

A Genetic Algorithm with Best Combination Operator for the Traveling Salesman Problem

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Abstract—In this research, we propose a genetic algorithm with best combination operator ($BC_{x,y}O$) for the traveling salesman problem. The idea of best combination operator is to find the best combination of some disjoint sub-solutions (also the reverse of sub-solutions) from some known solutions. We use $BC_{2,1}O$ together with a genetic algorithm. The proposed genetic algorithm uses the swap mutation operator and elitism replacement with filtration for faster computational time. We compare the performances of GA (genetic algorithm without $BC_{2,1}O$), $IABC_{2,1}O$ (iterative approach of $BC_{2,1}O$), and $GABC_{2,1}O$ (genetic algorithm with $BC_{2,1}O$). We have tested GA, $IABC_{2,1}O$, and $GABC_{2,1}O$ three times and pick the best solution on 50 problems from TSPLIB. From those 50 problems, the average of the accuracy from GA, $IABC_{2,1}O$, and $GABC_{2,1}O$ are 65.12%, 94.21%, and 99.82% respectively.

Index Terms—Traveling salesman problem, genetic algorithm, operator, best combination.

I. INTRODUCTION

THE traveling salesman problem is a famous combinatorial problem which has been studied by many researchers. TSP has many applications in vehicle routing problem [1], transport routes optimization [2], air logistics [3], chemical shipping [4], bioinformatics [5], and many others.

There are a lot of methods that had been developed to solve the TSP. The easiest one is the nearest neighbor algorithm (always choose the next closest node). The nearest neighbor algorithm usually produce a sub-optimal route (except in trivial cases). Dynamic programming algorithm can find an optimal solution for small TSP. The idea is that in an optimal solution, the path through the remaining subset must be optimal [6], [7]. Lin-Kernighan heuristic algorithm makes a great improvement in the quality of solutions provided by another heuristic methods [6], [8]. Heuristic algorithms are often used because they are able to provide solutions in a faster time [9].

Population-based algorithms, such as genetic algorithms [10], are also widely used today. These algorithms can obtain a better solution than heuristic algorithms. Usually these algorithms use certain operators to get new solutions from existing solutions.

In this research, we propose a genetic algorithm with best combination operator ($BC_{x,y}O$) for the traveling salesman problem.

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II. THE TRAVELING SALESMAN PROBLEM

Suppose there are some nodes that are labeled by $1, 2, \dots, n$ and $d_{i,j}$ represents the distance from node i to node j . In general, the distance can be obtained from traveling time, traveling distance, traveling cost, Euclidean distance, or other relations. The objective of the traveling salesman problem (TSP) is to find the shortest route that visits each node exactly ones and returns to the origin city.

A solution of a TSP can be written as a permutation $p_1 p_2 \dots p_n$ of the elements $1, 2, \dots, n$. The distance of $p_1 p_2 \dots p_n$ is calculated by

$$\sum_{i=1}^n d_{p_i, p_{i+1}} \quad (1)$$

where $p_{n+1} = p_1$ and $d_{p_i, p_{i+1}}$ is the distance from node p_i to node p_{i+1} .

In this research, we focus on symmetric TSP, i.e. the distance from node i to node j is equal to the distance from node j to node i .

A. TSPLIB

Gerhard Reinelt published the TSPLIB in 1991 [11]. It is a collection of benchmark instances of varying difficulty, which has been used by many research groups for comparing results.

For a TSP with EUC_2D type, d_{ij} is calculated by

$$d_{ij} = \left\lfloor \sqrt{(x_i - x_j)^2 + (y_i - y_j)^2 + 0.5} \right\rfloor \quad (2)$$

where $\lfloor x \rfloor$ is floor function.

The remaining types of TSP in TSPLIB and how to calculate the distances, can be read in [11], [9].

III. BEST COMBINATION OPERATOR

The idea of best combination operator is to find the best combination of some disjoint sub-solutions (also the reverse of sub-solutions) from some known solutions. We introduce an abbreviation $BC_{x,y}O$, where $x \geq 2$ and $y \geq 1$, to represent the best combination of x disjoint sub-solutions from y known solutions. It is the general form of best combination operator. The simplest one is $BC_{2,1}O$.

A. Example of $BC_{2,1}O$

Suppose that there is a TSP consisting of $n = 6$ nodes, and the node coordinates are shown in TABLE I and Fig. 1.

