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Transactions on Engineering Technologies

World Congress on Engineering and Computer Science 2014

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Preface

A large international conference on Advances in Engineering Technologies and Physical Science was held in San Francisco, California, USA, October 22–24, 2014, under the World Congress on Engineering and Computer Science (WCES 2014). The WCECS 2014 is organized by the International Association of Engineers (IAENG). IAENG is a nonprofit international association for the engineers and the computer scientists, which was founded originally in 1968 and has been undergoing rapid expansions in recent few years. The WCECS Congress serves as an excellent platform for the engineering community to meet with each other and to exchange ideas. The Congress has also struck a balance between theoretical and application development. The conference committees have been formed with over two hundred members who are mainly research center heads, deans, department heads/chairs, professors, and research scientists from over 30 countries. The full committee list is available at the congress' Web site: www.iaeng.org/WCECS2014/committee.html. The Congress is truly an international meeting with a high level of participation from many countries. The response to the conference call for papers was excellent with more than 600 manuscript submissions for the WCECS 2014. All submitted papers went through the peer review process, and the overall acceptance rate was 51.28 %.

This volume contains 39 revised and extended research articles, written by prominent researchers participating in the congress. Topics covered include engineering mathematics, electrical engineering, circuits, communications systems, computer science, chemical engineering, systems engineering, manufacture engineering, and industrial applications. This book offers the state of the art of tremendous advances in engineering technologies and physical science and applications, and also serves as an excellent source of reference for researchers and graduate students working with/on engineering technologies and physical science and applications.

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The original version of the book frontmatter was revised: The spelling of the last editor's name was corrected. The erratum to the book frontmatter is available at
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Contents

Genetic Algorithm for Energy Consumption Variance Minimisation in Manufacturing Production Lines Through Schedule Manipulation

Chris Duerden, Lik-Kwan Shark, Geoff Hall and Joe Howe

Abstract The typical manufacturing scheduling algorithms do not account for the energy consumption of each job when devising a schedule. This can potentially lead to periods of high energy demand which can be problematic for manufacturers with local infrastructure having limited energy distribution capabilities. In this book chapter, a genetic algorithm based schedule modification algorithm is introduced to optimise an original schedule such that it produces a minimal variance in the total energy consumption in a multi-process manufacturing production line. Results show a significant reduction in energy consumption variance can be achieved on schedules containing multiple concurrent jobs without breaching process constraints.

Keywords Energy consumption prediction · Energy consumption variance · Genetic algorithm · Peak energy minimisation · Production scheduling · Real value encoding

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1 Introduction

In the manufacturing sector, high throughput combined with efficient use of resources is critical for achieving an optimal cost-benefit ratio. During the generation of a production schedule the manufacturing jobs needing to be processed are assigned to the limited machinery and equipment available in such a way to ensure resource availability is never exceeded, and the scheduling constraints are satisfied [1]. Despite the crucial role it plays, many scheduling algorithms do not consider the energy demand. As jobs are executed, their demand for energy can change depending on the elemental operation they are currently performing. If this is not considered when the schedule is generated, there is the potential for very high peaks in energy demand due to the sum demand of many individual jobs running concurrently. As there is always a finite delivery rate in the energy infrastructure, this can potentially limit the availability and capacity of a manufacturing production line. Several researchers have discussed methods for including additional energy-based objectives for traditional schedulers to optimise. Fang et al. and Pechmann et al. both present methodologies for production schedules which aim to also minimise peak energy consumption [2–4]. As does the commercial scheduling software E-PPS by Transfact [5]. While the work of Fang et al. and Pechmann et al. shows promising results, it is concluded by Fang et al. that finding the optimal schedule is difficult due to the complexity and NP-hard nature of the problem. Another promising research focus is the development of intelligent machine controllers which aim to reduce overall manufacturing energy consumption by reducing the idling times of machines by putting them into energy saving modes or shut them down entirely [6–8]. As certain machines may have lengthy or costly start-up procedures, manufacturers typically leave machines idling when not in operation. In the proposed systems, by intelligently deciding when to shut down a machine or put it into an energy saving mode, the total energy consumption for the production line can be reduced.

