to the next node. The smallest weight is the most significant chance of choosing the next node. The minimum use of spanning tree is mostly done in real life. It is related to the cost of raw materials used to build a communication network. For example, to install fiber optic cables between buildings or cities requires proper optimization to avoid excessive use of cables [21]–[23]. If there are savings made in cable purchases, the budget used for the project is getting smaller. The economic principle says, the less material used, the less financial expenditure [24]–[32]. The following figure explains why a minimum spanning tree is required.

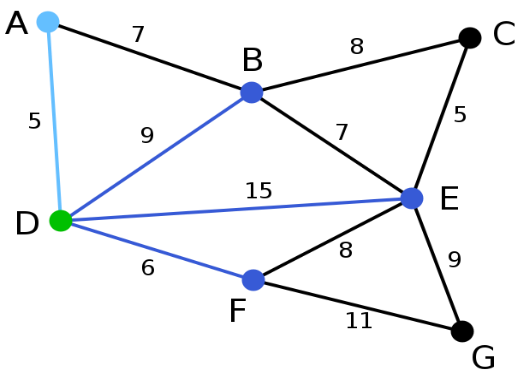

Fig. 1: Multiple Possible Spans.

Some opportunities can be made to connect "A" to "G." Several circuits occur in graph form in figure 1 [33]. In the simple graph, weights can be calculated manually. However, on a graph with a huge number of nodes, weights must be calculated by the computer. Genetic and Prim Algorithms can calculate the optimal weight used in a graph. Both of these algorithms have different techniques. The genetic algorithm uses a probability system to increase the minimum weight prediction while the Prim refers to the backtracking system on the minimum weight search [34]–[36]. The occurrence of backtracking due to a final condition is not fulfilled [37]. This study tries to compare the performance of both algorithms to see which algorithm is better to determine the minimum spanning tree in a graph.

2. Related works

2.1. Yumnah research

Yumnah conducted this research as a computer science thesis. This research is about Knapsack problem using the genetic algorithm. Genetic algorithms can optimize the needs based on the constrained weights [38][39]. In the Knapsack problem, not all nodes can be explored. Successfully visited nodes must match the specified criteria. Knapsack Problem has an essential role in limiting the number of nodes that must be neglected in the case of Travelling Salesman Problem. All nodes will be explored to get the most optimal value for a given generation. Knapsack is applied at least have two parameters to run correctly. Knapsack has two parameters, the number of nodes and the distance weight [40]. Optimization is done by calculating the distance weights to have the same value with the value of the proposed solution. The number of nodes affects how many coordinate points are visited. The optimal value of this problem depends on the technique performed on the mutation process. The dynamic mutation method aims to determine the value of mutation rate in each population [41][42]. The state of the population in each generation will affect the outcome of the genetic process. The author said that technique would approach the results of a generation approaching completion [43].
Population taking is determined on a sustained basis at this point. Testing is done by taking 30 nodes as a weighted graph form as shown in Figure 2. Knapsack problem will take ten nodes to be optimized with specific weights. Target is a goal that will be achieved in Knapsack problem. The fundamental difference to Knapsack is that nodes are captured not all of the existing nodes are different from the travelling salesman problem model. The number of nodes in Knapsack is determined based on the input weight. In a travelling salesman problem, all created nodes must be visited and returned to the initial node. Minimal distance is the optimal result obtained by using the genetic algorithm. The author tries to test ten nodes with weights of 400.

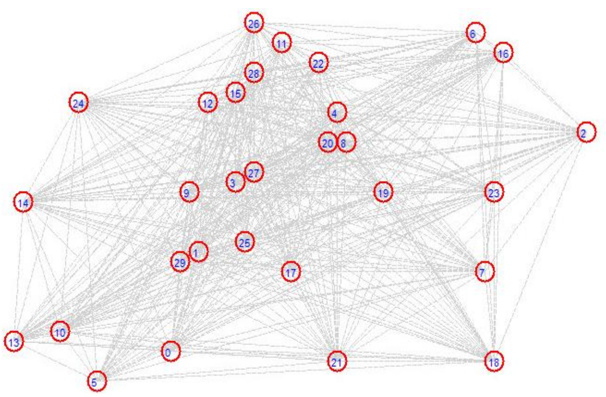

Fig. 2: Random Node.

