Definition of Flexible Transfer Line with Rework Paths and Its Simulator for Optimal Production Design

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Abstract: The buffer size decision for the flexible transfer line (FTL) gains more and more importance because of growing FTL complexity. The buffer size in front of the bay of machines in the FTL is still one of the major optimization problems faced by production engineers. In this paper, we attempt to find the near optimal design of buffer size for flexible transfer line with rework paths (FTL-RP) that achieves the best throughput of the FTL-RP. A genetic algorithm (GA) is presented to find buffer size of FTL-RP. For the performance evaluation of the FTL-RP, the well known aggregation technique is used to find the throughput of the FTL-RP at a given buffer size. In order to achieve the efficient use of the GA, we propose the multiple vectors distribution method (MVDM) for the genes arrangement. An application example was developed and after a number of operations based on GA, the sizes of all buffers for the FTL-RP could be found.

Keywords: Flexible transfer line, buffer size, rework path, GA

1. Introduction

Production lines that have complicated structures such as parallels, reworks, feed-forward, etc. are widely used in high volume industries (Gershwin, 1994; Burman, 1995). Among them, the flexible transfer line with rework path (FTL-RP) is one of the common production styles in the modern industries. The buffer size decision for the production lines has gained more and more importance because of growing production lines complexity. The buffer size is still one of the major optimization problems faced by production engineers.

Many articles and researches related to buffer size have been published (Bulgak et al., 1995; Hillier et al., 1993; Gershwin and Schor, 1997; Enginarlar et al., 2002). To solve the buffer size problem, two requirements need to be considered. The first requirement is a search method used to solve the buffer size problem (Vouros and Papadopoulos, 1998; Spinellis and Papadopoulos, 2000; Mechatronics Engineering Department Philadelphia University, P.O. Box 1, Amman 19392, Jordan

Jafari and Shanthikumar, 1989). One of the methods used for studying the buffer size in production lines is genetic algorithm (GA) (Goldberg, 1989; Lawrence,

1991). GA is a global optimization technique used for various optimization problems, such as the buffer size problem. The second requirement is a model or approach that can be can used to evaluate and measure production performance (Askin and Standrige, 1993: line Papadopoulos et al., 1993; Buzacott and Shanthikumar, 1993; Perros, 1994; Gershwin, 1994; Altiok, 1997; Dallery and Gershwin, 1992; Papadopoulos and Heavey, 1996). However, despite the many existing buffer size methodologies, many research studies have focused on the buffer size problem for a serial production line, and there is a lack in the literature of studies that look at the buffer size of the complex production system such as FTL-RP.

In this paper, we attempt to find the near optimal buffer size for FTL-RP. We applied a GA for FTL-RP to find its buffer size that achieves the best throughput of the FTL-RP. For the performance evaluation of the FTL-RP, a well known aggregation technique (Li, 2003) is used as an evaluative method. This method finds the throughput of the FTL-RP at given buffer size. In order to achieve the efficient use of the GA, a multiple vectors distribution method (MVDM) is propose for the genes arrangement.

Before going through GA characteristics, the basic concepts of the FTL-RP are introduced.

2. Definition Of FTL with Rework Paths

FTL-RP is one of the major forms of a production system widely used in high volume industries. In the rework path, rejected parts are repaired. Then their fault is remedied. The parts will join the FTL again for re-processing once rework is completed. The part which is sent back to the FTL proceeds at the same course as the original one. The effect of the rework path is to increase the FTL throughput and reduce scrap, cost, etc. One of the widely used of rework paths appears in automotive paint shops. Defective parts are repaired in the rework path and sent back to the painting station for re-painting. To manage,

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operate, and improve the performance of FTL-RP, optimizing the buffer size of the whole system (FTL and its rework path) is necessary and important.

The FTL-RP studied in this paper is shown in Figure 1.

The FTL-RP model consists of main production line and rework path. The following assumptions are introduced to model FTL-RP this paper this paper deals with.



Figure1 Flexible Transfer Line with single rework path

- The FTL-RP consists of a main production line with k1 machines (M1, M2, ..., Mk1) arranged serially and (k1-1) buffers (B1, B2, ..., Bk1-1) separating each consecutive pair of machines. The rework path consists of k2 machines (M1, M2, ..., Mk2), each pair of machines separated by buffer, in addition to one buffer in front of the first machine and another buffer next to the last machine, thus the total buffers in the rework path is (k2+1) buffers (B1, B2, ..., Bk2, ..., Bk2+1).
- 2. Each machine M_i , i=1, ..., k1 and \hat{M}_j , j=1, ..., k2, has two states: up and down. When the machine is down, no production takes place. When up, machine is capable of production.
- 3. Production rate is 1 part per unit of time (cycle). In other words, identical cycle time is assumed.

