BASE: a bacteria foraging algorithm for cell formation with sequence data

ABSTRACT

A cellular manufacturing system (CMS) is considered an efficient production strategy for batch type production. A CMS relies on the principle of grouping machines into machine cells and grouping parts into part families on the basis of pertinent similarity measures. The bacteria foraging algorithm (BFA) is a newly developed computation technique extracted from the social foraging behavior of Escherichia coli (E. coli) bacteria. Ever since Kevin M. Passino invented the BFA, one of the main challenges has been employment of the algorithm to problem areas other than those for which the algorithm was proposed. This research work studies the first applications of this emerging novel optimization algorithm to the cell formation (CF) problem considering the operation sequence. In addition, a newly developed BFA-based optimization algorithm for CF based on operation sequences is discussed. In this paper, an attempt is made to solve the CF problem, while taking into consideration the number of voids in the cells and the number of inter-cell travels based on operational sequences of the parts visited by the machines. The BFA is suggested to create machine cells and part families. The performance of the proposed algorithm is compared with that of a number of algorithms that are most commonly used and reported in the corresponding scientific literature, such as the CASE clustering algorithm for sequence data, the ACCORD bicriterion clustering algorithm and modified ART1, and using a defined performance measure known as group technology efficiency and bond efficiency. The results show better performance of the proposed algorithm.

Keyword: Cellular manufacturing system; Bacteria foraging algorithm; Cell formation