

Multi-objective assembly line balancing using genetic algorithm

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ABSTRACT

One of the primary issues in line balancing problems is the uncertainty associated with the processing times. There are different reasons for having uncertain processing times such as task deterioration, failure in machines, etc. On the other hand, there are different objectives, such as cycle time, number of workstations in an assembly line balancing. In this paper, we present a multi-objective decision making assembly line balancing which minimizes different objectives such as cycle time and number of workstations. The resulted problem is formulated based on Lp-norm mixed integer programming and a meta-heuristic approach is also presented to solve the resulted model. The problem formulation is solved for some test examples and the results are discussed under different conditions.

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1. Introduction

Line balancing has been one of the most important factors for reducing the cost of production. There are different forms of line balancing but the classical form has been the basis for many two sides and U-shape problems. One of the issues on line balancing is to consider task deterioration. Browne and Yechiali (1990) first presented a model for deteriorating jobs where processing time is an increasing function of their starting time. There are other related line balancing works such as Shahanaghi et al. (2010), Emrani Noshabadi et al. (2011) and Toksar et al. (2010) but all these works considered the problem with single objectives. There are several attempts to solve line balancing problem with heuristic or meta-heuristic methods. Jin and Wu (2002) presented a heuristic algorithm called ‘variance algorithm’ for mixed assembly line balancing. Krzysztof et al. (2003) presented a heuristic algorithm and new reduction techniques for type 1 assembly line balancing. Scholl and Becker (2006) presented a heuristic algorithm and a comprehensive survey of SALBP. In the field of goal programming Kara et al. (2009) proposed a binary fuzzy goal programming using the methodology which was originally introduced by Chang (2007) where the cycle time and the number of work stations were minimized. Ozcan and Toklu (2009) presented a goal programming and a fuzzy goal programming model for two sided assembly line balancing. The number of mated-stations, cycle time and the number of tasks assigned per station are considered as goals. In their paper, they minimized the number of mated-stations as the primary objective and the number of stations as the secondary

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objective for a given cycle time by presenting a mathematical model. Gokcen et al. (2006) presented new procedures and a mathematical model on the single model assembly line balancing problem with parallel lines. Simaria and Vilarinho (2007) developed an ant colony optimization algorithm for two sided assembly line balancing problem and the primary goal was to minimize the number of work stations. Agpak and Gokcen (2005) presented a new approach on assembly line balancing problem. They developed a mathematical formulation to the balancing assembly line to minimize the number of work stations and resources. Bautista and Cano (2008) presented some procedures to minimize work over load in the mixed-model assembly lines. Peeters and Degraeve (2006) presented a new lower bound, namely the LP relaxation of an integer programming formulation based on Dantzig–Wolfe decomposition. In addition, they developed a branch and bound algorithm to solve the simple assembly line balancing (SALB) problem. Lapierre et al. (2006) developed a tabu search algorithm for balancing assembly lines. In the field of scheduling and balancing assembly lines, Tadeusz Sawik (2002) presented a monolithic and a hierarchical approach for assembly lines. The objective he considered was to determine an assignment of assembly tasks to stations and an assembly schedule for all products to complete the products in minimum time. Andre's et al. (2008) considered the balancing and scheduling tasks in assembly lines, simultaneously. They added the sequence-dependent set up times to the SALB problem. They assumed that if a task assigned next to another task at the same workstation, the set up time should be added to compute the cycle time. They also presented a mathematical model along with some heuristic procedures. Toksari et al. (2008, 2010) studied scheduling and balancing assembly lines by considering the learning effect in the assembly lines. They showed that polynomial solutions can be obtained for both straight and U-shaped assembly line balancing with learning effect. Also Emrani Noshabadi et al. (2011) considered the simple assembly line balancing problem with additional scheduling issue based on the tasks deterioration element, they considered the single objective of number of workstations.