Coordinate creation should not have the same value on the X-axis and the Y-axis at the same time. There should be no exact coordinates of value. Problems encountered if two nodes have the same coordinates is no movement on the nodes. However, this has a tiny chance because the generated value is a random value. If multiple nodes have the same value on either X axis or Y axis, it will not affect the process of Knapsack calculation [44].

Table 1: Random Populations

Population	N1	N2	N3	N4	N5	N6	N7	N8	N9	N10
0	22	8	12	4	13	3	14	11	26	10
1	4	29	0	18	22	26	12	14	23	27
2	1	4	22	16	10	8	19	6	20	28
3	19	16	1	27	13	14	9	21	8	7
4	24	7	4	26	15	16	3	1	20	17
5	15	28	21	8	18	19	14	25	24	3
6	15	5	23	27	19	16	28	3	2	8
7	15	24	3	14	2	25	28	26	0	21
8	3	16	15	2	12	23	26	21	7	25
9	28	14	23	5	21	17	12	7	3	27

Table 1 describes the formation of 10 generated populations obtained from the population generation process. Population from population 0 to 9 will be calculated for getting fitness value. Fitness that approaches the target has a greater chance to be a parent in the selection and mutation process.
Table 2 describes the calculation of ten generations produces the best value of Fitness = 1 where the target is obtained according to the desired target. The population that has the value of Fitness = 1 there are three among others Population [0], Population [5] and Population [8]. Trajectory in this population is as follows:
22 - 7 - 19 - 16 - 23 - 2 - 8 - 24 - 18 - 11 – 22

Table 2: Genetic Algorithm Result

Population	N1	N2	N3	N4	N5	N6	N7	N8	N9	N10
0	22	7	19	16	23	2	8	24	18	11
1	18	19	2	8	23	24	11	16	22	7
2	24	23	8	19	2	22	7	11	16	18
3	8	7	11	23	22	16	18	24	19	2
4	23	18	16	22	2	7	11	8	19	24
5	22	7	19	16	23	2	8	24	18	11
6	8	7	11	23	22	16	18	24	19	2
7	8	7	11	23	22	16	18	24	19	2
8	22	7	19	16	23	2	8	24	18	11
9	18	19	2	8	23	24	11	16	22	7

2.2. Muhammad Iqbal research

The study, titled "Prim's Algorithm for Optimizing Fiber Optic Trajectory Planning" discusses how to optimize fiber optic cabling. The price of the fiber optic cable is high, so it takes an algorithm that can determine the minimum length used for a particular area of the area. The author uses the Prim algorithm to perform the optimization process. Determining the number of cables manually is a difficult thing to do. The prim algorithm can help the analyst to determine the required cable length accurately. This algorithm works by calculating the minimum spanning tree in the area to be installed [45]. The algorithm also streamlines and accelerates the transmission of data from source to destination [21].
The researchers used 24 nodes in the minimum spanning tree track test. Some of the nodes are the circuit. A circuit is a condition where the nodes are connected in a circle. Several nodes are interconnected; it should be determined which node is shorter than others. Figure 3 is the sample of 24 nodes.

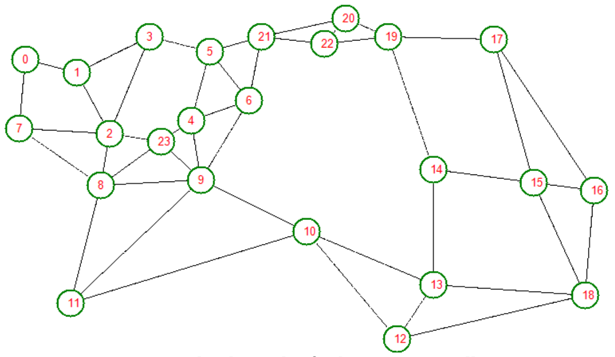

Fig. 3: Weighted Graph of Fiber Optic Installation.

Table 3 illustrates the location of the coordinates to which the fiber optic cable will be installed. Figure 4 is the result of the calculation of the Prim algorithm that produces the minimum spanning tree.

