

行政院國家科學委員會專題研究計畫 成果報告

作業時間不固定下之裝配線平衡與排序:新數學模型與方法

計畫類別：個別型計畫

計畫編號：NSC91-2416-H-002-006-

執行期間：91年08月01日至92年07月31日

執行單位：國立臺灣大學工商管理學系

計畫主持人：賴聰乾

報告類型：精簡報告

處理方式：本計畫可公開查詢

中 華 民 國 92 年 9 月 15 日

行政院國家科學委員會補助專題研究計畫成果報告

作業時間不固定下之裝配線平衡與排序：

新數學模型與方法

New Mathematical Models and Methods for Assembly Line Balancing
and Sequencing with Random and Bounded Operations Times

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計畫主持人：賴聰乾

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執行單位：台大工商管理系

中華民國 92 年 9 月 10 日

一、摘要

本報告呈現關於雙機串聯排序問題方面之有趣(值得發表於國際刊物)研究結果。該問題中, 雙機之任一部機器皆有可能存在若干個非可用時段, 作業目標在使作業全程最小。機器之非可用時段係裝配排程常見之限制條件。只要存在有一非可用時段(不論是發生於第一或第二部機器), 該問題便是 binary NP-hard。對給定之非可用時段個數 w , 就 Johnson 排序之最適狀態, 推導充分與必要條件。亦對該問題從事穩定度分析, 並從事計算實驗, 實驗範圍: 工作數介於 5 至 10000 間且非可用時段個數介於 1 至 1000。

關鍵詞: 雙機, 排序, 非可用時段, 穩定度分析, 作業全程, NP-難度。

Abstract

This report presents an interesting research result, which seems publishable in a well-recognized international journal, on a sequencing problem of minimizing the makespan in the two-machine-in-series n -job with w non-availability intervals on each of the two machines. The non-availability of a machine often occurs in the scenarios of assembly line sequencing. This problem is binary NP-hard even if there is only one non-availability interval either on the first or the second machine. Sufficient conditions are derived for optimality of Johnson's permutation in the case of the given $w \geq 1$ non-availability intervals. A stability analysis is conducted and demonstrated on a huge number of randomly generated problem instances with n between 5 and 10000, and w between 1 and 1000.

Keywords: *two-machine, sequencing, non-availability intervals, stability analysis, makespan, NP-hard.*

二、緣由與目的

A number of recent papers have been devoted to the makespan minimization for two-machine-in-series sequencing problem with $w \geq 1$ non-availability intervals. It was shown that this problem is unary NP-hard if an arbitrary number w of non-availability intervals occur on one of two machines (Kubiak et al. 2002). It was also shown to be binary NP-hard even if there is a single non-availability interval ($w=1$) on either machine 1 or machine 2 (Lee 1997). In the case of $w=0$, however, Johnson's permutation is optimal (Johnson 1954).

The aim of this research is to use the stability analysis of an optimal sequence for the two-machine-in-series problem with limited machine availability, which often occurs in the scenarios of assembly line sequencing. The influence of possible variations of the processing times on the optimality of a schedule was investigated in Sotskov (1991) where the stability radius of an optimal schedule was studied for a job-shop problem with $m \geq 2$ machines. Necessary and sufficient conditions for a schedule in a job-shop to have an infinitely large stability radius were proven by Kravchenko et al. (1995).

三、成果與討論

It is computed in this project for the stability polytope and stability radius of Johnson's permutation, which is the minimum of maximal possible enlargements r_{ij} of jobs i ($i=1, 2, \dots, n$) on machine j ($j=1, 2$). The stability polytope and stability radius can be computed in $O(n)$ time. It is also computed for the enlargement polytope and enlargement radius of the processing times of the operations on the machine j , which is the maximum of possible enlargements d_{ij} of time intervals used for job i on machine j caused by non-availability intervals. It is shown that a permutation remains optimal if $d_{ij} \leq r_{ij}$ for all i ($i=1, 2, \dots, n$) and j ($j=1, 2$). The enlargement polytope and radius q_j can be computed in $O(w^2 + n \log n)$ time. Intensive computational experiments are also conducted.

It should be noted that the stability analysis may also be used for other sequencing problems with limited machine availability if an optimal schedule for the corresponding pure setting of the problem can be constructed applying a priority rule to jobs such as SPT, LPT and so on. Moreover, one can use the above results for some kind of online settings of sequencing problems when there is no prior information about the exact location of the non-availability intervals on the time axis but values d_{ij} or values q_j , ($i=1, 2, \dots, n$ and $j=1, 2$), are known before sequencing.

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