2. Problem description

2.1. Problem definition

Consider a line-balancing problem where there are N dependent tasks, which should be assigned and scheduled in workstations. These tasks have deterioration trait and deteriorate if there is a delay in their starting time. Tasks deteriorate while waiting to be processed. By the effect of task deterioration, task's processing time increase if it is processed with delay. Thus, the processing time of each task depends on its starting time and the available time of that task. There is k undetermined work stations $s_1, s_2 \dots s_k$ and the sequence of these stations in straight assembly lines is based on their number of indexes (i.e. s_1 stands before s_2 and s_2 stands before s_3 and so on). Maximum number of work stations is equal to number of all tasks (every task in one separate work station) and the minimum number of workstations is equal to 1 (all tasks are in the one work station). We schedule and assign these tasks in stations by considering precedence relationships with objective function of minimizing the cycle time, number of stations and work load deviation which are considered for the first time simultaneously in this paper. For more details regarding to problem assumptions see (Emrani Noshabadi et al., 2011).

3. Mathematical formulation

3.1. Notation

$N :$	The number of all tasks	$PS_k :$	The processing time of station k
$Z :$	Number of work stations	$T_k :$	The starting time of station k
$k :$	$k \in Z = \{1 \dots Z_{\max}\}$, It designate the work	$Co_i :$	Completion time of task i
$j :$	It designates the position of job in the sequence. $j \in SE = \{1 \dots L\}$, $L = N$	$St_j :$	starting time of job that is assigned in sequence j , $j \in SE = \{1, \dots, L\}$
$i :$	$\in I = \{1, \dots, N\}$ Designate the task.	$p_i :$	processing time of job i ,
$Ep_i :$	Set of immediate predecessors of job i .	$C_j :$	Completion time of job that is in

J_p :	Set of jobs that have predecessor	b_i :	The growth rate of the processing
N_p :	Set of tasks that have no predecessor	a_i :	Total processing time of station k
AV_i :	The available time of task i	a_i^* :	Fixed part of the processing time of
S_i :	The starting time of task i	M :	A large positive number

3.2. Formulation

Using the above notations, the mathematical model for simple straight assembly line balancing problem is developed as follows:

Decision variable

$$x_{i,j,k} = \begin{cases} 1 & \text{if task } i \text{ in sequence } j \text{ assign in station } k \\ 0 & \text{other wise} \end{cases}$$

There are three objective functions of f_1, f_2 and f_3 associated with the proposed model of this paper and we use L_p -norm to find Pareto-optimal solutions as follows,

$$u = w_1 \left(\frac{f_1 - f_1^*}{f_1^*} \right) + w_2 \left(\frac{f_2 - f_2^*}{f_2^*} \right) + w_3 \left(\frac{f_3 - f_3^*}{f_3^*} \right), \quad (2)$$

where f_1, f_2 and f_3 are CT, Z and W.D, respectively representing the cycle time, the number of work stations and the work load deviation, respectively. The weights for each objective are shown with w , which are determined by decision maker.

$$Ct \geq \sum_{j=1}^L \sum_{i=1}^N (x_{ijk} * p_i) \quad k \in m \text{ and } k \leq Z_{\max} \quad (3)$$

$$WD = \frac{\sum_{k=1}^Z y_k (Ct - q_k)}{Z} \quad k \in m \text{ and } k \leq Z_{\max} \quad (4)$$

$$\sum_{k=1}^Z \sum_{j=1}^L x_{ijk} = 1 \quad i \in I, \quad Z \leq Z_{\max} \quad (5)$$

$$\sum_{k=1}^Z \sum_{i=1}^N x_{ijk} = 1 \quad j \in SE, \quad Z \leq Z_{\max} \quad (6)$$

$$\sum_{j=1}^L \sum_{i=1}^N x_{ijk} \geq 0 \quad k \in m \quad k \leq Z_{\max} \quad (7)$$

$$q_k = \sum_{i=1}^N \sum_{j=1}^L (x_{ijk} * p_i) \quad k \leq Z_{\max} \quad (8)$$

$$C_j + M(1 - x_{ijk}) \geq St_j + p_i \quad i \in I, j \in SE, k \in m \quad (9)$$