Table 3: Graph Coodinate

No.	X	Y	Branches
0	22	29	1, 7
1	39	34	0, 2, 3
2	50	58	1, 3, 7, 8, 23
3	63	20	1, 2, 5
4	77	53	5, 6, 9, 23
5	83	26	4, 6, 21
6	96	45	4, 5, 9, 21
7	20	56	0, 2, 8
8	47	78	2, 7, 9, 11, 23
9	80	76	4, 6, 8, 10, 11, 23
10	115	96	9, 11, 12, 13
11	37	124	8, 9, 10
12	145	138	10, 13, 18
13	157	117	10, 14, 18
14	157	72	13, 15, 19
15	190	77	14, 16, 17, 18
16	210	80	15, 17, 18
17	177	21	15, 16, 19
18	207	121	12, 13, 15, 16
19	142	20	14, 17, 20, 22
20	128	13	19, 21, 22
21	100	20	5, 6, 20, 22
22	121	23	19, 21
23	67	61	2, 4, 8, 9

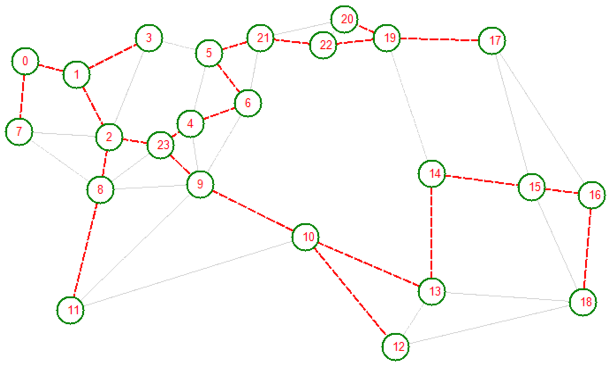

Fig. 4: Minimum Spanning Tree Result.

3. Methodology

This part is the design of graph formation. Some graph models will be created to test the ability of both algorithms in determining minimum spanning tree. The following image is the model graph used.

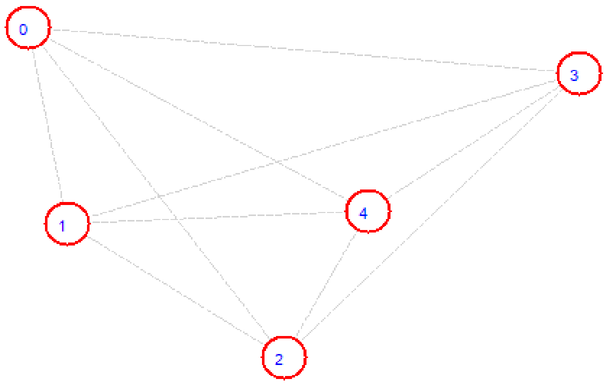

Fig. 5: Initial Graph Model.

Figure 5 describes five nodes connected to each other. Each node has different coordinate location as shown in the following table. Table 4 describes the position of the points described in Figure 5.

Table 4: Node Coordinate

Node	X	Y
0	38	29
1	46	76
2	90	108
3	150	40
4	107	73

4. Result and discussion

Each node has a certain distance from another node. The distance calculation is obtained by using Euclidean Distance. The following illustration is the distance of each node.

Coordinate [0] to Coordinate [1] = 47,68
Coordinate [0] to Coordinate [2] = 94,58
Coordinate [0] to Coordinate [3] = 112,54
Coordinate [0] to Coordinate [4] = 81,84
Coordinate [1] to Coordinate [0] = 47,68
Coordinate [1] to Coordinate [2] = 54,41
Coordinate [1] to Coordinate [3] = 110,05
Coordinate [1] to Coordinate [4] = 61,07
Coordinate [2] to Coordinate [1] = 54,41
Coordinate [2] to Coordinate [0] = 94,58
Coordinate [2] to Coordinate [3] = 90,69
Coordinate [2] to Coordinate [4] = 38,91
Coordinate [3] to Coordinate [1] = 110,05
Coordinate [3] to Coordinate [2] = 90,69
Coordinate [3] to Coordinate [0] = 112,54
Coordinate [3] to Coordinate [4] = 54,2
Coordinate [4] to Coordinate [1] = 61,07
Coordinate [4] to Coordinate [2] = 38,91
Coordinate [4] to Coordinate [3] = 54,2
Coordinate [4] to Coordinate [0] = 81,84

The earlier calculation shows the distance values between nodes shown in the following figure.

