Appeared in Fundamenta Informaticae 182(3): 257–283 (2021). Available at IOS Press through: https://doi.org/10.3233/FI-2021-2073

# Efficient Algorithms for Maximum Induced Matching Problem in Permutation and Trapezoid Graphs

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Abstract. We first design an  $\mathcal{O}(n^2)$  solution for finding a maximum induced matching in permutation graphs given their permutation models, based on a dynamic programming algorithm with the aid of the sweep line technique. With the support of the disjoint-set data structure, we improve the complexity to  $\mathcal{O}(m+n)$ . Consequently, we extend this result to give an  $\mathcal{O}(m+n)$  algorithm for the same problem in trapezoid graphs. By combining our algorithms with the current best graph identification algorithms, we can solve the MIM problem in permutation and trapezoid graphs in linear and  $\mathcal{O}(n^2)$  time, respectively. Our results are far better than the best known  $\mathcal{O}(mn)$  algorithm for the maximum induced matching problem in both graph classes, which was proposed by Habib et al.

Keywords: permutation graph, trapezoid graph, induced matching, sweep line, disjoint set

## 1. Introduction

The maximum matching problem is one of the most fundamental and applicable problems in graph theory. Given a graph G = (V, E), a maximum matching is a subset  $M \subseteq E$  of maximum size so that every two distinct edges in M do not share a common vertex. Its applications can be found everywhere, from VLSI circuit design [1] to archaeology and chemistry [2]. The best-known algorithm

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for the maximum matching problem in general graphs is  $\mathcal{O}(\sqrt{VE})$  [3]. However, we can achieve better running time on many special graph classes thanks to their particular properties.

If every two distinct edges in a matching M are not connected by an edge in G, then M is called an *induced matching*. Recently, the maximum induced matching (MIM) problem has drawn enormous attention among researchers because of its importance in many fields such as artificial intelligence (cooperative path-finding problem [4], neural information processing [5]), VLSI design [6], and marriage problems [7]. The problem is proved to be NP-hard in general graphs [7]. Some exponential time algorithms for the MIM problem in general graphs are proposed recently by Chang et al. [8] and Xiao et al. [9]. Besides, it is known for polynomial-time maximum induced matching on special graph classes such as co-comparability graphs (including circular-arc graphs [10], interval graphs [11], etc.), circular-convex bipartite and triad-convex bipartite graphs [12], AT-free graphs [13] and hexagonal graphs [14]. In chordal graphs, finding a MIM can be done in linear time [15].

Dagan et al. [1] introduced trapezoid graphs in 1988. Given two parallel horizontal lines, a trapezoid is formed by two points on the upper line and two points on the lower line. A trapezoid graph is an intersection graph, *i.e.*, a graph representing the pattern of intersections of a family of sets, built from such a set of trapezoids. A trapezoid representation (or trapezoid model) of a trapezoid graph includes two such horizontal lines and the set of trapezoids, which is used to forms that trapezoid graph. A permutation graph is a particular case of trapezoid graphs, in which the two intervals that define each trapezoid in the trapezoid representation shrink into two points only. Therefore, a permutation representation can be represented as a permutation of the first n positive integers.

Permutation graphs, as well as trapezoid graphs, are weakly chordal graphs [16]. They are also Asteroidal-Triple-free (AT-free) graphs. In [13], by applying the result from [17], MIM was solved in polynomial time for AT-free graphs. In [18], the authors proposed a linear time algorithm for MIM on bipartite permutation graphs (which are bipartite AT-free graphs).

Denote n and m as the number of vertices and edges in a graph, respectively. Do et al. [19] introduced an efficient algorithm to find a maximum matching in trapezoid graphs in  $\mathcal{O}(n(\log n)^2)$ . On the other hand, Rhee et al. [20] proposed an  $\mathcal{O}(n \log \log n)$  algorithm for such problems in permutation graphs. However, to the best of our knowledge, the MIM problem has not been mentioned with specific algorithms on permutation graphs. The best-known algorithm for finding a weighted induced matching for all co-comparability graphs, which are a superclass of permutation graphs and trapezoid graphs, has time complexity of  $\mathcal{O}(mn)$  [21]. So far, there is no other superclass of permutation graphs and trapezoid graphs on which the MIM problem is proved to be solvable in faster time than  $\mathcal{O}(mn)$ . Consequently, we can consider  $\mathcal{O}(mn)$  the fastest time complexity to find a MIM on a permutation graph or a trapezoid graph.

In this paper, we introduce more efficient algorithms for the MIM problem in both permutation graphs and trapezoid graphs. We first design in Section 2 an  $O(n^2)$  algorithm and then an  $O(m \log \log n + n)$  algorithm for finding a MIM in permutation graphs given their permutation models. These algorithms are based on a dynamic programming method with the aid of the sweep line technique on a geometry representation of permutation graphs. Our approach is to construct the longest chain of ordered edges, which form an induced matching. A sweep line moving from right to left correctly determines the order of dynamic processes. The edge set of the given permutation graph can be built from the vertex set of that graph in O(m + n) time by employing the benefits of the linked list

data structure. Especially, with the support of the disjoint-set data structure, we improve the overall running time for finding a MIM to  $\mathcal{O}(m+n)$  time in permutation graphs. Furthermore, in Section 3, we generalize this algorithm with the same running time  $\mathcal{O}(m+n)$  to trapezoid graphs given trapezoid models. With the combination of our algorithms and the current best graph identification algorithms that generate presentation models for permutation graphs and trapezoid graphs, we can solve the MIM problem in permutation and trapezoid graphs in linear and  $\mathcal{O}(n^2)$  time, respectively. Our results are far better than the best known  $\mathcal{O}(mn)$  algorithm [21] in both graph classes. This paper is the complete version including preliminary results of our conference papers [22] and [23].

## 2. Fundamental definitions

## 2.1. Maximum induced matching

A subset  $M \subseteq E$  is an induced matching of graph G = (V, E) if for every two distinct edges  $e_1 = u_1v_1$  and  $e_2 = u_2v_2$  in M we have  $u_1u_2 \notin E$ ,  $u_1v_2 \notin E$ ,  $v_1u_2 \notin E$  and  $v_1v_2 \notin E$ . We denote L(G) as the line graph of G, *i.e.*, each vertex of L(G) represents an edge of G. Two vertices in L(G) are adjacent if and only if their corresponding edges share a common endpoint in G. We also denote  $G^2$  as the graph having the same vertex set as G and two vertices are adjacent if their distance, *i.e.*, the number of edges in a shortest path connecting them, is at most 2 in G. Then, the problem to find an induced matching of maximum cardinality is exactly the maximum independent set problem on  $L(G)^2$ .

## 2.2. Permutation graph

Let  $\pi = (\pi(1), \pi(2), ..., \pi(n))$  be a permutation of the first *n* positive integers. We build an undirected graph  $G(\pi) = (V, E)$  in which the vertex set  $V = \{1, 2, ..., n\}$  and an edge  $uv \in E$  if and only if  $(u - v)(\pi^{-1}(u) - \pi^{-1}(v)) < 0$ , where  $\pi^{-1}(i)$  is the position of *i* in  $\pi$ . An undirected graph *G* is called a *permutation graph* if there is a permutation  $\pi$  such that  $G(\pi)$  is isomorphic to *G* (see Figure 1 for an example), and  $\pi$  is called a *permutation representation* (or *permutation model*) of *G*.

## 2.3. Trapezoid graph

We assume that a trapezoid model is given by a set of trapezoids  $\tau$ . Given two parallel horizontal axes: x-axis and y-axis, each trapezoid  $A \in \tau$  is given by four values  $x_1, x_2, y_1, y_2$  ( $x_1 \leq x_2, y_1 \leq y_2$ ) such that  $[x_1, x_2]$  and  $[y_1, y_2]$  are the two intervals on these two axes that form the trapezoid A. The segment connecting the point  $x_1$  on the x-axis and the point  $y_2$  on the y-axis is called a *diagonal* of A. Similarly, the segment connecting the point  $x_2$  on the x-axis and the point  $y_1$  on the y-axis is another diagonal of A. A trapezoid has at most two diagonals and at least one diagonal (when  $x_1 = x_2$  and  $y_1 = y_2$ ). We assume that all corners of each trapezoid in the model have mutually different x- and ycoordinates. Otherwise, we may obtain this property by perturbing the corner points without changing the relationship between trapezoids [24]. Therefore, we can assume that all x- and y-coordinates are integers in the interval [1, 2n], where  $n = |\tau|$  is the number of trapezoids by mapping each coordinate to an integer in this interval and keeping their cardinality order (see Figure 6 for an example).