While all these show promising results, the problem with generating energy optimised schedules has received little attention and appears to be plagued by its NP-hard nature. The use of artificial intelligence in the generation of manufacturing schedules has shown some promising results. Genetic algorithms appear to be a popular choice for solving scheduling optimisation which can include multi-objective [9, 10] and multi-project [11] problems.

In this work, a genetic algorithm is developed to modify the starting times of scheduled jobs, in order to minimise the variance in production line energy consumption without exceeding the process constraints [12]. The technique used is inspired by load-shifting, a traditional energy optimisation method in which energy intensive jobs are scheduled to run during times of low energy tariffs [13]. While the optimisation algorithm discussed below can be applied to all forms of energy consumption, in the context of this work, only electrical power is considered. Following the methodology described in Sect. 2, experiments and results are presented in Sect. 3 to demonstrate the level of potential reduction in energy consumption variance.

2 Methodology

Prior to any energy-based optimisation, a manufacturing schedule is initially generated for a list of jobs using a traditional scheduling algorithm. This will typically output a schedule optimised for processing time. Additionally, factors such as optimal intra-process job order and machine assignment have been determined by a piece of software trusted by the manufacturer. The schedule modification algorithm is then applied. This references job-specific energy profiles and alters the original job starting times in an attempt to minimise the production line energy consumption variance. Because the job start times must represent a valid schedule, not all possible combinations of job start times will be usable. To traverse such a volatile search space a genetic algorithm was selected as the basis for this schedule modification algorithm. This is a popular population-based evolutionary algorithm which has been applied to many complex optimisation problems.

A. Gene Representation and Chromosome Generation

In order for the genetic algorithm to optimise the schedules job start times, the start times themselves must be encoded into a form suitable for the algorithm to efficiently process. For this, real value encoding [14] was selected with the value of each gene in the chromosome representing the start time for a particular job. As such, for a schedule containing N jobs, the genetic algorithm will operate on a population consisting of multiple N length chromosomes. Each chromosome consists of an encoded candidate solution and an associated fitness value which represents the optimality of the candidate solution to the proposed problem. To convert job start times between the chromosome domain G and the time domain S, specialised encoding (1) and decoding (2) functions are used. Here s_e is the earliest starting time in the original schedule and it is used as a reference point for encoding and decoding job start time s_i to or from gene g_i. T is the minimum time alteration that can be applied to the job start time.

Encoding:

$$g_i = (s_i - s_e)/T \tag{1}$$

Decoding:

$$s_i = s_e + (g_i \times T) \tag{2}$$

The scheduling paradigm followed by this schedule modification algorithm defines manufacturing processes as independent of one another, allowing them to run in parallel. However intra-process jobs must be executed sequentially. At the beginning of the algorithms execution, the initial population comprises of $Np-1$ randomly generated chromosomes, where Np is the population size, along with the original encoded schedule. To ensure that the genes of each chromosome comply with this paradigm and the original job order, a relation seed is generated prior to

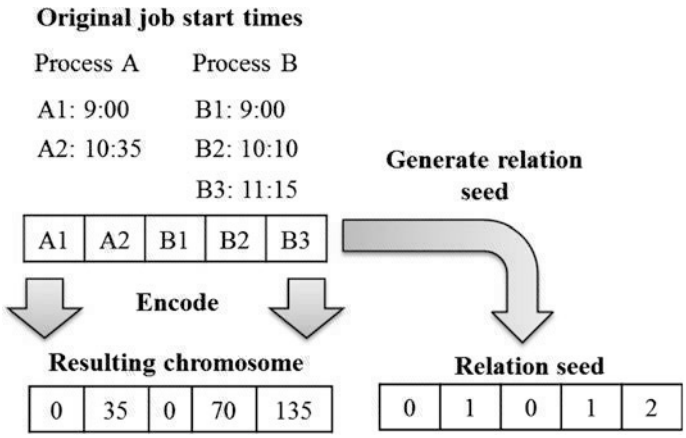

Fig. 1 Diagram showing how the original schedule is used to encode the initial chromosome and generate the relation seed. In this example, the earliest start time s_e is A1/B1, and T is set to 00:01:00