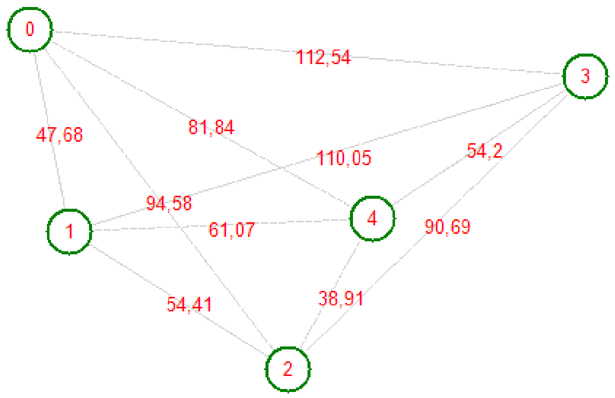

Fig. 6: Weighted Graph.

4.1. Genetic algorithm test

The test results using genetic algorithms always have different results on each test. It happens because the genetic algorithm uses random numbers as the population initialization and selection process. The random numbers generated are always different in each generation. Implementation of the genetic algorithm is not always successful. It needs multiple experiments to find the most optimal conditions. The following example is the first test using the genetic algorithm.

Inital Population

2	3	4	0	1
3	1	2	4	0
4	3	2	0	1
3	0	2	4	1
0	4	2	1	3

The test uses "Generation = 8" and "Population = 5". The final result can be seen in the following illustration.

Generation = 8

4	2	0	1	3
1	0	4	2	3
1	0	4	2	3
1	0	4	2	3
0	1	3	4	2

Fitness Calculation

Population [0]
Distance : 203
Fitness : 0,00505050505050505
Population [1]
Distance :215
Fitness:0,00537634408602151
Population [2]
Distance: 215
Fitness : 0,00537634408602151
Population [3]
Distance : 215
Fitness: 0,00537634408602151
Population [4]
Distance: 298
Fitness: 0,00970873786407767

Population After Selection

4	2	0	1	3
1	0	4	2	3
1	0	4	2	3
0	1	3	4	2
1	0	4	2	3

Population After Mutation

4	2	0	1	3
2	1	3	4	0
4	1	3	2	0
0	3	1	4	2
2	1	3	4	0

Fitness After Elitism

Population [0]
Distance: 203
Fitness: 0,00505050505050505
Population [1]
Distance: 299
Fitness :0,00980392156862745
Population [2]
Distance : 290
Fitness: 0,00900900900900901
Population [3]
Distance: 307
Fitness:0,0106382978723404
Population [4]
Distance : 299
Fitness : 0,00980392156862745

Population After Elitism

4	2	0	1	3
2	1	3	4	0
4	1	3	2	0
0	3	1	4	2
2	1	3	4	0

The last generation shows the most optimum results for the whole generation and population. It is visible from the displayed list. Population [0] is the best value of the five populations. The route obtained is "4-2-0-1-3" which has a distance of 203 as shown in the following figure.

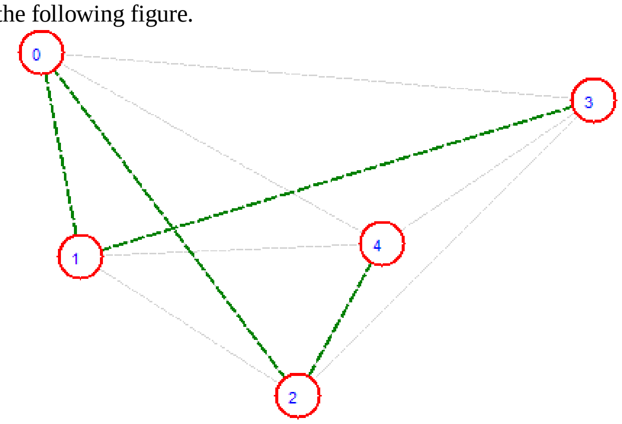

Fig. 7: Route of the First Test.

The following example is the second test using the genetic algorithm

Inital Population

3	1	0	4	2
3	1	0	4	2
2	4	3	0	1

The test uses "Generation = 3" and "Population = 3". The final result can be seen in the following illustration.