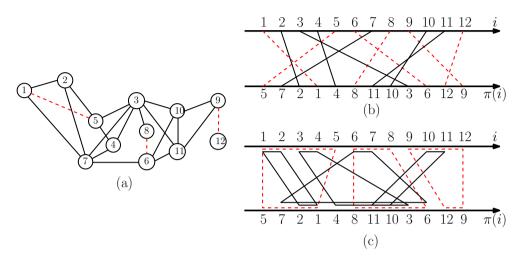


Figure 1: A permutation graph G (a) and one of its corresponding permutation representation (b), which has  $\pi = (5, 7, 2, 1, 4, 8, 11, 10, 3, 6, 12, 9)$ . A trapezoid model of the trapezoid graph  $L(G)^2$ , partially shown in (c), can be constructed from the permutation representation of G. A maximum induced matching for G is  $M = \{(1, 5), (6, 8), (9, 12)\}$ , also seen as a maximum independent set of  $L(G)^2$ .

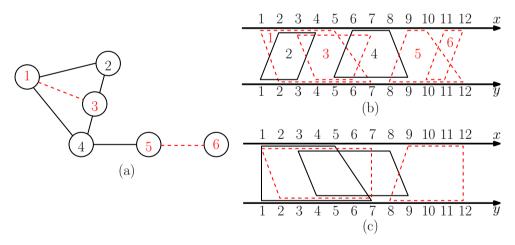


Figure 2: A trapezoid graph G (a) and one of its corresponding trapezoid representations (b). A trapezoid model of  $L(G)^2$ , partially shown in (c), can be constructed from the trapezoid representation of G. A maximum induced matching for G is  $M = \{(1,3), (5,6)\}$ , also seen as a maximum independent set of  $L(G)^2$ .

We construct an undirected graph  $G(\tau) = (V, E)$  by setting the vertex set  $V = \{1, 2, ..., |\tau|\}$  and labeling each trapezoid in  $\tau$  as a distinct number from 1 to  $|\tau|$ . Then, AB is an edge of  $G(\tau)$  if and only if trapezoid  $A \in \tau$  and trapezoid  $B \in \tau$  intersect (i.e. when a diagonal of A intersects with a diagonal of B). An undirected graph G is a trapezoid graph if there exists a set  $\tau$  such that G is isomorphic to  $G(\tau)$ .

# 3. Maximum induced matching in permutation graphs

## **3.1.** An $\mathcal{O}(n^2)$ maximum induced matching algorithm in permutation graphs

Permutation  $\pi^{-1} = (\pi^{-1}(1), \pi^{-1}(2), ..., \pi^{-1}(n))$  can be represented as points on 2-dimensional SPACE $(\pi^{-1})$  with horizontal axis *i* and vertical axis  $\pi^{-1}$ . Each element  $\pi^{-1}(i)$  corresponds to the point  $(i, \pi^{-1}(i))$  on SPACE $(\pi^{-1})$ . An edge xy of  $G(\pi)$  (or equivalently, vertex xy of  $L(G)^2$ ) is described as a rectangle whose sides are parallel to the axes and having two opposite corners  $(x, \pi^{-1}(x))$  and  $(y, \pi^{-1}(y))$  (see Figure 3 for an example). The problem could be viewed from a different angle as finding a longest sequence of disjoint rectangles such that the next rectangle is completely at the top-right of the previous rectangle in the sequence, since such a sequence corresponds to a maximum independent set in  $L(G)^2$  and vice versa. This geometric representation reveals special benefits based on the *sweep line technique* This geometric representation reveals special benefits based on the sweep line technique that plays an essential role in our algorithms. A sweep line moving from right to left on SPACE $(\pi^{-1})$  determines the order of dynamic programming processes, which helps to find a MIM correctly and efficiently.

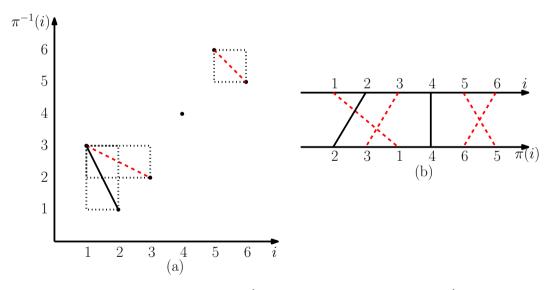


Figure 3: The presentation of permutation  $\pi^{-1} = (3, 1, 2, 4, 6, 5)$  on SPACE $(\pi^{-1})$  (a) and the corresponding diagram of permutation  $\pi$  (b). There are three matches: (1, 2), (1, 3) and (5, 6). Match (5, 6) is greater than the other two matches. A longest chain of length 2 is (1, 3), (5, 6).

We first briefly describe an algorithm that finds a MIM on  $G(\pi)$  in  $\mathcal{O}(n^2)$  time. Let  $G(\pi) = (V, E)$  where  $\pi$  is a permutation of length n and E is the edge set of size m. We show some following definitions.

**Definition 3.1.** An ordered pair (x, y) is called a *match* if  $1 \le x < y \le n$  and  $\pi^{-1}(x) > \pi^{-1}(y)$ . For a match (x, y), x is called the *left end* and y is called the *right end* of the match.

One can see that each match (x, y) corresponds to the edge xy of  $G(\pi)$ , so the number of distinct matches in SPACE $(\pi^{-1})$  is m. Denote by E' the set of all matches in SPACE $(\pi^{-1})$ . In our algorithms, the term *match* is used instead of *edge*. The utilization of *match* in place of *edge* is necessary to help our sweep line correctly determine the order of the dynamic programming process lately described.

**Definition 3.2.** Given two matches e = (x, y) and e' = (x', y'), we define e < e' if y < x' and  $\pi^{-1}(x) < \pi^{-1}(y')$ . We say that e is *smaller* than e' and e' is *greater* than e.

**Definition 3.3.** A sequence of matches  $e_1, e_2, ..., e_k$  is called a *chain* if  $e_i < e_{i+1}$  for all  $1 \le i < k$ . The *length* of the chain is k, and the match  $e_1$  is the *smallest match* of the chain.

Since a chain corresponds to a maximum independent set in  $L(G)^2$  and vice versa, the MIM problem in permutation graphs turns out to be finding the longest chain on SPACE $(\pi^{-1})$ . It could be solved by computing a function  $f: E' \to \mathbb{N}$ , where f(e) is the length of the longest chain having e as the smallest match. One can see that the maximum value of f(e) among all matches e is the size of a MIM on  $G(\pi)$ , which is what we need. We also compute a function  $link : E' \to E'$ , where link(e) is a match such that f(e) = f(link(e)) + 1 and the match e is smaller than link(e). This link function is utilized to construct a MIM in the end.

The whole algorithm can be summarized as follow:

#### Steps to find a MIM in $G(\pi)$ :

1. Construct all matches that exist on SPACE( $\pi^{-1}$ ) and store them in adjacent lists.

2. Calculate two functions f and link for all matches e.

3. Build a MIM based on functions f and link calculated in step 2.

## **3.1.1.** Construct all matches that exist on SPACE $(\pi^{-1})$

Throughout this paper, we denote  $A \cdot x$  as the value x of an object A.

In the first step, we construct all matches that exist on SPACE $(\pi^{-1})$ . Let Match(x), where  $1 \le x \le n$ , be the list of all y  $(1 \le y < x)$  having  $\pi^{-1}(y) > \pi^{-1}(x)$ . The set  $\{(y, x) \mid y \in Match(x)\}$  is the set of all matches with the right end x. These sets are pairwise disjoint for different values of x and the union of them is all the matches that exist on SPACE $(\pi^{-1})$ . Match lists can be considered as adjacent lists of the permutation graph, except that each edge is stored in only one list.

