Arbitrary Rectilinear Block Packing Based On Sequence Pair Structure

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Abstract

Due to layout or specific physical requirements, macro blocks can be in an arbitrary rectilinear shape. Block packing problem will no longer be limited to the rectangle packing. So far no efficient algorithm has been proposed to solve the general rectilinear block packing problem. This paper presents a novel representation method for arbitrary shaped rectilinear blocks in a sequence pair structure. A sequence pair is *feasible* if an optimal packing of arbitrary rectilinear blocks can be guaranteed for the given sequence pair regardless of the dimensions of the blocks. In this paper, three conditions are derived on a sequence pair which are necessary and sufficient for a sequence pair to be feasible.

Furthermore this paper shows that there always exists a feasible sequence pair for a packing of convex rectilinear blocks. As such, the optimal solution for convex rectilinear block packing can be found by exhausting the finite number of feasible sequence pairs. Three sequence pair operations are developed to incrementally change a solution. Each operation takes linear time and generates a feasible sequence pair. An important theoretical result demonstrates that the optimal solution can always be reachable through a finite times of the sequence pair operations. Therefore a stochastic search based on the three operations can search the feasible solution space both continuously and exhaustively. In such a way, for the first time, the arbitrary shaped rectilinear block packing is solved by using a sequence pair structure.

1 Introduction

Most of the traditional floorplanning or placement algorithms considered only rectangular shaped macro blocks. The slicing structure was proposed to represent the block placement by recursively dissecting the rectangular plane into two parts using either horizontal or vertical line [1]. Corresponding to the slicing structure, Wong and Liu proposed a data representation called *normalized Polish expression*, which enables the efficient local search [2]. As the increase of routing layers, most of channel routing is being replaced by area routing. A block placement becomes more like a block packing problem, and the wasted

area introduced by a slicing structure becomes more evident. As such, the non-slicing block packing becomes more attractive.

Murata et al. [3] introduced a sequence pair (SP), and Nakatake et al. [4] proposed a bounded slicing grid structure (BSG) to represent the general rectangle packing. Both SP and BSG define the binary relationship for each pair of rectangular blocks, and provide a way to independently compact the x and y direction.

Due to layout or specific physical requirements, macro blocks can be in an arbitrary rectilinear shape. Few previous works have studied the rectilinear shaped blocks where the most noticeable one is the *bounded 2D contour searching algorithm* proposed by [5]. The arbitrarily rectilinear shaped blocks are represented by a set of four linear profiles, each one of them specifies the profile viewed from one side of the block. Given the original placement of blocks, the algorithm iteratively compacts the blocks along a certain direction, in which the 2D contour searching is carried out on the profiles of the compacted design. As we can see, this compaction method cannot be applied on block packing problem due to the complicated geometrical calculation.

A BSG-based method was proposed by [6] to pack rectangular, L-shaped, T-shaped, and soft blocks. The complicated relationship among rectilinear blocks was indicated and a SP-based algorithm was presented by [7]. Unfortunately the algorithm does not converge to the feasible solutions, overlaps may exist in the packing solution. Most recently, an algorithm based on both BSG and SP structures was proposed by [8], in which the topology constrained block packing can be handled given that blocks belong to a specific class of convex rectilinear shapes. An SP-based algorithm was proposed by [9] to pack the mountain-shaped blocks. However it was not guaranteed that the algorithm could always terminate. Based on BSG structures, an algorithm was proposed by [10] where each block is sliced into a set of rectangular sub-blocks, one of them is selected to be a *master* and the others *slaves*. Only the master sub-block is assigned into BSG domain. After the compaction, the slaves are attached with the master. A post-process eliminates overlaps by pushing the neighboring blocks away. Obviously the optimal solution is not guaranteed to be included, and the post process takes much more time than the BSG compaction itself.

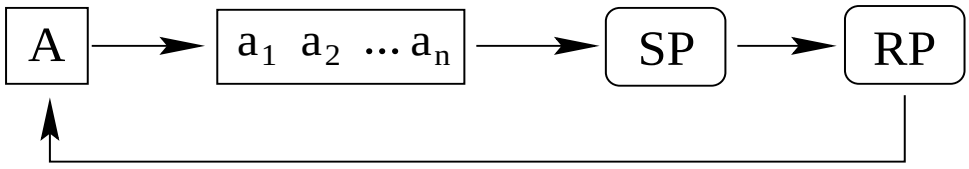


Figure 1: Each rectilinear shaped macro block, A, is partitioned into a set of rectangular sub-blocks : $a_1\ a_2\ \cdots\ a_n$, each of them is individually represented in a sequence pair as a unit block. After the unit blocks are compacted in the x and y directions, a post process aligns the x and y coordinates of the sub-blocks such as to recover the original macro shapes.

In this paper, a novel representation method is proposed for arbitrary shaped rectilinear blocks in a sequence pair structure. A sequence pair is *feasible* if an optimal packing of arbitrary rectilinear blocks for the given sequence pair can always be guaranteed regardless of the dimensions of the blocks. Three conditions on sequence pair are derived which are necessary and sufficient for a sequence pair to be feasible. The theoretical proof points

out that there always exists a feasible sequence pair corresponding to a packing of the convex rectilinear blocks. As such, an optimal solution for the convex block packing can be found by enumerating the finite feasible sequence pairs. Stochastic search is applied, and three sequence pair operations are defined such as to continuously search the feasible solution space. An important theorem shows that starting from any feasible sequence pair, the feasible sequence pair which yields the optimal packing can always be reachable through a finite steps of the operations. Therefore the stochastic search based on the three operations searches the feasible solution space both continuously and exhaustively.

In the following, the sequence pair structure is first introduced in Section 2. Then Section 3 describes the representation method for arbitrary rectilinear blocks in a sequence pair. The concept of feasible sequence pairs is defined, and three conditions on a sequence pair are presented. Section 4 shows that the three conditions are necessary and sufficient for a sequence pair to be feasible. In Section 5, it is proven that there always exists a feasible sequence pair for a packing of convex rectilinear blocks. Based on this fact, Section 6 applies a stochastic search on the convex block packing. The experimental results are reported in Section 7 followed by the conclusion of this paper.

2 Sequence Pair (SP) Structure

To clarify the notation, we call the rectangular blocks represented in sequence pair *unit blocks*. A *sequence pair* for a set of n unit blocks is a pair of sequences of n symbols which represent the unit blocks : (Γ_1, Γ_2). Given a sequence pair ($a\ b\ d\ e\ c\ f$, $c\ b\ f\ a\ d\ e$) , an oblique grid can be constructed as shown in Fig. 2 (a) : 45^0 slope lines are named from left to right by the symbols in the first sequence Γ_1, and -45^0 slope lines are similarly named by the symbols in the second sequence Γ_2. Each unit block is placed at the cross of the two slope lines which are named by the same symbol corresponding to the unit block. As shown in Fig. 2 (b), the plane can be divided by the two crossing slope lines into four cones for any unit block b. Unit a is in the upper cone of b, then a is above b. Similarly, unit d, e and f is in the right cone of b, then they are right to b. In general, the sequence pair imposes the relationship between each pair of unit blocks as follows :

$$\begin{aligned} (\cdots a \cdots b \cdots, \quad \cdots a \cdots b \cdots) \quad &\Rightarrow \quad a \textit{ is left to } b, \\ (\cdots b \cdots a \cdots, \quad \cdots a \cdots b \cdots) \quad &\Rightarrow \quad a \textit{ is below } b. \end{aligned}$$

Given the sequence pair, a horizontal directed graph G_h is derived as shown in Fig. 3 (a). Each vertex corresponds to a unit block, there is an arc from unit a to d if and only if a is left to d. In particular, there is a source s_h connected to each leftmost unit and a sink t_h connected from each rightmost unit. Each vertex has a weight which equals to the width of the corresponding unit block. The vertical graph G_v can be similarly derived as shown in Fig. 3 (b).

Both G_h and G_v are vertex weighted directed acyclic graphs, the packing of unit blocks can be obtained by simply applying the well-known *longest path algorithm* on both graphs. The x and y coordinates of each unit block are determined by the longest path from source to the vertex of the unit in G_h and G_v, respectively. Similarly, the width and height of the overall packing can be determined by the source-to-sink longest path of G_h and G_v.

For any two unit blocks, there is always an arc in either G_h or G_v, but not both. Due to this fact, the x and y coordinates can be independently determined, and the resultant packing is guaranteed not to contain any overlap. Since the width and the height are independently minimum, the resultant packing is optimal for the given sequence pair. The longest path calculation can be done in the time proportional to the number of arcs in the graphs.

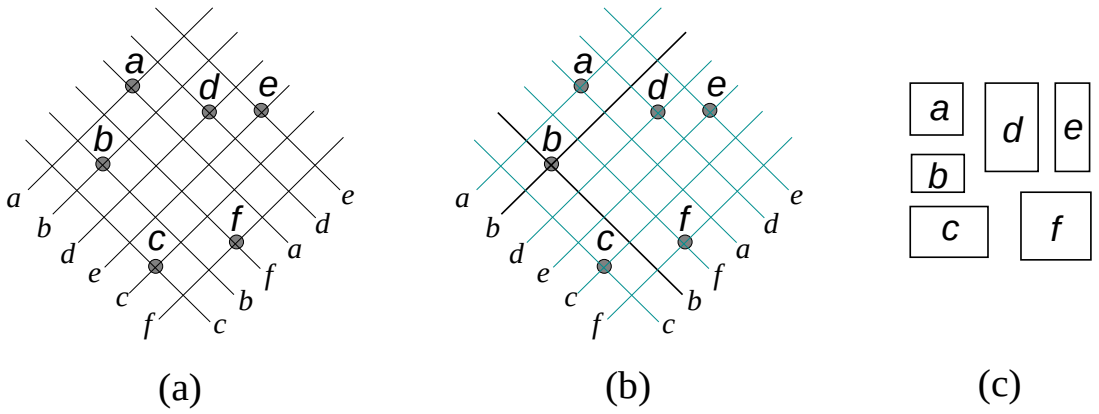


Figure 2: (a) Oblique grid of $(a\ b\ d\ e\ c\ f\ ,\quad c\ b\ f\ a\ d\ e)$, (b) the four cones of block b, and (c) the corresponding packing of the six blocks.

