

Genetic Algorithm to Optimize Routing Problem Modelled As the Travelling Salesman Problem

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#### ABSTRACT

This study presents genetic algorithm (GA) to solve routing problem modelled as the travelling salesman problem (TSP). Genetic algorithm conceptually follows steps inspired by the biological process of evolution. GA is following the ideas of "survival of the fittest" which meant better and better solution evolves from previous generations until a near optimal solution is obtained. In TSP, There are cities and distance given between the cities. The salesman needs to visit all the cities, but does not to travel so much. This study will use PCB component placement which is modelled as TSP. The objective is to find the sequence of the routing in order to minimize travelling distance. The GA with Roulette wheel selection, linear order crossover and inversion mutation is used in the study. The computational experiment was done using several randomly generated data with different GA parameter setting. The optimal distance obtains for 40 component placements is 8.9861 mm within 6.751 seconds .The results from the experiments show that GA used in this study is effective to solve PCB component placement which is modelled as TSP.

#### ABSTRAK

Kajian ini membentangkan algoritma genetik (GA) untuk menyelesaikan masalah laluan dimodelkan sebagai masalah jurujual kembara (TSP). Konsep algoritma genetic berikut adalah mengikut langkah-langkah yang diilhamkan oleh proses perkembangan biologi. GA mengikut idea-idea "yang kuat terus hidup" bermakna yang lebih baik dan penyelesaian yang lebih baik akan berkembang dari generasi yang sebelumnya sehingga memperolehi penyelesaian yang optimum atau hampir optimum. Dalam TSP, terdapat bandar-bandar dan juga jarak di antara bandar-bandar. Jurujual dikehendaki melawat semua bandar-bandar dengan perjalanan yang sedikit. Kajian ini akan menggunakan penempatan komponen pada PCB yang dimodelkan sebagai TSP. Tujuannya adalah untuk mencari urutan laluan dalam usaha untuk mengurangkan jarak perjalanan. Algoritma genetic dengan pemilihan roda Roulette, penyilangan perintah linear dan penyongsangan mutasi telah digunakan dalam kajian ini. Kajian ini dijalankan dengan menggunakan beberapa data yang dijanakan secara rawak dengan penetapan parameter GA yang berbeza. Jarak optimum yang diperolehi bagi 40 penempatan komponen adalah 8.9861 mm dalam masa 6.751 saat. Keputusan daripada eksperimen menunjukkan bahawa GA yang digunakan dalam kajian ini adalah berkesan untuk menyelesaikan penempatan komponen pada PCB yang dimodelkan sebagai TSP.

### TABLE OF CONTENTS

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CHAPTER	TITLE	PAGE
	SUPERVISOR'S DECLARATION	ii
	STUDENT DECLARATION	iii
	DEDICATED	iv
	ACKNOLEDGEMENTS	v
	ABSTRACT	vi
	ABSTRAK	vii
	TABLE OF CONTENTS	viii
	LIST OF TABLES	xi
	LIST OF FIGURES	xii
CHAPTER 1	INTRODUCTION	
1.1	BACKGROUND OF STUDY	1
1.2	PROBLEM STATEMENT	2
1.3	OBJECTIVES	2
1.4	SCOPE OF STUDY	2
1.5	METHODOLOGY OF STUDY	2
1.6	SUMMARY	3
CHAPTER 2	LITERATURE REVIEW	
2.1	INTRODUCTION	4
2.2	GENETIC ALGORTIHM	4
	2.2.1 Encoding	5
	2.2.2 Evolution	5

