

CHAPTER 1

INTRODUCTION

CHAPTER 1: INTRODUCTION

1.1. Assembly line balancing

An assembly line is a production system which is flow-oriented where stations are the productive units performing the operations, are in a serial manner. The work pieces go through stations successively as they are supposed to move along the line which is some kind of transportation system, e.g., a conveyor belt. Every assembly line consists of workstations, which are arranged along a conveyor belt or a similar material handling equipment generally mechanical. The workpieces, also called as jobs, are consecutively pass down the line and are moved from one station to next station. At each station, some operations are performed repeatedly regarding the cycle time which is maximum or average time available for each work cycle.

Assembly line balancing i.e. ALB as well as sequencing is an expanding area of optimization research in the field of operations management. Generally interchangeable parts of the final products are assembled in sequences using best possibly designed logistics in an ALB. The initial stage of configuration and design of an AL was focused on the cost efficient mass production of nearly standardized products. Manufacturing of a product on any assembly line requires division of the total amount of work into number of elementary operations which are called as tasks. Performing such a task takes a task time and it requires certain equipments of machines as well as skills of workers. The total workload measured is necessary to be by the sum of task times for assembling a work piece . There is also a need to

observe precedence constraints between the tasks due to technological and organizational conditions.

Classification of assembly line balancing problems on the basis of objective function used:

- Type-1: The objective in this type of problem is to minimize the number of workstations when cycle time is given
- Type-2 : The objective in this type of problem is to minimize the cycle time when number of workstations is given
- Type-3 : The objective in this type of problem is to maximize the workload smoothness
- Type-4 : The objective in this type of problem is to maximize work relatedness
- Type-5 : The objective in this type of problem is to optimization of more than one objectives
- Type-E : The objective in this type of problem is maximization of the line efficiency by simultaneous minimization of the cycle time and a number of workstations

1.2 Types of the assembly line balancing

1.Simple assembly line balancing problems (SALBP):

The simple assembly line balancing problems (SALBP) are relevant for assembly lines which are straight and of single product where only precedence constraints between tasks of the problem are considered. As mentioned above,

Type 1 of this basic problem (SALBP-1) consists of assigning of the tasks to work stations so that the total number of stations is minimized while maintaining the given production rate. The objective in Type 2 problem (i.e. SALBP-2) is to maximize the production rate, and simultaneously, to minimize the sum of idle times for a given number of stations. The general type of problem (SALBP-G) is obtained with minimization of the sum of idle times which is subjected to different production rates and the numbers of stations.

2.U shaped line balancing problem (UALBP):

The U shaped line balancing problem (UALBP) takes into consideration the case of U-type assembly lines generally used for single product, the stations are arranged on a narrow U line. As a result, worker is allowed to work on both sides of the U shape, i.e. on early as well as late tasks in the process of production at the same time. Therefore, precedence constraints have to be modified and observed accordingly. As done with SALBP, different types of problems can be distinguished from this form of assembly line.

3.GALBP:

All the problems of different types which generalize i.e. remove one or more assumptions of SALBP are called as generalized assembly line balancing problems i.e. GALBP. The class of such problems is very huge and contains almost all problem extensions which are relevant in practice which includes the equipment selection, the processing alternatives, the assignment restrictions and so on.

At the time of design stage of every assembly line, some limitations must be observed while grouping of work elements or tasks, they are

1. Precedence constraints.
2. The total number of work elements or tasks cannot be more than that of the number of workstations as well as the minimum possible number of workstations is 1.
3. The cycle time which is nothing but the amount of time allowed at each station which is equal to that of the time between successive products coming out of the assembly line, is not less than that of the maximum of any station time which means the station time of any station is not allowed to be more than the cycle time.

1.3. The Two sided Assembly line

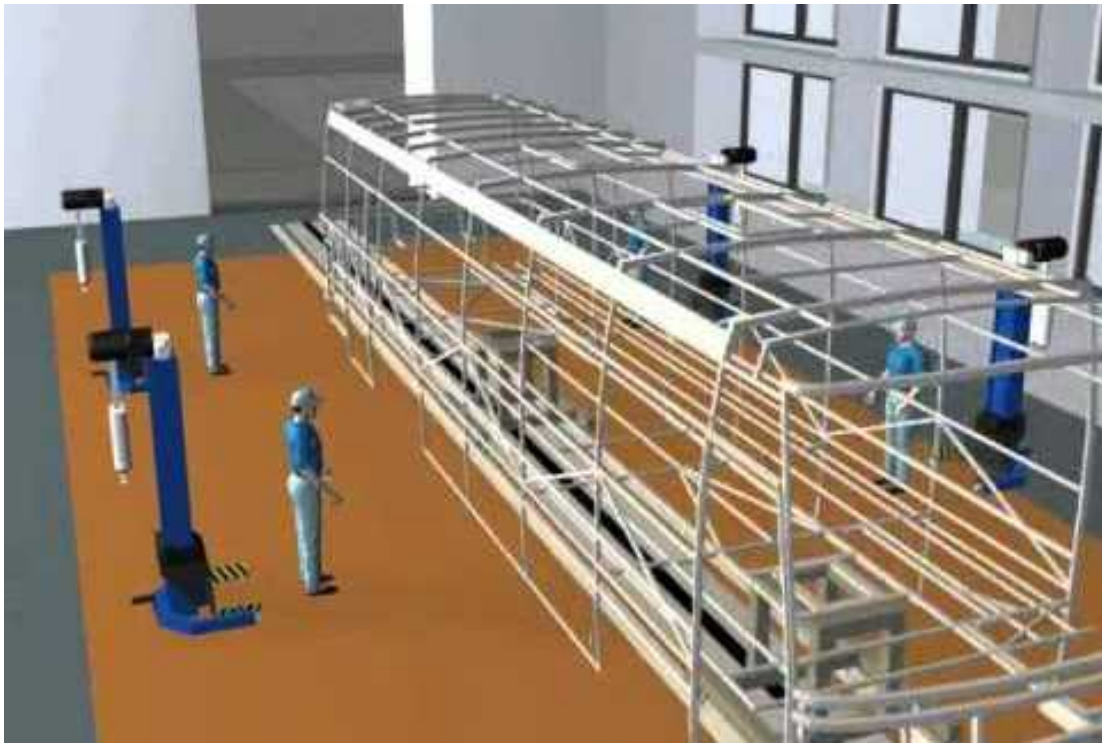


Figure1. Assembly line with Two Sides

Every two-sided assembly line is nothing but a type of production line in which all the tasks are performed at both sides of the line and that too in parallel. Generally such line is used to produce the large products like that of trucks and buses.

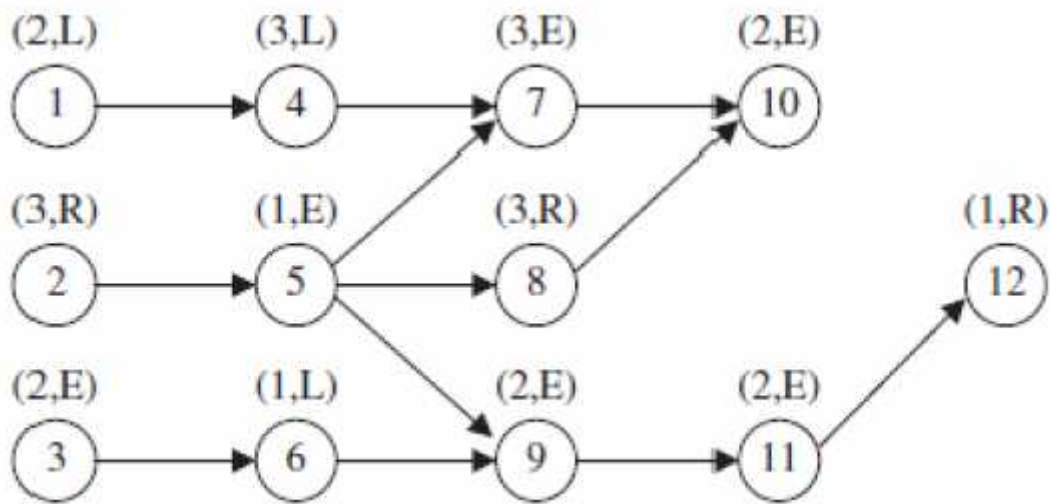


Figure2. Precedence diagram for assembly in two sides

The precedence diagram is a diagram which defines the precedence relationships of the tasks. For every such task the operation time and the direction of operation i.e. whether it is Right, Left or Either are indicated on the precedence diagram as shown in the figure.

