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Multi-objective optimization of a two-dimensional cutting problem using genetic algorithms

S. Tiwari [a], N. Chakraborti [b,*]

[a] Department of Mechanical Engineering, Indian Institute of Technology, Kanpur 208016, Uttar Pradesh, India
[b] Department of Metallurgical and Materials Engineering, Indian Institute of Technology, Kharagpur 721302, West Bengal, India

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Abstract

The work presented here describes a method of optimizing the layout of rectangular parts placed on a rectangular sheet to cut out various parts. Two types of cutting problems have been investigated (i) in which guillotine cutting (cutting from edge to edge) is required (mostly metallic sheets where each cut is made individually for one single sheet), and (ii) the one in which guillotine cutting is not essential (e.g. cuts which can be made using a punch) i.e. for materials like paper or rubber where the sheets to be cut can be laid side by side or on top of one another and one single cut can be made. The optimization of the layout of rectangular parts is achieved with respect to two design objectives involving minimization of (i) the length of the mother sheet required, and (ii) also the total number of cuts required to obtain all the parts from the mother sheet. A tree encoded multi-objective genetic algorithm has been used to study both guillotine and non-guillotine cutting cases, using a binary representation of the variables, and it is shown for the known cases that the globally optimum solutions are obtained.

Keywords: Guillotine cutting; Metal cutting; Genetic algorithms; Multi-objective optimization

1. Introduction

The applications of genetic algorithms [1–5] are now ubiquitous in the studies related to materials and manufacturing [6,7]. Some typical examples would include studies on mechanical working of metals [8–15] and their machining [16–18], alloy development [19–20], casting and solidification [21,22], hot and cold rolling [23,24]. Although these biologically inspired techniques are quite new entrants in these areas of research, in recent times genetic algorithms were applied to determine the optimized layout of rectangular parts related to metal cutting problems [25–28]. Without an exception, single objective optimization procedures were adopted in these studies. For example, the design objective considered was the length of the mother sheet required, from which the rectangular parts were to be cut, or effectively it was the total trim loss that was ultimately minimized. However, the number of cuts (or the total length of the cut) required for the cutting process is crucial to the tool life, and also is an important aspect in determining the cost and efficiency of the cutting operation, a comprehensive optimization methodology should take into account the number of cuts required for the process as well. Therefore, in this study, the number of cuts required was taken as a second design objective. What is proposed here is a multi-objective optimization procedure using genetic algorithms for optimizing the layout of rectangular parts so as to minimize the required sheet length (or the trim loss) as well as the number of cuts (or the total length of the cut required) to achieve the cutting process.

Two types of cutting frameworks are investigated here: (i) Non-guillotine cutting framework, where after each cut the detached parts are not considered as separate entities and a common cut can be made to both the parts. Also, the cuts made need not necessarily be from edge to edge. (ii) Guillotine cutting framework, where once a cut is made, the detached parts are treated as separate entities and guillotine cut again needs to be individually applied to them. Thus, in this case, every single cut has to be from edge to edge for any particular rectangular part.

* Corresponding author. Tel.: +91 3222 283286; fax: +91 3222 282280.
E-mail address: nchakrab@iitkgp.ac.in (N. Chakraborti).

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This article begins with further details of the two-dimensional formulation. A three-dimensional extension of the guillotine-cutting problem is presented elsewhere [29].

2. Formulation of the layout problem

In this study an inverse Polish notation has been used to represent the *gene*, formed by concatenation of the part numbers and two operators 'H' (implying a horizontal arrangement) and 'V' (implying a vertical arrangement), which determine the relative arrangement of the rectangular parts on the mother sheet [25]. Furthermore, each rectangular part individually could either be horizontal or vertical. Throughout in this study the horizontal state was denoted as '0' and the vertical state as '1', in order to uniquely determine any particular configuration. The basic methodology of genetic encoding is further illustrated below. Many aspects of it are actually similar to the earlier work of Ono and Ikeda [25].

2.1. Illustration of gene encoding and decoding

Consider a sequence of the form '1, 2, H' where 1 and 2 (both are taken in state '0' for simplicity) are part numbers and H is the operator representing a horizontal arrangement. Here the gene '1, 2, H' essentially denotes that rectangle number 2 is arranged at the right side of rectangle 1 as shown in Fig. 1.