We use the linked list data structure to construct all matches that exist on SPACE $(\pi^{-1})$  in  $\mathcal{O}(m+n)$  time (see Procedure 1 below). We create a linked list LL of n nodes numbered from 1 to n, where node n is the head of LL, and the next node of node i is node (i-1) for all  $1 < i \leq n$ . Initially, we set  $Match(x) = \emptyset$  for all x. We make a loop from a = n to a = 1. For each a, we start the visiting process from the head of LL. When a node p is visited, if  $p > \pi(a)$ , then we add  $\pi(a)$  to Match(p) and move to the next node, else we remove p from LL.

For readability and simplicity, we only show a brief version of Procedure 1 here. For the complete version of Procedure 1, please see *Appendix A*.

**Procedure 1:**  $buildAllMatches(\pi)$ 

**Description:** Step 1: Construct all matches that exist on SPACE( $\pi^{-1}$ ) and store them as adjacent lists. 1 /\* initialize \*/ 2 Create linked list LL of n nodes numbered from 1 to n, where LL.head = n, and i.next = i - 1 for all 1 < i < n3  $Match(x) \leftarrow \emptyset$  for all  $1 \le x \le n$ 4 5 /\* build Match lists \*/ 6 for  $a \leftarrow n$  down to 1 do  $p \leftarrow LL.head$ 7 while  $p > \pi(a)$  do 8 add  $\pi(a)$  to Match(p)9  $p \leftarrow p.next$ 10 11 remove node p from LL 12 13 return { $Match(x) \mid 1 \le x \le n$ }

**Lemma 3.4.** Procedure buildAllMatches correctly constructs the list Match(x) for all  $1 \le x \le n$ .

#### **Proof:**

Because the nodes in the linked list LL are sorted in decreasing order from head to tail and there are n distinct nodes at the beginning, the while-loop on line 8 always terminates when  $p = \pi(a)$ . Therefore, when a = i for some  $1 \le i \le n$ , only the nodes  $\pi(n), \pi(n-1), ..., \pi(i+1)$  are removed from LL. It means that when a = i, we have  $\pi^{-1}(\pi(a)) = a = i > \pi^{-1}(p)$  for all  $p > \pi(a)$ . Consequently, all the elements added to the list Match(p) on line 9 are valid.

On the other hand, suppose that when a = i for some  $1 \le i \le n$ , there is some removed node q where  $(\pi(a), q)$  is a match, we will show a contradiction. Indeed, if q is removed before, q must belong to the set  $\{\pi(n), \pi(n-1), ..., \pi(i+1)\}$ . It leads to the fact that  $\pi^{-1}(q) \ge i+1 > i = a = \pi^{-1}(\pi(a))$ , so  $(\pi(a), q)$  is not a match, contradicts with the assumption. Hence, when a = i, all the nodes p where  $(\pi(a), p)$  is a match still remain in the linked list LL. The while-loop on line 8 can iterate through all such nodes since  $p > \pi(a)$  when  $(\pi(a), p)$  is a match as definition.

Based on these two conclusions, for all  $1 \le x \le n$ , Procedure *buildAllMatches* correctly constructs the list Match(x).

**Lemma 3.5.** Procedure buildAllMatches takes  $\mathcal{O}(m+n)$  time.

### **Proof:**

The time complexity of procedure buildAllMatches is the LL's building time plus the number of times we add a new element to a *Match* list. Since each *Match* list does not have duplicate elements and each match corresponds to a unique edge in  $G(\pi)$ , this procedure takes  $\mathcal{O}(m+n)$  time.

#### **3.1.2.** Calculate two functions f and link

In the second step, we calculate two functions f and link. We make a sweep line L moving from right to left and visit every coordinate i = x  $(1 \le x \le n)$ . On L, we maintain n memory units called *cells*. Each time when L stays at i = x, each cell  $L_y$   $(1 \le y \le n)$  is a pair (len, trace), where len is the length of a longest chain where the smallest match is any match trace = (z, t) satisfying z > x and  $\pi^{-1}(t) = y$ . An algorithm to calculate the function f can be built with the aid of the sweep line L. First of all, let  $S_x$  be a list, which stores pairs of match e and its corresponding f(e), for all matches e having x as its left end. The  $S_x$  lists are needed later for the cell updating process in our dynamic algorithm. Initially, we set  $S_x = \emptyset$ , also set all  $L_y$  to be (0, NULL). Then, we start to move the sweep line L. When reaching the coordinate i = x, we calculate f(e) and link(e) for all matches e = (y, x)where  $y \in Match(x)$  by the following formulae:

•  $f(e) = 1 + \max_{j > \pi^{-1}(y)} L_j.len$ •  $link(e) = L_j.trace_{j > \pi^{-1}(y), f(e) = L_j.len+1 \ (*)}$  (for an arbitrary j satisfies (\*))

After having f(e), we add (f(e), e) into the list  $S_y$ . After the calculations of f(e) and link(e) for all e having x as their right end, we start to update cells on L. This process is done by going through all elements in the list  $S_x$ : for each element (f(e), e) where e = (x, a), if  $L_{\pi^{-1}(a)}$ . len < f(e), we set  $L_{\pi^{-1}(a)} = (f(e), e)$  (see Figure 4b for an example). In the end, when all x are swept by L, we will have the answer for the MIM problem by looking up the functions f and link.

A naive algorithm based on this method takes  $\mathcal{O}(mn)$  time to run. Indeed, to calculate f(e) and link(e) for each e, a single loop that runs in  $\mathcal{O}(n)$  is required. As the number of matches is m, it takes  $\mathcal{O}(mn)$  overall. The main problem which causes the algorithm slow is the requirement of an  $\mathcal{O}(n)$  loop to calculate each match.

However, it is noticeable that the elements in each list Match(x) are arranged in decreasing order of the function  $\pi^{-1}$  applying to them, *i.e.*, element *a* is added before element *b* in Match(x) if  $\pi^{-1}(a) > \pi^{-1}(b)$ . The following lemma will prove this argument.

**Lemma 3.6.** The elements of each list Match(x) are arranged in decreasing order of the function  $\pi^{-1}$  applying to them.

### **Proof:**

Consider any pair (p, q) of elements in Match(x), suppose that  $p = \pi(i)$  is added before  $q = \pi(j)$ , we can see that i > j since the for-loop iterator a in buildAllMatches decreases. Therefore,  $\pi^{-1}(p) = \pi^{-1}(\pi(i)) = i > j = \pi^{-1}(\pi(j)) = \pi^{-1}(q)$ , the lemma is proven.

By Lemma 3.6, we can reduce running time by using just  $\mathcal{O}(n)$  operations to calculate f(e) and link(e) for all e with the right end x. Hence, we have an  $\mathcal{O}(n^2)$  algorithm overall. We maintain a decreasing-pointer z and two variables maxLen and trace where maxLen is  $\max_{i>z}(L_i.len)$  and trace is the corresponding  $L_i.trace$  when  $L_i.len$  reaches maximum. These two variables maxLen and

trace are updated each time we decrease z (see Figure 4a for an example). The following procedure calculateFAndLink will represent step 2. For readability and simplicity, we only show a brief version of Procedure 2 here. For the complete version of Procedure 2, please see *Appendix B*.

**Procedure 2:** calculateFAndLink( $\pi^{-1}$ , Match)

**Description:** Step 2: Calculate two functions f and link for all matches e. 1 /\* initialize \*/ 2 initialize S and L3 4 /\* calculate functions f and link \*/5 for  $x \leftarrow n \ down \ to \ 1$  do 6 calculate f and link for all matches (\*, x) with pointer z decreasing from n7 update elements in  $S_x$  to L8 9 return (f, link)

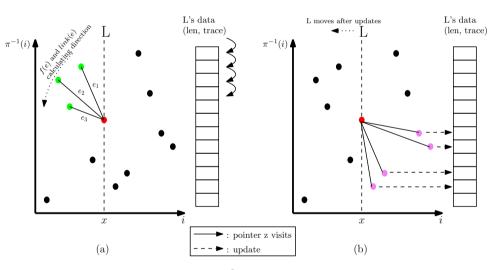


Figure 4: Calculate f and link in  $G(\pi)$  in  $\mathcal{O}(n^2)$  time.

