Hybrid Genetic Algorithm for Packing Segments of Decommissioned Nuclear Reactor Components

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1. Introduction

As Kori unit 1 and Wolsung unit 1 were permanently shut down for decommissioning, estimating the disposal amount of waste from decommissioned nuclear reactors has become one of the pressing issues. Recently, waste disposal amount of Kori unit 1 reactor vessel has been evaluated for various options of disposal containers [1], and a segmentation and packaging plan for reactor vessel and reactor vessel internals of Kori unit 1 has been proposed in a more comprehensive perspective [2].

In order to reduce the storage cost of radioactive wastes in the disposal facility, it is desirable to maximize the volume utilization of the disposal containers. The components of the nuclear reactors are segmented into various number of pieces according to the decommissioning plans of nuclear power plants. In past decommissioning cases, the number of segments of reactor vessels (RVs), for example, varied from 17 to 172 pieces [2]. Waste pieces cut into smaller sizes were more advantageous for packaging with better volume utilization [1]. However, few of the prior researches discuss optimal packing of segments of reactor components.

On the other hand, finding optimal packing arrangements in the enclosed build container has been the prime issue in additive manufacturing (AM), also known as 3D printing. The primary goal of AM is to maximize build volume utilization, which is essentially the same goal as packing segments of reactor components. One of the dominant strategies for packing problems in AM has been the deepest bottom left with fill (DBLF) heuristic combined with genetic algorithm (GA) [3].

This study proposes a packing placement design method of waste segments from nuclear reactor components by applying a hybrid genetic algorithm [4-6] for cuboidal disposal containers.

2. Packing placement design method

2.1 Problem Objective

The packing optimization problem can be formulated as a three-dimensional irregular packing problem, which is a combinatorial optimization problem where a set of arbitrary volumetric items must be placed into the given containers in such a way that the total empty space is minimized. This will lead to minimizing the number of containers to accommodate the given segments, which can be translated as the minimum number of containers to be stored in the disposal facility.

2.2 Hybrid genetic algorithm (HGA) method

HGA is a hybridization of GA and some problem-dependent heuristics. DBLF [4] was adopted as the heuristic for this packing problem. The HGA in this study uses a diploid representation of individual boxes to be packed, where one chromosome denotes the packing sequence of boxes and another chromosome denotes the rotations of the corresponding boxes, and DBLF finds the placing positions of boxes in the container such that each pair of packed boxes do not overlap. For applying DBLF algorithm, segments are modeled in the STL file format and enclosed by orthogonal bounding boxes. Fig. 1 shows the overall flowchart of the method, and some details about the algorithm are described in the following subsections.

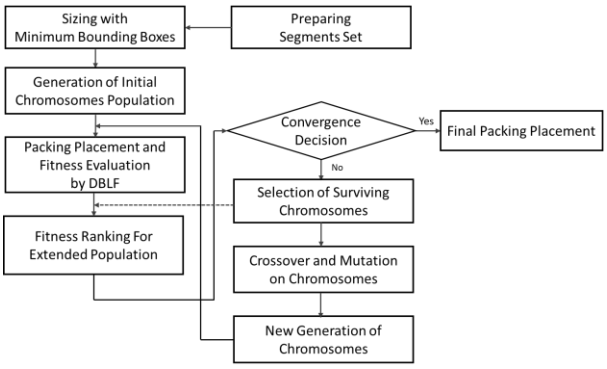

Fig. 1. Overall flowchart of packing placement design.

2.2.1. Deepest bottom left with fill (DBLF) heuristic. Once the sequence of boxes is decided, the initial dimensions of box i is (l_i, w_i, h_i) in the Cartesian coordinate system. Box i can be placed with 6 different rotations of r_i. The value of r_i can be equal to 0, 1, 2, 3, 4, or 5, and the responding deposited dimensions are (l_i, w_i, h_i), (l_i, h_i, w_i) (h_i, w_i, l_i), (w_i, l_i, h_i), (w_i, h_i, l_i), and (h_i, l_i, w_i), respectively.