Thus, in this case a genetic representation of the form '1, 2, H' decodes as an integrated rectangle with length as $l = l_1 + l_2$ and breadth as $b = \max(b_1, b_2)$ and a new part number was assigned to it.

Similarly, if one considers a sequence of the form '1, 2, V' where 1 and 2 (both are assumed to be in state '0' for simplicity) are part numbers and V is the operator (representing vertical arrangement) then it simply means that rectangle number 2 is arranged on top of rectangle 1 as shown in Fig. 2.

Hence a genetic representation of the form '1, 2, V' when taken as input returns an integrated rectangle with length as $l = \max(l_1, l_2)$ and breadth as $b = b_1 + b_2$ and as before, a new part number was assigned to it.

Next consider a string of the form '1, 2, H, 3, 4, H, V, 5, 6, V, 7, 8, V, H, H'. This is a gene representing the solution set. This however does not represent the orientation of rectangles and hence is incomplete. Therefore, in this case one also needs to have a gene, which represents the orientation of every rectangle either as '0' or '1'. Let the gene representing the orientation of rectangles be '0, 1, 1, 0, 0, 0, 1, 0'. The two combined represents our solution set uniquely and unambiguously. The arrangement denoted by these genes is shown in Fig. 3.[1]

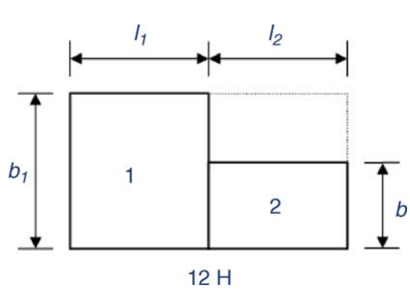

Fig. 1. The horizontal stacking of rectangles.

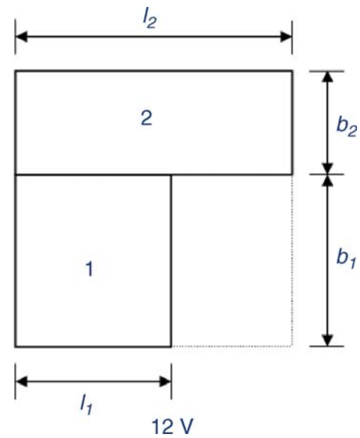

Fig. 2. The vertical stacking of rectangles.

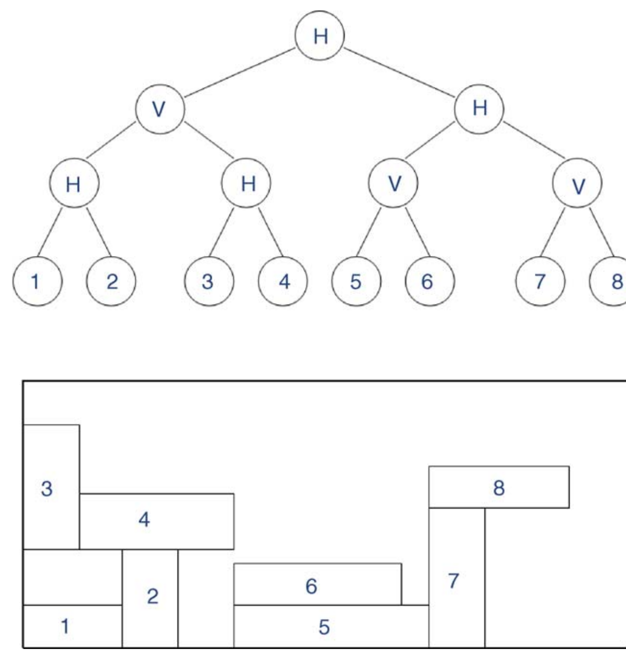

Fig. 3. Tree representation of the arrangement of the parts in the mother sheet (top) and the corresponding pictorial view (bottom).

It should be noted at this point that representing the gene either in form of a string or in form of a tree are essentially the same and the string can be reproduced from the tree by traversing recursively along the root of the tree in a way that first one traverses along the left child of any node, followed by the right child and finally to the node itself. The basic algorithm to achieve this is provided in Table 1.

Genetic operators like mutation and crossover can be applied to both the gene and the tree structures, and will result in the same solution. Both form of representation have restrictions on the

[1] For the sake of the clarity of pictorial representation, here we have taken the lengths of the rectangles to be greater than their breadths. This is, however, not a necessary condition as the length and breadth need not be related.