		2.2.3	Crossover	5		
		2.2.4	Mutation	5		
		2.2.5	Decoding	6		
	2.3	CHROMOSOME REPRESENTATION IN GA				
	,	2.3.1	Binary Representation	6		
		2.3.2	Path Representation	8		
	2.4	CHRO	MOSOME EVOLUTION & SELECTION	9		
		2.4.1	Evolution Process	9		
		2.4.2	Roulette Wheel Selection	10		
		2.4.3	Tournament Selection	11		
	2.5	CROS	SOVER MECHANISM	12		
		2.5.1	Order Crossover (OX)	12		
		2.5.2	Linear Order Crossover (LOX)	13		
		2.5.3	Partially Mapped Crossover (PMX)	14		
		2.5.4	Cycle Crossover (CX)	14		
	2.6	MUTA	TION MECHANISM	15		
		2.6.1	Inversion Mutation	15		
		2.6.2	Insertion Mutation	15		
		2.6.3	Displacement Mutation	16		
		2.6.4	Exchange Mutation	16		
	2.7	TRAV	ELLING SALESMAN PROBLEM	16		
	2.8	SIMPL	LE PROBLEM	17		
	2.9	GA IN	SEQUENCING ROUTING IN TSP	20		
	2.10	SUMM	IARY	21		
CHAPTE	R 3	MET	HODOLOGY			
	3.1	INTRO	DUCTION	22		
	3.2	PROJI	ECT FLOW CHART	23		
	3.3	GA PA	ARAMETER	24		
	3.4	GA M	ETHOD	24		
		3.4.1	Initialization and Representation	24		
		3.4.2	Selection	25		
		3.4.3	GA Operators	25		
			•			

	3.4.4	Termination	26
3.5	GENE	RAL PROCESS OF GA	26
3.6	PROC	ESS FLOW OF GA FOR TSP	27
3.7	COMF	PANY VISIT	28
3.8	TOOL		28
3.9	SUMN	1ARY	28
CHAPTER 4	RESU	LTS AND DISCUSSION	
4.1	INTRO	DUCTION	29
4.2	CASE	STUDY: K. E. MANUFACTURING SDN. BHD.	29
	4.2.1	SMT Machine	29
	4.2.2	Component Placement Process	30
4.3	EXPE	RIMENT SETUP	33
	4.3.1	Control Parameters	34
	4.3.2	Computational Experiments	35
4.4	RESUI	LT AND DISCUSSION	35
	4.4.1	1 <sup>st</sup> Ran of GA Program	36
	4.4.2	2 <sup>nd</sup> Run of GA Program (variable rate of crossover)	37
	4.4.3	3 <sup>rd</sup> Run of GA Program (variable rate of mutation)	38
	4.4.4	4 <sup>th</sup> Run of GA Program (variable rate of pop_size)	39
	4.4.5	5 <sup>th</sup> Run of GA Program (variable rate of max gene)	40
CHAPTER 5	CONC	LUSION AND RECOMMENDATION	
5.1	INTRC	DUCTION	41
5.2	SUMM	IARY AND CONCLUSION	41
5.3	RECO	MMENDATION	42
REFERENCES			43
APPENDIX			
Α	Gantt C	Chart of The Project	44

**B**Example of Programming Code44

### LIST OF TABLE

.

TABLE NO.	TITLE	PAGE
2.1	Binary Number Representation	8
2.1	The Initial Randomly Generated Population	19
	Of Chromosome	
4.1	GA Parameters Explanation	34
4.2	GA Parameters Setup	35

### LIST OF FIGURE

FIGURE NO.	TITLE	PAGE
2.1	Example of Path Representation Problem	9
2.2	Illustration of Roulette Wheel	11
2.3	Roulette Wheel	20
3.1	Project Flow Chart	23
3.2	General Process of GA	26
3.3	Process Flow of GA for TSP	27
4.1	SMT Machine	30
4.2	SMT Solder Print Machine	31
4.3	Metal Mask	31
4.4	Bare PCB	31
4.5	PCB with Solder Printing	31
4.6	Solder Paste	31
4.7	SMT Placement Machine	32
4.8	Component Placed on PCB	32
4.9	Different Size of Nozzles	32
4.10	Reflow Oven	33
4.11	PCB after Reflow Process	33
4.12	1 <sup>st</sup> Run	36
4.13	2 <sup>nd</sup> Run	37
4.14	3 <sup>rd</sup> Run	38
4.15	4 <sup>th</sup> Run	39
4.16	5 <sup>th</sup> Run	40

### **CHAPTER 1**

### **INTRODUCTION**

### 1.1 BACKGROUND OF STUDY

The Traveling salesman problems (TSP) is one of the most widely studied problems in combinatorial optimization (Chatterjee *et. al*, 1995). The TSP idea is to find a tour of a given number of cities, visiting each city exactly once and returning to the starting city where the length of this tour is minimized. The travelling salesman problem (TSP) is an NP-hard problem in combinatorial optimization studied in operations research and theoretical computer science. This complexity can solve by given n is the number of cities to be visited, the total number of possible routes covering all cities can be given as a set of feasible solutions of the TSP and is given as (n-1)!/2.

