Scheduling in a micro-biological laboratory: heuristics for sequencing food sample tests, to co-ordinate with production of perishable media materials

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1 Abstract

This paper explores the scheduling issues associated with co-ordinating two key processes in a food testing micro-biology laboratory. Most of the microbiology tests in the laboratory are carried out on glass dishes, in an agar compound. The type of agar employed is very specific to the nature of the test. Each food sample requires a whole suite of tests to be performed successfully in order to be certified fit for consumption. Thus the sequence of samples determines parallel demand for a range of agars. A major complication is the limited lifetime over which the agars are effective. The co-ordination of scheduling test samples with production of agars in batches on identical, parallel machines, is the topic of interest.

We focus on sequencing of test samples in such a way as to ensure that agars are consumed as quickly as possible since their usage starts. Therefore, the problem of sequencing test samples reduces to one of sequencing their agar combinations. A sequence of agar combinations can be represented as a (0,1)-matrix which columns correspond to agar types and rows specify agar combinations for test samples. Hence, the problem can be formulated in the following way: given a binary matrix, find a permutation of its rows such that the total number of zero-entries situated between the blocks of consecutive ones in the columns of the permuted matrix is minimized. Such a formulation has other important applications in the design of the efficient storage schemes for sparse matrices, and in the physical mapping of chromosomes in computational biology. The problem is proved to be NP-hard and no effective solution methods are known from the literature. It is, however, related to the Consecutive Ones Problem which is studied in the literature.

In this paper, we present an optimization approach for the problem described above, which is based on indirect enumeration of the solution space. The idea behind the technique is to define classes of solutions by specifying their common structures. Then, an optimal solution within each class is determined and the best of these provides an optimal solution to the original problem. Although this approach is more efficient than complete enumeration of all
feasible solutions, i.e., all possible permutations of rows of the original matrix, it can only be applied to matrices with a small number of columns. Therefore, we develop two heuristic algorithms which quickly construct feasible solutions to the problems. The first heuristic is a greedy insertion algorithm while the second one is a more complicated technique which constructs a solution matrix in two directions, from the top and the bottom.

We report the results of our algorithms for a wide range of randomly generated problem instances. We show that the first heuristic works well for small instances and the second one is able to produce optimal or near-optimal outcomes for the whole range of problem instances. In addition, we show how our structural insights into the problem enable data from the microbiological laboratory to be represented as relatively small problem instances, which can then be efficiently tackled by our exact algorithm.