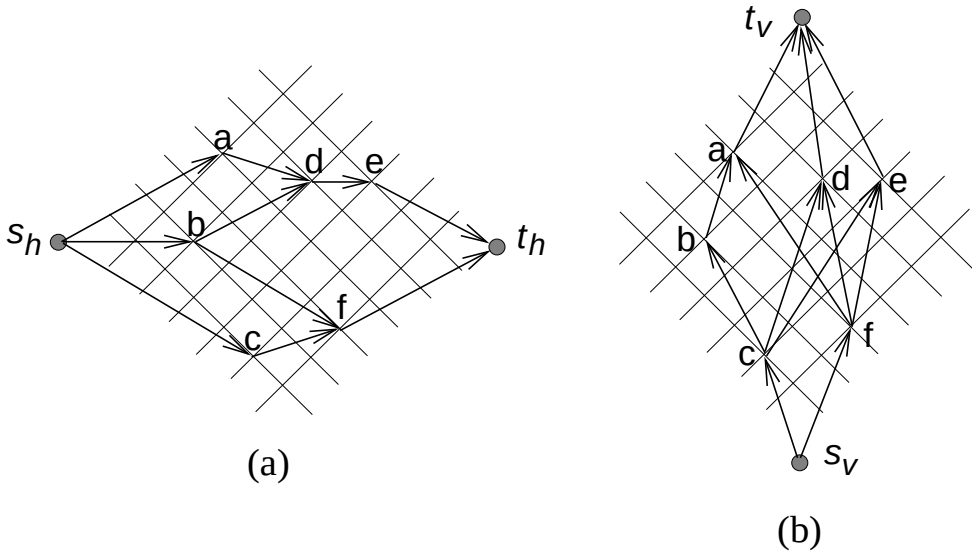


Figure 3: The two vertex weighted directed acyclic graphs derived from the sequence pair $(a\ b\ d\ e\ c\ f\ ,\quad c\ b\ f\ a\ d\ e)$, in which the transitive arcs are deleted for the simplification.

As a coding scheme, sequence pair becomes an ideal data representation of rectangular block packing due to following facts [3] :

- Quick evaluation of packing area based on sequence pair : $O(n^2)$ time where n is the number of unit blocks.
- Easy incremental change of packing topology using sequence pair : switch two units in the first or second sequence.
- There always exists a sequence pair corresponding to a rectangle packing, and vice versa.

Therefore the optimal packing can always be found by exhausting the finite number $(n!)^2$ of sequence pairs.

3 Arbitrarily Rectilinear Blocks in Sequence Pair

3.1 H, V-Partition

Let A denote an arbitrary shaped rectilinear macro block. A can be partitioned into a set of rectangular sub-blocks by slicing A from the left to right along every vertical boundary of A. As shown in Fig. 4 (a), the partition is referred to as a *horizontal partition* or *H-partition*. Similarly A can be *vertically partitioned* or *V-partitioned* as shown in Fig. 4 (b). Given that A is H-partitioned or V-partitioned into $a_1,\ a_2,\ \cdots a_n$, each sub-block $a_i \in A$ is individually represented in SP as a unit block. We call the pair of permutations on $a_i \in A$ in the sequence pair a *permutation pair of A*.

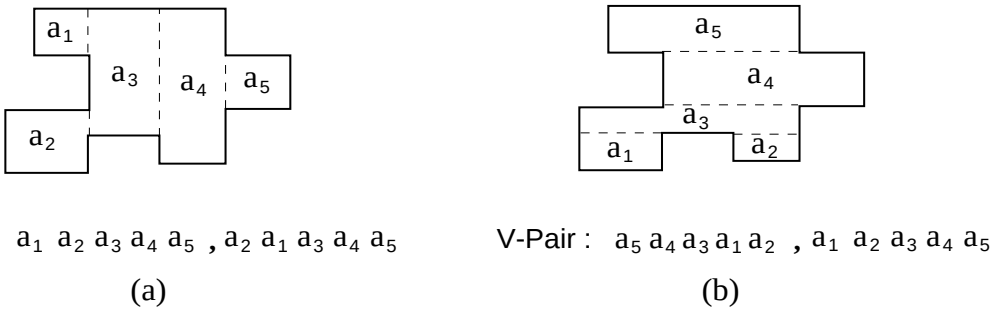


Figure 4: (a) H-partition slices block A on every vertical boundary from the left to right. (b) V-partition slices block A on every horizontal boundary from the bottom to top.

For any two unit blocks a and b placed in a plane without overlaps, let u_a and l_a denote the upper and lower boundary of block a, respectively. Block a is left of b if the right boundary of a is left of the left boundary of b. If $[l_a, u_a] \cap [l_b, u_b] \neq \phi$ as shown in Fig. 5 (a), a is *strictly* left of b. The permutation pair of $a,\ b$ is $(a\ b,\ \ a\ b)$. Otherwise $[l_a, u_a] \cap [l_b, u_b] = \phi$ as shown in Fig. 5 (b), a is both left of and below b, and two permutation pairs of $a,\ b$ are possible.

Given that macro block A is either H-partitioned or V-partitioned, the topology between the sub-blocks of A is strictly defined. Accordingly there is exactly one permutation pair of A corresponding to the partition. The following Lemma is true :

Lemma 1 *Given an arbitrary rectilinear macro block A, there exists only one permutation pair of A corresponding to the H-partition of A, which is referred to as an* H-pair *of A. Similarly*

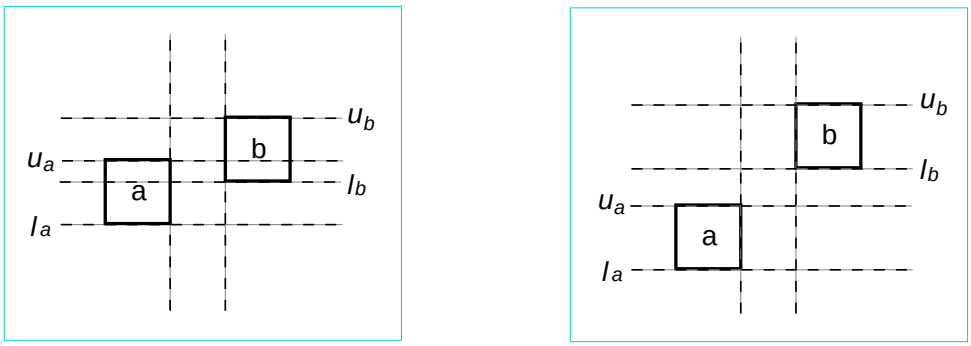


Figure 5: For any two unit blocks a and b placed in a plane without overlaps, a is left of b if the right boundary of a is left of the left boundary of b. In (a), $[l_a, u_a] \cap [l_b, u_b] \neq \phi$, a is *strictly* left of b. The permutation pair of a, b is $(a\ b,\ \ a\ b)$. In (b), $[l_a, u_a] \cap [l_b, u_b] = \phi$, a is both left of and below b, and two permutation pairs are possible.

there exists only one permutation pair of A corresponding to the V-partition of A, which is referred to as a V-pair.

In the example shown in Fig. 4, the H-pair of A is $(a_1\ a_2\ a_3\ a_4\ a_5,\ \ a_2\ a_1\ a_3\ a_4\ a_5)$ and V-pair is $(a_5\ a_4\ a_3\ a_1\ a_2,\ \ a_1\ a_2\ a_3\ a_4\ a_5)$.

3.2 X, Y-Alignment

Given a sequence pair representing topological relationships among unit blocks of rectilinear macro blocks, the unit blocks are compacted left and downward using the longest path algorithm in the x and y directions, respectively. If any unit block is further moved left or downward after the compaction, overlaps will occur. In other words, X, Y-alignment can only move unit blocks right and upward. Given a macro block A is H-partitioned as shown in Fig. 6 (a), and the sequence pair is $(c\ a_1\ a_2\ e\ a_3\ a_4\ d\ a_5\ f,\ \ e\ a_2\ a_1\ a_3\ f\ c\ a_4\ a_5\ d)$, the unit blocks are compacted as shown in Fig. 6 (b). In the x direction, a_5 is the right-most sub-block of A. X-Alignment(A) freezes a_5 and moves a_4 to the right until it hits a_5, then moves a_3 to the right until it hits a_4, and so on. After the right move of a_1 and a_2, the sub-blocks of A are aligned together in the x direction as shown in Fig. 6 (c). In the y direction, the highest sub-block of A is a_4. Y-Alignment(A) freezes a_4, and moves the other sub-blocks of A upward to align with a_4 as shown in Fig. 6 (d). When macro block A is V-partitioned, X, Y-alignment can be symmetrically carried out. Obviously the following Theorem is true :

Theorem 1 *Given a sequence pair representing topological relationships among unit blocks of rectilinear macro blocks, X, Y-Alignment yields an optimal packing for the sequence pair.*

Given a sequence pair, the shapes of macro blocks may not be recovered by X, Y-Alignment.

Definition 1 *A sequence pair is* feasible *if after X, Y-Alignment, the shapes of rectilinear blocks are guaranteed to be recovered regardless of the dimensions of the blocks.*

Definition 2 *A sequence pair is* infeasible *if it is not feasible, e.g. the shapes of rectilinear blocks may not be recovered after X, Y-Alignment.*

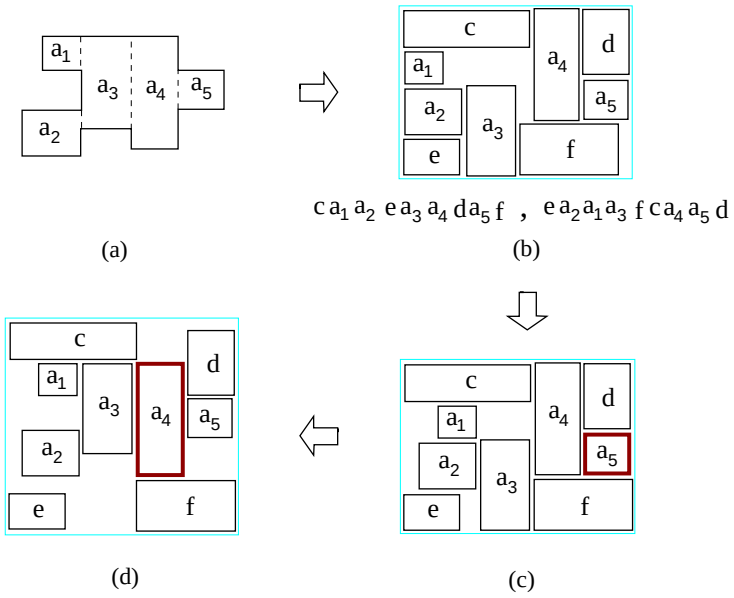


Figure 6: (a) Macro block A is H-partitioned into a_1 a_2 a_3 a_4 a_5. (b) Given a sequence pair (c a_1 a_2 e a_3 a_4 d a_5 f, e a_2 a_1 a_3 f c a_4 a_5 d), the unit blocks are compacted left and downward using the longest path algorithm in the x and y directions, respectively. (c) In the x direction, a_5 is the right-most sub-block of A. X-Alignment(A) freezes a_5 and moves a_4 to the right until it hits a_5, then moves a_3 to the right until it hits a_4, and so on. After the right move of a_1 and a_2, the sub-blocks of A are aligned together in the x direction. (d) In the y direction, the highest sub-block of A is a_4. Y-Alignment(A) freezes a_4, and moves the other sub-blocks of A upward to align with a_4.

