

A New Packing Method for Two Dimensional Rectilinear Polygons using Genetic Algorithm

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ABSTRACT

This paper proposes a new placement method for two dimensional rectilinear polygons. The proposed method is based on the idea of corner junction method and uses only genetic algorithm approach with a new hierarchical chromosome structure to pack rectilinear polygons on container. Experimental results show the proposed method is succeeded in placement of some complicated two dimensional rectilinear polygons in feasible time.

Categories and Subject Descriptors

I.2.8 [Artificial Intelligence]: Problem Solving, Control Methods, and Search - *Heuristic methods*

General Terms

Algorithms, Theory, Verification.

Keywords

Two dimensional polygon packing problem, Strip packing problem, Genetic algorithm, Corner junction method.

1. INTRODUCTION

Packing and layout problems are common in both engineering and non-engineering applications, which aims high packing density as the main objective without overlaps by objects to be layout or to be packed. New packing method for tow dimensional rectilinear polygons is introduced in this paper.

2. PACKING METHOD AND MATERIALS

2.1 Genetic Algorithm Based Packing Method and Corner Junction Method

Although there are a lot of heuristic and hybrid approaches for solving two dimensional strip-packing problems [1], the application of the method based on GA is not so many. In this paper the method embedded in a double chromosome structure is enhanced and applied to pack irregular shaped objects containing four or more right angles. The proposed method does not belong to any of the existing irregular object packing techniques. GA-based approach with a single straight chromosome structure using CJ method was introduced in [2]. A double chromosome structure using CJ method is proposed in [3], which obtains good results in

search time and the quality of solutions in comparison with [2]. Figure 1 shows the relationship between corner junction points and junction genes. The corners of rectangle are identified by the numbers $\{0,1,2,3\}$. The junction genes are identified by the numbers $\{0,1,2,3,4,5,6,7\}$. These eight values cover the eight allowable junctions of rectangles.

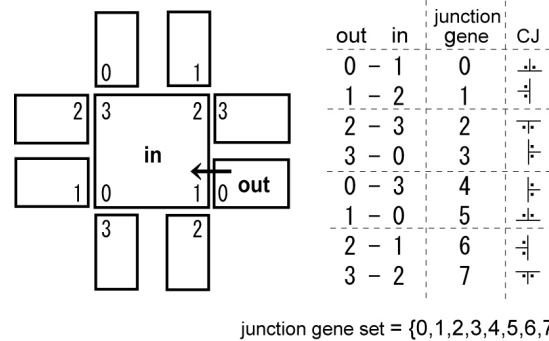


Figure 1. Illustration of junction genes and the corner junction (CJ) representation with dots [3].

2.2 Proposed Chromosome Structure for GA

Figure 2 shows the relationship of the rectilinear polygons, polygon chromosome and double chromosome structure for GA.

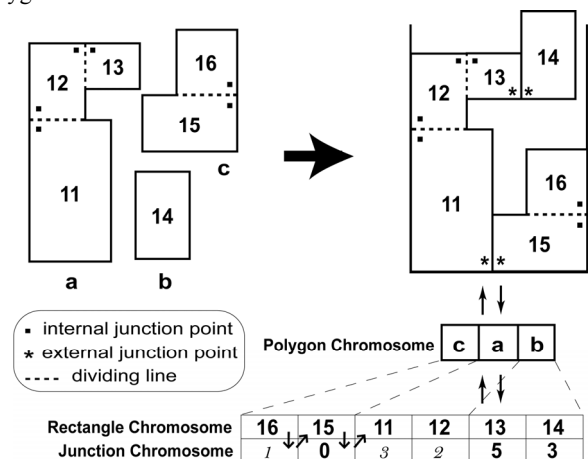


Figure 2. Illustration of hierarchical chromosome structure.

2.3 Genetic Operators

Four genetic operations were used in this paper: elite selection, cyclic crossover, mutation, and local search method.

1) Selection: The elite selection strategy retains the elite to the next generation.

2) Crossover: CX (Cyclic Crossover). CX is directly applies only to polygon chromosomes. The less fit parent is replaced by the offspring. After the crossover of polygon chromosomes, rectangle chromosome and junction chromosome are produced.

3) Mutation: All chromosomes except the elite were subject to mutation. For this study, rectilinear polygon exchange mutation and external junction gene change mutation are used.

4) Local search method (LS): All chromosomes including the elite were subject to mutation. LS is used for keeping improvement which was obtained by the same processes of mutation. The move strategy for LS is the first admissible move strategy.