(a) When L stays at i = x, for all matches e = (y, x), f(e) and link(e) are calculated in decreasing order of  $\pi^{-1}(y)$ . To obtain f(e) and link(e), every  $L_z$  such that  $\pi^{-1}(y) < z \leq n$  is visited. Then (f(e), e) is added to the list  $S_y$ .

(b) Each element (f(e), e) having e = (x, y) in  $S_x$  is updated to the cell  $L_{\pi^{-1}(y)}$ . After all, the sweep line L moves to the coordinate i = x - 1.

### 3.1.3. Build a maximum induced matching

Let startChain be a match where f(startChain) is the maximum among all f(e). Consequently, a MIM on  $G(\pi)$  will have the cardinality of f(startChain). Such a MIM could be built by tracing the link function in  $\mathcal{O}(|\text{MIM}|)$  which is  $\mathcal{O}(n)$ . Step 3 is implemented in Procedure buildMIM below.

**Procedure 3:** buildMIM(*f*, *link*)

```
Description: Step 3: Build a MIM based on functions f and link calculated in step 2.
 1 /* initialize */
2 MIM \leftarrow \emptyset
3 startChain \leftarrow a (for an arbitrary a where f(a) is maximum)
4 e \leftarrow startChain
5
 6 /* build a MIM */
 7 while e \neq NULL do
        (x, y) \leftarrow e
8
        \texttt{MIM} \leftarrow \texttt{MIM} \cup xy
9
        e \leftarrow link(e)
10
11
12 return MIM
```

### 3.1.4. Summary

Given a permutation model  $\pi$ , a MIM of permutation graph  $G(\pi)$  can be found by calling the following procedure maxInducedMatching.

```
Procedure 4: maxInducedMatching(\pi)

Description: Finding a MIM in G(\pi)

1 Match \leftarrow buildAllMatches(\pi)

2 (f, link) \leftarrow calculateFAndLink(\pi^{-1}, Match)

3 return buildMIM(f, link)
```

**Theorem 3.7.** A maximum induced matching in permutation graph  $G(\pi)$  can be found in  $\mathcal{O}(n^2)$  time.

## **Proof:**

Procedure 4 returns a MIM of permutation graph  $G(\pi)$ . The first function *buildAllMatches* takes  $\mathcal{O}(m+n)$  time, proved by Lemma 3.5. The second function *calculateFAndLink* runs in  $\mathcal{O}(n^2)$ , as shown in Section 3.1.2. The last function *buildMIM* takes  $\mathcal{O}(n)$  time to run, as shown in Section 3.1.3. Therefore, Procedure 4 a maximum induced matching on  $G(\pi)$  in  $\mathcal{O}(n^2)$  time.

## 3.2. Faster maximum induced matching algorithms in permutation graphs

With the aid of a segment tree [25], we can build an  $\mathcal{O}(m \log n + n)$  algorithm for MIM in permutation graphs from the  $\mathcal{O}(n^2)$  algorithm. Unlike the  $\mathcal{O}(n^2)$  algorithm in which the sweep line L stores an array of cells, L here stores a segment tree. All operations, including updating a cell and finding the maximum cell within an interval, are done in  $\mathcal{O}(\log n)$  time per each operation. As we mentioned, a MIM on permutation graph G can be seen as a maximum independent set on trapezoid graph  $L(G)^2$ . Actually, this  $\mathcal{O}(m \log n + n)$  algorithm is similar to the maximum independent set algorithm for

trapezoid graph in [24], which could be improved to an  $\mathcal{O}(m \log \log n + n)$  solution by using vEB tree in [26]. A Van Emde Boas tree (or Van Emde Boas priority queue), also called vEB tree, supports searching, inserting and deleting an element in  $\mathcal{O}(\log \log M)$ , where  $M = 2^m$  is a fixed number indicating the maximum number of nodes to be stored in the tree, and the elements are integers in  $\{1, 2, ..., M\}$ . A vEB tree implements an associative array of m-bit integer keys in  $\mathcal{O}(M)$  space.

We shall not show this algorithm in detail since our following O(m + n) algorithm does not use the idea of segment tree nor vEB tree.

## **3.3.** An $\mathcal{O}(m+n)$ maximum induced matching algorithm in permutation graphs

To the best of our knowledge, there has not been existed any data structure that supports both query and update operations in  $\mathcal{O}(1)$  applicable for this problem. Therefore, improving an  $\mathcal{O}(n^2)$  algorithm in Section 3.1 into an  $\mathcal{O}(m+n)$  algorithm only by applying different data structures in Step 2 is quite an impossible work.

Let pay attention to procedure maxInducedMatching. Although the idea of pointer z is essential to make the running time  $\mathcal{O}(n^2)$ , it consumes  $\mathcal{O}(n)$  calculations for each x from n to 1, and becomes the most time-consuming part of the whole algorithm. Instead of  $\mathcal{O}(n)$ , if we can turn it to  $\mathcal{O}(|Match(x)|)$  for each x, we will acquire an  $\mathcal{O}(m+n)$  for the overall algorithm. We show next the most critical points for an  $\mathcal{O}(m+n)$  solution.

Assume that  $L_y$  now stores 3 values (*len*, *trace*, *swept*) in place of a pair (*len*, *trace*), where *swept* equals to 1 if the sweep line L has passed the coordinate  $i = \pi(y)$  ( $L_y$  is called a *swept cell*) or equal to 0 ( $L_y$  is called an *unswept cell*) otherwise. Some operations of our  $\mathcal{O}(n^2)$  algorithm are going to be changed.

### 3.3.1. Adjustment of formulae

We call  $\varphi(a)$  the greatest number smaller than a having  $L_{\varphi(a)}$ .swept = 0 (if such  $\varphi(a)$  does not exist then we assume  $\varphi(a) = 0$ ). To calculate f(e) and link(e) for all matches e = (y, x) where  $y \in Match(x)$ , their formulae are also adjusted as below:

• $f(e) = 1 + \underset{j \ge \pi^{-1}(e)}{j \ge \pi^{-1}(e)}$	$\max_{J_j, L_j.swept=0} L_j.len$	
• $link(e) =$	$L_j.trace$ , $L_j.swept=0, f(e)=L_j.len+$	• •

With the new formulae, we do not need the pointer z decreasing from n anymore. We just need to iterate through all  $L_{\pi^{-1}(z)}$  where  $n \ge \pi^{-1}(z) > \pi^{-1}(x)$  and  $L_{\pi^{-1}(z)}$ .swept = 0 (see Figure 5a for an example). In this occasion,  $L_{\pi^{-1}(z)}$ .swept = 0 also means z < x, because  $L_{\pi^{-1}(z')}$ .swept is set to 1 for all z' > x when sweep line L stays at coordinate i = x. Amazingly, if we have  $\pi^{-1}(z) > \pi^{-1}(x)$  and z < x, then (z, x) is a match. Therefore, the number of  $L_{\pi^{-1}(z)}$  we need to check for each x is exactly  $\mathcal{O}(|Match(x)|)$  as we need.

When going through all elements of the list  $S_x$  in the updating process, for each element (f(e), e)where e = (x, a), we will update  $L_{\varphi(\pi^{-1}(a))}$  instead of  $L_{\pi^{-1}(a)}$ . If  $L_{\varphi(\pi^{-1}(a))}$ . len < f(e) then we set  $L_{\varphi(\pi^{-1}(a))}$ . len = f(e) and  $L_{\varphi(\pi^{-1}(a))}$ . trace = e (see Figure 5b for an example).