In the DBLF heuristic, the first step is to generate a series of potential positions (PPs) for the boxes to be packed. As illustrated in Fig. 2, the initial PP list is started with only one position (0, 0, 0). As box i in the sequence is placed with its left-bottom-back corner at (x_i, y_i, z_i) in the container, new PPs are generated and added in the list. Two PPs are generated by projecting (x_i+Δx, y_i, z_i) and (x_i, y_i+Δy, z_i) on the boxes between the bottom of the container and box i or on the container bottom,

where Δx and Δy are the dimensions of the rotated box i in the x- and y- directions. If there is more than one box under box i, the position is projected on the box that is the nearest to box i. The third PP is $(x_i, y_i, z_i+\Delta z)$, where Δz is the dimension of the rotated box i in the z-direction. And an additional position is obtained at $(x_i+\Delta x, 0, 0)$, if the current $(x_i+\Delta x)$ is greater than all the previous $(x+\Delta x)$ [5].

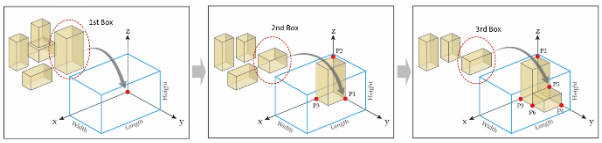

Fig. 2. Illustration of sequence of boxes and generation of potential positions in the container.

In the second step, the positions in the PP list are sorted in the deepest-bottom-left order. A box is tried at potential positions of the PP list in ascending order, and placed in a position, if it does not overlap any other box that has been packed into the container and it does not penetrate the boundary surfaces of the container. When a box is placed at one position, the position is removed from the PP list. The placing process terminates when either all boxes are placed in the container or the current box finds no available positions in the PP list that satisfy the above constraints.

2.2.2. Genetic algorithm. As shown in Fig. 3, a chromosome is coded with two rows and n columns when there are n boxes to be packed. Each gene of the chromosome consists of box index and rotation. The packed positions are determined by DBLF for the given chromosome, where the position of the first box of the sequence is (0, 0, 0) as discussed previously. This matrix in 5×n completely describes a feasible packing solution for a container.

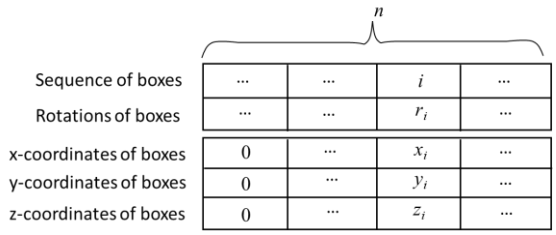

Fig. 3. Illustration of a chromosome and the corresponding solution of placed positions.

The initial population of chromosomes is created by random permutations of {1, 2, ⋯, n} for sequences and all rotations are set to 0. However, to guarantee a certain quality of optimization, the boxes with large volumes should be packed into the container first and, therefore, special chromosomes created by sorting the sequence genes in descending orders of volume, length, width, and height of boxes are added in the initial population.

Given the fitness values for the population of the chromosomes, surviving chromosomes are selected based on the fitness rankings of the chromosomes. Pairs of chromosomes among these survivors are designated as parents, P_1 and P_2, for two-point crossover for generating children, C_1 and C_2. In crossover, two cutting sites i and j are randomly selected, $i < j$. Referring to Fig. 4, the genes $P_l(i)$ ... $P_l(j)$ are copied into $C_1(i)$ ... $C_1(j)$. Then, P_2 is swept circularly from the $(j+1)$-th gene onward to complete C_l with the missing genes and C_l is filled circularly from the $(j+1)$-th gene. The other child C_2 can be obtained in the same way by exchanging the roles of P_1 and P_2.

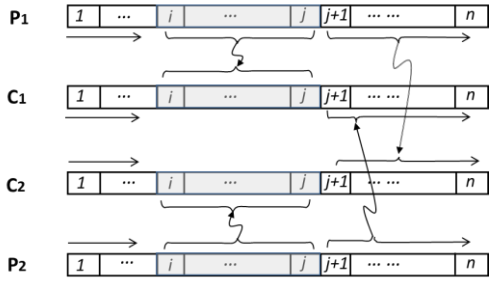

Fig. 2. Concept of crossover operated on a pair of parent chromosomes.

After the crossover is executed, a two-step mutation is performed. In the first mutation, two random sites i and j are selected in C, and then the genes C(i) ... C(j) are inversed with probability P_{m1}. In the second mutation step, each rotation of C is changed randomly with probability P_{m2}.

When the new generation of population is obtained through crossover and mutation, DBLF is used to determine packing positions and fitness values. Then, the surviving chromosomes are selected according to the fitness rankings from the extended population that include the new and old generations.