4. Each buffer
$$B_i, \forall i = 1, ..., kl - l$$
 and B

j = 1, ..., k2 + 1 is characterized by its capacity S_i , $0 < S_i < \infty$.

- 5. The rework path may start after any machine in the main production line and end after any machine that's located before the start point of the rework path.
- 6. Each machine in main production line and rework path is starved at time *t* if the buffer in front of its bay is empty at time *t*. Machine M_1 is never starved. The merge machine, M_i is starved if both B_{i-1} and B_{k2+1} are empty.
- 7. Each machine in main production line and rework path is blocked at time *t* if the buffer located after it is full at time *t*. Machine M_{kl} is never blocked. The split machine, M_j is blocked by the main line if it produces a good part and B_j is full, while machine M_j is blocked by the rework path if it produces a defective part and \hat{B}_l is full.
- 8. The good part is sent to B_j if it is not full and the defective part is sent to \hat{B}_l if it is not full. A part is defective with probability α , $0 < \alpha < 1$. A part will continue to circulate in the system until it satisfies the

quality requirements.

9. Machine M_i always takes part from rework path first if it is not empty. Machine M_i can take one part each cycle either from upstream of main production line or from the rework path.

In this paper, GA is introduced to find the buffer size for FTL-RP defined by assumptions (1-9).

3. GA ant its MVEM

GA is a global optimization technique used for various optimization problems. GA differ from other search techniques which depend on natural genetic evaluation process, start with an initial set of solutions selected randomly called *population* and follow the biological evolution process to improve upon them. The solution set in the population, called as *chromosome* or *individual*, represents a solution to the optimization problem. Each individual contains a number of genes. The individuals in the initial population are *evaluated* to measure its *fitness*. Based on the individuals' fitness, some individuals are selected from the current population as parents. GA operations like crossover and mutation are then applied to the parents to generate new individuals, called offspring's. These offspring's are then evaluated. A new population can be generated by selecting some of the parents and offspring's. The iteration, called a generation will continue until the fitness reaches its maximum value. The best overall solution becomes the candidate solution to the problem. In this paper, we present the determination of a near optimal design for an S-PPL. The arrangement of genes in individuals is different from that obtained using the conventional arrangement methods. The operations for our GA are also different. The characteristics of the GA are described in sections 3-1 ~ 3-6.

3.1 GA Outline

The GA can be executed by using the flow chart in Figure

2. The index I in the flow chart refers to an individual in a population of N size and the variable Gen is the current generation number. As shown in Figure 2, the initial population is randomly selected. After the fitness evaluation for each individual in the population, the GA operations are carried out to generate the next generation.



Figure 2 GA flow chart

3.2 Multiple Vector Distribution method

The goal of our research is to determine buffer size in front of the bay of each machine in the FTL-RP. We adopt the GA to determine the buffer size. One of the important jobs to use GA is how to express a chromosome. The conventional GA operation is generally based on an individual with a linear gene arrangement. In the case of FTL-RP, it is difficult to use a linear arrangement of genes in individuals to find a buffer size. This is because the FTL-RP buffers are arranged in more than one line, and it is impossible to express such arrangement with conventional gene arrangement methods. In order to solve this problem, we propose MVDM as new individual expression of genes. MVDM expresses the individuals with multi vectors; each vector represents one part of the production line buffers. For the production system we are studying here, that is FTL-RP, 2 vectors will be used, one vector represents the main production line buffers, and another vector represents the rework path buffers. According to this arrangement method the buffer size

arrangement of FTL-RP shown in Figure 1 can be defined as the following equation.

$$BS = \left\{ \begin{bmatrix} B_1 & B_2 & \dots & B_{kl-2} & B_{kl-1} \end{bmatrix} \\ \begin{bmatrix} \widehat{B}_1 & \widehat{B}_2 & \dots & \widehat{B}_{k2} & \widehat{B}_{k2+1} \end{bmatrix} \right\}, \quad kI > k2$$
(1)

Each buffer size in FTL-RP represents a gene, thus the individuals used in our GA can be coded by replacing buffer sizes B_i and \hat{B}_j in Equation (1) with genes G_i and \hat{G}_j respectively, $\forall i = 1, 2, ..., kl - 1$ and $\forall j = 1, 2, ..., k2 + 1$. The individual using MVEM is defined as follows.

$$individual = \left\{ \begin{bmatrix} G_1 & G_2 & \dots & G_{k\,l-1} \\ \hat{G}_1 & \hat{G}_2 & \dots & \hat{G}_{k\,2+1} \end{bmatrix} \right\}, \ kl > k2 \quad (2)$$

The number of vectors of the individual is not limited, which means that any production system with any number of rework paths can be dealt with.