Finally, before moving the sweep line L to the coordinate i = x - 1, we set  $L_{\pi^{-1}(x)}$ .swept = 1,  $L_{\pi^{-1}(x)}$  becomes a swept cell. In addition, if  $L_{\pi^{-1}(x)}$ .len >  $L_{\varphi(\pi^{-1}(x))}$ .len, then we set  $L_{\varphi(\pi^{-1}(x))} = (L_{\pi^{-1}(x)}$ .len,  $L_{\pi^{-1}(x)}$ .trace, 0) (see Figure 5b for an example).

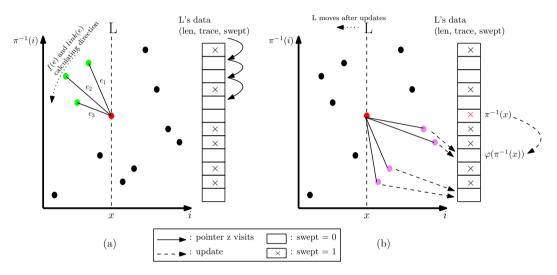


Figure 5: Calculate f and link in  $G(\pi)$  in  $\mathcal{O}(m+n)$  time.

(a) When L stays at i = x, for all matches e = (y, x), f(e) and link(e) are calculated in decreasing order of  $\pi^{-1}(y)$ . To obtain f(e) and link(e), every  $L_z$  such that  $\pi^{-1}(y) \le z \le n$  and  $L_z$ .swept = 0 is visited. Then (f(e), e) is added to the list  $S_y$ .

(b) Every element (f(e), e) having e = (x, y) in  $S_x$  is updated to the cell  $L_{\varphi(\pi^{-1}(y))}$ . Then  $L_{\pi^{-1}(x)}$ .swept is set to 1;  $L_{\pi^{-1}(x)}$ .len and  $L_{\pi^{-1}(x)}$ .trace are updated to  $L_{\varphi(\pi^{-1}(x))}$ . After all, the sweep line L moves to the coordinate i = x - 1.

Let  $\psi(y)$  be the smallest number such that  $n \ge \psi(y) > y$  and  $L_{\psi(y)}.swept = 0$ , if such  $\psi(y)$  does not exist then we assume  $\psi(y) = n$ . We will prove the correctness of all these changes above through Lemma 3.8.

**Lemma 3.8.** For all  $1 \le x \le n$ , when the sweep line L moves from coordinate i = x+1 to coordinate i = x, each cell  $L_y$   $(1 \le y \le n)$  where  $L_y.swept = 0$  contains 3 variables (*len*, *trace*, *swept*) that:

- $L_y$ .len is the length of a longest chain among all chains having their smallest match (a, b) satisfies a > x and  $y < \pi^{-1}(b) \le \psi(y)$ .
- $L_y.trace$  is the smallest match of such a chain (if there are multiple choices,  $L_y.trace$  can be any match).
- $L_y.swept = 0.$

### **Proof:**

We will prove this lemma using the induction hypothesis as follows.

- The lemma is true for x = n since for all  $1 \le y \le n$ ,  $L_y = (0, \text{NULL}, 0)$ .
- Suppose that the lemma is true for some x = t + 1 where 1 ≤ t < n, we will prove that the lemma is correct for x = t. Indeed, suppose that π<sup>-1</sup>(t + 1) = k, we will have φ(ψ(k)) = φ(k) and ψ(φ(k)) = ψ(k) after all update operations are done and before the sweep line L moves from coordinate i = t + 1 to coordinate i = t. In addition, since we set L<sub>φ(k)</sub> = (L<sub>k</sub>.len, L<sub>k</sub>.trace, 0) if L<sub>k</sub>.len > L<sub>φ(k)</sub>.len before L's movement, the cell L<sub>φ(k)</sub> will satisfy all the three properties mentioned in Lemma 3.8. Therefore, each cell L<sub>y</sub> (1 ≤ y ≤ n) where L<sub>y</sub>.swept = 0 will also satisfy all these three properties.

By the induction hypothesis, we can conclude that the lemma applies for all  $1 \le x \le n$ .

The last issue is whether there is a data structure, which helps to calculate all the  $\varphi$  operations in  $\mathcal{O}(m+n)$ . Here the disjoint-set data structure does the job.

#### 3.3.2. Complexity improvement by the disjoint-set data structure

We consider a disjoint-set data structure d consists of n sets  $\{1\}, \{2\}, ..., \{n\}$ , where the name of the set containing i is also i at the beginning. Each set in the disjoint-set structure corresponds to either a single unswept cell or a set of consecutive swept cells on the sweep line L. The purpose of d is to quickly jump through sets of consecutive cells that are swept, thus lead to quickly calculate the function  $\varphi$ .

We define two operations on our disjoint-set data structure d as below:

- find(d, x): Return the name of the set containing x.
- union(d, x, y): Create a new set that is the union of the sets containing x and y. The name of the new set is the name of the old set containing x. This operation assumes that x and y are initially in different sets and destroys the old sets containing x and y.

In our algorithm, before moving the sweep line L from the coordinate i = x to the coordinate i = x-1, we set  $L_{\pi^{-1}(x)}$ .swept = 1. After this operation, if  $L_{\pi^{-1}(x)-1}$ .swept = 1, then the set containing  $\pi^{-1}(x)$  will be united with the set containing  $\pi^{-1}(x) - 1$  by calling union $(d, \pi^{-1}(x) - 1, \pi^{-1}(x))$ . Similarly if  $L_{\pi^{-1}(x)+1}$ .swept = 1, we unite two sets where  $\pi^{-1}(x)$  and  $\pi^{-1}(x) + 1$  belong to by calling union $(d, \pi^{-1}(x), \pi^{-1}(x) + 1)$ .

Since these are the only union operations in our algorithm, we can see that the name of the set containing x is always the minimum number in that set. Based on this observation, we have a simple way to calculate  $\varphi$  as follows. If  $L_{x-1}$ .swept = 0, then  $\varphi(x) = x - 1$ . Otherwise,  $\varphi(x)$  is exactly find(d, x - 1) - 1. This is correct since find(d, x - 1) is the smallest number in the set containing (x - 1). In general, the function  $\varphi(x)$  is calculated by the procedure  $cal\varphi$ .

<b>Procedure 5:</b> $cal\varphi(L, d, x)$
<b>Description:</b> Calculate $\varphi(x)$
1 <b>if</b> $x = 1$ or $L_{x-1}$ .swept = 0 <b>then</b>
2 return $x-1$
3 else
4 return find $(d, x - 1) - 1$

Thanks to the disjoint-set structure in [27], all find and union operations in our algorithm can be calculated in  $\mathcal{O}(m+n)$ . Because the total number of *union* and *find* operations in Procedure is  $\Theta(m+n)$ , and according to [27], in our case, the *union tree* T is the tree where node *i* is the parent of node (i + 1) for all  $i : 1 \le i < n$ . Therefore, the  $\mathcal{O}(m + n)$  algorithm can be built by a modification of the procedure calculateFAndLink, shown in Procedure 6 below. For readability and simplicity, we only show a brief version of Procedure 6 here. For the complete version of Procedure 6, please see *Appendix C*.

## **Procedure 6:** calculateFAndLink( $\pi^{-1}$ , Match)

```
Description: Step 2: Calculate two functions f and link for all matches e.

1 /* initialize */

2 initialize S, L and d

3

4 /* calculate functions f and link */

5 for x \leftarrow n \ down \ to \ 1 \ do

6 calculate f and link for all matches (*, x) with pointer z decreasing from \varphi(n + 1)

7 update elements in S_x to L

8 update L and d before L passes coordinate i = x

9

10 return (f, link)
```

**Theorem 3.9.** A maximum induced matching in permutation graph  $G(\pi)$  can be found in  $\mathcal{O}(m+n)$  time.

#### **Proof:**

All union and find operations take  $\mathcal{O}(m+n)$  time as shown. Therefore, the cost for Procedure 6 is  $\mathcal{O}(m+n)$ . By substituting Procedure 6 for Procedure 2, Procedure 4 can produce a maximum induced matching for  $G(\pi)$  in  $\mathcal{O}(m+n)$  time.