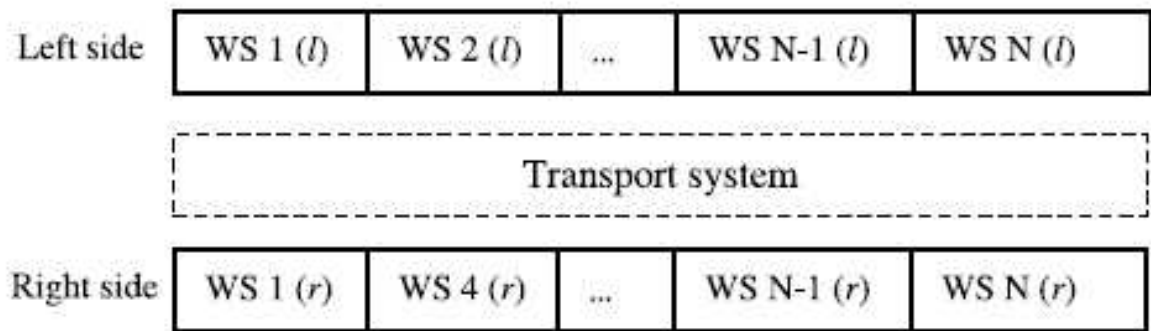


Figure3. Presentation of Two Sided Assembly Line

There are number of advantages that are offered by the two sided assembly lines, important of them are-

1. It facilitates the shorter line length.
2. It reduces the throughput time
3. It also lowers the cost of tools and fixtures.
4. It reduces material handling to a large extent

In this type of assembly line, the products or jobs wait at each mated-station where there are two operators who are working from the opposite sides of the assembly line in parallel performing the different tasks on the same individual job but in different directions. The tasks which are supposed to be performed according to definite sequence of operations and they may have restrictions on the directions in which they can be performed. Some such assembly operations are supposed to be performed on any of the two sides and remaining can be performed at single side of the assembly line. Therefore, all the tasks are divided into three groups of Left (L), Right (R), and Either (E) tasks.

1.4. Genetic Algorithm

1.4.1. Important terms popularly used in GA

Chromosome: It is the complete genetic description of each individual in the population. It is nothing but the collection of definite characteristics which are called as genes.

Gene: It is a single characteristic within every chromosome. It can assume any of several values which are called as alleles.

Allele: It is a definite value which can be taken by any gene. Various genes generally tend to have different alleles. For example, gene deciding the hair colour can have alleles of red, black, brown, etc.

Population: It is the total number of the chromosomes which form a single population generation.

Objective: It is a function which is decided for minimisation or maximisation of a certain criterion.

Fitness: It is a measurement of the quality of performance of a parameter set.

1.4.2. Principles on which GA works

A genetic algorithm is nothing but a set of procedures which on repeating, takes near the solutions of the specific problems which are to be searched. To achieve the such objectives, GA generates successive population generations of different solutions till a solution is obtained which gives optimum results. With every generation of successive population, betterments in the quality of the solutions in population are achieved. Like this, a GA quickly moves towards a successful outcome avoiding the examination of each possible solution of the problem. The procedure which is used in GA is identical with the fundamental process which controls the evolution of biological organisms, which is, natural selection and reproduction.

They together improve an ability of an organism to survive in its environment as given below:

1. Natural selection is determination of organisms which have the ability of reproduction and survival within its population.
2. Reproduction is combining the genes from two different individuals in order to form an offspring which will inherit the surviving characteristics of the parents.

The GA is an attempt to imitate the manner of reproduction of beneficial genes themselves by successive populations and therefore contribute to survival ability of an organism.

1.4.3.General steps of GA

Many functions are used for evaluating the objective criterion which measures fitness of every individual. There are many methods which are used for reproduction and mutation. The genetic optimisation which is achieved in the different steps is shown in figure-

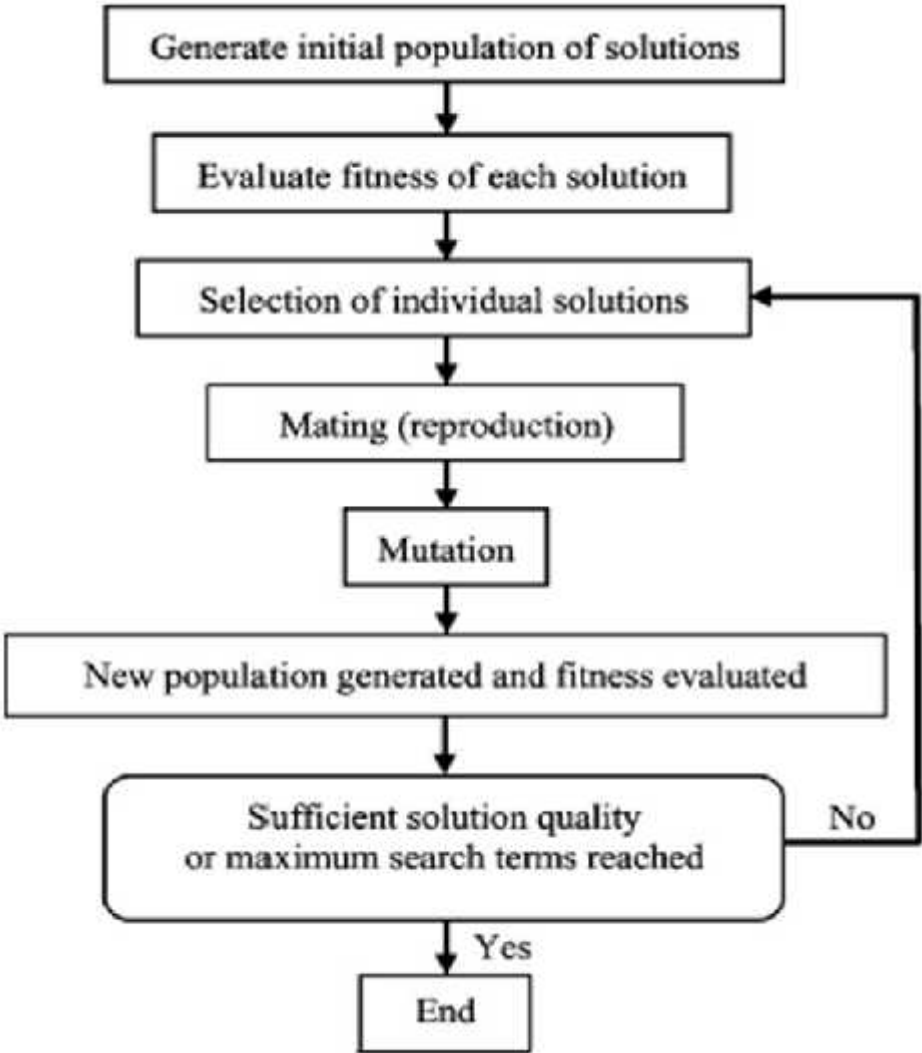


Figure 4. General scheme of GA

Initialise -the population: Generation of the initial population i.e. set of solutions.

Evaluate- It is the computation of the fitness value, which is measured as by the wellness of the individual in optimising the function. Testing every individual in population for the objective function.

Select the Parents: Choosing the pairs of individuals in from the generation of population so that fitter the individual more the copies are generated.

Reproduce: It is generating the offspring from every pair of parents. Every such parent gives the part of its genetic format to its each offspring.

Mutate: Randomness in changing very small part of genetic make-up of every child. It completes one generation after which new one starts.