Accordingly we define the necessary and sufficient conditions on sequence pair as follows:

Definition 3 *A condition is* necessary **iff** *when the condition is not satisfied, the sequence pair is infeasible.*

Definition 4 *A set of conditions are* sufficient **iff** *when the set of conditions are satisfied, the sequence pair is feasible.*

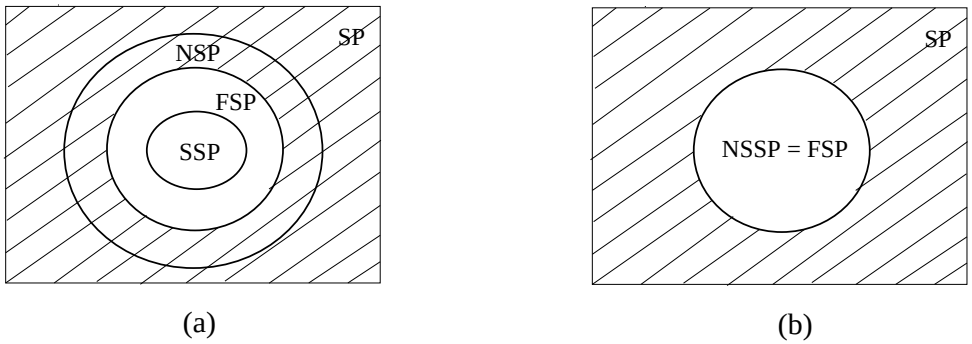


Figure 7: (a) Let FSP denote a set of feasible sequence pairs, NSP the sequence pairs which satisfy the necessary conditions, and SSP the sequence pairs which satisfy the sufficient conditions, then $SSP \subseteq FSP \subseteq NSP$. (b) If we can derive a set of conditions which are necessary and sufficient, the solution space for feasible sequence pairs can be completely characterized by the necessary and sufficient conditions: a sequence pair is feasible if the conditions are satisfied, otherwise infeasible.

Let FSP denote a set of feasible sequence pairs, NSP the sequence pairs which satisfy the necessary conditions, and SSP the sequence pairs which satisfy the sufficient conditions, then $SSP \subseteq FSP \subseteq NSP$ as shown in Fig. 7 (a). If the necessary conditions are not met, the sequence pair is infeasible. If the necessary conditions are met, the sequence pair may or may not be feasible. On the other hand, if the sufficient conditions are met, the sequence pair is feasible. If the sufficient conditions are not met, the sequence pair may or may not be feasible. As such, necessary conditions can not completely characterize the solution space for feasible sequence pairs, neither can sufficient conditions.

If we can derive a set of conditions which are necessary and sufficient, as shown in Fig. 7 (b), the solution space for feasible sequence pairs can be completely characterized by the necessary and sufficient conditions: a sequence pair is feasible if the conditions are satisfied, otherwise infeasible. In the following, we first present three conditions on sequence pair, and later we will prove that the three conditions are both necessary and sufficient.

3.3 Three Conditions on Sequence Pairs

Before presenting the detailed conditions, we first define four relations for the unit blocks in a sequence pair.

– Given three unit blocks $a_i,\ a_j \in A$ and $c \notin A$, if c is between a_i and a_j in both sequences, for example $(a_i\ c\ a_j,\ \ a_i\ c\ a_j)$. we call c *interrupts* a_i and a_j.

– Given two pairs of unit blocks $a_i,\ a_j \in A$ and $b_i,\ b_j \in B$, $A \neq B$. In the first sequence :

$a_i\ \cdot\cdot\ a_j\ \cdot\cdot\ b_i\ \cdot\cdot\ b_j$, we call $(a_i,\ a_j)$ and $(b_i,\ b_j)$ as *separates* of each other.

$a_i\ \cdot\cdot\ b_i\ \cdot\cdot\ a_j\ \cdot\cdot\ b_j$, we call $(a_i,\ a_j)$ and $(b_i,\ b_j)$ as *interleaves* of each other.

$a_i\ \cdot\cdot\ b_i\ \cdot\cdot\ b_j\ \cdot\cdot\ a_j$, we call $(a_i,\ a_j)$ as *covering* $(b_i,\ b_j)$.

– Similarly, the *separate*, *interleave* and *cover* relations can be defined in the second sequence.

The first condition is referred to as *condition-1* :

> For any H-partitioned macro A, the permutation pair of A equals the H-Pair of A, similarly for any V-partitioned A, the permutation pair of A equals the V-pair of A.

The second condition is referred to as *condition-2* :

> Any two units $a_i,\ a_j \in A$ are not interrupted by a unit $c\ \notin\ A$.

Finally the third condition is referred to as *condition-3* :

> Any two pairs of unit blocks $a_i,\ a_j \in A$ and $b_{i'},\ b_{j'} \in B$, $A \neq B$. $(a_i,\ a_j)$ separates $(b_{i'},\ b_{j'})$ in the first or second sequence.

Overall the three conditions are called *3-conditions*.

4 3-Conditions Are Necessary and Sufficient

4.1 3-Conditions Are Necessary

Given the sequence pair which does not satisfy condition-1, without loss of generality, we assume the permutation pair of an H-partitioned macro block A does not equal the H-pair of A. There must exist two sub-blocks $a_i,\ a_j \in A$, whose permutations in SP are different from those in the H-pair of A. For example, sub-block a_1 is left of a_2 in the H-partitioned A, the H-pair of A is $(a_1\ a_2\ ,\ \ a_1\ a_2)$. On the other hand, the permutations of $a_1,\ a_2$ in the sequence pair is $(a_1\ a_2\ ,\ \ a_2\ a_1)$. X, Y-Alignment preserve the topological relationships defined in the sequence pair, block a_1 will be above a_2 after the alignment and the shape of macro block A cannot be recovered. Therefore condition-1 is a necessary condition.

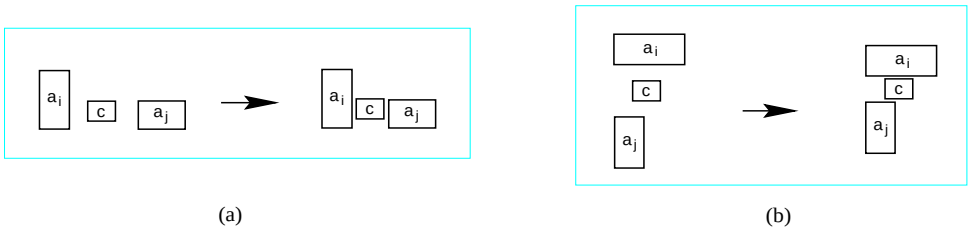


Figure 8: (a) Unit block c is right of a_i while left of a_j, a_i and a_j may not be aligned in the x direction. (b) Block c is below a_i while above a_j, a_i and a_j may not be aligned in the y direction.

Given the sequence pair does not satisfy condition-2, there must exist two unit blocks $a_i,\ a_j \in A$ interrupted by a unit block $c \notin A$. The sequence pair will be either $(a_i \cdot\cdot c \cdot\cdot a_j\ ,\ \ a_i \cdot\cdot c \cdot\cdot a_j)$ or $(a_i\ \cdot\cdot c\ \cdot\cdot a_j\ ,\ \ a_j\ \cdot\cdot c\ \cdot\cdot a_i)$. In the first case, c is right of a_i while left of a_j, a_i and a_j may not be aligned in the x direction as shown in Fig. 8 (a). While in the second case, c is below a_i while above a_j, a_i and a_j may not be aligned in the y direction as shown in Fig. 8 (b). Therefore condition-2 is also a necessary condition.

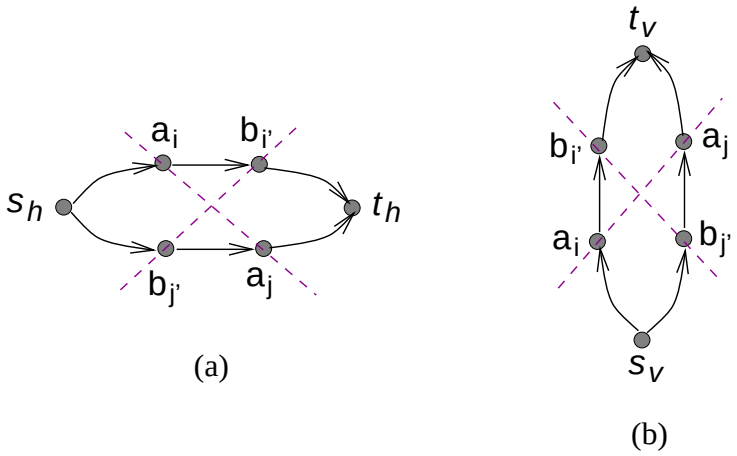


Figure 9: (a) In the horizontal graph G_h, if unit block $a_i \in A$ is left of unit $b_{i'} \in B$, $A \neq B$, and unit block $a_j \in A$ is right of unit $b_{j'} \in B$, $a_i,\ a_j$ and $b_{i'},\ b_{j'}$ are *H-crossed* to each other. (b) In the vertical graph G_v, if a_i is below $b_{i'}$, and a_j is above $b_{j'}$, $a_i,\ a_j$ and $b_{i'},\ b_{j'}$ are *V-crossed* to each other.