McConnell and Spinrad [28] introduced an algorithm to construct a permutation model from a permutation graph in linear time. This leads to a linear-time algorithm for the MIM problem in permutation graphs by first generate a permutation model  $\pi$  from permutation graph G, and then find a MIM in  $G(\pi)$  in  $\mathcal{O}(m+n)$  time. Based on this result and Theorem 3.9, we conclude the section by the following corollary.

Corollary 3.10. A maximum induced matching in a permutation graph G can be found in linear time.

## 4. Maximum induced matching in trapezoid graphs

Trapezoid graphs are a superclass of permutation graphs. Algorithms for solving the MIM problem in trapezoid graphs, which will be proposed later in this paper, are pretty similar to those of permutation graphs. Despite that, our procedures in Section 3 still need a huge modification in order to be applicable in trapezoid graphs.

## **4.1.** An $\mathcal{O}(m+n)$ maximum induced matching algorithm in trapezoid graphs

A trapezoid graph can be represented as rectangular boxes on 2-dimensional SPACE( $\tau$ ) in which each trapezoid corresponds to a unique box. A trapezoid which is made by two intervals  $[x_1, x_2]$  and  $[y_1, y_2]$ , where  $x_1 \leq x_2$  and  $y_1 \leq y_2$ , is described as a unique rectangle having bottom-left corner  $(x_1, y_1)$ , top-right corner  $(x_2, y_2)$  and edges parallel to x- and y-axis.

An edge AB of  $G(\tau)$  (or equivalently, a vertex of  $L(G)^2$ ) is described as a *big rectangle* whose sides are parallel to the axes and having two opposite corners  $(min(A.x_1, B.x_1), min(A.y_1, B.y_1))$ and  $(max(A.x_2, B.x_2), max(A.y_2, B.y_2))$  (see Figure 6 for an example). The problem could be viewed as finding a longest sequence of the disjoint big rectangles such that the next rectangle is completely at the top-right of the previous rectangle in the sequence, since such a sequence corresponds to a maximum independent set in  $L(G)^2$  and vice versa. We shall show some definitions similar to Section 3.

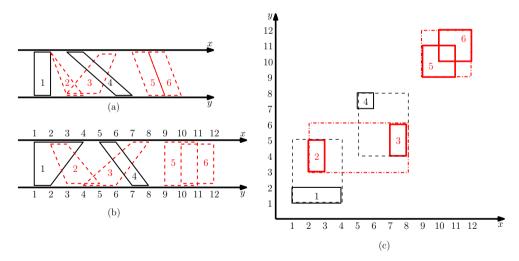


Figure 6: Trapezoids with duplicate x- and y-coordinates (a) can be mapped to a new set of trapezoids without duplicate x- or y-coordinates (b) and can be represented as boxes in 2-dimensional space (c). All x- and y-coordinates lie inside [1, 2n]. There are four matches in this figure: (2, 1), (2, 3), (4, 3) and (5, 6). Match (5, 6) is greater than all other matches. A longest chain of length 2 is (2, 3), (5, 6).

**Definition 4.1.** An ordered pair of trapezoids (A, B) is called a *match* if  $A.x_2 < B.x_2$  and either  $A.x_2 \ge B.x_1$  or  $A.y_2 \ge B.y_1$ . For a match (A, B), A is called the *left end* and B is called the *right end* of the match. The ordered pair (B, A) is called a *reversed match*.

One can see that each match (A, B) corresponds to the edge AB of  $G(\tau)$ , so the number of distinct matches is equal to m. In our algorithm, the term *match* is used instead of *edge*.

**Definition 4.2.** Given two matches e = (A, B) and e' = (A', B'), we define e < e' if  $\max(A.x_2, B.x_2) < \min(A'.x_1, B'.x_1)$  and  $\max(A.y_2, B.y_2) < \min(A'.y_1, B'.y_1)$ . We say that e is *smaller* than e' and e' is *greater* than e.

In other words, e = (A, B) < e' = (A', B') if and only if the big rectangle C' that covers A' and B' is completely at the *top-right* of the big rectangle C that covers A and B in SPACE( $\tau$ ).

**Definition 4.3.** A sequence of matches  $e_1, e_2, ..., e_k$  is called a *chain* if  $e_i < e_{i+1}$  for all  $1 \le i < k$ . The *length* of the chain is k, and the match  $e_1$  is the *smallest* match of the chain.

Since a chain corresponds to a maximum independent set in  $L(G)^2$  and vice versa, the MIM problem in trapezoid graphs turns out to be the problem of finding the longest chain on SPACE( $\tau$ ). We introduce an  $\mathcal{O}(m + n)$  algorithm for MIM problem in  $G(\tau)$  where  $n = |V| = |\tau|$  and m = |E|using the same idea but a little bit more tricky than the permutation one. As well as in the permutation case, we first build adjacent lists from pairs of intersecting trapezoids. Then, we calculate f and link functions for all these pairs. Finally, we construct a MIM based on the functions we calculated.

## Steps to find a MIM in $G(\tau)$ :

1. Construct all matches that exist on SPACE( $\tau$ ) and store them in adjacent lists.

2. Calculate two functions f and link for all matches e.

3. Build a MIM based on functions f and link calculated in step 2.

### **4.1.1.** Construct all matches on SPACE $(\tau)$

For each trapezoid A, let Match(A) be the list of all trapezoids B so that (B, A) is a match. Trapezoids in Match(A) are sorted in decreasing order of their  $y_2$  coordinate. It is noticeable that two trapezoids A, B intersect if and only if there is a diagonal of A intersects with a diagonal of B. Since x- and y-coordinates of all trapezoids are distinct as we assumed, all trapezoid diagonals form a permutation graph, so Match lists can be constructed by a nearly similar algorithm written in procedure buildAllMatches from Section 3.1.1. We present procedure buildAllMatches for the trapezoid case as below. For readability and simplicity, we only show a brief version of Procedure 7 here. For the complete version of Procedure 7, please see Appendix D.

As we assumed, x-coordinates and y-coordinates of all trapezoids are distinct and lie inside the range [1, 2n]. Hence we can make an  $\mathcal{O}(n)$  pre-process step to find in  $\mathcal{O}(1)$  the trapezoid to which a x- or y-coordinate belongs. Although a trapezoid B could appear many times in a list revMatch(A), the number of B's appearances is at most 4 since A and B have only two diagonals each. Therefore, the number of elements in all revMatch lists is at most 4m, which leads to  $\mathcal{O}(m+n)$  running time of procedure buildAllMatches.

## **Procedure 7:** $buildAllMatches(\tau)$

**Description:** Step 1: Construct all matches on SPACE( $\tau$ ) and store them as adjacent lists. 1 /\* initialize \*/ 2 Create linked list LL of n nodes numbered from 1 to 2n, where LL.head = 2n, and i.next = i - 1 for all 1 < i < 2n3 set  $revMatch(A) \leftarrow \emptyset$  and  $Match(A) \leftarrow \emptyset$  for all  $1 \le x \le 2n$ 4 5 /\* build reversed match lists with possibly duplicate elements \*/ 6 for  $y \leftarrow 2n$  down to 1 do  $p \leftarrow LL.head$ 7 suppose that  $y = R.y_1$  or  $y = R.y_2$  for some  $R \in \tau$ 8 while true do 9 suppose that  $p = A.x_1$  or  $p = A.x_2$  for some  $A \in \tau$ 10 if A = R then 11 if  $(p = R.x_1 \text{ and } y = R.y_2)$  or  $(p = R.x_2 \text{ and } y = R.y_1)$  then 12 break 13 else if  $A.x_2 < R.x_2$  then add R to revMatch(A)14 else add A to revMatch(R)15  $p \leftarrow p.next$ 16 remove node p from LL 17 18 19 build Match lists from revMatch lists 20 return { $Match(A) \mid A \in \tau$ }

## **4.1.2.** Calculate two functions f and link

The procedure calculateFAndLink (see Procedure 8) can be reused from Section 3.1.2 by applying some minor adjustments without changing the time complexity (see Figure 7). For readability and simplicity, we only show a brief version of Procedure 8 here. For the complete version of Procedure 8, please see *Appendix E*.