To determine the convergence of the GA loop, the degree of convergence is evaluated using the diversity index(η), which is defined as follows.

$$\eta = \frac{(f_{best} - f_{worst})}{f_{best}/2}, \quad (1)$$

where f indicates the fitness value of the best or worst chromosome in the current population. Here, the fitness is defined as the volume utilization rate of the container. When the diversity index becomes sufficiently small or the number of generations reaches the preset limit, GA loop is terminated with the final packing solution which is the best solution in the population.

When there are more boxes left after packing a container, the same HGA can be repeated for the next container with the remained boxes.

3. Numerical Experiments

3.1 Verification of HGA

The proposed HGA method was implemented in C++ and verified using a known box packing problem with the optimal solution of 100% volume utilization [6].

The population size of chromosomes was selected to be 400, and mutation probabilities were set at 0.2 and 0.02 for P_{m1} and P_{m2}, respectively.

A perfect packing solution with 100% volume utilization has been obtained with several trials of random seeds. Fig. 5 shows how the best and worst solutions in generations converged into an optimal solution.

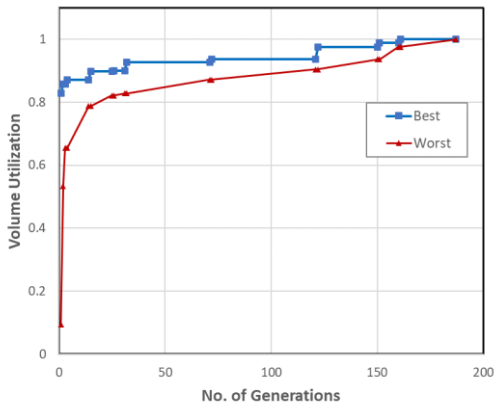

Fig. 5. Convergence results of a known packing problem.

3.2 Preparation of the segment packing test case

The developed method was tested for cutting and packing of a sample reactor vessel. An RV model has been prepared in STL file format, and subsidiary programs have been developed for visualization and cutting.

The RV model was cut into 7 pieces in axial direction and then 18 pieces in azimuthal direction, generating 126 segments that are quite heterogeneous. Fig. 6 shows the RV model used and its cut segments. The height of the model was set at 200 (unitless) and the used container was sized with 60x60x60, each dimension of which was determined to be larger than the maximum length of the segments.

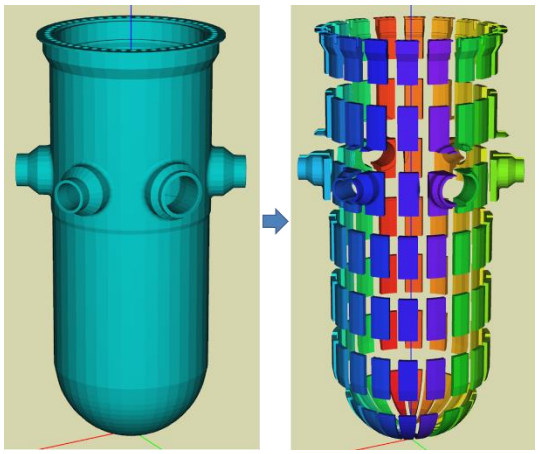

Fig. 6. A sample RV model and its cut segments.

The minimum bounding boxes (MBBs) were sized for the resulting segments so that the MBBs have the minimum cuboidal volumes encapsulating the corresponding segments. Fig. 7 illustrates one of the segments shown with MBB oriented in six ways of rotation.

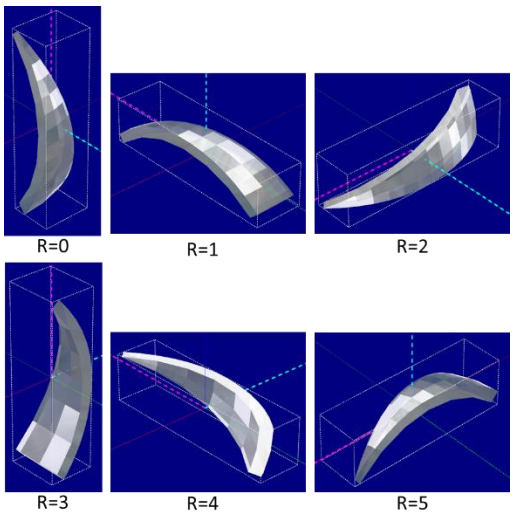

Fig. 7. Illustration of a segment with six rotations.