In the following, we refer two unit blocks $a_i,\ a_j \in A$ as *a-pair*. Similarly two unit blocks $b_{i'},\ b_{j'} \in B$ as *b-pair*, where $A \neq B$. If a_i is left of $b_{i'}$ while a_j is right of $b_{j'}$ as shown in Fig. 9 (a), we call a-pair and b-pair *H-crossing* each other. In X-Alignment(A), the right move of a_i may push unit $b_{i'}$ to the right. Then $b_{j'}$ has to be moved to the right along with $b_{i'}$, which may push unit a_j to the right. Again a_i is moved to the right along with a_j and so on ... , the x alignment might continue infinitely. When the similar situation happens in the vertical dimension as shown in Fig. 9 (b), we call a-pair and b-pair *V-crossing* each other, and Y-Alignment might continue infinitely. We can conclude the following fact :

Lemma 2 *If two pairs of unit blocks are H-crossed or V-crossed to each other, the shapes of the corresponding macro blocks may not be recovered after X, Y-Alignment.*

Given the sequence pair does not satisfy condition-3, there must exist a-pair and b-pair which do not separate each other in either sequence. Without loss of generality, we assume a_i is before a_j, and $b_{i'}$ is before $b_{j'}$ in the first sequence Γ_1. Then Γ_1 will be either $a_i\ b_{i'}\ a_j\ b_{j'}$, or $a_i\ b_{i'}\ b_{j'}\ a_j$. When the first sequence is $a_i\ b_{i'}\ a_j\ b_{j'}$, the second sequence Γ_2 is enumerated in Fig. 10. Since a-pair does not separate b-pair in Γ_2, the second sequence can not be the case (1.1.1), (1.1.2), (1.3.3), (1.3.4), (2.1.3), (2.1.4), (2.3.1) or (2.3.2). On the other hand, if the second sequence is the case (1.1.4), (1.3.1), (1.3.2), (2.1.1), (2.3.3) or (2.3.4), condition-2 will be violated. Therefore Γ_2 can only be case (1.1.3) or (2.1.2). The two corresponding sequence pairs are :

1. $(a_i\ b_{i'}\ a_j\ b_{j'}\ ,\ \ b_{i'}\ a_i\ b_{j'}\ a_j)$
2. $(a_i\ b_{i'}\ a_j\ b_{j'}\ ,\ \ a_j\ b_{j'}\ a_i\ b_{i'})$

When the first sequence Γ_1 is $a_i\ b_{i'}\ b_{j'}\ a_j$, the second sequence is enumerated in Fig. 11. Since a-pair does not separate b-pair in Γ_2, the second sequence can not be the case (1.1.1), (1.1.2), (1.3.3), (1.3.4), (2.1.3), (2.1.4), (2.3.1) or (2.3.2). On the other hand, if the second sequence is the case (1.1.3), (1.3.2), (2.1.2) or (2.3.3), condition-2 will be violated in the sequence pair. Therefore Γ_2 can only be case (1.1.4), (1.3.1), (2.1.1) or (2.3.4). The four corresponding sequence pairs are :

3. $(a_i\ b_{i'}\ b_{j'}\ a_j\ ,\ \ b_{i'}\ a_i\ a_j\ b_{j'})$
4. $(a_i\ b_{i'}\ b_{j'}\ a_j\ ,\ \ b_{j'}\ a_i\ a_j\ b_{i'})$
5. $(a_i\ b_{i'}\ b_{j'}\ a_j\ ,\ \ b_{i'}\ a_j\ a_i\ b_{j'})$
6. $(a_i\ b_{i'}\ b_{j'}\ a_j\ ,\ \ b_{j'}\ a_j\ a_i\ b_{i'})$

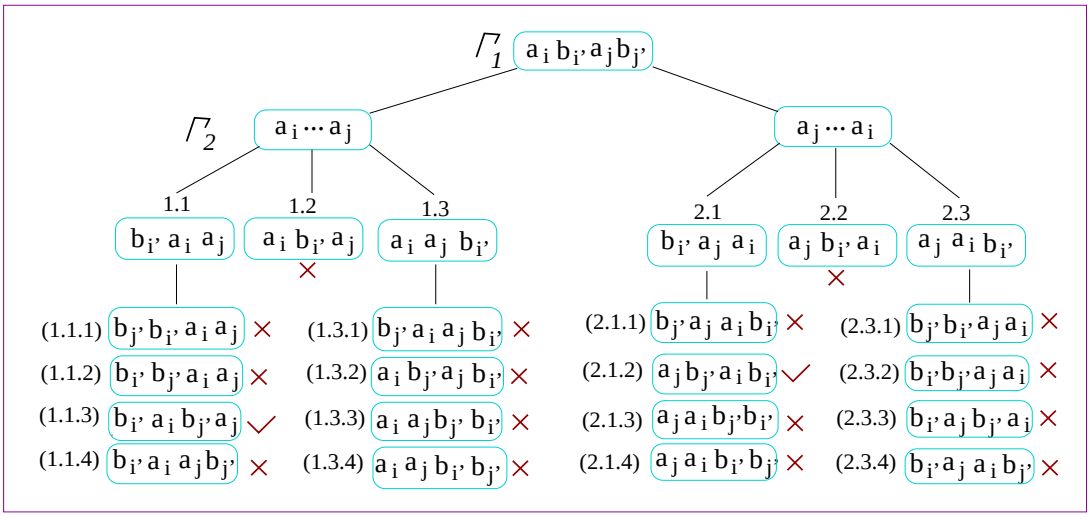


Figure 10: Given a-pair does not separate b-pair in either sequence, and the first sequence is $a_i\ b_{i'}\ a_j\ b_{j'}$. The second sequence Γ_2 is enumerated in this Figure. Since a-pair does not separate b-pair in Γ_2, the second sequence can not be the case (1.1.1), (1.1.2), (1.3.3), (1.3.4), (2.1.3), (2.1.4), (2.3.1) or (2.3.2). On the other hand, if the second sequence is the case (1.1.4), (1.3.1), (1.3.2), (2.1.1), (2.3.3) or (2.3.4), condition-2 will be violated. Therefore Γ_2 can only be case (1.1.3) or (2.1.2).

In each of the above six sequence pairs, a-pair and b-pair are either H-crossed or V-crossed to each other, the corresponding sequence pair is infeasible. Therefore condition-3 is a necessary condition.

Lemma 3 *The 3-conditions are necessary for a sequence pair to be feasible.*

Based on the similar analysis, we can derive the following property :

Lemma 4 *Given condition-3 is satisfied in the sequence pair, any two pairs of unit blocks* $a_i,\ a_j \in A$ *and* $b_{i'},\ b_{j'} \in B$, $A \neq B$, *are neither H-crossed nor V-crossed to each other.*

4.2 3-Conditions Are Sufficient

Given 3-conditions are satisfied in the sequence pair, the following Lemma is true :

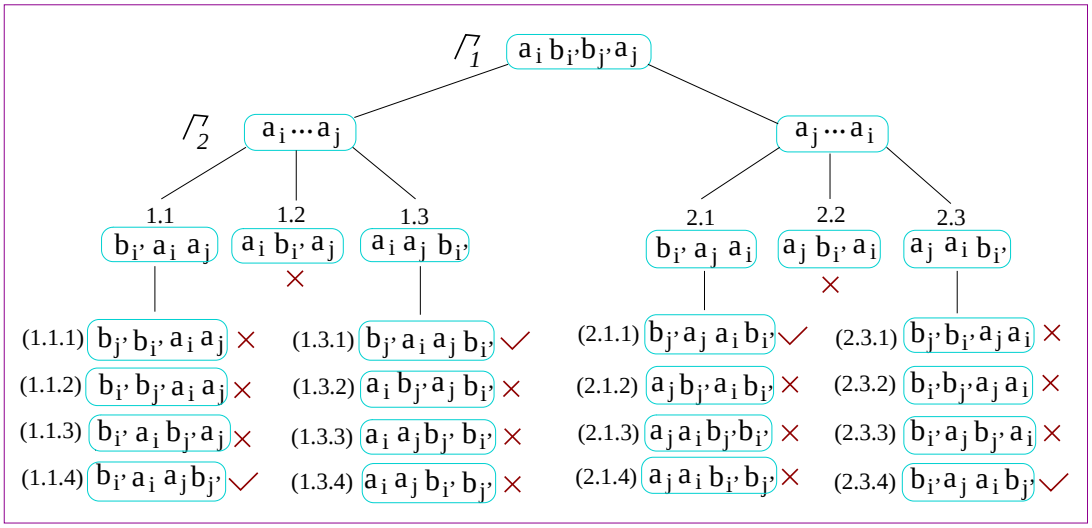


Figure 11: Given a-pair does not separate b-pair in either sequence, and the first sequence is $a_i\ b_{i'}\ b_{j'}\ a_j$. The second sequence Γ_2 is enumerated in this Figure. Since a-pair does not separate b-pair in Γ_2, the second sequence can not be the case (1.1.1), (1.1.2), (1.3.3), (1.3.4), (2.1.3), (2.1.4), (2.3.1) or (2.3.2). On the other hand, if the second sequence is the case (1.1.3), (1.3.2), (2.1.2) or (2.3.3), condition-2 will be violated. Therefore Γ_2 can only be case (1.1.4), (1.3.1), (2.1.1) or (2.3.4).

Lemma 5 *If a unit block $a_i \in A$ is left of a unit $b_{i'} \in B$, $A \neq B$, then no unit of A is right of a unit of B. Similarly, if a_i is below $b_{i'}$, no unit of A is above a unit of B.*

Lemma 5 can be proven by the contradiction. Let's assume that a_i is left of $b_{i'}$, and a unit block $a_j \in A$ is right of a unit $b_{j'} \in B$. If $a_i = a_j$ or $b_{i'} = b_{j'}$, we can easily derive that a_i interrupts $(b_{i'},\ b_{j'})$ or $b_{i'}$ interrupts $(a_i,\ a_j)$ in the sequence pair, which contradicts the assumption. Thus $a_i \neq a_j,\ b_{i'} \neq b_{j'}$. As such a-pair and b-pair are H-crossed to each other, then a-pair does not separate b-pair in either sequence. Again the assumption that sequence pair satisfies the 3-conditions is contradicted. Therefore Lemma 5 is true. Based on this property, we can sort the macro blocks in x and y direction, respectively :

x-order : macro block A is before macro block B if a unit of A is left of a unit of B;

y-order : macro block A is before macro block B if a unit of A is below a unit of B.

In the following, we show that the shapes of macro blocks can be exactly recovered by applying X, Y-Alignment on each macro block in x and y-order, respectively. Based on the horizontal graph G_h, X-Alignment(A) is carried out, a unit $a_i \in A$ is moved right, the unit $b_{i'} \in B$ is pushed to the right by a_i only when $b_{i'}$ is right of a_i and $B \neq A$, as shown in Fig. 12 (a). The right move of $b_{i'}$ may further affect the unit blocks of A if and only if:

1. a unit block $a_j \in A$ is right of $b_{i'}$, or
2. a unit block $a_j \in A$ is right of another unit block $b_{j'} \in B$.