1.4.4. Advantages of GA

Genetic Algorithms is a particularly very different and attractive approach of solving optimization problem as it is very effective in faster global search of a vast, non-linear and poorly understood solution spaces. Genetic algorithms have received very much attention of the the researcher community as it gives an alternative to the traditional optimization techniques by using the direction and random search to find the optimum solution in complex solution space.

CHAPTER 2
LITERATURE REVIEW

CHAPTER 2: LITERATURE REVIEW

The two-sided assembly lines are the lines in which tasks on the same job are performed parallel at both sides of the line. Its benefits include the shorter line length, reduced throughput time, lower cost of tools and fixtures, and less material handling.

Bartholdi [1] was the first to take up the problem in 1993 with the objective of minimization of the number of stations applying a simple assignment rule.

Lee et al. [2] have developed a group assignment procedure for TALBP in which the assignments were made on the basis of the task groups instead of individual tasks so as to maximize work relatedness and work slackness. As a fitness function, they used work relatedness and work slackness. Though, these criteria generally are in conflict with the traditional criteria like number of stations and cycle time. Thus, improving the work relatedness and slackness may sometimes result into sacrifice of traditional criteria. Such sacrifice is justified on significance of new criteria as it improves efficiency, helps to demarcate responsibility for the completion of the related tasks and also helps to give workers more job satisfaction.

Hu et al. [3] have developed a station-dependent assignment procedure to solve the TALBP. The experimental results proved the efficiency of the proposed procedure.

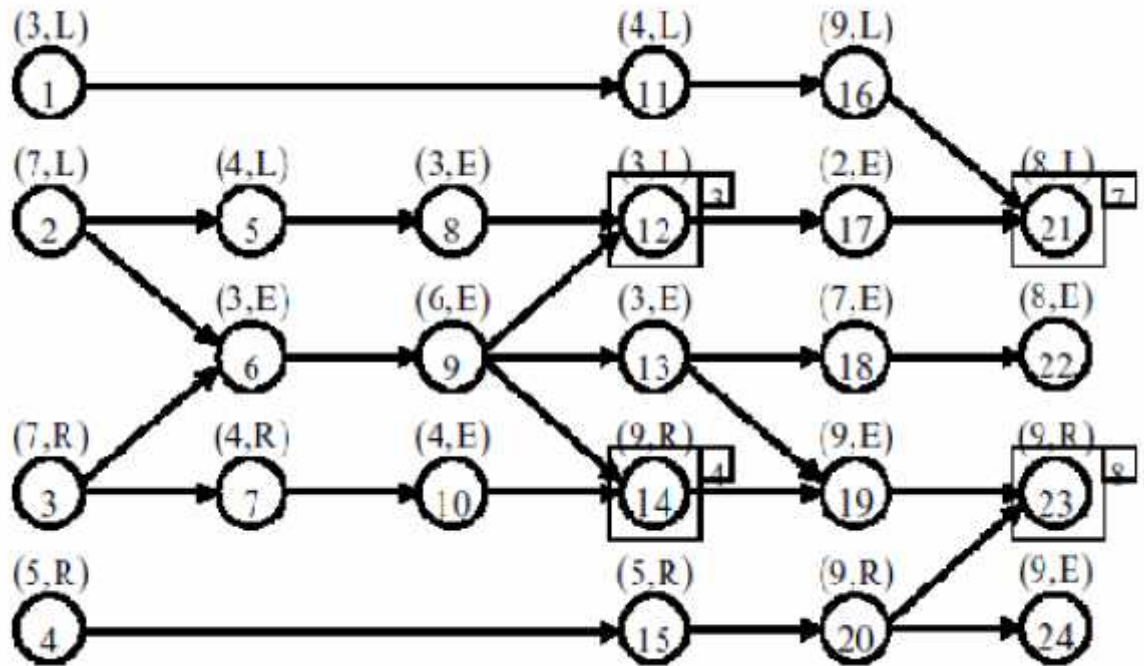


Figure 5: Problem with positional constraints

Kim et al.[4] started the use of GA or solving the TALBP with an objective of minimization of the number of stations with the constrain of cycle time as well as positional constraints. The efficiency of the proposed GA was improved than that of the mathematical model which was proposed by Kim et al. [5], and also the heuristic method proposed by Bartholdi [1].

Kim et al. [2] have proposed a mathematical model as well as a Genetic Algorithm to solve TALBP for the minimization of the cycle time. The strategy they adopted is the strategy of localized evolution as well as steady state reproduction in order to facilitate population diversity and improve the search efficiency. The proposed mathematical model was successful in finding the optimal solutions especially for small sized problems. The results from

experiments showed that the proposed GA performed better than the compared algorithms as it improved the solution quality as well as convergence speed.

There are different techniques which are used to solve the TALBP, the use of diverse methods in problem formulation used in each research. Some researchers have used the popular priority rules in order to assign the priority values each of the task and find an initial solution at the same time the solution is improved by the application of different meta-heuristic techniques.

In most of the TALBP research available, they considered the random method of selection of the side in order to assign the tasks which can be processed in either direction. Though convenient, this method is not efficient mainly in case of large problems which can result in large number of possible solutions that is difficult to cover for even a meta-heuristic technique and therefore it results in sacrifice of some important and optimal solutions. Raghda B. Taha et al.[6] have proposed the new kind of set of rules in order to assign the “Either” tasks to the best possible direction efficiently. The new set of rules are formulated to ensure that the best side assignment is considered for each sequence. These rules reduce the solution space and the number of iterations needed since for each sequence there is only one assignment. These rules are mainly related to the workloads of the current mated station and to the predecessors of that task.

Raghda B. Taha et al.[6] have used the precedence preservative crossover operator which is having great importance in line balancing problems where potential solutions generated after crossover should not violate the precedence restrictions. The scheme of this crossover operator is shown in figure:

Binary vector

0	1	0	0	1	0	1	0	1
---	---	---	---	---	---	---	---	---

Parent-1

2	1	5	4	3	8	6	7	9
---	---	---	---	--------------	--------------	--------------	---	--------------

Parent-2

3	2	6	1	5	4	8	9	7
---	--------------	---	--------------	--------------	---	---	---	--------------

Offspring

2	3	1	5	6	4	8	7	9
---	---	---	---	---	---	---	---	---

Figure 6: Precedence preservative crossover

The works in which minimization of number of work station was the objective, mostly task based representation is used as it is shown in figure

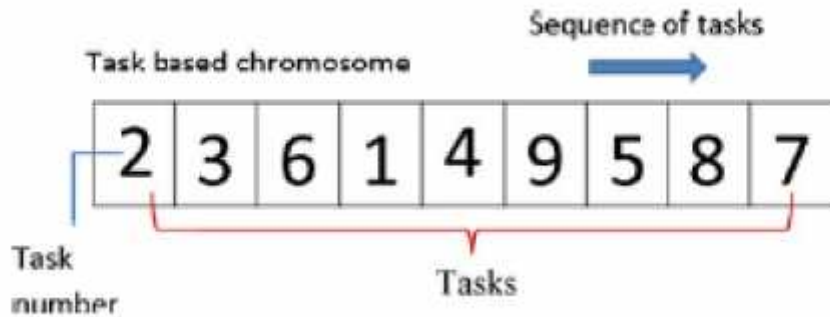


Figure 7: Task based representation

A new measure called the measure of similarity is introduced in Raghda B. Taha et al.[6]. This measure is expected to be a good representation of the population diversity. The similarity is assumed to be the probability of having similar chromosomes in the same population. A zero similarity means that all the chromosomes are different and a gene does not repeat its position more than once in the whole population. A similarity of 100% means that all the chromosomes are similar, i.e. genes are located in the same position in any chromosome in the population under consideration. To measure the similarity between individuals, the similarity of the chromosomes in the initial population is measured following the procedure shown in table below

Chromosome1	1	3	2	4	6	5	8	7	9
Chromosome2	2	1	3	4	5	6	8	9	7
Similar genes	0	0	0	1	0	0	1	0	0

$$\text{Similarity percentage } 2/9 = 22.2$$

Table 1: Calculation of Similarity measure

Many researchers have used elitist strategy for selection of chromosomes for crossover and mutation. “Elitism” improves the performance of GA with retention of the best individual in every generation to the next generation. It helps to ensure that a fit individual solution is not lost or wasted in the process of crossover and mutation .