Figure 3 MA of the individuals

3.3 Crossover by MVEM

The arrangement of genes in individuals using MVDM is different from that which is obtained using the conventional arrangement method. The crossover operations for our GA are also different. The main difference between the MVDM crossover and the conventional methods crossover is that MVDM crossover applies to each vector in the individual independently using a different crossover point for each vector. The crossover of our GA is carried out by using the following steps.

Step1: Choose two individuals randomly from the current population according to their fitness.

Step2: Select two crossover points randomly, [number of crossover points equals the number of vectors in the individuals, and its 2 here as defined in Equation (2)]. The two crossover points, CP_1 , CP_2 are selected as follows

 $CP_i \leftarrow random[1, ..., i, ..., kl - 2]$, *i* refer to the position between genes G_i and G_{i+1} .

 $CP_2 \leftarrow random[1, ..., j, ..., k2]$, *j* refer to the position between genes G_j and G_{j+1} .

Step3: Swap the genes after the crossover point CP_1 in the first vector among the two individuals. Similarly, swap the genes after the crossover point CP_2 in the second vector among the two individuals. Figure 5 shows the crossover graphically.

3.4 Mutation by MVEM

The mutation of our GA is different because the gene expression adopts MVDM. The characteristic of the mutation is to change the value of one gene for each vector in the individual. The mutation is carried out using the following steps.

Step1: Choose an individual randomly from the current population

Step2: Select mutation places randomly, [number of mutation places equals the number of vectors in the individual, one mutation place for each vector, and its 2 here as defined in Equation (2)].

The two mutation places, MP_1 , MP_2 are selected as follows

 $MP_{1} \leftarrow random[1, ..., k1 - 1]$ $MP_{2} \leftarrow random[1, ..., k2 + 1].$

3.5 Implementation of GA

Step3: Replace each gene in the selected places with a new value; the new values are randomly selected from $(1 \sim S)$, where S is the maximum buffer capacity. Figure 6 shows the mutation graphically. Assume that the two mutation places, MP1, MP2 are selected randomly as 3, 2 respectively.

Before describing our implementation of the GA, the following notations are defined.

- *N* Number of individuals in the population
- *s* Number of individuals that select on elitist strategy
- P_i Selection probability of individual i
- F_i Fitness of individual i
- C_r Crossover rate.
- M_r Mutation rate.

[Algorithm to implement the GA]

Step 1 [Initialization]: Randomly select the initial population.

Step 2 [Elitist selection]: Select *s* individuals that have high fitness based on elitist strategy and send the selected individuals to the next generation.

Step 3 [Crossover]: Randomly select a pair of individuals from the current population by the selection probability based on fitness and carry out crossover operation.

Step 4 [Mutation]: Randomly select an individual from the current population based on fitness and carry out mutation operation.

Step 5: Apply the following rule:

if $(C_r \times N + M_r \times N) = N - s$, *then*, continue to step 7, *if not*, return to step 4.

Step 6: Regard *N* individuals acquired in steps 2-6 as the next generation population.

Step 7: Loop until fitness reaches its maximum value.

$\begin{cases} A & CP_1 & B \\ \hline G_1 & G_2 & \dots & \hline G_{kl-2} & G_{kl-1} \\ \hline G_2 & G_{kl-2} & G_{kl-1} \\ \hline G_{kl-2}$



Figure 6 Individual after and before mutation



Figure 7 The data flow chart of the GA

The data flow chart of the GA is shown in Figure 7.

4. Throughput evaluation of the FTL-RP

To evaluate the performance of a FTL-RP, an estimation of production rate of a serial line is needed. However, no closed form expression for performance of a serial line with more than two (non-identical) machines is available.

4.1 Serial production Lines

Consider a serial line with N machines, defined by assumption (1-9) without rework path. The aggregation the first two machines into a single machine, M_2^f , with downtime parameter r_2^f defined as

$$r_2^f = r_2 [1 - Q(p_1, r_1, p_2, r_2, N_1)]$$
(3)

And the uptime parameter p_2^f selected so that

$$\frac{r_2^f}{p_2^f + r_2^f} = \frac{r_2}{p_2 + r_2} [1 - Q(p_1, r_1, p_2, r_2, N_1)]$$
(4)

Thus, the uptime parameter p_2^f is

$$p_2^f = p_2 + r_2 Q(p_1, r_1, p_2, r_2, N_1)$$
(5)

$$\begin{aligned}
\mathcal{Q}(p_{l},r_{l},p_{2},r_{2},N_{l}) &= \begin{cases} \frac{(l-e_{l})(l-\Phi)}{l-\Phi e^{-\rho N}+r_{2}}, & \text{if } \frac{p_{l}}{r_{l}} \neq \frac{p_{2}}{r_{2}} \\
\frac{p_{l}(p_{l}+p_{2})(r_{l}+r_{2})}{(p_{l}+r_{1})[(p_{l}+p_{2})(r_{l}+r_{2})+p_{2}r_{l}(p_{l}+p_{2}+r_{l}+r_{2})N]}, & \text{if } \frac{p_{l}}{r_{l}} = \frac{p_{2}}{r_{2}} \\
\text{where} \\
e_{l} &= \frac{r_{l}}{p_{l}+r_{l}}, i = l, 2, \quad \Phi = \frac{e_{l}(l-e_{1})}{e_{2}(l-e_{1})} \text{ and } \beta = \frac{(p_{l}+p_{2}+r_{l}+r_{2})(p_{l}r_{2}-p_{2}r_{l})}{(p_{l}+p_{2})(r_{l}+r_{2})} \end{aligned}$$
(6)