$$St_j + p_i + M(1 - x_{ijk}) \geq C_j \quad i \in I, j \in SE, k \in m \quad (10)$$

$$St_j = C_{j-1} \quad j \geq 2, j \in SE \quad (11)$$

$$P(i) = a(i) + b(i) \times (St(i) - AV(i)) \quad i \in I \quad (12)$$

$$S_i + M(1 - x_{ijk}) \geq St_j \quad i \in I, j \in SE, k \in m \quad (13)$$

$$St_j + M(1 - x_{ijk}) \geq S_i \quad i \in I, j \in SE, k \in m \quad (14)$$

$$T_k + M(1 - x_{ijk-1}) \geq C_j \quad i \in I, j \in SE, k \in m, k \geq 2 \quad (15)$$

$$St_j + M(1 - x_{ijk}) \geq T_k \quad i \in I, j \in SE, k \in m \quad (16)$$

$$S_i \geq S_g + p_g \quad i \in Jp, g \in Ep_i \quad (17)$$

$$y_k \geq x_{ijk} \quad k \in m, i \in I, j \in SE \quad (18)$$

$$y_k \geq y_{k+1} \quad k \in m, k \leq Z_{\max} - 1 \quad (19)$$

$$Z = \sum_{k=1}^z y_k \quad (20)$$

$$AV_i = 0 \quad i \in NP \quad (21)$$

$$AV_i = \max \{C_r\} \quad i \in Jp, r \in Ep_i \quad (22)$$

$$CO_i = p_i + S_i \quad i \in I \quad (23)$$

$$y_k = \{1, 0\} \quad k \in m \quad (24)$$

$$C(j), P(i) \geq 0, St(1) = 0.$$

Eq. (2) shows the objective function, Eq. (3) describes the cycle time and Eq. (4) shows the workload deviation formulation. Eq. (5) and Eq. (6) state that each job and sequence occur once. Eq. (7) shows that some stations could be free of tasks (maximum number of stations is equal to number of all tasks). Eq. (9) and Eq. (10) describes the completion time of job in sequence j . Eq. (15) and Eq. (16) state that the starting time of station k is greater or equal to completion time of former station. Eq. (17) shows the precedence relations among tasks. Eq. (18) and Eq. (19) describe that task assigning process starts from early stations to last ones where there is no any vacant station between two busy stations. Eq. (20) shows the number of workstations. Eq. (21) and Eq. (22) describe the formulation of available time. Eq. (23) shows the formulation of task completion time.

4. Solution methodology

4.1. LP-metric

Lp-metric method is one of the prominent MCDM methods to address multi-objective problems with inconsistent objectives (Aryanezhad, et al., 2009; Mazdeh, et al., 2010). In this paper, a multi-objective integer programming model is developed to minimize the cycle time, workload and number of workstations. Mazdeh et al. (2010) recommended the LP-metric method to demonstrate the importance of two objectives in a bi-criteria parallel machines scheduling problem. Lp-norm has different forms of norm one, two and the norm one is the simplest form which helps us integrate different objectives. Suppose f_1^*, f_2^* and f_3^* are the best values of three objective functions for our proposed model. The LP-metric objective function can be constructed as follows:

$$u = w_1 \left(\frac{f_1 - f_1^*}{f_1^*} \right) + w_2 \left(\frac{f_2 - f_2^*}{f_2^*} \right) + w_3 \left(\frac{f_3 - f_3^*}{f_3^*} \right), \quad (10)$$

where w_1 , w_2 and w_3 are the weights of the objective functions determined by the decision maker. In other word, the proposed model of this paper is first solved using each objective function, separately and then they are integrated using different weights with the utility function given in Eq. (10) into a single objective function and the problem is solved using different weights.