TABLE I: The coordinates of the nodes

i	x_i	y_i
1	0	10
2	10	10
3	20	10
4	20	0
5	10	0
6	0	0



Fig. 1: The coordinates of the nodes

From those coordinates, we can use (2) to obtain the following distance matrix

$$D = \begin{pmatrix} 0 & 10 & 20 & 22 & 14 & 10 \\ 10 & 0 & 10 & 14 & 10 & 14 \\ 20 & 10 & 0 & 10 & 14 & 22 \\ 22 & 14 & 10 & 0 & 10 & 20 \\ 14 & 10 & 14 & 10 & 0 & 10 \\ 10 & 14 & 22 & 20 & 10 & 0 \end{pmatrix} \quad (3)$$

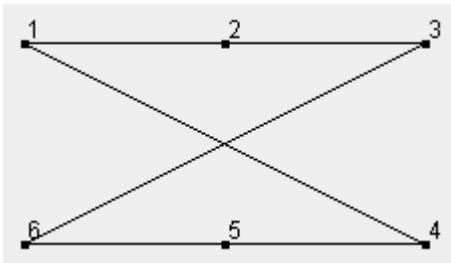


Fig. 2: Example of TSP solution

Suppose that 123654 is a random solution for the TSP. Using (1), the distance of this solution is equal to 84. First, we take all sub-solutions of length 2, 3, or 4 from 123654 as shown in Table II. The reverse of those sub-solutions are shown in Table III.

TABLE II: Sub-solutions of 123654

Sub-solution of		
length 2	length 3	length 4
12	123	1236
23	236	2365
36	365	3654
65	654	6541
54	541	5412
41	412	4123

To obtain different solutions from the initial solution, we search pairs of two disjoint sub-solutions from Table II and Table III.

TABLE III: The reverse of sub-solutions of 123654

The reverse of sub-solution of		
length 2	length 3	length 4
21	321	6321
32	632	5632
63	563	4563
56	456	1456
45	145	2145
14	214	3214

TABLE IV: Pairs of two disjoint sub-solutions and the new solutions

Sub-solution from		New Solution
Table II	Table III	
12	4563	124563
23	1456	231456
36	2145	362145
65	3214	653214
54	6321	546321
41	5632	415632
123	456	123456
236	145	236145
365	214	365214
654	321	654321
541	632	541632
412	563	412563
1236	45	123645
2365	14	236514
3654	21	365421
6541	32	654132
5412	63	541263
4123	56	412356

Since we focus on symmetric TSP, there is some equal new solutions in Table IV, i.e. 124563 is equal to 365421, 123456 is equal to 654321, and so on. If we remove unnecessary solutions, and then count the distance of the remaining solutions, we will get results as shown in Table V. Because the best solution is 123456, we pick it as a new solution. Its distance is equal to 60.

This is an example of $BC_{2,1}O$. We can use $BC_{x,y}O$ for two or more solutions using similar steps as before.

B. $BC_{2,1}O$ Simplification

We can make a simplification for $BC_{2,1}O$. The purpose of the simplification is to reduce the computational time. We write again the solutions listed in Table V. It is easy to see the difference between the initial solution and new solutions in Table VI. The second and third column have same solutions, we just change the starting node and the direction.

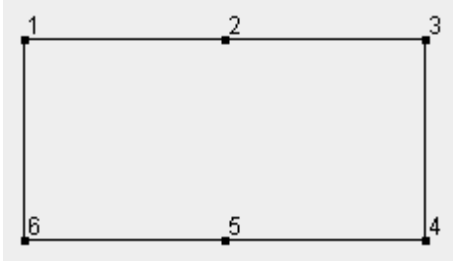
The first six new solutions are obtained by reversing a sub-solutions of length 2. The remaining three new solutions are obtained by reversing sub-solutions of length 3.

From Table IV, V, and VI, it can be seen that we will get all of the different new solutions by reversing a sub-solutions of length 2 and 3. If we have a TSP with n nodes, then we need to reverse sub-solutions of length 2, 3, ..., and $n/2$.