**Procedure 8:** calculateFAndLink( $\tau$ , Match)

**Description:** *Step 2:* Calculate 2 functions *f* and *link* for all matches *e*. 1 /\* initialize \*/ 2 initialize S, L and d3 /\* calculate functions f and link \*/4 for  $x \leftarrow 2n$  down to 1 do if  $x = A.x_2$  for some  $A \in \tau$  then 5 calculate f and link for all matches (\*, x) with pointer z decreasing from  $\varphi(2n+1)$ 6 update the L and d before L passes coordinate i = x7 else //  $x = A.x_1$  for some  $A \in \tau$ 8 9 update elements in  $S_x$  to L 10 return (f, link)

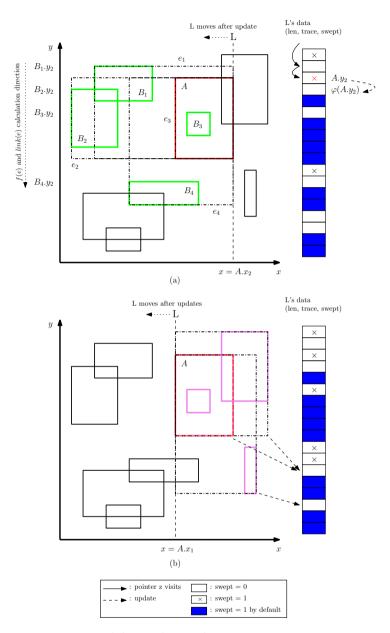


Figure 7: Calculate f and link in  $G(\tau)$  in  $\mathcal{O}(m+n)$  time.

(a) For all matches e = (B, A) where  $A.x_2 = x$ , f(e) and link(e) are calculated in decreasing order of  $B.y_2$ . To obtain f(e) and link(e), every  $L_z$  such that  $\max(A.y_2, B.y_2) \le z \le 2n$  and  $L_z.swept = 0$  is visited. Then (f(e), e) is added to the list  $S_{\min(A.x_1, B.x_1)}$ . After all,  $L_{A.y_2}.swept$  is set to 1;  $L_{A.y_2}.len$  and  $L_{A.y_2}.trace$  are updated to  $L_{\varphi(A.y_2)}$ ; and the sweep line L moves to the coordinate i = x - 1.

(b) Every element (f(e), e) in  $S_x$  having e = (A, B) and  $A.x_1 = x$  is updated to the cell  $L_{\varphi(\min(A,y_1,B,y_1))}$ . After all, the sweep line L moves to the coordinate i = x - 1.

### 4.1.3. Build a maximum induced matching

The last procedure buildMIM from Section 3.1.3 can be completely reused.

### 4.1.4. Summary

All three main procedures have  $\mathcal{O}(m+n)$  time complexity. Therefore, given  $\tau$ , we can find a MIM of trapezoid graph  $G(\tau)$  in  $\mathcal{O}(m+n)$  time by calling the procedure maxInducedMatching below.

$\textbf{Procedure 9:} \texttt{maxInducedMatching}(\tau)$		
<b>Description:</b> Finding a MIM in $G(\tau)$		
$\texttt{1} Match \leftarrow \texttt{buildAllMatches}(\tau)$		
2 $(f, link) \leftarrow \texttt{calculateFAndLink}(\tau, Match)$		
3 return $buildMIM(f, link)$		

We summarize our approach in Theorem 4.4.

**Theorem 4.4.** A maximum induced matching in trapezoid graph  $G(\tau)$  can be found in  $\mathcal{O}(m+n)$  time.

### **Proof:**

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We can use the same technique in the proof of Theorem 3.9 to show that the overall running time of Procedure 8 is  $\mathcal{O}(m+n)$ . In addition, since Procedure 7 runs in  $\mathcal{O}(m+n)$  time and Procedure buildMIM runs in  $\mathcal{O}(n)$  time, Procedure 9 can produce a maximum induced matching for  $G(\tau)$  in  $\mathcal{O}(m+n)$  time.

By exploiting Cogis' result [29] and matrix multiplication properties, Ma and Spinrad [30, 31, 32] created an algorithm that can recognize whether an undirected graph is a trapezoid graph or not in  $\mathcal{O}(n^2)$ . This algorithm is by far the fastest trapezoid graph recognition algorithm, and it can be modified to give a trapezoid model in  $\mathcal{O}(n^2)$ .

Based on this result and Theorem 4.4, we conclude the section by the following corollary.

**Corollary 4.5.** A maximum induced matching in a trapezoid graph G can be found in  $\mathcal{O}(n^2)$  time.

## 5. Conclusion

We have introduced efficient algorithms for the MIM problem in both permutation graphs and trapezoid graphs based on the combined technique of dynamic programming and geometrical sweep line. This method is promising to apply to optimization problems in various special graph classes. We finally summarize the main results in Table 1.

Input for G Class of G	$\pi$ or $ au$	V and $E$
Permutation graph	$\mathcal{O}(m+n)$	$\mathcal{O}(m+n)$
Trapezoid graph		$O(n^2)$

Table 1: Time complexity to find a MIM in particular graph classes.

#### Acknowledgment

This research is funded by Vietnam National Foundation for Science and Technology Development (NAFOSTED) under grant number 102.01-2019.302.

Viet Dung Nguyen was funded by Vingroup Joint Stock Company and supported by the Domestic Master/PhD Scholarship Programme of Vingroup Innovation Foundation (VINIF), Vingroup Big Data Institute (VINBIGDATA), code VINIF.2020.ThS.BK.05.

## References

- Dagan I, Golumbic MC, Pinter RY. Trapezoid graphs and their coloring. *Discrete Applied Mathematics*, 1988. 21(1):35–46. doi:10.1016/0166-218X(88)90032-7.
- [2] Golumbic MC. Algorithmic graph theory and perfect graphs. Elsevier, 2004.
- [3] Micali S, Vazirani VV. An O(√|V|.|E|) algorithm for finding maximum matching in general graphs. In: Foundations of Computer Science, 1980., 21st Annual Symposium on. IEEE, 1980 pp. 17–27. doi: 10.1109/sfcs.1980.12.
- [4] Surynek P. Compact representations of cooperative path-finding as SAT based on matchings in bipartite graphs. In: Tools with Artificial Intelligence (ICTAI), 2014 IEEE 26th International Conference on. IEEE, 2014 pp. 875–882. doi:10.1109/ictai.2014.134.
- [5] Kocaoglu M, Shanmugam K, Bareinboim E. Experimental design for learning causal graphs with latent variables. In: Advances in Neural Information Processing Systems. 2017 pp. 7018–7028. doi:10.5555/ 3295222.3295445.
- [6] Golumbic MC, Lewenstein M. New results on induced matchings. *Discrete Applied Mathematics*, 2000. 101(1-3):157–165. doi:10.1016/S0166-218X(99)00194-8.
- [7] Stockmeyer LJ, Vazirani VV. NP-completeness of some generalizations of the maximum matching problem. *Information Processing Letters*, 1982. 15(1):14–19. doi:10.1016/0020-0190(82)90077-1.
- [8] Chang MS, Chen LH, Hung LJ. Moderately exponential time algorithms for the maximum induced matching problem. *Optimization Letters*, 2015. 9(5):981–998. doi:10.1007/s11590-014-0813-z.
- [9] Xiao M, Tan H. Exact algorithms for Maximum Induced Matching. *Information and Computation*, 2017. 256:196–211. doi:10.1016/j.ic.2017.07.006.