The Genetic algorithms are relatively new optimization technique which can be applied to various problems, including those that are NP-hard. This genetic algorithms technique does not ensure an optimal solution, however it usually gives good come up in a reasonable amount of time. This, therefore, would be a good algorithm to try on the traveling salesman problem, one of the most famous NP-hard problems. Genetic algorithms are loosely based on natural evolution and use a "survival of the fittest" technique, where the best solutions survive and are varied until we get a good result.

The MATLAB is a tool which is used to develop a program for GAs which will be used to solve TSP. MATLAB is a special-purpose computer program optimized to perform engineering and scientific calculations. It is high-performance language for technical computing. MATLAB combine the computation, visualization, and programming in an easy-to-use environment where problems and solution are expressed in familiar mathematical notation.

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### **1.2 PROBLEM STATEMENTS**

Modern production factories, which want to obtain high profits, usually maximize their productivity. The latter goal can be achieved, among others, by optimal or almost optimal scheduling of jobs in the production process. The problem is to get the optimum result for routing distances same like TSP. This includes getting the shortest distance and time taken to visit all the cities and return back to original position. The constraint is there is no shorter way to solve the problem. Travelling salesman has to visit each city with different sequence and compare the result and choose the most optimum result. The genetic algorithm method is a one of the tools used to solve optimization problems. Remember in mind that the longer the distance taken will cause the more time taken to complete.

### **1.3 OBJECTIVES**

The objectives are:

- To find the optimum route that minimizes the travelling distance / cost / time.
- To develop TSP fitness function and to use GA programming to solve TSP.

### **1.4 SCOPES OF STUDY**

- To apply TSP concept using GA to one of the case study (real application in industry case).
- To use MATLAB to simulate and to solve problem.

### 1.5 METHODOLOGY OF STUDY

This study is conducted under three main steps. The first step is the literature review. In literature review, the previous method that used to solve routing problem

modelled as the travelling salesman problem and simulated to ensure the algorithm are working as reported in scientific literatures. Then, the existing algorithms limitations are identified.

From the previous limitations method, a new sequencing problem is developed as the purpose solution to optimize the routing problem. In order to prove that genetic algorithm was one of the methods that could solve routing distance problem, various kind of problem will be perform. The results of the performance will be analyst as the final step of this study.

### 1.7 SUMMARY

This chapter discussed about the project background such as the important of this routing distance optimization and study in other to know which type of algorithm that can be applied to a wide variety problem. It is also described the problem statement of this project, the important to the study, the objective, the scope of the project and the methodology of study.

### **CHAPTER 2**

### LITERATURE REVIEW

#### 2.1 INTRODUCTION

This chapter explains the study and methods that used to solve optimization problem such as Travelling Salesman Problems (TSP). There was also an explanation of the genetic algorithm (GA) method and the steps that need to follow to solve the problem using the GA method. At the end of this chapter, it is shown how the GA method can be used to get the optimum or near the optimum result for TSP.

### 2.2 GENETIC ALGORITHM

Genetic Algorithm (GA) is an optimization technique, based on natural evolution. It was introduced by John Holland in 1975 (Othman 2002). This technique copied the biological theory, where the concept of "survival of the fittest" exits. GA provides a method of searching which does not need to explore every possible solution in the feasible region to obtain a good result (Othman 2002).

In nature, the fittest individuals are most likely to survive and mate. Therefore the next generation should be fitter and healthier because they were raised from healthy parents. This same idea is applied to a problem by first "guessing" solution and then combining the fittest solutions to create a new generation. The genetic algorithm consist five steps, that is:

- 1. Encoding
- 2. Evaluation
- 3. Crossover

- 4. Mutation
- 5. Decoding

#### 2.2.1 Encoding

A suitable encoding is found for the solution to a problem so that each possible solution has a unique encoding and the encoding is some form of string. Many possible solution need to be encoded to create a population. The traditional way to represent a solution is with a string of zeroes (0) and ones (1). However genetic algorithms are not restricted to this encoding (Chatterjee et.al 1996).