Suppose that there is a solution $p_1 p_2 \dots p_n$ and its distance is x . If we reverse the order of $p_i p_{i+1} \dots p_{j-1} p_j$, in $p_1 p_2 \dots p_n$, we will get

TABLE V: The new solutions

Solution	Distance
124563	86
231456	86
362145	92
653214	86
546321	86
415632	92
123456	60
236145	84
365214	84


 Fig. 3: New solution obtained by $BC_{2,1}O$

$$p_1 p_2 \dots p_{i-1} p_j p_{j-1} \dots p_{i+1} p_i p_{j+1} \dots p_n$$

and its distance is equal to

$$x - d_{p_{i-1}, p_i} - d_{p_j, p_{j+1}} + d_{p_{i-1}, p_j} + d_{p_i, p_{j+1}} \quad (4)$$

Using this simplification, the objective of $BC_{2,1}O$ is to find the best i and j so that the value obtained by (4) is as small as possible. The pseudocode of $BC_{2,1}O$ can be seen in Algorithm 1.

C. Iterative Approach of $BC_{2,1}O$

After we get a new solution from $BC_{2,1}O$, we can apply the same process again to the new solution. That operator can be used iteratively until there is no further improvement. The initial solution can be any random permutation. Usually, we will get different final solutions if the initial solutions are not equal.

D. Proposed Genetic Algorithm

It is not enough to solve the traveling salesman problem only using $BC_{2,1}O$ or the iterative approach, so we use the help of a genetic algorithm. The proposed genetic algorithm uses the swap mutation operator and elitism replacement with filtration for faster computational time.

Suppose that there is a solution $p_1 p_2 \dots p_n$ and random different values i and j , where $i, j \in \{1, 2, \dots, n\}$. The swap mutation is done by swapping the position of p_i and p_j , i.e. if the initial solution is $p_1 p_2 \dots p_{i-1} p_i p_{i+1} \dots p_{j-1} p_j p_{j+1} \dots p_n$, then the new solution is $p_1 p_2 \dots p_{i-1} p_j p_{i+1} \dots p_{j-1} p_i p_{j+1} \dots p_n$. In this research, every solution in the population is mutated to produce a new solution.

To get N solutions for a new population, where N is the size of the population, we use elitism replacement with filtration. First, we put together N solutions from the initial population

TABLE VI: The initial and new solutions

Initial Solution	New Solution	
123654	124563	213654
	231456	132654
	362145	126354
	653214	123564
	546321	123645
	415632	423651
	123456	123456
	236145	523614
	365214	143652

```

input :  $n$  (the number of nodes),
           $p_1 p_2 \dots p_n$  (a solution)
output:  $p_1 p_2 \dots p_n$  (new solution)

1 for  $i \leftarrow 2$  to  $n/2$  do
2   for  $j \leftarrow 1$  to  $n$  do
3      $a \leftarrow (j-1+n) \bmod n$ ;
4      $b \leftarrow j$ ;
5      $c \leftarrow (j+i-1) \bmod n$ ;
6      $d \leftarrow (j+i) \bmod n$ ;
7      $e \leftarrow p_a$ ;
8      $f \leftarrow p_b$ ;
9      $g \leftarrow p_c$ ;
10     $h \leftarrow p_d$ ;
11     $s_{i,j} \leftarrow -d_{e,f} - d_{g,h} + d_{e,g} + d_{f,h}$ ;
12  end
13 end
14  $(i, j) \leftarrow \text{IndexOfMinimumElement}(s)$ ;
15  $q_1 q_2 \dots q_n \leftarrow p_1 p_2 \dots p_n$ ;
16 for  $k \leftarrow 2$  to  $i/2$  do
17    $a \leftarrow (j+k) \bmod n$ ;
18    $b \leftarrow (j+i-k-1) \bmod n$ ;
19    $c \leftarrow q_a$ ;
20    $q_a \leftarrow q_b$ ;
21    $q_b \leftarrow c$ ;
22 end
23  $p_1 p_2 \dots p_n \leftarrow q_1 q_2 \dots q_n$ ;
    
```

Algorithm 1: Pseudocode of $BC_{2,1}O$

and N new solutions obtained by swap mutation. If there are two identical solutions in the population, we pick one of them and remove the other one. With these steps, it can be guaranteed that all solutions are different. Then, we sort them according to their distance. And then we pick N best solutions for the new population.