Various stopping criteria are used to stop the genetic algorithm, for example the criteria of maximum generations allowed which is nothing but the maximum number of iterations of the GA that will be performed, also there is another criteria of number of stalled generations allowed which is the number of iterations in which there is no improvement in the best fitness value of the solution.

Problem identification: Though Genetic algorithms are receiving an increased attention of the research community as it helps to provide an better alternative to the traditional optimization methods by the use of directed as well as the random search in order to locate optimum solution in large, complex as well as least understood solution space and the performance of various genetic algorithms developed is encouraging, there is little done on the front of generation of initial population. There is a need to involve different heuristics as well as techniques to maximise the diversity in the initial population considering the effect it is having on the performance of the GA.

CHAPTER 3

EXPERIMENTATION

CHAPTER 3: EXPERIMENTATION

3.1. Methodology

As earlier discussed the chromosomes generated in forward direction have more randomness in the initial part while the chromosomes generated in backward direction have more randomness in later part of the chromosome.

The new measure developed by Raghda B. Taha et al. is good representation of the population diversity. It is an important tool to measure the performance of the technique used for generating initial population in terms of diversity it provided in the initial population. The similarity is assumed to be the probability of having similar chromosomes in the same population. A zero similarity means that all the chromosomes are different and a gene does not repeat its position more than once in the whole population. A similarity of 100% means that all the chromosomes are similar, i.e. genes are located in the same position in any chromosome in the population under consideration.

To measure the similarity between individuals, the similarity of the chromosomes in the initial population is measured following the procedure shown below:

Chromosome1	1	3	2	4	6	5	8	7	9
Chromosome2	2	1	3	4	5	6	8	9	7
Similar genes	0	0	0	1	0	0	1	0	0

Similarity percentage $2/9 = 22.2$

Table 1: Calculation of Similarity measure

If one gene in the chromosome under consideration is repeated in another chromosome in the same position, then this chromosome is considered similar to the other chromosome by 1 over the chromosome length. This process is repeated for each gene in the chromosome. Each chromosome is compared with the rest of the chromosomes in the population and the value of the chromosome similarity is the similarity to each chromosome divided by the population size. The average similarity is then calculated for the whole population.

The similarity measure is used to study the effect of the proposed method in generating the initial population on the population diversity when applied on two problems with 9 and 16 tasks.

The population size is kept constant to 10. Initial population is produced in forward direction, in backward direction and in random (forward or backward) direction. A random binary matrix is generated for the purpose. The procedure is shown below:

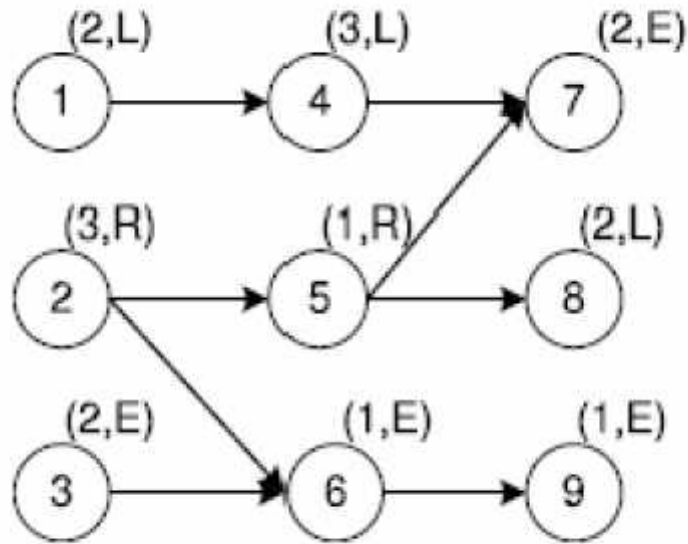


Figure 8: Problem with 9 tasks

If the Random Binary Vector generated is as below =

1 0 1 0 1 1 0 1 0

It indicates the sequence of allotting the tasks in following manner

Direction sequence =

F₁ B₂ F₃ B₄ F₅ F₆ B₇ F₈ B₉

It suggests that out of 9 tasks to be appointed in the Chromosome, first will selected out of tasks 1 , 2 and 3; after allotment of task the next task will be allotted in the backward direction i.e. out of 7, 8 and 9. The procedure is repeated to get the 10 chromosomes in initial population.

3.2. Problem with 9 tasks

3.2.1. Forward direction:

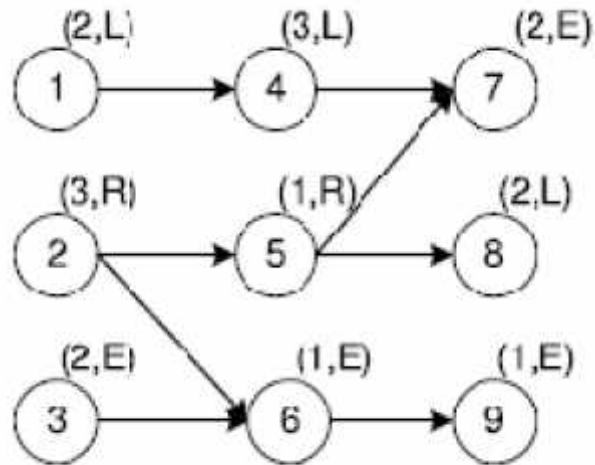


Figure 8: Problem with 9 tasks

Table 2: Initial population



Ch = Chromosome

Ch 1	2	3	6	1	5	4	7	8	9
Ch 2	2	3	1	4	6	9	5	7	8
Ch 3	1	3	2	4	5	6	7	9	8
Ch 4	2	5	1	3	6	9	4	7	8
Ch 5	3	1	2	4	6	5	7	9	8
Ch 6	2	3	5	1	4	7	8	6	9
Ch 7	1	3	2	5	6	4	7	9	8
Ch 8	2	1	3	6	5	4	8	7	9
Ch 9	3	1	2	6	5	4	9	8	7
Ch10	2	1	3	5	4	6	8	7	9

Table 2 shows the set of chromosomes generated as an Initial Population. The Population size is maintained at 10.

Table 3: Calculation

-	Chr 1	Chr 2	Chr 3	Chr4	Chr 5	Chr 6	Chr 7	Chr 8	Chr 9	Chr10	Avg
Ch 1	-	22.22	33.33	11.11	11.11	44.44	33.33	44.44	33.33	22.22	28.4
Ch 2	22.22	-	33.33	66.66	33.33	22.22	33.33	22.22	0	22.22	28.4
Ch 3	33.33	33.33	-	11.11	55.55	11.11	66.66	11.11	22.22	11.11	28.4
Ch 4	11.11	66.66	11.11	-	22.22	11.11	22.22	22.22	0	22.22	21
Ch 5	11.11	33.33	55.55	22.22	-	0	55.55	11.11	33.33	11.11	25.9
Ch 6	44.44	22.22	11.11	11.11	0	-	11.11	33.33	0	44.44	19.8
Ch 7	33.33	33.33	66.66	22.22	55.55	11.11	-	11.11	22.22	11.11	29.6
Ch 8	44.44	22.22	11.11	22.22	11.11	33.33	11.11	-	44.44	66.66	29.6
Ch 9	33.33	0	22.22	0	33.33	0	22.22	44.44	-	11.11	18.5
Ch10	22.22	22.22	11.11	22.22	11.11	44.44	11.11	66.66	11.11	-	24.7

All digits showing similarity between chromosomes in %

Table 3 shows the calculations done for calculating the similarity measure. As shown in the table, first, the similarity measure of each chromosome is calculated with the remaining chromosomes. The average of these 9 values gives the similarity measure of the single chromosome. To get the final similarity measure of the Initial population, average of these ten values is calculated.

$$\begin{aligned}
 \text{Final similarity measure in forward direction} &= [28.4 + 28.4 + 28.4 + 21 + 25.9 + 19.8 \\
 &\quad + 29.6 + 29.6 + 18.5 + 24.7] / 10 \\
 &= \mathbf{25.43\%}
 \end{aligned}$$