3.3 Test Results and Analysis

The population size of chromosomes for the test case was also selected to be 400, and mutation probabilities were set at 0.2 and 0.02 for P_{m1} and P_{m2}, respectively.

Fig. 8 shows the convergence results of the developed HGA represented in MBB volume utilization. During the HGA process, fitness of a solution was evaluated by the MBB volume utilization rate, where MBB was specified to differentiate it from the volume utilization by segments.

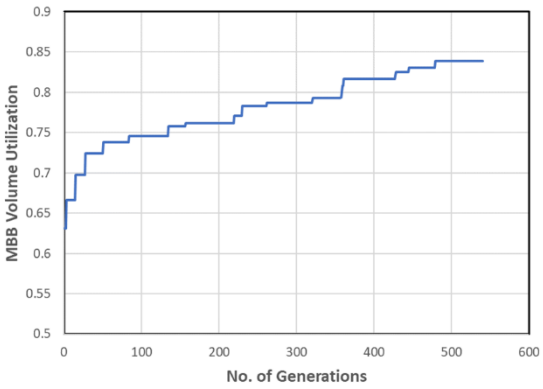

Fig. 8. Convergence results of the developed HGA.

By applying the HGA process successively, a packing placement solution was obtained for the 126 segments. The 126 segments were packed in three containers as shown in Fig. 9, where numbers of segments packed,

MBB volume utilizations, and volume utilizations by segments are indicated alongside.

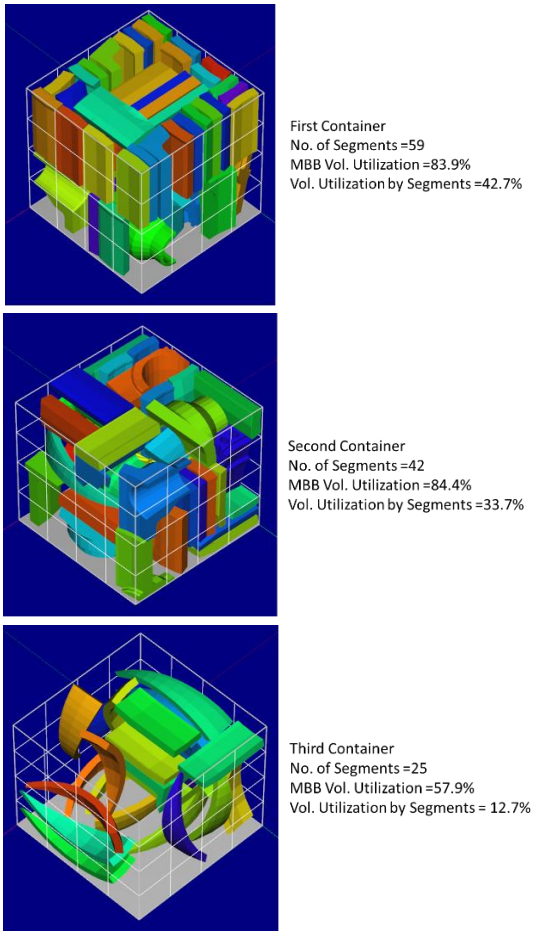

Fig. 9. A packing placement solution for the test case.

MBB volume utilizations were over 80% in the first and second containers. The volume utilizations by segments of the first and second containers were 42.7% and 33.7%, respectively, which are generally far better than that of packing solutions which could be obtained through laborious manual trials. The volume utilization by segments is expected to improve towards the MBB volume utilization, if cutting is more carefully planned to have higher solidity in MBBs.

The packing solution for the last container was not quite optimized by the algorithm, because the container volume is sufficiently large compared to the volume sum of the remained segments and the fitness value was kept constant regardless of the packing placements.

4. Concluding remarks

With the growing interest in the decommissioning of nuclear power plants, optimal packing of segments of decommissioned reactor components is an imminent challenge. This work provides a packing placement method for waste segments from nuclear reactor components based on a hybrid genetic algorithm.

The developed packing placement method was verified using a known packing problem and tested on a sample model of reactor vessel. It was successfully demonstrated that the proposed method can provide near-optimal packing placement solutions for packing problems in the nuclear reactor decommissioning.

As the packing problems are dependent on the decommissioning policy and conditions, the developed method is expected to be flexibly applicable for various cases of segments with different numbers and sizes and various containers, and to provide excellent solution guides in packing placement planning for decommissioning of nuclear reactors.

ACKNOWLEDGMENT

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