There are two stopping conditions used in this research. The first one, GA will stop if he has found the optimal solution. We can use this stopping condition because of the optimal solution of every problem in TSPLIB is known. The second one, GA will stop if the maximum computational time is reached. The maximum computational time used in this research is 100 seconds.

You can access the source code used in this research freely on <https://github.com/mlshahab/gabcotsp>.

```

input :  $N$  (the size of population),
          $P$  (initial population),
          $p^i$  ( $i$ -th solution in  $P$ ),
          $q$  (optimum solution)
output:  $P$  (new population)

1  $p^* \leftarrow \text{Fittest}(P)$  ;
2 while  $p^* \neq q$  and  $\text{time} < 100$  do
3    $Q \leftarrow P$  ;
4   for  $i \leftarrow 1$  to  $N$  do
5      $a \leftarrow \text{Mutate}(p^i)$  ;
6      $\text{Add}(Q, a)$  ;
7   end
8    $\text{Sort}(Q)$  ;
9    $R$  (new empty population) ;
10   $n \leftarrow 1$  ;
11   $\text{Add}(R, q^n)$  ;
12   $i \leftarrow 2$  ;
13  while  $n < N$  do
14    if  $q^i \neq r^n$  then
15       $n \leftarrow n + 1$  ;
16       $\text{Add}(R, q^n)$  ;
17    end
18     $i \leftarrow i + 1$  ;
19  end
20  for  $i \leftarrow 1$  to  $N$  do
21    if  $\text{CanBeImproved}(r^i)$  then
22       $r^i \leftarrow \text{BC}_{2,1}\text{O}(r^i)$  ;
23    end
24  end
25   $P \leftarrow R$  ;
26   $p^* \leftarrow \text{Fittest}(P)$  ;
27 end

```

Algorithm 2: Pseudocode of The Genetic Algorithm with $\text{BC}_{2,1}\text{O}$

IV. RESULTS AND DISCUSSIONS

In this research, we use 50 problems from TSPLIB. The smallest one is burma14 that has 14 nodes and the biggest one is gr202 that has 202 nodes. We compare the performances of GA (genetic algorithm without $\text{BC}_{2,1}\text{O}$), $\text{IABC}_{2,1}\text{O}$ (iterative approach of $\text{BC}_{2,1}\text{O}$), and $\text{GABC}_{2,1}\text{O}$ (genetic algorithm with $\text{BC}_{2,1}\text{O}$). For $\text{IABC}_{2,1}\text{O}$, we use $12 \dots n$ as its initial solution. For GA and $\text{GABC}_{2,1}\text{O}$, the size of population used is 100.

For every problem, we test GA, $\text{IABC}_{2,1}\text{O}$, and $\text{GABC}_{2,1}\text{O}$ three times and pick the best solution (the solution with smallest distance). This test is done using the Java programming language on Netbeans IDE. The computer use an Intel I5 Processor and 4GB RAM.

We show the results of GA, $\text{IABC}_{2,1}\text{O}$, and $\text{GABC}_{2,1}\text{O}$ in TABLE VII. The first column is the name of the problem. The second column is the best known distance for the problem. It is available online on <http://elib.zib.de/pub/mp-testdata/tsp/tsplib/stsp-sol.html>. The third, fifth, and seventh column are the distance obtained by GA, $\text{IABC}_{2,1}\text{O}$, and $\text{GABC}_{2,1}\text{O}$ respectively. The fourth, sixth, and eighth column

are the accuracy of the distance obtained by GA, $\text{IABC}_{2,1}\text{O}$, and $\text{GABC}_{2,1}\text{O}$ respectively. The accuracy is calculated by

$$\left(1 - \frac{d_i - d_i^*}{d_i^*}\right) 100\% \quad (5)$$

where $1 \leq i \leq 50$, d_i is the distance of i -th problem obtained by GA, $\text{IABC}_{2,1}\text{O}$, or $\text{GABC}_{2,1}\text{O}$ and d_i^* is the best known distance of i -th problem.

From those 50 problems, the average of the accuracy from GA, $\text{IABC}_{2,1}\text{O}$, and $\text{GABC}_{2,1}\text{O}$ are 65.12%, 94.21%, 99.82% respectively. We can see that for every problem, the distance obtained by $\text{GABC}_{2,1}\text{O}$ is less than or equal to the distances obtained by GA and $\text{IABC}_{2,1}\text{O}$. It can also be seen in the table, the distances obtained by $\text{GABC}_{2,1}\text{O}$ are equal to the best known distances for 37 different problems.