In the first case, $b_{i'}$ is right of a_i while left of a_j as shown in Fig. 12 (b). Then b_i interrupts $a_i,\ a_j$ in the sequence pair, condition-2 is violated. In the second case, $a_i,\ a_j$ and $b_{i'},\ b_{j'}$ are H-crossed to each other as shown in Fig. 12 (c). Then a-pair does not separate b-pair in either sequence

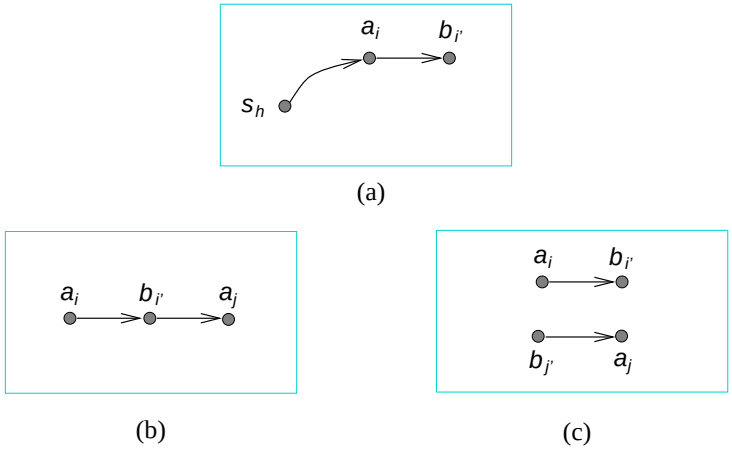


Figure 12: (a) In X-Alignment(A), unit block $a_i \in A$ is moved to the right, a unit $b_{i'} \in B$ is pushed to the right by a_i only when $b_{i'}$ is right of a_i and $B \neq A$. The right move of $b_{i'}$ may further affect the unit blocks of A if and only if : (b) a unit block $a_j \in A$ is right to $b_{i'}$, or (c) a unit block $a_j \in A$ is right of a unit block $b_{j'} \in B$.

and condition-3 is violated. Due to the assumption that sequence pair satisfies the 3-conditions, neither case 1 nor case 2 will happen. In other words, the right move of a_i in x-align(A) will not affect any other unit of A. X-Alignment(A) exactly aligns the x coordinates of A.

On the other hand, when X-Alignment is carried out on macro B after X-Alignment(A), no unit of B can be left of a unit of A due to the x-order. As such, the right move of unit blocks in X-Alignment(B) will not affect macro block A. It implies that once X-Alignment(A) is carried out, the x coordinates of A will not be affected later. We can conclude the following Lemma :

Lemma 6 *The 3-conditions are sufficient for a sequence pair to be feasible.*

Followed by Lemma 3 and Lemma 6, we can conclude :

Theorem 2 *The 3-conditions are necessary and sufficient for a sequence pair to be feasible.*

5 Convex Rectilinear Block Packing

A rectilinear block is called *convex* if any two points in the block have a shortest Manhattan path inside the block, as shown in Fig. 13 (a). Otherwise the block is called *concave*, as shown in Fig. 13 (b). It can be observed that some packing of concave blocks can not be represented by the feasible sequence pair. For example, in the packing of Fig. 13 (c), block c is right of block a_1 while left of a_3, then c must interrupt a_1, a_3 in the corresponding sequence pair.

Let Π denote an arbitrary convex block packing. By H- or V-partitioning the rectilinear macro blocks, Π becomes a rectangle packing. The corresponding sequence pair $SP(\Pi)$ can be easily derived, in which the sub-blocks are treated as individual unit blocks. Obviously condition-1 is satisfied in $SP(\Pi)$.

If condition-2 is not satisfied in the sequence pair, there exist two unit blocks a_i, $a_j \in A$ interrupted by a unit $c \notin A$. It can be easily derived that A has concave shape, which contradicts the convex assumption. Therefore condition-2 is also satisfied in $SP(\Pi)$.

If the condition-3 is not satisfied in the sequence pair $SP(\Pi)$, there exist a_i, $a_j \in A$ and $b_{i'}$, $b_{j'} \in B$ such that a-pair does not separate b-pair in either sequence. According to the

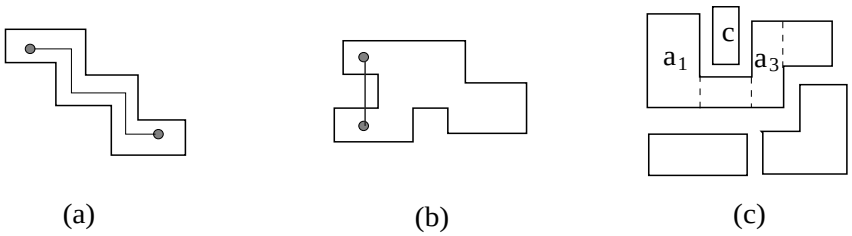


Figure 13: (a) Any two points of the convex rectilinear block have a shortest Manhattan path inside the block. (b) At least two points in the concave block have no shortest Manhattan path located inside the block. (c) The packing of concave blocks can not be representable by feasible sequence pairs.

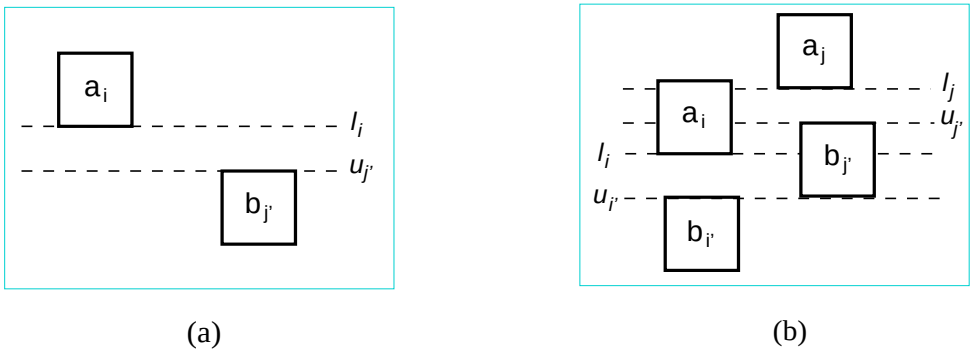


Figure 14: Let l_i and u_i denote the lower and upper boundary of unit a_i, respectively. Given sequence pair $SP(\Pi) = (a_i\ b_{i'}\ a_j\ b_{j'},\ \ b_{i'}\ a_i\ b_{j'}\ a_j)$, a_i is above $b_{i'}$ and a_j is above $b_{j'}$. Then in the packing Π, $l_i \geq u_{i'}$ and $l_j \geq u_{j'}$. (a) $l_i \geq u_{j'}$: block a_i is both left of and above $b_{j'}$. Then $SP(\Pi)$ can be transformed to $(a_i\ b_{i'}\ a_j\ b_{j'},\ \ b_{i'}\ b_{j'}\ a_i\ a_j)$. (b) $l_i < u_{j'}$: $l_j \geq u_{j'} > l_i \geq u_{i'}$, then $l_j > u_{i'}$. Block a_j is both right of and above $b_{i'}$ in the packing Π. $SP(\Pi)$ can be transformed to $(a_i\ a_j\ b_{i'}\ b_{j'},\ \ b_{i'}\ b_{j'}\ a_i\ a_j)$.

analysis of Fig. 10 and Fig. 11, a total of six non-symmetrical sequence pairs are possible. When the sequence pair is the first case, $SP(\Pi) = (a_i\ b_{i'}\ a_j\ b_{j'},\ \ b_{i'}\ a_i\ b_{j'}\ a_j)$, a_i is above $b_{i'}$ and a_j is above $b_{j'}$. Let l_i and u_i denote the lower and upper y coordinate of a_i, respectively. Then $l_i \geq u_{i'}$ and $l_j \geq u_{j'}$. If $l_i \geq u_{j'}$ as shown in Fig. 14 (a), a_i is both left of and above $b_{j'}$, $SP(\Pi)$ can be transformed as follows:

$$(a_i\ b_{i'}\ a_j\ b_{j'},\ \ b_{i'}\ a_i\ b_{j'}\ a_j)\ \Rightarrow\ (a_i\ b_{i'}\ a_j\ b_{j'},\ \ b_{i'}\ b_{j'}\ a_i\ a_j) \tag{1}$$

Otherwise $l_i < u_{j'}$ as shown in Fig. 14 (b), $l_j \geq u_{j'} > l_i \geq u_{i'}$, then $l_j > u_{i'}$. Block a_j is both right of and above $b_{i'}$ in the packing Π. Thus $SP(\Pi)$ can be transformed as follows :

$$(a_i\ b_{i'}\ a_j\ b_{j'},\ \ b_{i'}\ a_i\ b_{j'}\ a_j)\ \Rightarrow\ (a_i\ a_j\ b_{i'}\ b_{j'},\ \ b_{i'}\ b_{j'}\ a_i\ a_j). \tag{2}$$

Obviously the transformation will not cause any violation of 3-conditions, a-pair will separate b-pair in at least one sequence of $SP(\Pi)$, meanwhile the topology defined by the sequence pair is consistent with the packing Π. For case 2 through case 6, $SP(\Pi)$ can be similarly transformed. In such a way, a feasible sequence pair can be eventually achieved, that is

Lemma 7 *There always exists a feasible sequence pair corresponding to a packing of convex rectilinear blocks.*

For M convex macro blocks, each of them includes at most n rectangular sub-blocks, the optimal solution for convex rectilinear block packing can be found by exhausting the finite number $O((nM)!^2)$ of feasible sequence pairs.

When a convex macro block A is H-partitioned as shown in Fig. 15 (a), a_i denotes the i^{th} leftmost sub-block, the H-pair of A is $(a_1\ \cdot\cdot\ a_i\ a_{i+1}\ \cdot\cdot\ a_m,\ \ a_1\ \cdot\cdot\ a_i\ a_{i+1}\ \cdot\cdot\ a_m)$. When A is V-partitioned as shown in Fig. 15 (b), a_i denotes the i^{th} lowest sub-block, the V-pair of A is $(a_m\ \cdot\cdot\ a_{i+1}\ a_i\ \cdot\cdot\ a_1,\ \ a_1\ \cdot\cdot\ a_i\ a_{i+1}\ \cdot\cdot\ a_m)$.

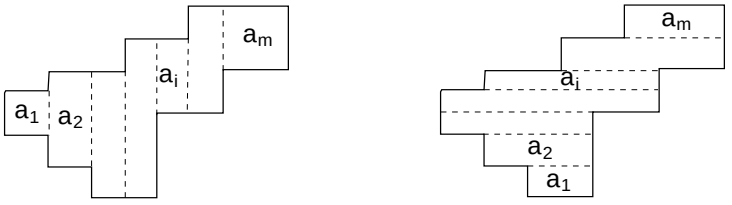


Figure 15: (a) Convex block A is H-partitioned where a_i is the i^{th} leftmost sub-block of A. The H-pair of A equals to $(a_1\ \cdot\cdot\ a_i\ a_{i+1}\ \cdot\cdot\ a_m,\ \ a_1\ \cdot\cdot\ a_i\ a_{i+1}\ \cdot\cdot\ a_m)$. (b) When A is V-partitioned, a_i is the i^{th} lowest sub-block of A. The V-pair A equals to $(a_m\ \cdot\cdot\ a_{i+1}\ a_i\ \cdot\cdot\ a_1,\ \ a_1\ \cdot\cdot\ a_i\ a_{i+1}\ \cdot\cdot\ a_m)$.