Generation = 6

4	1	0	2	3
0	2	4	1	3

0	2	4	1	3

Fitness Calculation

Population [0]
Distance: 207
Fitness:0,005154639175257773
Population [1]
Distance: 217
Fitness: 0,005434782608695650
Population [2]
Distance: 217
Fitness: 0,005434782608695650

Population After Selection

4	1	0	2	3
0	2	4	1	3
4	1	0	2	3

Population After Mutation

4	1	0	2	3
1	2	3	4	0
1	3	0	2	4

Fitness After Elitism

Population [0]
Distance :207
Fitness :0,005154639175257773
Population [1]
Distance :296
Fitness :0,009523809523809520
Population [2]
Distance :282
Fitness :0,008403361344537810

Population After Elitism

4	1	0	2	3
1	2	3	4	0
1	3	0	2	4

The last generation shows the most optimum results for the whole generation and population. It is visible from the displayed list. Population [0] is the best value of the five populations. The route obtained is "4-1-0-2-3" which has a distance of 207 as shown in the following figure. There are slightly different routes in the first and second experiments. In the first experiment, the route traversed was "4-2-0-1-3" while in the second experiment, the route traversed was "4-1-0-2-3".

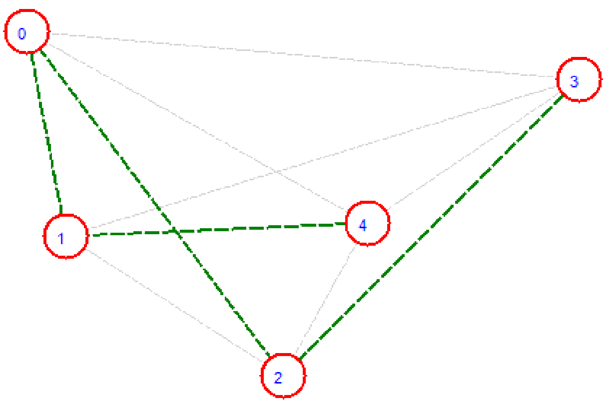

Fig. 8: Route of the Second Test.

The following example is the third test using the genetic algorithm Inital Population

4	1	0	2	3
2	0	3	4	1
2	3	1	0	4
4	2	0	1	3
1	3	0	2	4
4	2	1	0	3
1	0	3	4	2
3	2	4	1	0
4	2	1	0	3
1	2	0	3	4

The test uses "Generation = 20" and "Population = 10". The final result can be seen in the following illustration.

Generation = 6

3	1	0	2	4
2	1	0	4	3
4	3	2	0	1
3	0	4	1	2
3	0	2	1	4
3	4	1	0	2
4	3	2	0	1
0	1	4	3	2
4	2	0	3	1
3	0	4	1	2

Fitness Calculation

Population [0]
Distance : 203
Fitness : 0,005050505050505050
Population [1]
Distance : 216
Fitness : 0,005405405405405410
Population [2]
Distance : 277
Fitness : 0,008064516129032260
Population [3]
Distance : 225
Fitness : 0,005681818181818180
Population [4]
Distance :210
Fitness :0,005235602094240840
Population [5]
Distance : 211
Fitness : 0,005263157894736840
Population [6]
Distance : 277
Fitness : 0,008064516129032260
Population [7]
Distance : 302
Fitness : 0,010101010101010100
Population [8]
Distance : 282
Fitness : 0,008403361344537810
Population [9]
Distance :225
Fitness:0,005681818181818180

Population After Selection

3	1	0	2	4
4	3	2	0	1
3	0	4	1	2
2	1	0	4	3
4	2	0	3	1
3	4	1	0	2
0	1	4	3	2
4	2	0	3	1

4	3	2	0	1
4	3	2	0	1

Population After Mutation

3	1	0	2	4
0	3	2	4	1
3	2	0	1	4
3	1	2	4	0
4	3	2	1	0
0	1	4	3	2
0	4	1	2	3
4	3	2	1	0
3	2	1	0	4
3	2	1	0	4

Fitness After Elitism

Population [0]
Distance:203
Fitness :0,00505050505050505
Population [1]
Distance :304
Fitness :0,0103092783505155
Population [2]
Distance :207
Fitness :0,00515463917525773
Population [3]
Distance :222
Fitness :0,00558659217877095
Population [4]
Distance :292
Fitness :0,00917431192660551
Population [5]
Distance :302
Fitness :0,0101010101010101
Population [6]
Distance :226
Fitness :0,00571428571428571
Population [7]
Distance :292
Fitness :0,00917431192660551
Population [8]
Distance :212
Fitness :0,00529100529100529
Population [9]
Distance :212
Fitness : 0,00529100529100529

Population After Elitism

3	1	0	2	4
0	3	2	4	1
3	2	0	1	4
3	1	2	4	0
4	3	2	1	0
0	1	4	3	2
0	4	1	2	3
4	3	2	1	0
3	2	1	0	4
3	2	1	0	4