5. Genetic algorithm

Since the mathematical models does not give optimum solutions for large-scale problems in a reasonable amount of time, Meta-heuristic methods are exerted for these large problems to reach a near optimal solutions. Genetic algorithm (GA) raises a couple of important features. First it is a *stochastic* algorithm; randomness as an essential role in genetic algorithms. Both selection and reproduction needs random procedures. A second very important point is that genetic algorithms always consider a population of solutions. GA can recombine various solutions to get better ones and it uses the benefits of assortment. A population base algorithm is also very amenable for parallelization. The *robustness* of the GA methods is mentioned as something essential for the algorithm success which is the ability to perform consistently well on a broad range of problem types.

There is no particular requirement on the problem before using GAs, so it can be applied to resolve any problem.

5.1. GA for multi objective SALB problem

This paper presented a GA for the simple straight assembly line balancing problem with deteriorating tasks. In the case of assembly line balancing Kim et al. (2009) developed a genetic algorithm for two-sided assembly line balancing called neighborhood GA (n-GA). They used straight forward encoding scheme called *group-number* encoding. The individual they proposed was a string of length m (the number of tasks), each element of which is an integer between 1 and n (the number of mated-stations). Three main objective functions are considered in this paper as follows:

$$\begin{aligned} \min f_1 &= ct && \text{Minimizing the cycle time} \\ \min f_2 &= M && \text{Minimizing the number of work stations} \\ \min f_3 &= wd && \text{Minimizing the work load deviation} \end{aligned}$$

Minimizing the work load deviation will balance the assembly line and minimize the idle times in the work stations. The general procedure of the GA that used in this paper is as follows:

Step 1: Initial population of chromosomes is generated in size p ,

Step 2: Compute the fitness values of each chromosome,

Step 3: Choose a pair of chromosomes as parents by using the roulette wheels selecting method, generate offspring by doing crossover and then mutation with a probability of p_m (mutation probability).

Step 4: Insert the new population in to the new pool.

Step 5: If the stopping conditions are met, stop the searching process, select and decode the best chromosome and choose it as a the best solution. Otherwise, generate a new population and replace it with the former one and return to the step 3.

5.1.1. Representation

In this paper, each gene includes an integer number. Let n be the number of tasks in assembly line, each gene in chromosome includes an integer from 0 to n , also the number of all genomes in each chromosome which is against the zero is equal to number of all tasks which exists in the line. The position of gene in the chromosome, when a gene in a chromosome takes integer i not equals to zero, shows that task i is in which workstation and in what sequence is placed. As we can see from Fig.1, the number of genes in each chromosome is n^2 . Each n gene in the chromosome represents one workstation W_i . For an example, according to Fig. 1, task 1 is assigned to station 1 at the first sequence and task i is assigned to position $n+1$ and task k to $n+5$ shows that task i is assigned in station 2 before task k . Each chromosome should include integer numbers from 1 to n only for ones.

Assigning integer i at the t 'th gene shows that task i is assigned to station $\left[\frac{t}{n}\right]+1$. The maximum

number of workstations is equal to the number of all tasks, each task is assigned to separate one workstation, and the minimum number of workstations is equal to 1 if all tasks are assigned in one station. Assigning integer 0 for the last n genomes of the chromosome shows that the n 'th station is eliminated. Generally, if all last kn ($k < n$) genomes are 0, the number of k work stations are free of task and the number of stations in the system is computed as $M = n - k$, where M is the number of work stations. If task j depends on task i and to the one of the successors of task i , integer j cannot be placed at a gene that is in earlier position than the genome that task i is placed in it. Otherwise, the feasibility conditions do not hold and the chromosome is discarded.

1	2	n	n+1	n+5	n ² -1	n ²
1	0	...	0	i	0	k	...	0

W_1 W_2

Fig.1. An example of a chromosome

To prevent of creating vacant extra workstations between two occupied workstations, a checking process needs to be performed. In case the genomes from $kn+1$ to $2kn$ are zero, this means that no task is assigned to this station and we can eliminate the genomes and shift all the previous genome by kn .