#### 2.2.2 Evaluation

The fitness of each individual in the population is then computed; this is how well the individual fits the problem and whether it is near the optimum compared to other individuals in the population. This fitness is used to find the individual's probability of crossover. Evaluation function is used to decide how good a chromosome is. This function is also known as objective function (Bryant 2001).

### 2.2.3 Crossover

Crossover is where the two individuals are recombined to create new individuals which are copied into the new generation. Not every chromosome is used in crossover. The evaluation function gives each chromosome a 'score' which is used to decide the chromosome's probability of crossover. The crossover operator randomly chooses a crossover point where two parent chromosomes 'break' and then exchanges the chromosome parts after that point (Negnevitsky 2002).

### 2.2.4 Mutation

Mutation, which is rare in nature, represents a change in gene. It may lead to a significant improvement in fitness, but more often has rather more harmful results. Mutation is used to avoid getting trapped in a local optimum. The chromosome is

naturally near the local optimum and very far from the global optimum (possible solution) due to the randomness process. Some individuals are chosen randomly to be mutated and then a mutation point is randomly chosen. Mutation causes the character in the corresponding position of the string changed (Negnevitsky 2002).

### 2.2.5 Decoding

On all the four processes are done, a new generation has been formed and the process is repeated until some stopping criteria have been reached. At this point the individual who is closest to the optimum is decoded and the process is complete (Bryant 2000).

### 2.3 CHROMOSOME REPRESENTATION IN GA

In genetic algorithms, each individual that is a member of the population represents a potential solution to the problem. This solution information is coded in the associated chromosome of that individual. A chromosome is a string of *gene* positions, where each *gene* position holds an *allele* value that constitutes a part of the solution to the problem. Allele value at a gene position represents an element from a finite alphabet. This alphabet depends on the nature of the problem. There are number of possible chromosome representations, due to vast variety of problem types. However there are two representation types which are most commonly used: binary representation and path/permutation representation (Bryant 2000).

### 2.3.1 Binary Representation

In binary representation, the finite alphabet domain which allele at each gene position takes its value from is the set  $\{0, 1\}$ . An example of problem to minimize the function of,  $f(x) = 3x^3 + 4x^2 - 7x + 1$  over the integers in set  $\{0, 1, ..., 15\}$ . The binary number for the integer set was represented in **table 2.1**. The possible solution for the problem are obviously just numbers, so the representation is simple the binary form of each number. For example, the binary representation of 8 and 14 are 1000 and 1110

respectively. For initial chromosomes (1000 and 1110) which represent value 8 and 14, the evaluations are performing by calculating the fitness function above.

$$f(8) = 3(8^{3}) + 4(8^{2}) - 7(8) + 1$$
  
= 1737  
$$f(14) = 3(14^{3}) + 4(14^{2}) - 7(14) + 1$$
  
= 8919 (2-1)

Obviously 8 is better solution than 14 (since f(8) is lower than f(14)) and would therefore have a lower fitness. The initial chromosomes then are being regenerated by using simple crossover.

$$P1 = 1000$$
  
 $P2 = 1110$ 

Then the crossover point is randomly chosen. In this example, the crossover point is after the second gene.

$$P1 = 1000$$
  
 $P2 = 1110$ 

Therefore the new offspring are 10 and 12. This number will be evaluated as above. These procedures are continuous to evaluate and re-generate new offspring until a termination criteria is satisfied (Bjarnadottir 2004).