The last generation shows the most optimum results for the whole generation and population. It is visible from the displayed list. Population [0] is the best value of the five populations. The route obtained is “3-1-0-2-4” which has a distance of 203 as shown in the following figure. There are slightly different routes in the first, second and last experiments. In the first experiment, the route traversed was “4-2-0-1-3” while in the second experiment, the route traversed was “4-1-0-2-3”, and the third is “3-1-0-2-4”. There is no difference of route on first and third try. The results of these two experiments show that the optimum distance is 203. However, both have differences at the beginning of the end of the route. It means that the most optimum value for a genetic algorithm can generate is 203. Although "Generation" and "Population" are extended to infinity, this will not create a more optimum value anymore.

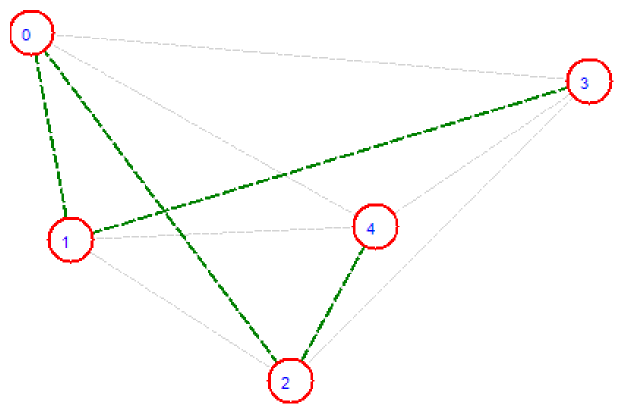

Fig. 9: Route of the Third Test

4.2. Prim algorithm test

This algorithm works greedily. If there are several nodes as an alternative, then the selected node is the shortest node from the beginning.

Table 5: Distance of Each Node

	N1	N2	N3	N4	N5
N1	0	47.68	94.58	112.54	81.84
N2	47.68	0	54.41	110.05	61.07
N3	94.58	54.41	0	90.69	38.91
N4	112.54	110.05	90.69	0	54.2
N5	81.84	61.07	38.91	54.2	0

The following table is the result of the calculation of Prim algorithm. The trip was made from N1 to N5. In N1, four possible nodes are the next destination. Each node will be compared where the distance of the node is the shortest from the beginning; the node is the next selected trip.

Table 6: Prim Algorithm Test Result

N1	0	N2 N3	47.68 94.58	47.68	N2
		N4 N5	112.54 81.84		
N2	0	N3 N4 N5	54.41 110.05 61.07	54.41	N3
N3	0	N4 N5	90.69 38.91	38.91	N5
N5	0	N4	54.2	54.2	N4

The following figure is the result of graph formation based on the results obtained in the previous calculation.

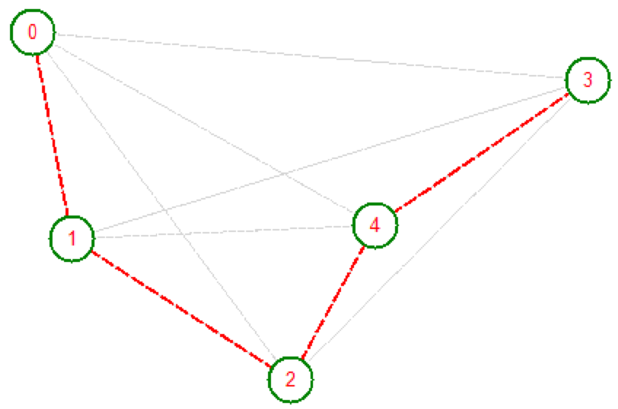

Fig. 10: Route of Prim Algorithm Test.

5. Conclusion

Prim and Genetic Algorithms can be used to optimize minimum spanning tree and travelling salesman problem. The fundamental difference is that the genetic algorithm cannot find the smallest distance as the Prim algorithm does. Another weakness of genetic algorithm is that crossover process cannot be done without changing the exchange system between parent and child. The genetic algorithm also can not do branching on the node as Prim does. It can determine the minimum weight of spanning tree maximal. This algorithm can also be used in the case of travelling salesman problems, but this requires little modification to route back to the starting point. The second test of this algorithm states that the Prim algorithm is better than Genetic algorithm because the minimum spanning tree process is a definite case. Genetic algorithms are better used for large cases that can not be done with brute-force techniques.

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