3.2.2. Backward direction

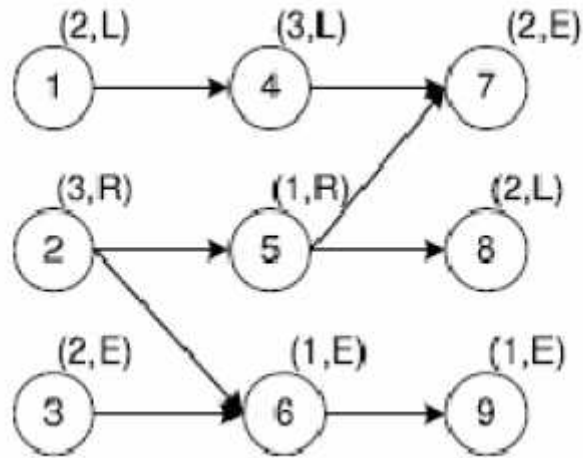


Figure 8: Problem with 9 tasks

Table 4: Initial population



Ch 1	1	3	2	6	4	5	7	8	9
Ch 2	3	1	2	6	4	5	7	8	9
Ch 3	2	3	1	5	4	6	8	7	9
Ch 4	2	3	1	5	4	6	7	8	9
Ch 5	3	2	1	6	5	4	9	8	7
Ch 6	1	2	3	5	4	6	7	9	8
Ch 7	3	1	2	6	4	5	8	7	9
Ch 8	2	1	3	6	4	5	9	7	8
Ch 9	1	3	2	4	6	5	7	9	8
Ch10	2	3	1	5	6	4	8	9	7

Ch = Chromosome

Table 4 shows the set of chromosomes generated as an Initial Population. The Population size is maintained at 10.

Table 5: Calculation

-	Chr 1	Chr 2	Chr 3	Chr 4	Chr 5	Chr 6	Chr 7	Chr 8	Chr 9	Chr10	Avg
Ch 1	-	77.77	33.33	55.55	22.22	33.33	55.55	33.33	55.55	11.11	42
Ch 2	77.77	-	22.22	44.44	33.33	22.22	77.77	44.44	33.33	0	39.4
Ch 3	33.33	22.22	-	77.77	11.11	33.33	44.44	33.33	11.11	55.55	33.3
Ch 4	55.55	44.44	77.77	-	22.22	44.44	22.22	22.22	22.22	44.44	39.4
Ch 5	22.22	33.33	11.11	22.22	-	11.11	22.22	22.22	0	33.33	19.6
Ch 6	33.33	22.22	33.33	44.44	11.11	-	11.11	33.33	44.44	22.22	28.3
Ch 7	55.55	77.77	44.44	22.22	22.22	11.11	-	55.55	22.22	11.11	35.7
Ch 8	33.33	44.44	33.33	22.22	22.22	33.33	55.55	-	22.22	11.11	30.7
Ch 9	55.55	33.33	11.11	22.22	0	44.44	22.22	22.22	-	33.33	27
Ch10	11.11	0	55.55	44.44	33.33	22.22	11.11	11.11	33.33	-	24.6

All digits showing similarity between chromosomes in %

Table 5 shows the calculations done for calculating the similarity measure. As shown in the table, first, the similarity measure of each chromosome is calculated with the remaining chromosomes. The average of these 9 values gives the similarity measure of the single chromosome. To get the final similarity measure of the Initial population, average of these ten values is calculated.

$$\begin{aligned}
 \text{Final similarity measure backward direction} &= [42 + 39.4 + 33.3 + 39.4 + 19.6 + 28.3 \\
 &\quad + 35.7 + 30.7 + 27 + 24.6] / 10 \\
 &= \mathbf{32\%}
 \end{aligned}$$

3.2.3. Random direction

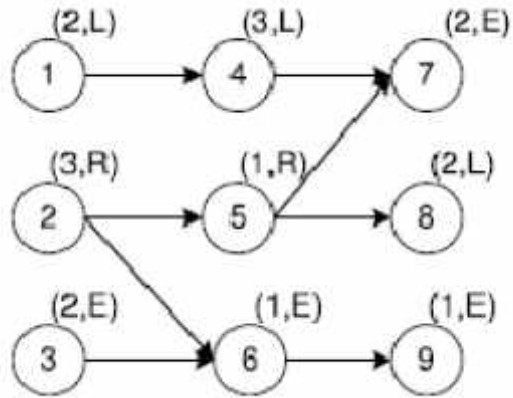


Figure 8: Problem with 9 tasks

Random binary matrix:

1	0	1	0	1	0	0	1	1
1	0	0	1	0	0	1	1	1
0	0	1	1	0	1	0	1	1
0	0	1	1	1	0	1	0	0
1	0	1	0	0	0	1	1	0
1	0	1	0	1	0	1	0	1
1	1	0	0	1	0	1	1	0
0	1	1	0	1	0	1	0	0
1	1	0	1	0	1	1	1	0

Table 6 : Initial Population



Ch 1	1	4	2	5	3	6	7	9	8
Ch 2	2	3	5	1	4	6	8	7	9
Ch 3	3	2	1	6	9	5	4	8	7
Ch 4	2	3	1	5	8	4	7	6	9
Ch 5	3	2	6	5	9	8	1	4	7
Ch 6	1	4	2	5	7	3	8	6	9
Ch 7	2	5	3	1	4	7	6	9	8
Ch 8	3	2	1	6	5	4	9	8	7
Ch 9	2	5	1	4	3	6	9	8	7
Ch10	3	1	2	6	5	8	9	4	7

Ch = Chromosome

Table 7: Calculation

-	Chr 1	Chr 2	Chr 3	Chr 4	Chr 5	Chr 6	Chr 7	Chr 8	Chr 9	Chr10	Avg
Ch 1	-	11.11	0	22.22	11.11	44.44	22.22	0	22.22	11.11	16
Ch 2	11.11	-	0	33.33	0	22.22	33.33	0	22.22	0	13.5
Ch 3	0	0	-	11.11	44.44	0	0	66.66	33.33	33.33	20.8
Ch 4	22.22	33.33	11.11	-	11.11	33.33	11.11	22.22	22.22	0	18.4
Ch 5	11.11	0	44.44	11.11	-	11.11	0	33.33	11.11	44.44	18.4
Ch 6	44.44	22.22	0	33.33	11.11	-	0	0	0	11.11	13.5
Ch 7	22.22	33.33	0	11.11	0	0	-	0	22.22	0	9.6
Ch 8	0	0	66.66	22.22	33.33	0	0	-	44.44	55.55	24.6
Ch 9	22.22	22.22	33.33	22.22	11.11	0	22.22	44.44	-	22.22	22
Ch10	11.11	0	33.33	0	44.44	11.11	0	55.55	22.22	-	19.6

All digits showing similarity between chromosomes in %

Table 7 shows the calculations done for calculating the similarity measure. As shown in the table, first, the similarity measure of each chromosome is calculated with the remaining chromosomes. The average of these 9 values gives the similarity measure of the single chromosome. To get the final similarity measure of the Initial population, average of these ten values is calculated.

$$\begin{aligned} \text{Final similarity measure in random direction} &= [16 + 13.5 + 20.8 + 18.4 + 18.4 + 13.5 \\ &\quad + 9.6 + 24.6 + 22 + 19.6] / 10 \\ &= \mathbf{17.64\%} \end{aligned}$$