V. CONCLUSIONS AND FUTURE WORKS

In this research, we proposed a genetic algorithm with $\text{BC}_{x,y}\text{O}$ for the traveling salesman problem. The idea of $\text{BC}_{x,y}\text{O}$ is to find the best combination of x disjoint sub-solutions (also the reverse of sub-solutions) from y known solutions.

In this research, we only use $\text{BC}_{2,1}\text{O}$. It is the simplest and the fastest one. It is still challenging to find $\text{BC}_{x,y}\text{O}$ simplification for $x \geq 3$ or $y \geq 2$. We are sure that better results will be obtained if we use bigger value of x and y .

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TABLE VII: The results of GA, IABC_{2,1}O, and GABC_{2,1}O

Problem	Best Known Distance	GA		IABC _{2,1} O		GABC _{2,1} O	
		Distance	Accuracy	Distance	Accuracy	Distance	Accuracy
burma14	3323	3323	100	3461	95.85	3323	100
ulysses16	6859	6859	100	7076	96.84	6859	100
gr17	2085	2090	99.76	2211	93.96	2085	100
gr21	2707	2707	100	2801	96.53	2707	100
ulysses22	7013	7013	100	7163	97.86	7013	100
gr24	1272	1272	100	1278	99.53	1272	100
fri26	937	959	97.65	937	100	937	100
bayg29	1610	1610	100	1686	95.28	1610	100
bays29	2020	2048	98.61	2108	95.64	2020	100
dantzig42	699	766	90.41	699	100	699	100
swiss42	1273	1390	90.81	1410	89.24	1273	100
att48	10628	10937	97.09	11045	96.08	10628	100
gr48	5046	5627	88.49	5278	95.4	5046	100
hk48	11461	12180	93.73	11718	97.76	11461	100
eil51	426	463	91.31	460	92.02	426	100
berlin52	7542	8297	89.99	8492	87.4	7542	100
brazil58	25395	29586	83.5	27397	92.12	25395	100
st70	675	765	86.67	712	94.52	675	100
eil76	538	602	88.1	587	90.89	538	100
pr76	108159	129164	80.58	121232	87.91	108159	100
gr96	55209	71200	71.04	58601	93.86	55209	100
rat99	1211	1503	75.89	1257	96.2	1211	100
kroA100	21282	29754	60.19	22926	92.28	21282	100
kroB100	22141	29938	64.78	24237	90.53	22141	100
kroC100	20749	28149	64.34	22773	90.25	20749	100
kroD100	21294	28303	67.08	23268	90.73	21294	100
kroE100	22068	33621	47.65	23401	93.96	22068	100
rd100	7910	9859	75.36	8607	91.19	7910	100
eil101	629	762	78.86	699	88.87	629	100
lin105	14379	21847	48.06	14962	95.95	14379	100
pr107	44303	77314	25.49	47706	92.32	44303	100
gr120	6942	9713	60.08	7475	92.32	6942	100
pr124	59030	106506	19.57	63234	92.88	59030	100
bier127	118282	156361	67.81	124191	95	119566	98.91
ch130	6110	8514	60.65	6524	93.22	6139	99.53
pr136	96772	151803	43.13	102668	93.91	97324	99.43
gr137	69853	111523	40.35	71883	97.09	69853	100
pr144	58537	115406	2.85	58812	99.53	58537	100
ch150	6528	9892	48.47	7037	92.2	6554	99.6
kroA150	26524	38934	53.21	28665	91.93	26620	99.64
kroB150	26130	42767	36.33	28289	91.74	26141	99.96
pr152	73682	185734	-52.08	77039	95.44	73826	99.8
u159	42080	66668	41.57	42981	97.86	42080	100
si175	21407	24354	86.23	21570	99.24	21414	99.97
brg180	1950	3840	3.08	1990	97.95	1950	100
rat195	2323	3754	38.4	2397	96.81	2347	98.97
d198	15780	26498	32.08	16692	94.22	15855	99.52
kroA200	29368	51289	25.36	31231	93.66	29826	98.44
kroB200	29437	47128	39.9	31853	91.79	29929	98.33
gr202	40160	58869	53.41	43012	92.9	40555	99.02