An Efficient Assignment Sequence Algorithm for the Multi-Stage Shelf Allocation Problem

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Abstract

Shelf allocation is one of the most important issues in retailing business, because different displaying strategies can directly impact customers' purchasing decision. In most previous researches, items are allocated into shelf space according to their item similarity only, so that items in the same categories (or sub-categories) might be assigned in very different shelf. However, in practical retailing environment, items with the same category and sub-category should be allocated into adjacent shelf space. In addition, several researchers develop different heuristic algorithms for solving complicated shelf allocation problems. Although these methods are significant, the solution quality and computation efficiency of theses algorithms can be further improved.

In this thesis, this research develops a multi-stage shelf allocation method, which allocates items into the shelf spaces based on their category similarity, sub-category similarity, and item similarity, sequentially. There are three tasks in each level of the proposed shelf allocation method. First, the required shelf spaces for every item are obtained based on their facing length and sales volumes. Second, an assignment sequence algorithm applied the association clustering analysis is proposed to derive a nice initial solution setting. Finally, genetic algorithms with the initial solution setting derived in the second task are used to solve this shelf allocation problem.

Based on the experiment result, the multi-stage method can obtain better shelf space

allocation solution than one-stage shelf allocation method. In addition, the method with initial solution setting can not only obtain a better shelf space allocation solution but also less computation cost. The experiment shows that the proposed multi-stage shelf allocation method with initial solution setting is a nice method for solving the shelf allocation problems.

Keywords: Shelf Allocation Assignment Sequence Multi-Stage Method Genetic Algorithms Association Clustering Analysis