Where Q(p_1, r_1, p_2, r_2, N_1) is the probability that machine M_2 is starved and is defined in Equation (6) (Chiang et al., 2000). Next, M_2^{f} is aggregated with M_3 to result in M_3^{f} , and so on until all N machines are aggregated in a single one, M_N^{f} . This constitutes the forward aggregation (superscript *f* is used to denote this fact). Then, in the backward aggregation, the last machine, M_N , is aggregated with M_{N-1} to result in M_{N-1}^{b} and so on until all machines are aggregated in a single machine, M_1^{b} . The procedure is repeated until a convergence is satisfied. Follows the Procedure for serial line in (LI J., 2004), the production rate can be approximated as follows.

$$PR(p_1, r_1, \dots, p_N, r_N, N_1, \dots, N_{N-I}) = \frac{r_N^f}{p_N^f + r_N^f} = \frac{r_I^b}{p_I^b + r_I^b}$$

4.2 Production line with rework path

The FTL-RP decomposes to 4 serial production lines. Line 1 consists of machines and buffers from the start of main production line till the merge machine and the last is included in this line. Line 2 consists of machine and buffers from the merge machine to the split machine, merge and split machines are include in this line. Line 3 consists of machines and buffers from the split machine to the end of the main production line. Finally Line 4 is represented by the rework path in addition to the merge and split machines.

Since merge machine and split machine are included in more than one serial line, this decomposition includes overlapping. Following the definitions and procedures described in (LI J., 2004), the FTL-RP production rate can be evaluated as:

$$PR = pr_3$$

In addition, the following relationships are hold:

$$pr_1 - pr_3;$$

$$pr_2 = pr_1 + pr_{4;}$$

where

 pr_i is production rate estimation of line i, i = 1, 2, 3, 4.



Figure 8 Flexible Transfer Line with rework path



Figure 9: Best Fitness Curve.

B ₁	B ₂	B ₃	B ₄	B ₅	B ₆	B ₇	B ₈	B ₉	B ₁₀	B ₁₁	B ₁₂	B ₁₃	B ₁₄	B ₁₅
5	8	6	5	3	7	8	9	4	7	6	7	8	3	8
B ₁₆	B ₁₇	B ₁₈	B ₁₉	B ₂₀	B ₂₁	B ₂₂	B ₂₃	B ₂₄	B ₂₅	B ₂₆	B ₂₇	B ₂₈	B ₂₉	B ₃₀
2	6	6	2	5	7	4	9	5	3	2	2	3	1	3

Table 1 Individual of the maximum fitness

5. Numerical Experiments

The FTL-RP we adopted has 30 machines (25 machines in main production line and 5 machines in rework path) as shown in Figure 8. The maximum buffer size in front of the bay of each machine is 10. In this example the parts variety is 50, each part have a different machining time for each machine and machining time is (15- 20 sec). Each machine stops 6 times an hour, stopping time is 15 sec, each machine stops for a quality check every 100 parts and one defective product is machined once an hour. 10% of the parts are reworked. The one cycle of the input parts sequence into the bay of the FTL is decided based on the one-to-one method (Yamamoto, 2000).

Figure 9 shows the best fitness curve with the generation. In this curve, the fitness increases with the generations until it reaches its maximum value. The fitness was improved from approximately 83 to more than 88. That means the buffer size was improved. In other words GA is useful for buffer size decisions in FTL-RP. Table 1 gives the buffer size acquired at the best fitness. In Table 1, the buffers $B_1 \sim B_{25}$ represent the main production line buffer sizes and the buffers $B_{26} \sim B_{30}$ represent the rework path buffer sizes.

6. Conclusions

This study introduced the GA to determine the buffer size in FTL-RP. The GA searches for the better buffer size which can aid in achieving maximum production rate. Applying the crossover and mutation techniques can discover the gene corresponding to the buffer size of FTL-RP. MVDM for genes is adopted for the genes arrangement in each individual. The aggregation technique is used as an evaluative method in conjunction with a GA. We applied GA to some FTL-RP examples. After a number of generations, the best buffer size of the FTL-RP could be found. The results of the study can be used to improve the production plan, and production engineers can use these results when making decisions on a buffer size.

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