3.3. Problem with 16 tasks

3.3.1. Forward direction

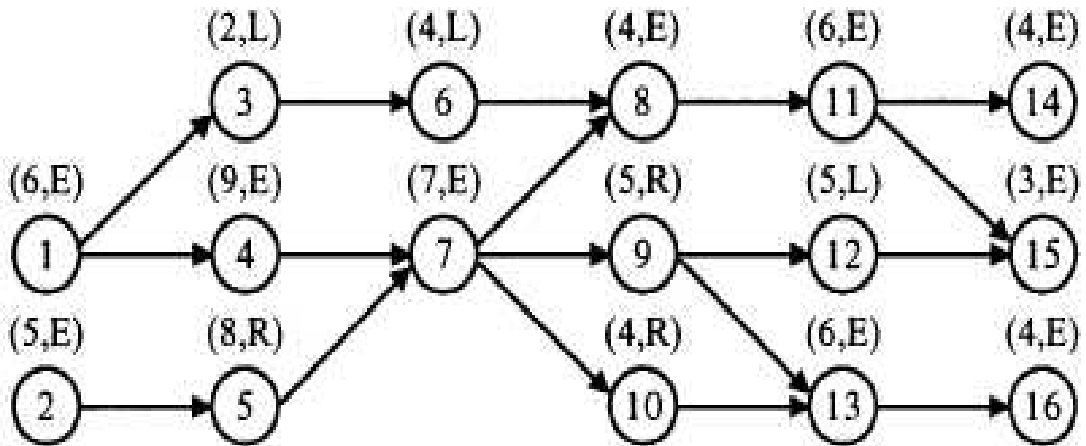


Figure 9: Problem with 16 tasks

Table 8: Initial Population



Ch 1	1	2	3	5	4	7	6	9	8	10	11	12	13	14	16	15
Ch 2	2	1	3	6	5	4	7	8	10	9	13	11	12	16	15	14
Ch 3	2	5	1	3	4	6	7	9	10	8	11	12	13	15	14	16
Ch 4	1	2	5	3	4	6	7	10	8	9	12	13	11	14	16	15
Ch 5	2	1	4	3	5	7	6	8	11	10	9	13	12	15	14	16
Ch 6	1	4	3	2	5	7	6	9	10	13	8	11	12	16	15	14
Ch 7	2	1	5	3	4	6	7	9	8	10	11	12	13	14	15	16
Ch 8	2	1	4	5	3	7	6	8	10	9	13	12	11	15	14	16
Ch 9	1	2	3	6	5	4	7	10	9	8	12	11	13	16	15	14
Ch10	1	2	4	5	3	6	7	10	8	11	9	13	12	15	14	16

Table 8 shows the set of chromosomes generated as an Initial Population. The Population size is maintained at 10.

Table 9: Calculation

	Chr 1	Chr 2	Chr 3	Chr 4	Chr 5	Chr 6	Chr 7	Chr 8	Chr 9	Chr10	Avg
Ch 1	-	6.25	31.25	43.75	18.75	31.25	50	25	25	25	28.5
Ch 2	6.25	-	18.75	12.5	31.25	50	25	37.5	56.25	12.5	27.7
Ch 3	31.25	18.75	-	25	31.25	12.5	62.5	37.5	18.75	31.25	29.8
Ch 4	43.75	12.5	25	-	12.5	6.25	43.75	12.5	31.25	43.75	25.7
Ch 5	18.75	31.25	31.25	12.5	-	25	31.25	56.25	6.25	43.75	28.5
Ch 6	31.25	50	12.5	6.25	25	-	12.5	18.75	43.75	12.5	23.6
Ch 7	50	25	62.5	43.75	31.25	12.5	-	25	18.75	25	32.6
Ch 8	25	37.5	37.5	12.5	56.25	18.75	25	-	0	37.5	27.7
Ch 9	25	56.25	18.75	31.25	6.25	43.75	18.75	0	-	25	25
Ch10	25	12.5	31.25	43.75	43.75	12.5	25	37.5	25	-	28.5

All digits showing similarity between chromosomes in %

Table 9 shows the calculations done for calculating the similarity measure. As shown in the table, first, the similarity measure of each chromosome is calculated with the remaining chromosomes. The average of these 9 values gives the similarity measure of the single chromosome. To get the final similarity measure of the Initial population, average of these ten values is calculated.

$$\begin{aligned}
 \text{Final similarity measure forward direction} &= [28.5 + 27.7 + 29.8 + 25.7 + 28.5 + 23.6 \\
 &\quad + 32.6 + 27.7 + 25 + 28.5] / 10 \\
 &= \mathbf{27.76 \%}
 \end{aligned}$$

3.3.2. Backward direction

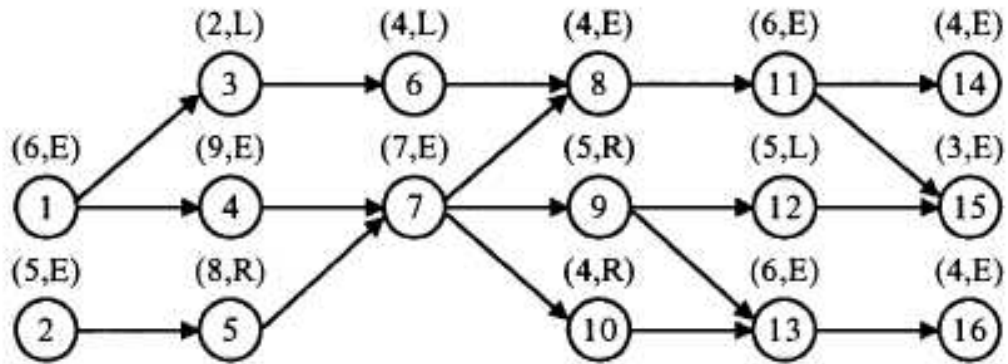


Figure 9: Problem with 16 tasks

Table 10: Initial Population



Ch 1	2	5	1	3	4	6	7	9	10	8	11	12	13	15	14	16
Ch 2	1	2	5	4	3	7	6	9	8	10	13	12	11	15	16	14
Ch 3	1	2	5	3	4	6	7	10	8	9	12	13	11	14	16	15
Ch 4	2	1	3	5	4	6	7	9	8	10	12	13	11	16	15	14
Ch 5	1	4	3	2	5	7	6	9	10	13	8	11	12	16	15	14
Ch 6	2	1	3	4	5	6	7	8	10	9	13	11	12	14	15	16
Ch 7	1	2	3	5	4	7	6	9	10	8	13	11	12	16	14	15
Ch 8	2	1	4	3	5	7	6	8	11	10	9	13	12	15	14	16
Ch 9	1	2	5	3	4	6	7	8	9	10	11	13	12	14	15	16
Ch10	2	1	5	3	4	6	7	9	8	10	11	12	13	14	15	16

Ch = Chromosome

Table 10 shows the set of chromosomes generated as an Initial Population. The Population size is maintained at 10.

Table 11: Calculation

-	Chr 1	Chr 2	Chr 3	Chr 4	Chr 5	Chr 6	Chr 7	Chr 8	Chr 9	Chr10	Avg
Ch 1	-	18.75	25	31.25	12.5	31.25	31.25	31.25	37.5	62.5	31.2
Ch 2	18.75	-	37.5	31.25	31.25	12.5	37.5	25	25	31.25	27.8
Ch 3	25	37.5	-	37.5	6.25	25	25	12.5	56.25	43.75	29.8
Ch 4	31.25	31.25	37.5	-	31.25	37.5	31.25	25	37.5	56.25	35.4
Ch 5	12.5	31.25	6.25	31.25	-	37.5	56.25	25	18.75	12.5	25.7
Ch 6	31.25	12.5	25	37.5	37.5	-	31.25	37.5	43.75	43.75	33.3
Ch 7	31.25	37.5	25	31.25	56.25	31.25	-	25	25	12.5	30.6
Ch 8	31.25	25	12.5	25	25	37.5	25	-	37.5	31.25	27.8
Ch 9	37.5	25	56.25	37.5	18.75	43.75	25	37.5	-	62.5	38.2
Ch10	62.5	31.25	43.75	56.25	12.5	43.75	12.5	31.25	62.5	-	39.6

All digits showing similarity between chromosomes in %

Table 11 shows the calculations done for calculating the similarity measure. As shown in the table, first, the similarity measure of each chromosome is calculated with the remaining chromosomes. The average of these 9 values gives the similarity measure of the single chromosome. To get the final similarity measure of the Initial population, average of these ten values is calculated.

$$\begin{aligned}
 \text{Final similarity measure backward direction} &= [31.2 + 27.8 + 29.8 + 35.4 + 25.7 \\
 &\quad + 33.3 + 30.6 + 27.8 + 38.2 + 39.6] / 10 \\
 &= \mathbf{31.94 \%}
 \end{aligned}$$