5.1.2. Initial population

Genetic algorithm starts by generating initial population of chromosomes. Every integer is assigned just for ones, next assigning 0 for the rest of the genes. This first population must offer a wide diversity of genetic materials. The gene pool should be as large as possible so that any solution of the search space can be engendered. For this aim the algorithm is done for several pool sizes and then results are checked. If all constrains hold for the generated chromosome it is added to the population and it is discarded, otherwise. For generating initial population, first the jobs with no predecessor are chosen for assigning randomly in chromosomes, next the chromosomes, which do not heed the precedence relations, are removed. After creating initial population, fitness value is computed for each chromosome. Fitness function is defined as follows:

$$\text{fitness} = \frac{1}{g}. \quad (25)$$

The g is defined as the following equation:

$$g = w_1 \left(\frac{\sum_{k=1}^Z (Ct - q_k)}{Z} - f_1^* \right) / f_1^* + w_2 (CT - f_2^*) / f_2^* + w_3 (M - f_3^*) / f_3^*. \quad (26)$$

The first statement in Eq. (26) minimizes the work load deviation between work stations. CT and M designate the cycle time and the number of workstations, respectively, q exhibits the total processing time of all tasks assigned to station k and w_i represents the weighting values of objectives. With this definition of the fitness function, the objective of the algorithm is to maximize the fitness value. The better fitness has bigger chance to enter the next population. The problem is tested by several different values and the results are compared. The weights used in this paper is just to show the effectiveness of the weights in objective values, for using the algorithm in real situations decision maker can choose the weights, which are better for the problem.

5.1.3. Selection operation

Selection is the process of choosing two parents from the population for crossing. The purpose of selection is to emphasize better chromosomes in the population with the hope that their offspring have better fitness. Chromosomes are selected from the initial population as parents for propagation. In this paper, the roulette wheel selecting method is used for selecting parents from the initial population. Roulette selection is one of the traditional GA selection techniques. The expected value of a chromosome is obtained from dividing the fitness by the actual fitness of the population. A slice of the roulette wheel is assigned to each chromosome, the size of the slice is commensurate to the chromosome's fitness which means that as the basic rule of the roulette wheel selection method, for every chromosome in the population, the rule gives a chance to these chromosomes to be selected in order to execute the crossover and mutation. These dedicated chances are calculated on the basis of fitness functions of the chromosomes. First summation of fitness values (T) of the chromosomes of a population are computed where the domain is defined in the interval of $[0, T]$. Next, a random number between 0 and T is chosen and the chromosome, which is associated with the fitness is

selected as a parent. For example, if a chromosome number 1 has the fitness function of 4 and the chromosome number 2 has the fitness function of 6, then chromosome number 1 has the domain of [0,4] from the domain [0,T] and the chromosome 2 has the part of (4,10] from the domain [0,T].

5.1.4. Crossover operation

Crossover operator is applied to the mating pool with the hope that it creates offspring with a better fitness. In this paper a crossover technique, which is similar to precedence preservative crossover (PPX) crossover method is applied for the recombination. After selecting two parents for generating off springs, at first, an integer 0 value for the number of $n^2 - n$ items is assigned randomly in genomes of the chromosome. Next for the rest of the genomes we repeat a method which is similar to PPX crossover method. For this aim, integer random numbers from the set of {1, 2} are produced and they are assigned to the remained vacant genomes. The genomes except the ones which are labeled by 0. As we can observe from Fig. 2, the random integers of 1, 2 and 1 are assigned to vacant genomes. Integer number 1 indicates that the position of this genome in the chromosome must be filled by the first sequenced available task from parent 1. As we can observe, task number 1 is assigned in that position, which is selected from the first task from parent 1, and integer 2 shows that this position in the chromosome should be filled by the first sequenced task from parent 2 if it did not assigned already. In case it did, then the next sequenced task from parent 2 is selected. According to Fig 2, the next generated integer is 2 so task 3 is selected from the first available task from parent 2. Finally, the final randomly generated number is 1, so a task is selected from the next sequence and not the assigned task from parent 1 (task 2). More details for the procedure of PPX crossover method are available on the work by Sivanandam and Deepa (2008).