Real Number	Dec	imal to Bi	nary Equa	Binary Number	
$10^0 = 1$	$2^3 = 8$	2 <sup>2</sup> =4	21=2	20=1	-
0	0	0	0	0	0000
1	0	0	0	1	0001
2	0	0	1	0	0010
3	0	0	1	1	0011
4	0	1	0	0	0100
5	0	1	0	1	0101
6	0	1	1	0	0110
7	0	1	1	1	0111
8	1	0	0	0	1000

**Table 2.1**Binary number representation

9	1	0	0	1	1001
10	1	0	1	0	1010
11	1	0	- 1	1	1011
12	1	1	0	0	1100
13	1	1	0	1	1101
14	1	1	1	0	1110
15	1	1	1	1	1111

#### 2.3.2 Path Representation

The path representation also called permutation representation is probably the most natural representation of a TSP tour. In path representation, the n cities that should be visited are put in order according to a list of n elements, so that if the city i is the j element of the list, city i is the j city to be visited. This representation has allowed a great number of crossover and mutation operators to have been developed. In TSP, there are a number of cities, where each pair of cities has a corresponding distance. The aim is to visit all the cities such that the total distance travelled will be minimized. Obviously, a solution, and therefore a chromosome which represents that solution to the TSP, can be given as an order, that is, a permutation, of the cities (Bryant 2000).

For example, an assembly process which contained 6 processes  $\{1, 2, 3, 4, 5, 6\}$  is represent in **Figure 2.1** below.



Figure 2.1: Example of path representation problems

The distance of each station can be calculated through the given scale. Let assume that the assembly process can be performed in any order. The scheduler need to determine the optimal sequence which comes out with minimum traveling distance. The initial chromosomes, which represent sequence of process, are given as follows:

. 4	1	3	5	2	6
2	6	3	1	4	5

From the chromosomes above, evaluation of travelling distance is performed

$$D_{1} \Rightarrow 4 \rightarrow 1 \rightarrow 3 \rightarrow 5 \rightarrow 2 \rightarrow 6$$
  
=  $\sqrt{1^{2} + 4^{2}} + \sqrt{2^{2} + 3^{2}} + \sqrt{1^{2} + 3^{2}} + \sqrt{4^{2} + 4^{2}} + \sqrt{5^{2} + 1^{2}} = 21.46$   
$$D_{2} \Rightarrow 2 \rightarrow 6 \rightarrow 3 \rightarrow 1 \rightarrow 4 \rightarrow 5$$
  
=  $\sqrt{1^{2} + 5^{2}} + \sqrt{4^{2} + 4^{2}} + \sqrt{3^{2} + 2^{2}} + \sqrt{1^{2} + 4^{2}} + \sqrt{1^{2} + 1^{2}} = 19.9$  (2-2)

The evaluation above shows that the second chromosome P2 is better than P1 because of smaller total traveling distance. These chromosomes are then being regenerated by using crossover and mutation operators, which will be described later (Bryant 2000).

### 2.4 CHROMOSOME EVALUTION AND SELECTION

Chromosome evaluation and selection is a mechanism to select individual in population for reproduction to create new offspring or to transfer a part of the existing population to the next generation is need. It is possible to perform the task of selection completely in a randomized fashion. This selection mechanism will eventually cause the algorithm to reach global minimum/maximum (ARSLANOĞLU, Yılmaz, 2006).

### 2.4.1 Evolution Process

A fitness function evaluation is incorporated to assigns a value to each organism, noted as fi. This fi value is a figure of merit which is calculated by using

7

any domain knowledge that applies. In principle, this is the only point in the algorithm that domain knowledge is necessary. Organisms are chosen using the fitness value as a guide, where those with higher fitness values are chosen more often.

Selecting organisms based on fitness value is a major factor in the strength of GAs as search algorithms. The method employed here was to calculate the total Euclidean distance Di for each organism first, then compute fi by using the following equation

$$fi = Dmax - DI$$
 (2.3)

where Dmax is the longest Euclidean distance over organisms in the population (M. Melanie, 1996).

### 2.4.2 Roulette Wheel Selection

In keeping with the ideas of natural selection, we assume that stronger individuals, that is, those with higher fitness values, are more likely to mate than the weaker ones. One way to simulate this is to select parents with a probability that is directly proportional to their fitness values. This method is called the roulette wheel method (ARSLANOĞLU, Yılmaz, 2006).

$$Pi = Fi / \sum_{j=1}^{n} Fj$$
(2.4)

The idea behind the roulette wheel selection technique is that each individual is given a chance to become a parent in proportion to its fitness. The chances of selecting a parent can be seen as spinning a roulette wheel with the size of the slot for each parent being proportional to its fitness. Obviously, those with the largest fitness (slot sizes) have more chance of being chosen. Consider a roulette wheel with a number of slices on it, each of which has an associated width as shown in **Figure 2.2**.