3.3.3. Random direction

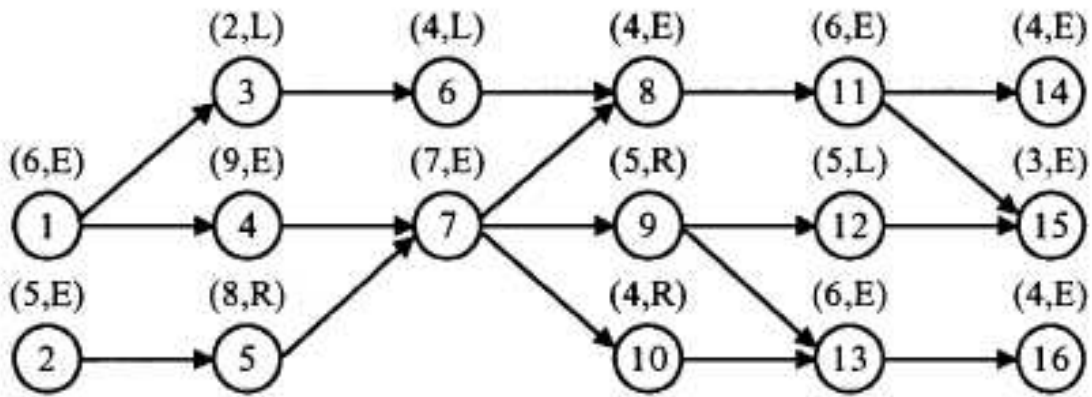


Figure 9: Problem with 16 tasks

Random binary matrix:

1	0	0	1	0	1	0	0	1	1	1	0	0	1	0	1
1	0	1	0	1	0	1	0	1	0	0	1	0	1	1	0
0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1
0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1
1	0	1	0	1	0	1	0	1	0	1	0	1	0	0	1
1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0
1	1	0	1	1	0	1	0	1	1	0	0	1	0	1	0
0	1	1	0	0	1	0	1	0	1	0	0	1	0	1	0
1	1	0	1	0	1	1	0	1	0	1	0	1	0	1	0
0	0	1	0	1	1	1	0	1	1	0	1	0	1	0	1

Table 12: Initial Population



Ch 1	1	3	6	4	2	5	7	8	11	14	9	12	15	10	13	16
Ch 2	2	5	1	4	7	9	10	3	13	6	8	11	14	12	16	15
Ch 3	1	4	2	3	6	5	7	9	12	8	11	10	13	16	14	15
Ch 4	2	1	4	3	5	7	6	8	11	14	9	12	15	10	13	16
Ch 5	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Ch 6	2	5	1	4	7	9	10	3	13	12	6	8	11	14	16	15
Ch 7	1	4	2	5	7	9	12	3	10	13	16	6	8	11	15	14
Ch 8	1	3	6	2	5	4	7	8	11	14	9	12	15	10	13	16
Ch 9	2	1	3	4	5	7	6	8	10	9	12	11	13	15	16	14
Ch10	1	2	4	3	5	7	6	8	9	12	10	13	16	11	14	15

Ch = Chromosome

Table 13: Calculations

-	Chr 1	Chr 2	Chr 3	Chr 4	Chr 5	Chr 6	Chr 7	Chr 8	Chr 9	Chr10	Avg
Ch 1	-	6.25	18.75	56.25	37.5	6.25	6.25	81.25	12.5	12.5	26.3
Ch 2	6.25	-	6.25	6.25	6.25	68.75	18.75	0	25	6.25	15.9
Ch 3	18.75	6.25	-	6.25	25	6.25	18.75	12.5	6.25	25	13.8
Ch 4	56.25	6.25	6.25	-	18.75	6.25	0	62.5	37.5	37.5	25.7
Ch 5	37.5	6.25	25	18.75	-	12.5	12.5	37.5	31.25	31.25	23.6
Ch 6	6.25	68.75	6.25	6.25	12.5	-	18.75	0	18.75	12.5	16.7
Ch 7	6.25	18.75	18.75	0	12.5	18.75	-	0	12.5	12.5	11.1
Ch 8	81.25	0	12.5	62.5	37.5	0	0	-	12.5	18.75	25
Ch 9	12.5	25	6.25	37.5	31.25	18.75	12.5	12.5	-	25	20.1
Ch10	12.5	6.25	25	37.5	31.25	12.5	12.5	18.75	25	-	20.1

Table 13 shows the calculations done for calculating the similarity measure. As shown in the table, first, the similarity measure of each chromosome is calculated with the remaining chromosomes. The average of these 9 values gives the similarity measure of the single chromosome. To get the final similarity measure of the Initial population, average of these ten values is calculated.

$$\begin{aligned} \text{Final similarity measure random direction} &= [26.3 + 15.9 + 13.8 + 25.7 + 23.6 \\ &\quad + 16.7 + 11.1 + 25 + 20.1 + 20.1] / 10 \\ &= \mathbf{19.83 \%} \end{aligned}$$

CHAPTER 4

RESULTS

CHAPTER 4: RESULTS

The two problems with 9 tasks and 16 tasks are solved using 3 directions of generation of initial population- forward direction, backward direction and random direction. The similarity measure is calculated in each of the case.

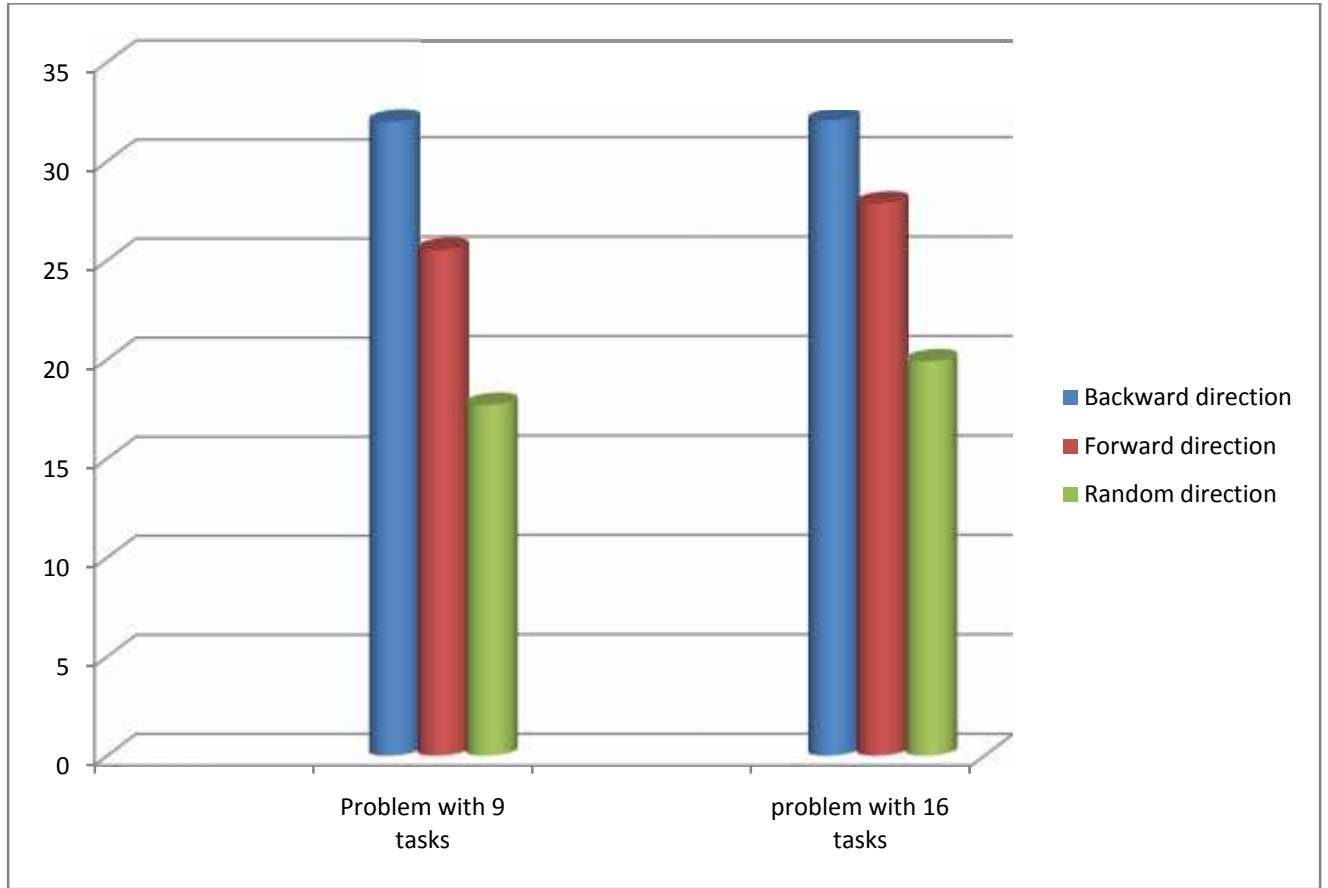
The initial population of 9 task problem shown 32% similarity measure on generating in backward direction, 25.43% on generating in forward direction and 17.64% on generating in random direction.