Parent 1	(0 1 0 0 0 2 0 3 0)
Parent 2	(3 0 0 1 0 0 0 2 0)
Random filling 0 in genomes	(0 0 0 0 0 0)
Random number {1, 2}	(1 2 1)
Child 1	(0 0 1 0 0 0 3 0 2)

Fig. 2. Crossover mechanism

Therefore, the first child is produced by performing the method explained earlier and the next child is produced using the proposed rule. In this paper, we define an alternative way to produce the second child. First, the alternative method assigns number 1 for the same position of produced random number 2 in child 1 and number 2 for the position of produced random number 1 in child 1. Therefore, the positions of genomes with zero value are fixed. In this paper, the crossover method is performed in three types shown in Table 1 by considering these two procedures of producing child 2 and by naming the regular one as procedure 1 and the presented inversing one as procedure 2.

Table 1

Three types of used crossover methods

Type 1	Produce child 1, next produce child 2 through the first procedure
Type 2	Produce child 1, next produce child 2 through the second procedure
Type 3	Apply type 1 and 2, then choose a pair of chromosomes from the set of $\{p_1, p_2, ch_1, ch_2\}$ by considering the fitness values

5.2.5. Mutation

The mutation occurs with the probability of p_m . Three kinds of mutation methods are considered in this paper. The first one is to select two integers from 1 to n (number of all tasks), which is located in the first sequence of a station and another one from the last sequence of that station and transfer them to the last sequence of former station and first sequence of frontier station, respectively. If just one task exists in the workstation, it is randomly transferred to the frontier station or to the former station. The method does not need to maintain the feasibility. The second method is to select one gene

randomly, which includes an integer between 1 to n and transfer it to the last sequence of former station or to the first sequence of the frontier station. The third one is to apply type 1 and 2 then choose a pair of chromosomes from the set of $\{p_1, p_2, ch_1, ch_2\}$ by considering the fitness values.

6. Computational results

We first implement the proposed GA for three small examples and we compare the results with the optimal solutions. The proposed model has been solved by Lingo 8 mathematical software and the program has been coded by Java language and with PC 3.2 GHz CPU and 1 GB of RAM. Fig. 3 shows the example used in this paper with 20 tasks, which is the same as the example given by Kim et al. (2009).

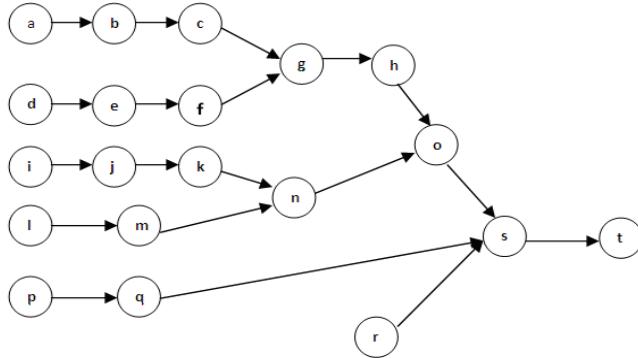


Fig. 3. precedence diagram of the example with 20 tasks

Table 2 shows the precedence, times and other information of this example. In our implementation, crossover-probability is 0.3, mutation probability is 0.05 and population size is 100. The maximum number of iteration is 1000, the running time is limited to only ten seconds, the maximum variance of population size is one and the number of program run for each scenario is limited to 10. Table 3 also shows the results of our implementation.

Table 2
Fixed processing time and deterioration rate

Task	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
Processing time	3	3	6	8	3	4	7	3	3	8	3	3	6	3	5	9	10	3	4	7
Deterioration rate	0.2	0.3	0.4	0.7	0.6	0.2	0.3	0.2	0.4	0.5	0.3	0.6	0.2	0.3	0.4	0.5	0.6	0.2	0.2	0.3