the population generation. The encoded job start times are ordered in the chromosome firstly by process, and secondly by intra-process order. The relation seed is a zero-based unit incrementing numeric vector of equal length to the chromosome, and denoted by $R = \{r_0, \ldots, r_{N-1}\}$. When an encoded job start time is the first in its process, its associated relation seed value is zero. The associated relation seed value following that is assigned a unit incrementing value until it reaches the end of that process. At this stage the count is reset to zero for the first job in the next process. An example relation seed can be seen in Fig. 1. The relation seed is subsequently utilised as one of many constraints by the random number generator to ensure job order is maintained. All these constraints aim to reduce the overall size of the search space and increase the probability of a candidate solution representing a valid schedule. For a job denoted by i and belonging to a process denoted by u with deadline d_u, then the candidate job start time is given by (3),

$$s_i = \left\{ \begin{array}{ll} 0 \leq random\ number \leq d_u & if\ r_i = 0 \\ s_{i-1} \leq random\ number \leq d_u & if\ r_i > 0 \end{array} \right\} \tag{3}$$

B. Algorithm Overview

Based on Darwinism, a genetic algorithm is designed to locate an optimal or near-optimal solution by evolving a population of chromosomes, which are our candidate schedule solutions. This evolutionary process consists of three steps—Selection, Crossover and Mutation. At the beginning of the process, selection is used to emulate 'survival of the fittest' to generate a reproducing population from the current population. This reproducing population is of size $Np-2$ to allow for two candidate elitism. Every chromosome has a non-equal chance of being selected, with fitter chromosomes having better odds. The selection algorithm used in this

implementation is tournament selection. Here a group of chromosomes are randomly selected and the fittest in the group is assigned to the reproducing population. This process is repeated until the reproducing population reaches the required size of $Np-2$. While there are a number of different selection algorithms available, tournament selection was used due to its simplicity, and as a result, computational efficiency. The reproducing population is then operated on.

Uniform crossover is then applied to generate the new population. Designed to emulate reproduction, chromosomes are grouped into couples and are split into two at the same random point. The two halves are then swapped between chromosomes and recombined to form two new chromosomes. An illustration of this can be found in Fig. 3. Next, each chromosome has a mutation operation applied to it. Here, each gene in the chromosome has a small probability of being mutated, where its value is randomly changed. This allows the algorithm to explore new areas of the search space. After each chromosome in the reproducing population has been operated on, the next generation of the population is constructed by combining the reproduced population with a copy of the two fittest candidates from the previous generation. These are saved via elitism. The fitness of each candidate in the new population is then calculated. In a standard genetic algorithm, this process is repeated either a predetermined number of times or until the optimal value (if known) has been found.

While the algorithms objective is to locate a combination of job start times which will generate a minimal variance in production line energy consumption, this combination of start times must also represent a valid schedule so that it could potentially be executed on the proposed production line. Despite the initial candidate generation constraints, there is the potential for a large percentage of candidates to represent invalid schedules in the population. To compensate for this, additional features have been added to increase the probability of candidates representing valid schedules.

A flow diagram of the algorithm can be seen in Fig. 2. The core of the genetic algorithm is located inside the inner loop. Here the standard operators manipulate the population with an aim to locate the global optimal solution. During the uniform crossover and mutation operations there is the potential for a valid candidate schedule to become invalidated. This is demonstrated in Fig. 3.

After crossover has been applied, each child chromosome is checked at the point of crossover to see if the job order has been breached. If it has, the affected job g_i is modified according to (4).

$$g_i = (g_{i-1} + C_{i-1} + 1) \tag{4}$$

where C_{i-1} is the makespan of the previous job represented by g_{i-1}. Similarly with the mutation operator, if a gene is selected for mutation the range of possible values is limited according to (5),

$$(g_{i-1} + C_{i-1} + 1) \leq g_i \leq (g_{i+1} - C_i - 1) \tag{5}$$