Figure 2.2 Illustration of Roulette Wheel

If a ball is put on this wheel and the wheel is rotated, the ball will finally stop on one of the slices, most probably on one of the widest ones. However, all slices have a chance, with a probability that is proportional to its width. By repeating this each time an individual needs to be chosen, the better individuals will be chosen more often than the poorer ones, thus fulfilling the requirements of survival of the fittest. The basic advantage of roulette wheel selection is that it discards none of the individuals in the population and gives a chance to all of them to be selected. Therefore, diversity in the population is preserved (ARSLANOĞLU, Yılmaz, 2006)..

#### 2.4.3 Tournament Selection

In tournament selection technique, n individuals are selected from the larger population, and the selected individuals compete against each other. The individual with the highest fitness wins. The tournament selection also gives a chance to all individuals to be selected and thus it preserves diversity, although keeping diversity may degrade the convergence speed. The number of individuals competing in each tournament is referred to as tournament size, commonly set to 2 (binary tournament). For example, let consider the previous problem shown in Figure 2.2. In this problem, the population size is 6 and the chromosomes are given as follows:

4	1	3	5	2	6
2	6	3	1	4	5
3	2	1	5	4	6

5	4	2	1	6	3
5	1	4	3	2	6
2	3	5	6	1	4

Evaluations of chromosomes are being performed and the fitness values for chromosomes are:

$C1 \rightarrow D1 = 21.64$	$C4 \rightarrow D1 = 19.63$
$C2 \rightarrow D1 = 19.90$	$C5 \rightarrow D1 = 22.53$
$C3 \rightarrow D1 = 17.29$	$C6 \rightarrow D1 = 21.63$

For example, n = 3, means three chromosomes will randomly selected from population. Let assume C5, C1 and C4 are selected. From the fitness value of chromosomes, C4 gives the minimum value. Therefore C4 is selected and placed in "mating-pool". Then, random selection of three chromosomes is repeated until the number of chromosomes in "mating-pool" is enough to perform crossover and mutation. Advantages to tournament selection include efficient time complexity, no requirement for fitness scaling or sorting (ARSLANOĞLU, Yılmaz, 2006).

### 2.5 CROSSOVER MECHANISM

A simple crossover reproduction scheme does not work as it makes the chromosomes inconsistent i.e. some cities may be repeated while others are missed out. To avoid these several types of special crossover operators reported for permutation problems are selected to be examined and used in the proposed TSP system. They are: *order crossover* (OX), *linear order crossover* (LOX), *partially mapped crossover* (PMX), and *cycle crossover* (CX), as described briefly below.

### 2.5.1 Order Crossover (OX)

The order crossover was proposed by (Davis, 1985). To apply OX, two random cross points are selected. Alleles from parent1 that fall between the two cross points are copied into the same positions of the offspring. The remaining allele order is determined by parent2. Non duplicative alleles are copied from parent2 to the offspring beginning at the position following the second cross point. Both the parent2 and the offspring are traversed circularly from that point. A copy of the parent's next non duplicative allele is placed in the next available child position. Ordered two-point crossover is used when the problem is of order based, for example in U-shaped assembly line balancing etc. given two parent chromosomes, two random crossover points are selected partitioning them into a left, middle and right portion. The ordered two-point crossover behaves in a following way: Child 1 inherits its left and right section from parent 1, and its middle section is determined by the genes in the middle section of parent 1 in the order in which the values appear in parent 2. A similar process is applied to child 2. This is shown in example below.



#### 2.5.2 Linear Order Crossover (LOX)

Example:

The linear order crossover (LOX) is a modified version of the order crossover operator proposed by Falkenauer and Bouffix (1987). Recall that the order crossover operator treats the chromosome as a circular string, in which it wraps around from the end of the chromosome back to the beginning. This circular assumption may not play a big role in the TSP. As such, the LOX operator treats the chromosome as a linear entity. For this operator, the swap occurs in the same fashion as it occurs in the OX operator, but when sliding the parent values around to fit in the remaining open slots of the child chromosome, they are allowed to slide to the left or right. This allows the chromosome to maintain its relative ordering and at the same time preserve the beginning and ending values. In the below example, after the values are swapped, there are two open spaces in the front of the chromosome and three open spaces at the end. The algorithm then goes through Parent 1 and finds the first two values that were not part of the swap, in this example they are 5 and 4. These values are shifted left to fill the first two chromosome locations. The final three locations are filled in a similar manner.