6 Stochastic Search on Convex Block Packing

In the following, a stochastic search is applied to the optimization of convex block packing. Three sequence pair operations are defined to incrementally change the feasible sequence pair : *rotation*, Γ_1-*mutation*, and Γ_2-*mutation*.

6.1 Rotation

Rotation rotates a macro block by 90^0 in the clockwise direction as shown in Fig. 16. Given macro block $A = \{a_1, a_2, \cdot\cdot, a_n\}$, $rotate(A)$ switches the height with the width for each unit block of A. The sequence pair is accordingly changed by switching unit a_i with a_{m+1-i}, $i \in [1,\ n]$, in the first sequence (90^0 to 180^0, 270^0 to 0^0) or the second sequence (0^0 to 90^0, 180^0 to 270^0). Rotation takes $O(n)$ time, which is close to constant time.

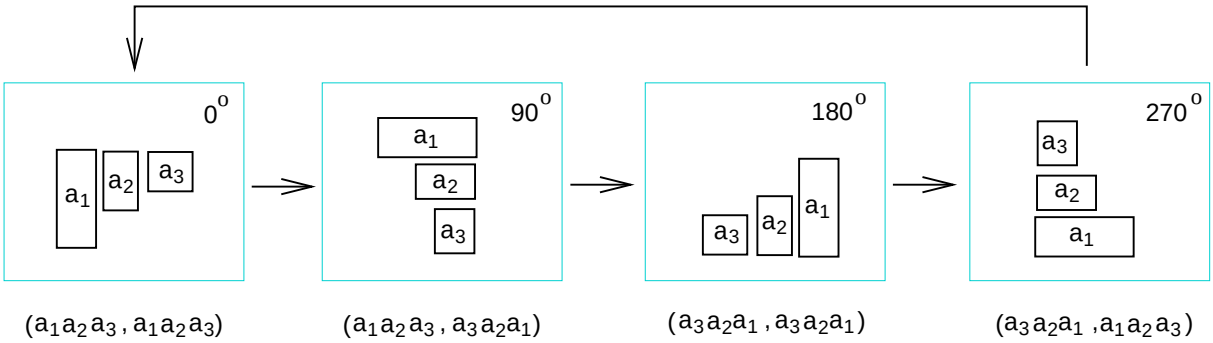


Figure 16: A macro block $A = \{a_1, a_2, a_3\}$ is rotated from 0^0 through 90^0 and 180^0 to 270^0 in the clockwise direction. $rotate(A)$ switches the height and width for each unit block of A, and changes the sequence pair by switching a_i with a_{m+1-i} in the first or second sequence.

Given a rotation is carried out on macro block A represented in a feasible sequence pair (Γ_1, Γ_2), only the permutation pair of A is changed from H-pair to V-pair, or vice versa. Accordingly the orientation of A is rotated such that the H-partition of A becomes the V-partition, or vice versa. As such, the resultant sequence pair $(\Gamma_1^{'}, \Gamma_2^{'})$ still satisfies condition-1.

If the resultant sequence pair does not satisfy condition-2, there exists a unit $c \in C$ between two units $b_i,\ b_j \in B$ in both $\Gamma_1^{'}$ and $\Gamma_2^{'}$, $C \neq B$. Three cases are possible :

1. $B \neq A$, $C \neq A$.
   The positions of $b_i,\ b_j$ and c in the resultant sequence pair are exactly the same with those in the original sequence pair. Thus c also interrupts $b_i,\ b_j$ in (Γ_1, Γ_2), which contradicts the feasible assumption.

2. $B \neq A$, $C = A$.
   Without loss of generality, we assume $c = a_k$, the resultant sequence pair is $(b_i\ a_k\ b_j,\ \ b_i\ a_k\ b_j)$. According to $rotate(A)$, the original sequence pair should be either $(b_i\ a_k\ b_j,\ \ b_i\ a_{m+1-k}\ b_j)$ or $(b_i\ a_{m+1-k}\ b_j,\ \ b_i\ a_k\ b_j)$. If $k = m + 1 - k$, then a_k interrupts $b_i,\ b_j$. Otherwise $a_k,\ a_{m+1-k}$ and $b_i,\ b_j$ will not separate each other in either sequence of $(\Gamma_1,\ \Gamma_2)$, then condition-3 is violated. Either case contradicts the feasible assumption of the original sequence pair.

3. $B = A$, $C \neq A$.
   Without loss of generality, we assume $b_i = a_i,\ b_j = a_j$ and the resultant sequence pair is $(a_i\ c\ a_j,\ \ a_i\ c\ a_j)$. According to $rotate(A)$, the original sequence pair should be either $(a_i\ c\ a_j,\ \ a_{m+1-i}\ c\ a_{m+1-j})$ or $(a_{m+1-i}\ c\ a_{m+1-j},\ \ a_i\ c\ a_j)$. Since the two cases are symmetrical, we only discuss the first one. Due to the feasible assumption, unit c can not appear between a_i and a_j in the second sequence Γ_2. Similarly, c can not appear between a_{m+1-i} and a_{m+1-j} in the first sequence Γ_1. Therefore the original sequence pair (Γ_1, Γ_2)

will be one of the four possible cases shown in Fig. 17. In each of them there are two units of A interrupted by unit c. A contradiction exists.

As such, we can derive that the resultant sequence pair also satisfies condition-2.

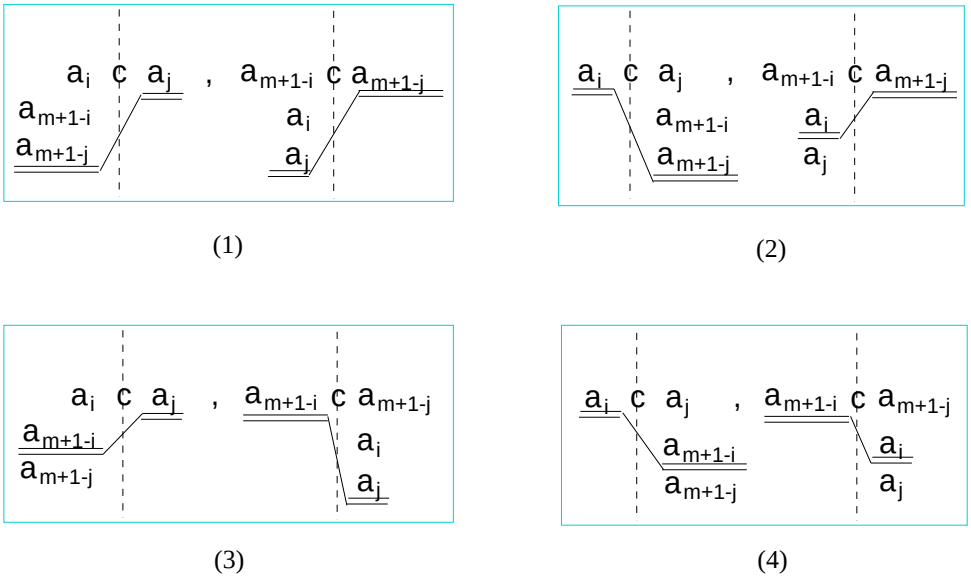


Figure 17: In a feasible sequence pair (a_i c a_j, a_{m+1-i} c a_{m+1-j}), a_i, a_j will be both before or both after c in the second sequence. Similarly a_{m+1-i}, a_{m+1-j} will be both before or both after c in the first sequence. As such, the sequence pair will be one of the four possible cases: (1) a_j, a_{m+1-j} are interrupted by c, (2) a_i, a_{m+1-j} are interrupted by c, (3) a_j, a_{m+1-i} are interrupted by c, (4) a_i, a_{m+1-i} are interrupted by c. The sequence pair can not be feasible.

If the resultant sequence pair does not satisfy condition-3, there exist b_i, $b_j \in B$ and c_k, $c_l \in C$, $B \neq C$, b-pair does not separate c-pair in either sequence of (Γ_1', Γ_2') When $B \neq A$, $C \neq A$, the original sequence pair will also violate condition-3. Thus let $B = A$, $b_i = a_i$, $b_j = a_j$. In the original sequence pair, a_i, a_j do not separate c_k, c_l in one sequence, say Γ_1, while a_{m+1-i}, a_{m+1-j} do not separate c_k, c_l in the other sequence, say Γ_2.

Due to the feasible assumption of (Γ_1, Γ_2), a_{m+1-i}, a_{m+1-j} must separate c_k, c_l in Γ_1. As shown in Fig. 18, we can draw a line to separate c_k, c_l from a_{m+1-i}, a_{m+1-j} in the first sequence Γ_1. Either a_i or a_j will be on the different side of a_{m+1-i}, a_{m+1-j}, otherwise a_i, a_j will separate c_k, c_l in the first sequence. In the second sequence Γ_2, we can derive the symmetrical situation. Then totally four cases are possible as shown in Fig. 18, in each of them condition-3 is not satisfied, and the original sequence pair could not be feasible. As such, we can derive that the resultant sequence pair satisfies condition-3. Overall we can conclude :

Lemma 8 *When a rotation is carried out on a macro block represented in a feasible sequence pair, the resultant sequence pair remains feasible.*

6.2 Γ_1-Mutation And Γ_2-Mutation

Γ_1-Mutation switches two adjacent unit blocks in the first sequence : $\cdots$ $\underline{a\ b}$ $\cdots$ $\Rightarrow$ $\cdots$ $\underline{b\ a}$ $\cdots$, in which $a \in A$, $b \in B$, $A \neq B$. Γ_2-Mutation is similarly carried out on the second sequence. Both operations take constant time. Since two mutations are symmetrical, we will only discuss Γ_1-mutation.

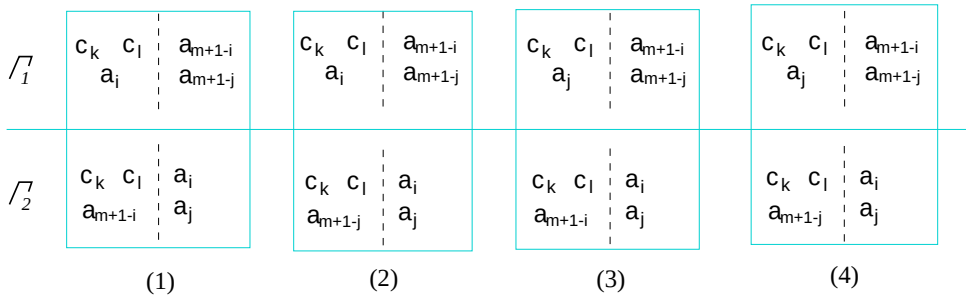


Figure 18: Given a feasible sequence pair (Γ_1, Γ_2) where $a_i,\ a_j$ do not separate $c_k,\ c_l$ in Γ_1, and $a_{m+1-i},\ a_{m+1-j}$ do not separate $c_k,\ c_l$ in Γ_2. Then $a_{m+1-i},\ a_{m+1-j}$ must separate $c_k,\ c_l$ in Γ_1. We can draw a line to separate $c_k,\ c_l$ from $a_{m+1-i},\ a_{m+1-j}$. Either a_i or a_j will be on a different side of $a_{m+1-i},\ a_{m+1-j}$, otherwise $a_i,\ a_j$ will separate $c_k,\ c_l$ in the first sequence. The similar case can be derived in the second sequence. Totally four cases are possible for the sequence pair : (1) $a_i,\ a_{m+1-i}$ and $c_k,\ c_l$, (2) $a_i,\ a_{m+1-j}$ and $c_k,\ c_l$, (3) $a_j,\ a_{m+1-i}$ and $c_k,\ c_l$, or (4) $a_i,\ a_{m+1-j}$ and $c_k,\ c_l$ violate condition-3. As such, the sequence pair can not be feasible.

