



An endosymbiotic evolutionary algorithm for the integration of balancing and sequencing in mixed-model U-lines

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Abstract

This paper proposes a new evolutionary approach to deal with both balancing and sequencing problems in mixed-model U-shaped lines. The use of U-shaped lines is an important element in Just-In-Time production. For an efficient operation of the lines, it is important to have a proper line balancing and model sequencing. A new genetic approach, called endosymbiotic evolutionary algorithm, is proposed to solve the two problems of line balancing and model sequencing at the same time. The algorithm imitates the natural evolution process of endosymbionts that is an extension of existing cooperative or symbiotic evolutionary algorithm. The distinguishing feature of the proposed algorithm is that it maintains endosymbionts that are a combination of an individual and its symbiotic partner. The existence of endosymbionts can accelerate the speed that individuals converge to good solutions. This enhanced capability of exploitation together with the parallel search capability of traditional symbiotic algorithms results in finding better quality solutions than existing hierarchical approaches and symbiotic algorithms. A set of experiments are carried out, and the results are reported.

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1. Introduction

This paper deals with balancing and sequencing problems in mixed-model U-shaped lines. As is well known, the use of U-shaped lines (hereafter called *U-lines*) is an important element in

Just-In-Time (JIT) production. A U-line often adopts the strategy of mixing product models. This helps manufacturers provide their customers with a variety of products in a timely and cost effective manner. For an efficient operation of the mixed-model U-line, it is important to have a proper line balancing and model sequencing [24]. Line balancing is a problem of assigning tasks to workstations (hereafter called *stations*), and model sequencing is a problem of determining a production sequence of models. This paper proposes a new method that can efficiently solve the two problems simultaneously.

The two problems of balancing and sequencing are tightly interrelated with each other in mixed-model production lines. The optimality of model sequencing depends on the results of line balancing, which is in turn affected by the model sequencing. However, many researches have treated the two problems separately. For traditional mixed-model straight lines (MMSLs), the line balancing has been studied by Thomopoulos [27], Macaskill [14], and Chakravarty and Shtub [4]. The model sequencing in MMSLs has been investigated by a number of researchers including Yano and Rachamadugu [29], Bard et al. [2], and Kim et al. [11]. For mixed-model U-lines (MMULs), Sparling and Miltenburg [24] is the only study we could find dealing with the line balancing. The model sequencing in JIT production systems has been addressed by Miltenburg [17] and Monden [18]. Recently, genetic algorithms have drawn a great amount of attention in this area [11,13,23], but most of them consider only one of the two problems.

There have been a few researches dealing with the two problems at the same time. Thomopoulos [26], Dar-El and Nadivi [6], and Merengo et al. [16] have proposed hierarchical approaches to solve the problem in MMSLs. Rekiek et al. [22] have proposed an iterative hierarchical procedure with feedback mechanism in MMSL. Kim et al. [12] have developed a special kind of genetic algorithm (GA), called symbiotic evolutionary algorithm, to deal with the integration of balancing and sequencing problems in MMUL. In the hierarchical approaches, one problem is solved first, and then the other under the constraint of the first

solution. Such an approach has been widely used to solve a complex problem that can be decomposed into several sub-problems. However, this approach cannot explore the solution space effectively, and is therefore limited in finding good solutions. A symbiotic evolutionary algorithm is a stochastic search algorithm that imitates the biological coevolution process through symbiotic interaction [20]. Kim et al. [12] have demonstrated that the genetic approach provides better solutions than a hierarchical approach.

In this paper, we develop a new algorithm, called endosymbiotic evolutionary algorithm, which simulates the endosymbiotic evolution process [15]. As the name implies, the new approach is an extension of symbiotic evolutionary algorithm. It can overcome some of the shortcomings found in the symbiotic evolutionary algorithm. This paper presents how the endosymbiotic evolutionary algorithm is applied to solving the integrated problem of balancing and sequencing in MMULs. The proposed algorithm is compared with existing evolutionary algorithms in terms of solution quality and convergence speed.

2. Balancing and sequencing MMULs

2.1. Operation of MMULs

It is assumed that the MMUL considered in this paper operates under the following conditions. First, tasks are assigned to a given number of stations that can cross from one side of the line to the other. Second, a combined precedence diagram [14] is employed, which synthesizes traditional precedence diagrams for every model. Third, each task type is assigned to only one station regardless of models. That is, tasks are not assigned to different stations for different models. Fourth, the line operates asynchronously and the time taken for a worker to move on the line is ignored. Finally, the line takes the strategy of cyclic production. Let M be the number of models that should be produced during a planning period. Let D_m ($m = 1, 2, \dots, M$) be the demand of model m during the period, and h be the greatest common divisor of D_1, D_2, \dots, D_M . Then, the vector,

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