2.4 Evolutionary Process

The flow of evolutionary process is roughly described as follows: GA starts from an initial set of a fixed number of individual chromosomes generated at random, and then is applied to above-mentioned 4 genetic operators repeatedly until the end conditions are satisfied. Individuals subject to mutation (excluding the elite) and Local search method are randomly selected from the population. If the value of the elite does not improve after a fixed number of generations, mutation process is then executed. Local search method is executed in each generation.

2.5 Fitness Function

The fitness function of the chromosome is shown as follows:

$$\min f(X,Y,C) = \text{If } (W-X < 0) \text{ then } X^2 Y^2 C \text{ else } Y^2 C. \quad (1)$$

$$X = \sum x_i, \quad i=1,2,\dots,n. \quad (2)$$

$$Y = \sum y_i, \quad i=1,2,\dots,n. \quad (3)$$

$$C = (m+1)^2 + 1 \quad (m \geq 0: \text{number of overlaps}) \quad (4)$$

Here, i is a given polygon of x width and y height, X is total width, Y is total height, W is the width of the container.

3. EXPERIMENT

3.1.1 Benchmark problems

The problems newly created as the benchmark and confirmation test are used in this paper. Figure 3 shows the rectilinear polygons of problem p5 and the one optimal packing solution. The rectilinear polygons in this study have neither acute angle nor obtuse angle, however only right angle of 90 degree corners hold.

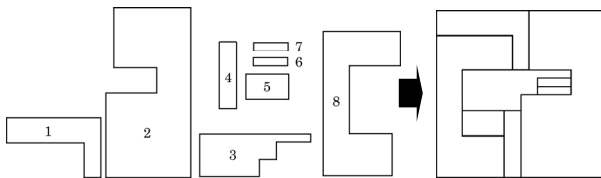


Figure 3. The illustration of polygons to be packed (right), and an optimal solution when all polygons were packed.

3.1.2 Experimental Environment

The experiment is conducted on a note PC with Windows7, Intel Core i5, 2.67GHz, two cores and four logical processors, and 3.8GByte RAM is available. The development language is Java

with no optimization. The population size is set at 5. The arbitrary number of mutations is 50% of the population, affecting 50% of the genes in each chromosome. The generation size is 50000. HDC (Hierarchical Double Chromosome) with CJ method (CJ+HDC) runs 100 times on each benchmark problem. Mutation is executed once in every 500 generations to randomly selected individuals excluding the elite.

3.1.3 Results

Table 1 shows the packing results of CJ+HDC. As can be seen, CJ+HDC found the optimal solutions in benchmark problem p3, p4 and p5. It means that some rectilinear polygon packing problems can be solved by CJ+HDC which uses only well known genetic algorithm operators. However, the search time and the unpacked area are larger than expectation. The quality of solution in terms of Gap is more than 15% for problem p1 and p2. These problems might be difficult problem. The average elapse time for best_found solutions is less than about 16 minutes.

Table 1. Results of CJ method with HDC

Problem (Polygons)	Optimum height	Average Height	Gap (%)	Time (min)
p1 (9)	20	26.69	20	15.24
p2 (8)	20	27.55	15	11.03
p3 (9)	20	26.94	0	12.23
p4 (10)	20	25.84	0	11.83
p5 (8)	20	24.79	0	10.33

Gap (%) = (best_found - optimum)*100/optimum.

Time (min) = The average elapsed time for best found solutions.

4. CONCLUSION

This paper proposes a hierarchical double chromosome structure for genetic algorithm to solve rectilinear packing problem. The proposed method embedded in hierarchical double chromosome structure uses only genetic operators such as selection, crossover, mutation, and local search method to solve rectilinear packing problem, and succeeded in getting optimum solution(s) for some benchmark problems.

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6. REFERENCES

- [1] Hopper, E., and Turton, B. C. H. An empirical investigation of meta-heuristic and heuristic algorithms for a 2D packing problem. In *European Journal of Operational Research*, 128, 1 (January 2001), 34-57.
- [2] Matayoshi, M. The 2D strip packing problem: a new approach with verification by EA. In *Proceedings of the 2010 IEEE International Conference on Systems, Man, and Cybernetic (SMC'10)* (Istanbul, Turkey, October 10-13), 2492-2499.
- [3] Matayoshi, M. Double Chromosome GA with Corner Junction for Solving the 2D Strip Packing Problem. In *The 36th Annual Conference of the IEEE Industrial Electronics Society (IECON'10)* (Glendale, AZ, November 7-10), 110-1116.