# 2.5.3 Partially Mapped Crossover (PMX)

The partially mapped crossover was suggested by Goldberg and Lingle (1985). PMX proceeds just as OX. Alleles from parent1 that fall between two randomly selected crossing sites are copied into the same positions of the offspring. The remaining allele positions are determined by parent2 during a two-step process. First, alleles in parent2 not within crossing sites are copied to the corresponding positions within the offspring. Next each allele of parent2 within the crossing sites is placed in the offspring at the position occupied in parent2 by the allele from parent1 that displaced it, see the example below. PMX can be applied usefully in the TSP. Indeed, TSP chromosomes are simply sequences of integers, where each integer represents a different city and the other represents the time at which the city is visited. Under this representation, known as permutation encoding, we are only interested in labels and not alleles. It may be viewed as a crossover of permutation that guarantees that all positions are found exactly once in each offspring.

Example:



### 2.5.4 Cycle Crossover (CX)

The cycle crossover operator was proposed by Oliver et al. (1987). CX performs recombination under the constraint that each allele value comes from one parent or the other. CX does not use crossing sites, but a cycle is defined in a manner similar to an algebraic permutation group, see the example below, Comparing the strings of parent1 with parent2, F displaces A, A displaces D, D displaces G, and displaces F. This forms the cycle FADG. The remaining alleles are filled from parent2 in the corresponding positions, BC, E, and H.



## 2.6 MUTATION MECHANISM

In order to avoid from getting stuck onto a local minimum, population diversity is required to be kept up to some extent. In genetic algorithms, this is achieved by the help of a mutation mechanism, which causes some sudden changes on the traits of individuals according to a predefined mutation probability parameter (Negnevitsky, 2011). A new offspring can be achieved by different ways either by flipping, inserting, swapping or sliding the allele values at two randomly chosen gene positions.

### 2.6.1 Inversion Mutation

The *inversion mutation* (flipping) operator (Michalewicz, 1996) randomly selects two cut points in the chromosome, and it reverses the subtour between these two cut points. Suppose that the first cut point is chosen between city 9 and city 5, and the second cut point between the 6<sup>th</sup> and 7<sup>th</sup> city. For example, consider the tour

Parent:	3	9	5	4	6	2	7	1	8
Offspring:	3	9	2	6	4	5	7	1	8

### 2.6.2 Insertion Mutation

The *insertion mutation* (Michalewicz, 1996) operator selects a gene at random and then inserts it at a random position. Suppose that the insertion mutation operator selects city 5, removes it, and randomly inserts it after city 7. For example, consider again the tour

Parent:	3	9	5	4	6	2	7	1	8
Offspring:	3	9	4	6	2	7	5	1	8

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# 2.6.3 Displacement Mutation

The *displacement mutation* (Michalewicz, 1992) operator first selects a subtour at random. This subtour is removed from the tour and inserted in a random place. For example, consider the tour represented as below and suppose that the tour (5 4 6) is selected. Hence, after the removal of the subtour we have (3 9 2 7 1 8), and suppose we randomly select city 7 to be the city after which the subtour is inserted. This result in



#### 2.6.4 Exchange Mutation

The *exchange mutation* (Michalewicz, 1996) operator, also known as reciprocal exchange mutation (swapping) randomly selects two cities in the tour and exchanges them. For example, consider the tour represented as below and suppose that third and the eighth city are randomly selected.



### 2.7 TRAVELLING SALESMAN PROBLEM

The travelling salesman problem (TSP) is one of the most widely discussed problems in combinatorial optimization. The most basic TSP involves finding an optimal route for visiting n cities exactly once and returning to the point of origin, where the inter-city distances is symmetric and known. Other variations of the TSP have also aroused interest. This problem has caught the intentions of the researcher