Given Γ_1-mutation is carried out on a feasible sequence pair, the permutation pair of every macro block will be preserved in the resultant sequence pair, as such condition-1 is satisfied after the operation. In the following, we assume $A = \{a_1\ a_2\ \cdot\cdot a_m\}$ and $B = \{b_1\ b_2\ \cdot\cdot b_n\}$. By relabeling the sub-blocks of A and B, a_i and b_i are the i^{th} sub-block of A and B in the first sequence Γ_1, respectively.

Lemma 9 *When Γ_1-mutation is carried out on a feasible sequence pair : $\cdot\cdot\ \underline{a_i\ b_j}\ \cdot\cdot\ \Rightarrow\ \cdot\cdot\ \underline{b_j\ a_i}\ \cdot\cdot$, the resultant sequence pair may violate condition-2 only when $a_i = a_m,\ b_j = b_1$. And the violation only happens on a_m and b_1.*

Given the resultant sequence pair violates condition-2, then $d \in D$ is between $c_u,\ c_v \in C$ in both sequences of $(\Gamma_1^{'},\ \Gamma_2^{'})$. According to Γ_1-mutation, $\Gamma_2^{'} = \Gamma_2$, then d is between c_u and c_v in Γ_2. On the other hand, if $d \neq a_i,\ d \neq b_j$, d is also between c_u and c_v in Γ_1, the original sequence pair violates condition-2. Thus d must be either a_i or b_j. Similarly we can derive that one unit of $(c_u,\ c_v)$ must be a_i or b_j. Therefore in the resultant sequence pair $(\Gamma_1^{'},\ \Gamma_2^{'})$, two cases are possible :

1. $a_x,\ a_i \in A$ is interrupted by b_j. Due to Γ_1-mutation, $\Gamma_1^{'}$ must be $\cdot\cdot\ a_x\ \cdot\cdot b_j\ a_i\ \cdot\cdot$, then $a_x = a_{i-k}$, where $k > 0$.

2. $b_y,\ b_j \in B$ is interrupted by a_i. Due to Γ_1-mutation, $\Gamma_1^{'}$ must be $\cdot\cdot\ b_j\ a_i\ \cdot\cdot b_y\ \cdot\cdot$, then $b_y = b_{j+l}$, where $l > 0$.

In the following, we assume that the resultant sequence pair is the first case. If $i < m$, the original first sequence Γ_1 will be $\cdot\cdot\ a_{i-k}\ \cdot\cdot a_i\ b_j\ \cdot\cdot a_m\ \cdot\cdot$. The original second sequence Γ_2 will be either $\cdot\cdot\ a_{i-k}\ \cdot\cdot b_j\ \cdot\cdot a_i\ \cdot\cdot a_m\ \cdot\cdot$ or $\cdot\cdot\ a_m\ \cdot\cdot a_i\ \cdot\cdot b_j\ \cdot\cdot a_{i-k}\ \cdot\cdot$. Then b_j will interrupt $a_{i-k},\ a_m$ in the original sequence pair. Therefore, i must equal m, i.e. $a_i = a_m$.

If $j > 1$, the original first sequence Γ_1 will be either $\cdot\cdot a_{i-k} \cdot\cdot b_1 \cdot\cdot a_i\ b_j \cdot\cdot$ or $\cdot\cdot b_1 \cdot\cdot a_{i-k} \cdot\cdot a_i\ b_j \cdot\cdot$. Due to condition-3, $a_{i-k},\ a_i$ and $b_1,\ b_j$ must separate each other in the original second sequence Γ_2. Since $\Gamma_2 = \Gamma_2^{'}$, b_j can not be between $a_{i-k},\ a_i$ in $\Gamma_2^{'}$, which contradicts the assumption that b_j interrupts a_{i-k} and a_i in the resultant sequence pair. Therefore j must equal 1, i.e. $b_j = b_1$. Similarly when the resultant sequence pair is the second case, we can derive that $a_i = a_m,\ b_j = b_1$. Therefore, Lemma 9 is true.

Lemma 10 *When Γ_1-mutation is carried out on a feasible sequence pair : $\cdots$ $\underline{a_i\ b_j}$ $\cdots$ $\Rightarrow$ $\cdots$ $\underline{b_j\ a_i}$ $\cdots$, the resultant sequence pair may violate condition-3 only when $a_i = a_m,\ b_j = b_1$. And the violation only happens on a_m and b_1.*

If the resultant sequence pair does not satisfy condition-3, there exist two pairs of unit blocks which separate each other in neither $\Gamma_1^{'}$ nor $\Gamma_2^{'}$. Since $\Gamma_2 = \Gamma_2^{'}$, the two pairs must separate each other in the first sequence Γ_1 due to the feasible assumption of the original sequence pair. Therefore the two pairs must include both a_i and b_j : $a_{i-k}, a_i \in A$ and $b_j, b_{j+l} \in B$, where $k,\ l > 0$.

If $i < m$, the original first sequence Γ_1 will be either $\cdots\ a_{i-k}\ \cdots a_i\ b_j\ \cdots a_m\ \cdots b_{j+l}\ \cdots$ or $\cdots\ a_{i-k}\ \cdots a_i\ b_j\ \cdots b_{j+l}\ \cdots a_m\ \cdots$. Due to the feasible assumption of the original sequence pair, in the second sequence Γ_2, both $a_{i-k},\ a_m$ and $a_i,\ a_m$ should separate $b_j,\ b_{j+l}$. Therefore $a_{i-k},\ a_i$ will separate $b_j,\ b_{j+l}$ in Γ_2. Since $\Gamma_2 = \Gamma_2^{'}$, $a_{i-k},\ a_i$ and $b_j,\ b_{j+l}$ satisfy condition-3 in the resultant sequence pair, which contradicts the assumption. So i must equal m, i.e. $a_i = a_m$. In the same way, we can derive that $b_j = b_1$. Therefore, Lemma 10 is true.

As we can see, an infeasible solution can be generated by a mutation. During the stochastic search, the infeasible solutions can be avoided by simply cancelling the operation. However the continuity of the local search may be destroyed, the optimal solution may not be reachable. Based on above analysis, the infeasible solution can only be generated when a mutation is carried out on $\cdots\ a_1\ a_2\ \cdots \underline{a_m\ b_1}\ b_2\ \cdots b_n\ \cdots$, where switching a_m with b_1 may cause the violation of condition-2 or condition-3. Due to this fact, we can develop a very simple procedure called *adaptation* to adapt the infeasible solution into a new feasible solution. In such a way, the continuous search of the feasible solution space can be guaranteed.

6.3 Adaptation

Given that Γ_1-mutation generates an infeasible solution, the original first sequence Γ_1 must be $\cdots\ a_1\ \cdots a_2\ \cdots \underline{a_m\ b_1}\ \cdots b_2\ \cdots b_n\ \cdots$. For example,

$$\Gamma_1 = a_1\ c\ a_2\ d\ e\ a_3\ f\ \underline{a_4\ b_1}\ g\ b_2\ h\ i\ j\ b_3 \tag{3}$$

We define *squeeze-to-right* $(\Gamma_1,\ A)$ as follows : applying Γ_1-mutation on a_3 and its right neighbor until a_3 is left adjacent to a_4, then applying Γ_1-mutation on a_2 and its right neighbor until a_2 is left adjacent to a_3, and so on ... :

$$\Gamma_1 = c\ d\ e\ f\ \underline{a_1\ a_2\ a_3\ a_4}\ b_1\ g\ b_2\ h\ i\ j\ b_3 \tag{4}$$

Based on the analysis of the mutations, it can be guaranteed that the intermediate sequence pairs generated during squeeze-to-right $(\Gamma_1,\ A)$ are always feasible. Similarly we define *squeeze-to-left* $(\Gamma_1,\ B)$ as follows : applying Γ_1-mutation on b_2 and its left neighbor until b_2 is right adjacent to b_1, then applying Γ_1-mutation on b_3 and its left neighbor until b_3 is right adjacent to b_2 :

$$\Gamma_1 = c\ d\ e\ f\ a_1\ a_2\ a_3\ a_4\ \underline{b_1\ b_2\ b_3}\ g\ h\ i\ j \tag{5}$$

The intermediate sequence pairs generated during squeeze-to-left $(\Gamma_1,\ B)$ are always feasible.

After the squeeze operations, the unit blocks of both A and B are consecutive in the first sequence. Then adaptation swaps A and B : $\cdots$ $\underline{a_1\ a_2\ \cdots a_m}$ $\underline{b_1\ b_2\ \cdots b_n}$ $\cdots$ $\Rightarrow$ $\cdots$ $\underline{b_1\ b_2\ \cdots b_n}$ $\underline{a_1\ a_2\ \cdots a_m}$ $\cdots$. Obviously no violation of 3-conditions can occur during the swapping, and the resultant sequence pair is feasible. In the above example, the first sequence is adapted to :

$$\Gamma_1 = c\ d\ e\ f\ b_1\ b_2\ b_3\ a_1\ a_2\ a_3\ a_4\ g\ h\ i\ j \tag{6}$$

In $O(m+n)$ time, adaptation generates a new feasible sequence pair which is different from the original one.

Lemma 11 *The resultant infeasible sequence pair after a mutation can always be transformed to a feasible sequence pair by the adaptation.*

As such, the local moves of the stochastic search are completed. Each local move (a rotation or a mutation followed by an adaptation) takes the time proportional to the number of unit blocks in a macro block, which is close to constant time. In addition, each local move generates a feasible sequence pair. In such a way, the feasible solution space can be continuously searched by the local moves.