Table 3
The Pareto-optimal results for different weights with $g = Ct + W.D + M$, $Ct, M, W.D$

size	$w_1 = w_2 = w_3 = 1/3$			$w_1 = 0.6, w_2 = 0.2, w_3 = 0.2$			$w_1 = 0.2, w_2 = 0.2, w_3 = 0.6$		
Solver	Lingo	GA		Lingo	GA		Lingo	GA	
P4	8.44	8.44		8.22	8.22		8.44	8.44	
Ct	6.4	6.4		6.2	6.2		6.4	6.4	
M	2	2		2	2		2	2	
W.D	0.04	0.04		0.2	0.2		0.04	0.04	
P5	8.2,	8.2		7.385	7.385		7.385	7.385	
Ct	6,	6		4.2	4.2		4.2	4.2	
M	2,	2		3	3		3	3	
W.D	0.2	0.2		0.185	0.185		0.185	0.185	
P5	9.33	9.33		9.75	9.75		9.33	9.33	
Ct	5.6	5.6		4.5	4.5		5.6	5.6	
M	3	3		4	4		3	3	
W.D	0.73	0.73		1.25	1.25		0.73	0.73	

We have used the proposed GA method for another example from the literature where the input information of the problems with 12 tasks is presented in Table 4 and the Pareto-optimal solutions are summarized in Table 5 for different crossover mutation types. The first three rows of the table represent the results for crossover type 1, the second three rows present the results for crossover type 2 and the last three rows present the results for crossover type 3. As we can observe from Table 5, we get the best results for all three objectives when we use crossover number having equal weight set for all objective functions. For crossover type 2 and type 3 we may not find the best solutions for different weights under various mutation types.

Table 4

Fixed processing time and deterioration rate of the problem with 12 tasks

Task	1	2	3	4	5	6	7	8	9	10	11	12
Processing time	3	1	1	2	1	2	1	2	2	2	2	3
Deterioration rate	0.4	0.3	0.3	0.1	0.1	0.5	0.3	0.1	0.2	0.2	0.1	0.5

Table 5

The results of GA for the example with 12 tasks and crossover type 1, 2, 3 and mutation types 1, 2 and 3

Crossover	$w_1 = w_2 = w_3 = 0.333$			$w_1 = 0.6, w_2 = 0.2, w_3 = 0.2$			$w_1 = 0.2, w_2 = 0.2, w_3 = 0.6$		
	C1, M1	C1, M2	C1,M 3	C1, M1	C1,M2	C1,M3	C1, M1	C1,M2	C1,M3
Cycle Time	7.04	6.8	6.8	6.8	4.6	8.3	4.98	5.2	12.02
NO. Stations	5	5	5	5	6	4	7	7	3
W.D	0.77	0.64	0.37	0.37	0.08	1.25	0.02	0.5	0.16
Crossover	C2, M1	C2, M2	C2,M 3	C2, M1	C2,M2	C2,M3	C2, M1	C2,M2	C2,M3
Cycle Time	6.6	6.32	6.8	4.4	5.1	4.9	7.36	6.6	11.1296
NO. Stations	5	5	5	9	8	9	5	5	3
W.D	0.17	0.40	0.38	0.18	0.42	0.3	0.00	0.021	0.06
Crossover	C3, M1	C3, M2	C3,M 3	C3, M1	C3,M2	C3,M3	C3, M1	C3,M2	C3,M3
Cycle Time	7.28	6.6	6.6	4.5	5.56	4.9	4.982784	7.20192	9.0784
NO. Stations	5	5	5	9	7	9	7	5	4
W.D	0.52	0.66	0.38	0.28	0.36	0.8	0.09312	0.059	0.254886

7. Conclusion

In this paper, simple straight assembly line balancing problem with deteriorating tasks have been considered. By existence of deteriorating tasks in assembly lines, the problem of assigning tasks to the workstations changes to scheduling and assigning tasks to the workstations. A mathematical model based on 0-1 integer programming model has been developed with the objective functions of minimizing the cycle time, number of work stations and work load deviation. Since these cases of problems fall in to class of NP-hard, mathematical model cannot be applied for large-scale problems. Therefore, we have proposed a genetic algorithm where three kinds of crossover and mutation methods are used. The implementation of the proposed model has been used for some well-known benchmark problems and the results have been discussed.

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