The initial population of 16 task problem shown 31.94% similarity measure on generating in backward direction, 27.76% on generating in forward direction and 19.83% on generating in random direction.

The comparison of similarity measures in different cases is shown in table 13 as well as in graph shown in figure 11.

Table 14: Similarity measures

	Backward Direction	Forward Direction	Random Direction
Problem with 9 tasks	32%	25.43%	17.64%
Problem with 16 tasks	31.94%	27.76%	19.83%



Y axis = Similarity measure in %

Figure 10: Comparison Chart

CHAPTER 5

CONCLUSIONS

CHAPTER 5: CONCLUSIONS

Genetic algorithms are widely being used for manufacturing optimization problems. A very common among these manufacturing optimization problems is the assembly line balancing problem, which is related to the allocation of the tasks with workstations in order to optimize objective function. As GAs are well known for their usefulness as optimization technique in the field of manufacturing, their application to assembly line balancing is expanding fast. Now it is also used to balance the two sided assembly lines of large sized products. After the study of literature and from the results of experimentation following conclusions can be made.

- Two sided assembly line balancing has large scope of experimentation. We can handle the real world problems in TALBP.
- Though diversity in population largely depends upon the precedence relations of the tasks in problem, it can vary to a great extent with the use of random direction of generation. It is evident from the results.
- In problem of 9 tasks similarity measure is reduced in random direction by 14.36% over backward direction and by 7.79% over forward direction.
- In problem of 16 tasks similarity measure is reduced in random direction by 12.11% over backward direction and by 7.93% over forward direction.

- The performance of the GA is dependent upon many parameters like genetic operators, encoding scheme, problem specifications.

- Initial population is one of the key features of GA. Performance of GA is very much dependent upon the method of generation of initial population. More diverse the initial population helps to prevent early convergence and local optimization.

- High diversity in initial population may lead to more computational time. This can be optimized using better performing selection criteria.

- Direction of generation can be treated as good tool to diversify the initial population along with different heuristic rules.

CHAPTER 6
FUTURE SCOPES

CHAPTER 6: FUTURE SCOPES

The application of genetic algorithms for optimization in manufacturing is increasing due to its own advantages. It will also increase in the field of two sided assembly lines. Considering this fact, there is a large scope for research in improving the performance of these algorithms.

Following are the major areas which need further attention in research

- Surprisingly, even after being critical feature of GA, initial population has received less attention in research. There is a need to explore different problem specific methods to generate initial population.
- Initial population can be diversified using different heuristic rules combined with different directions of generation. It can be further diversified by taking different proportions of initial populations using different methods.
- Different representation schemes can be used in order to bring the different real world situations in the ambit of algorithms.
- Though Two sided assembly line balancing is more in practice for the assembly of large sized products, it is comparatively less attended research area. There is need to explore the possibilities of different varieties of two sided assembly lines.

- Various real world constraints can be introduced in algorithm as it is done by Lee et al.[2] with work relatedness and slackness or with positional constraints by Kim et al.[11].

REFERENCES

REFERENCES

1. Bartholdi JJ. “Balancing two-sided assembly lines: a case study.” *International Journal for Production Research*;31:2447–61, 1993.
2. Lee TO, Kim Y, Kim YK. “Two-sided assembly line balancing to maximize work relatedness and slackness.” *Computational Industrial Engineering* ;40:273–92;2001.
3. Hindriyanto DP, Hui-MW, Hsin R. “Two-sided assembly lines balancing with assignment restrictions”. *Mathematical and Computer Modelling* 57;189–199; 2013.
4. Kim YK, Kim Y, Kim YJ. “Two-sided assembly line balancing: a genetic algorithm approach.” *Production Planning and Control*;11:44–53; 2000.
5. Kim YK, Kim Y, Lee TO. “Two-sided assembly line balancing models.” *Technical report*; 1998.
6. Raghda BT, Amin K, El-Kharbotly, Yomna MS, Nahid HA. “A Genetic Algorithm for solving two-sided assembly line balancing problems” *Ain Shams Engineering Journal*; 2, 227–240; 2011.
7. Ponnambalam SG, Aravindan P and Mogileeswar GN. “A Multi-Objective Genetic Algorithm for Solving Assembly Line Balancing Problem” *International Journal for Advanced Manufacturing Technology*; 16:341–352 , 2000.

8. Murata T, Ishibuchi H, Tanaka H. “Multi-objective genetic algorithm and its application to flowshop scheduling”, *Computers and Industrial Engineering*, 30(4), 957–968, 1996.
9. Michalewicz Z. “Genetic Algorithms + Data Structures = Evolution Programs”, Springer-Verlag, Berlin, 1992.
10. Kuan EC, Mohamed KO, Nooh AB. “Solving Assembly Line Balancing Problem using Genetic Algorithm with Heuristics-Treated Initial Population” *Proceedings of the World Congress on Engineering ,Vol II,WCE 2008*
11. Kim YK, Song WS, Kim JH. “A mathematical model and a genetic algorithm for two-sided assembly line balancing.” *Computational Operations Research*; 36:853–65; 2009.
12. Hu X, Wu E, Jin Y. “A station-oriented enumerative algorithm for two-sided assembly line balancing.” *European Journal of Operations Research*;186:435–40; 2008.
13. Goldberg, DE. “Genetic Algorithms in Search, Optimization & Machine Learning.”; Reading, MA: Addison–Wesley; 1989.
14. Helgeson WB, Birnie DP. “ Assembly line balancing using the ranked positional weight technique.” *Journal of Industrial Engineering* , 12, 394–398;1961.

15. Anderson EJ, Ferris MC. "Genetic algorithms for combinatorial optimization: the assembly line balancing problem." *Operations Research SAJ Computing* 6, 161–173; 1994.
16. Talbot FB, Patterson JH, Gehrlein WV. "A comparative evaluation of heuristic line balancing techniques." *Management Science*, 32, 430–454; 1986.
17. Ghosh S, Gagnon RJ. "A comprehensive literature review and analysis of the design, balancing and scheduling of assembly systems." *International Journal of Production Research*, 27, 637–670; 1989.
18. Fleszar K, Hindi KS. "An enumerative heuristic and reduction methods for the assembly line balancing problem." *European Journal of Operational Research* 145,606–620; 2003.
19. Buxey GM. "Assembly line balancing with multiple stations." *Management Science* 20 ;1010–1021; 1974.
20. Shtub A, Dar-El EM. "A methodology for the selection of assembly systems." *International Journal of Production Research* ;27; 175–186; 1989.
21. Boysen N, Fliedner M, Scholl A. "A classification of assembly line balancing problems." *European Journal of Operational Research* ,183; 674–689;2007.
22. Scholl A, Fliedner M, Boysen N. "ABSALOM: balancing assembly lines with assignment restrictions." *European Journal of Operation Research*, 688–701; 2010.

23. Becker C, Scholl, A. “A survey on problems and methods in generalized assembly line balancing.” *European Journal of Operational Research*, 168, 694–715; 2006.