6.4 Rotation + Mutations + Adaptation = Exhaustive Search

Theorem 3 *The optimal solution can always be reachable through a finite steps of the rotation and mutations followed by the adaptation.*

Given any two feasible sequence pairs ISP = (IΓ_1, IΓ_2) and OSP = (OΓ_1, OΓ_2), we can always find a search path from ISP to OSP, which consists of only a finite times of the local moves. In such way, the above Theorem can be proven. The path can be constructed by following four phases :

Phase 1 for every macro block A
rotate A until
the permutation pair of A in ISP equals that in OSP
endfor
Phase 2 for every macro block A
squeeze-to-right(IΓ_1, A)
squeeze-to-right(IΓ_2, A)
endfor
Phase 3 adjust IΓ_1 such that IΓ_1 equals OΓ_1
Phase 4 adjust IΓ_2 such that IΓ_2 equals OΓ_2

Phase 1 first applies the rotation in ISP such that the permutation pair of every macro block equals that in OSP. Given total M macro blocks, at most $3M$ times rotation are required, in which 3-conditions are always satisfied. In Phase 2, squeeze operation is applied in both sequences of ISP such that the unit blocks of each macro are consecutive in both IΓ_1 and IΓ_2. Based on the description of squeeze operations, Phase 2 includes mutations only, and the intermediate sequence pairs are always feasible. After Phase 2, for any unit blocks a_i, $a_j \in A$ and $b_k \in B$, $A \neq B$, b_k will not appear between a_i, a_j in either IΓ_1 or IΓ_2. Given total N unit blocks in the sequence pair, Phase 2 will take $O(N^2)$ times mutations.

In Phase 3, IΓ_1 is adjusted to OΓ_1 by applying Γ_1-mutations followed by adaptations. As shown in Fig. 19 (a), starting from $i = 0$, Phase 3 compares i^{th} unit of OΓ_1, u_i, with the i^{th} unit of IΓ_1, v_i. If $u_i = v_i$, i increases by one, i.e. Phase 3 compares the following units. Otherwise, the unit u_i is located in IΓ_1 : $u_i = v_{i+k}$, where k is a positive integer.

Let v_{i+k-1} denote the left neighbor of v_{i+k} in IΓ_1. Then in OΓ_1, v_{i+k-1} will be after u_i which equals v_{i+k}, as shown in Fig. 19 (b). If v_{i+k-1} and v_{i+k} belong to the same macro block V, the permutation of V in IΓ_1 is different from that in OΓ_1. Due to Phase 1, we can derive that v_{i+k-1} and v_{i+k} do not belong to the same macro. Therefore in IΓ_1, mutation can be applied on v_{i+k-1} and v_{i+k}. If the mutation generates a feasible sequence pair, the unit u_i will be moved to the left by one step in IΓ_1 : $u_i = v_{i+k-1}$ as shown in Fig. 19 (c). Otherwise, $v_{i+k-1} = a_m$, $v_{i+k} = b_1$.

If a_1 is before v_i in IΓ_1 as shown in Fig. 19 (d), then in OΓ_1, a_1 must be before $u_i = v_{i+k} = b_1$. Due to condition-2, b_1 can not be between a_1, a_m in the second sequence of OSP. If IΓ_2 has not been adjusted to OΓ_2 so far, b_1 will not be between a_1, a_m due to Phase 2. On the other hand,

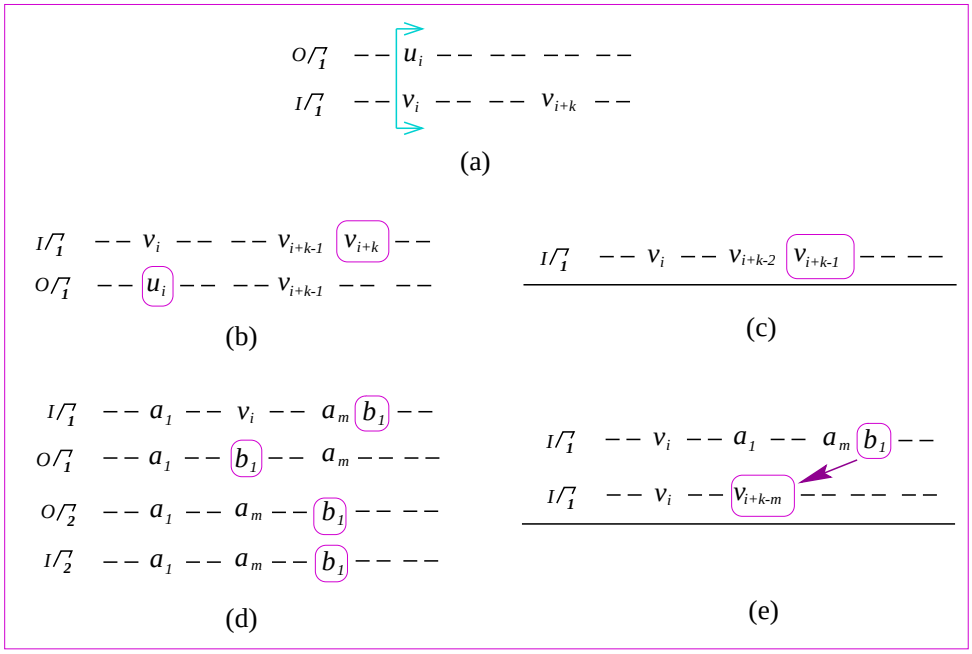


Figure 19: (a) Starting from $i = 0$, Phase 3 compares the i^{th} unit of OΓ_1, u_i, with the i^{th} unit of IΓ_1, v_i. If $u_i \neq v_i$, the unit u_i must be located in IΓ_1 as v_{i+k}, where $k > 0$. (b) Let v_{i+k-1} denote the left neighbor of v_{i+k} in IΓ_1. Then in OΓ_1, v_{i+k-1} will be after $u_i = v_{i+k}$. The permutation of v_{i+k-1} and v_{i+k} in OΓ_1 is different from that in IΓ_1. (c) If the mutation of v_{i+k-1}, v_{i+k} generates a feasible sequence pair, the unit u_i will be moved to v_{i+k-1} in IΓ_1. (d) If the mutation causes an infeasible solution, $v_{i+k-1} = a_m$ and $v_{i+k} = b_1$. If a_1 is before v_i in IΓ_1, then in OΓ_1, a_1 must be before $u_i = v_{i+k} = b_1$. Due to condition-2, b_1 can not be between a_1, a_m in OΓ_2. Then b_1 can not be between a_1, a_m in IΓ_1. The mutation of a_m, b_1 can not lead to an infeasible solution. (e) As such, in IΓ_1, a_1 must be after v_i. After the adaptation, unit u_i will be moved to the left by m steps in IΓ_1: $u_i = v_{i+k-m}$, where $i + k - m \geq i$.

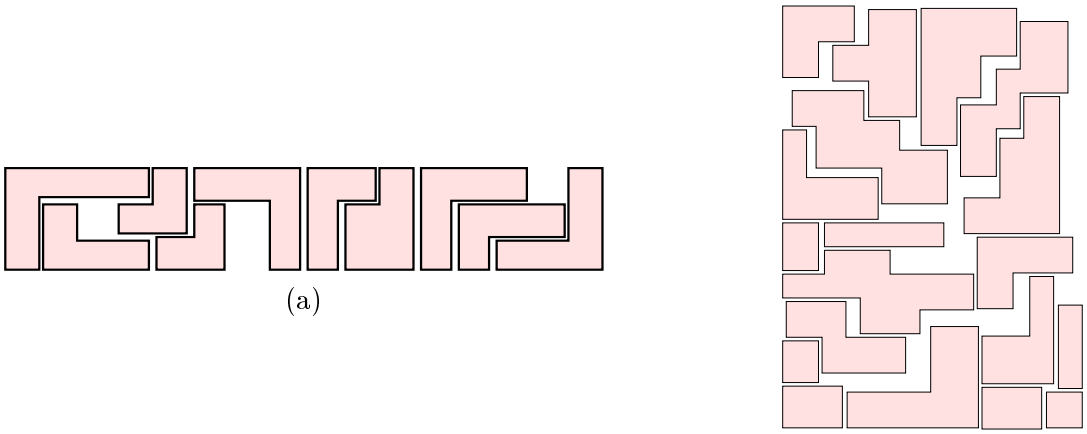
if $I\Gamma_2$ has been adjusted to $O\Gamma_2$, b_1 still can not be between a_1, a_m. As such, the mutation of a_m, b_1 can not lead to an infeasible solution. Therefore in $I\Gamma_1$, a_1 must be after v_i as shown in Fig. 19 (e). After the adaptation, unit u_i will be moved to the left by m steps in $I\Gamma_1$: $u_i = v_{i+k-m}$, where $i + k - m \geq i$.

Therefore in $I\Gamma_1$, the unit u_i is either moved to v_{i+k-1} as shown in Fig. 19 (c) or v_{i+k-m} as shown in Fig. 19 (e). In such way, u_i can be continuously moved to the left in $I\Gamma_1$ until $u_i = v_i$. Then i increases by one and Phase 3 visits the following unit u_{i+1} in $O\Gamma_1$. When i reaches N, the first sequence of ISP is adjusted to be $O\Gamma_1$, Phase 3 terminates. Phase 4 repeats the similar process on the second sequence of ISP. It can be easily derived that Phase 3 and Phase 4 take $O(N^2)$ times mutations and adaptations, together with the first two phases, the search path consists of at most $O(M + N^2)$ times of local moves.

7 Experimental Results and Conclusion

7.1 Packing Results

We have implemented the algorithm proposed in this paper using C language and tested it on SUN SPARC 20 workstation. The data are generated randomly. Figure 20 (a) gives the packing of ten L-shaped blocks, which takes about two minutes, the total packing area is 1.09 times of the total block area. On the other hand, Figure 20 (b) reports the packing result of 19 convex rectilinear blocks, which takes about 35 minutes, the total packing area is 1.13 times of the total block area. Due to the tight schedule, we have not enough time to refine the source code. We believe that the tradeoff of the packing quality and CPU time can be much improved, and we are working on this right now.



(a) (b)

Figure 20: (a) The packing of ten L-shaped blocks, which takes about two minutes, the total packing area is 1.09 times of total block area. (b) The packing result of 19 convex rectilinear blocks, which takes about 45 minutes, the total packing area is 1.13 times of total block area.

7.2 Concluding Remarks

In this paper, for the first time, we solve the arbitrary shaped rectilinear block packing problem. Rectilinear macro blocks are partitioned into a set of rectangular sub-blocks, each of them is individually represented as a unit block in the sequence pair. The feasible solution space is

defined. Three conditions on the sequence pair are derived, which are necessary and sufficient for a sequence pair to be feasible. Furthermore it is proven that there always exists a feasible sequence pair corresponding to a packing of convex rectilinear blocks. Based on this fact, a stochastic search is applied on the optimization of convex block packing. Local moves are defined to search the feasible solution space both continuously and exhaustively.

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