- [10] Golumbic MC, Laskar RC. Irredundancy in circular arc graphs. *Discrete Applied Mathematics*, 1993. 44(1-3):79–89. doi:10.1016/0166-218X(93)90223-B.
- [11] Cameron K. Induced matchings. Discrete Applied Mathematics, 1989. 24(1-3):97–102. doi:10.1016/ 0166-218X(92)90275-F.
- [12] Pandey A, Panda B, Dane P, Kashyap M. Induced matching in some subclasses of bipartite graphs. In: Conference on Algorithms and Discrete Applied Mathematics. Springer, 2017 pp. 308–319. doi: 10.1007/978-3-319-53007-9.
- [13] Köhler EG. Graphs without asteroidal triples. Cuvillier, 1999.
- [14] Erveš R, Šparl P. Maximum Induced Matching of Hexagonal Graphs. Bulletin of the Malaysian Mathematical Sciences Society, 2016. 39(1):283–295. doi:10.1007/s40840-015-0288-9.
- [15] Brandstädt A, Hoàng CT. Maximum induced matchings for chordal graphs in linear time. *Algorithmica*, 2008. 52(4):440–447. doi:10.1007/s00453-007-9045-2.
- [16] Cameron K, Sritharan R, Tang Y. Finding a maximum induced matching in weakly chordal graphs. *Discrete Mathematics*, 2003. 266(1-3):133–142. doi:10.1016/S0012-365X(02)00803-8.
- [17] Broersma H, Kloks T, Kratsch D, Müller H. Independent sets in asteroidal triple-free graphs. SIAM Journal on Discrete Mathematics, 1999. 12(2):276–287. doi:10.1137/S0895480197326346.
- [18] Chang JM. Induced matchings in asteroidal triple-free graphs. *Discrete Applied Mathematics*, 2003. 132(1-3):67–78. doi:10.1016/S0166-218X(03)00390-1.
- [19] Do PT, Le NK, Vu VT. Efficient maximum matching algorithms for trapezoid graphs. *Electronic Journal* of Graph Theory and Applications, 2017. **5**(1):7–20. doi:10.5614/ejgta.2017.5.1.2.
- [20] Rhee C, Liang YD. Finding a maximum matching in a permutation graph. Acta informatica, 1995.
   32(8):779–792. doi:10.1007/bf01178659.
- [21] Habib M, Mouatadid L. Maximum induced matching algorithms via vertex ordering characterizations. *Algorithmica*, 2020. 82(2):260–278. doi:10.1007/s00453-018-00538-5.
- [22] Nguyen VD, Pham BT, Tran VH, Do PT. A dynamic programming algorithm for the maximum induced matching problem in permutation graphs. In: Proceedings of the Ninth International Symposium on Information and Communication Technology. ACM, 2018 pp. 92–97. doi:10.1145/3287921.3287961.
- [23] Nguyen VD, Do PT. Quadratic time algorithm for maximum induced matching problem in trapezoid graphs. In: Proceedings of the 2019 2nd International Conference on Information Science and Systems. ACM, 2019 pp. 185–189. doi:10.1145/3322645.3322653.
- [24] Felsner S, Müller R, Wernisch L. Trapezoid graphs and generalizations, geometry and algorithms. *Discrete Applied Mathematics*, 1997. 74(1):13–32. doi:10.1016/S0166-218X(96)00013-3.
- [25] Bentley JL. Algorithms for Klee's rectangle problems. Technical report, Technical Report, Computer, 1977.
- [26] van Emde Boas P. Preserving order in a forest in less than logarithmic time and linear space. *Information processing letters*, 1977. 6(3):80–82. doi:10.1016/0020-0190(77)90031-X.
- [27] Gabow HN, Tarjan RE. A linear-time algorithm for a special case of disjoint set union. Journal of computer and system sciences, 1985. 30(2):209–221.
- [28] McConnell RM, Spinrad JP. Modular decomposition and transitive orientation. *Discrete Mathematics*, 1999. 201(1-3):189–241. doi:10.1016/S0012-365X(98)00319-7.

- [29] Cogis O. On the Ferrers dimension of a digraph. Discrete Mathematics, 1982. 38(1):47–52. doi:10.1016/ 0012-365X(82)90167-4.
- [30] Ma TH, Spinrad JP. On the 2-chain subgraph cover and related problems. *Journal of Algorithms*, 1994. 17(2):251–268. doi:10.1006/jagm.1994.1034.
- [31] Ma Th. Algorithms on special classes of graphs and partially ordered sets. Vanderbilt University, 1990.
- [32] Ma TH, Spinrad JP. Avoiding matrix multiplication. In: International Workshop on Graph-Theoretic Concepts in Computer Science. Springer, 1990 pp. 61–71. doi:10.1007/3-540-53832-1.

# Appendix A.

<b>Procedure 1:</b> buildAllMatches( $\pi$	-)	)
--	----	---

```
Description: Step 1: Construct all matches that exist on SPACE(\pi^{-1}) and store them as
                  adjacent lists.
1 /* initialize */
2 Create linked list LL of n nodes numbered from 1 to n, where LL.head = n, and
    i.next = i - 1 for all 1 < i \le n (the next node of node numbered 1 is NULL)
3 for x \leftarrow 1 to n do
       Match(x) \leftarrow \emptyset
4
5
6 /* build Match lists */
7 for a \leftarrow n down to 1 do
       p' \leftarrow \text{NULL}
                                                                                    // previous node
8
       p \leftarrow \text{LL.}head
                                                                                      // current node
9
       while p > \pi(a) do
10
           add \pi(a) to Match(p)
11
           p' \leftarrow p
12
           p \leftarrow p.next
13
       /* remove node p */
14
       if p' \neq \text{NULL} then
15
           p'.next \leftarrow p.next
16
       else
17
           LL.head \leftarrow p.next
18
19
20 return \{Match(x) \mid 1 \le x \le n\}
```

## Appendix B.

```
Procedure 2: calculateFAndLink(\pi^{-1}, Match)
```

```
Description: Step 2: Calculate 2 functions f and link for all matches e.
1 /* initialize S and L */
2 for x \leftarrow 1 to n do
3
       S_x \leftarrow \emptyset
       L_x \leftarrow (0, \text{NULL})
4
5
6 /* calculate functions f and link */
7 for x \leftarrow n down to 1 do
       /* calculate f and link for all matches (*, x) with pointer z
8
            decreasing from n * /
9
       z \leftarrow n
       maxLen \leftarrow 0
10
       trace \leftarrow \texttt{NULL}
11
       for y \leftarrow Match(x).begin to Match(x).end do
12
           while z > \pi^{-1}(y) do
13
                if L_z.len > maxLen then
14
                    maxLen \leftarrow L_z.len
15
                    trace \leftarrow L_z.trace
16
                z \leftarrow z - 1
17
           e \leftarrow (y, x)
18
            f(e) \leftarrow maxLen + 1
19
           link(e) \leftarrow trace
20
           add (f(e), e) to the list S_u
21
22
23
       /* update elements in S_x to L */
       for each (f(e), e) \in S_x where e = (x, a) do
24
           if L_{\pi^{-1}(a)}. len < f(e) then
25
                L_{\pi^{-1}(a)} \leftarrow (f(e), e)
26
27
28 return (f, link)
```

## Appendix C.

**Procedure 8:** calculateFAndLink $(\pi^{-1}, Match)$ 

```
Description: Step 2: Calculate 2 functions f and link for all matches e.
 1 /* initiallize S, L and d */
 2 d \leftarrow \{\{1\}, \{2\}, ..., \{n\}\}
 3 for x \leftarrow 1 to n do
        S_x \leftarrow \emptyset, L_x \leftarrow (0, \text{NULL}, 0)
 4
 5
 6 /* calculate functions f and link */
 7 for x \leftarrow n down to 1 do
        /* calculate f and link for all matches (*, x) with pointer z
 8
             decreasing from \varphi(n+1) */
        z \leftarrow \mathsf{cal}\varphi(L, d, n+1), maxLen \leftarrow 0, trace \leftarrow \mathsf{NULL}
 9
        for y \leftarrow Match(x).begin to Match(x).end do
10
            while z > \pi^{-1}(y) do
11
                 if L_z.len > maxLen then
12
                     maxLen \leftarrow L_z.len, trace \leftarrow L_z.trace
13
                 z \leftarrow \mathsf{cal}\varphi(L, d, z)
14
            e \leftarrow (y, x)
15
            f(e) \leftarrow maxLen + 1, link(e) \leftarrow trace
16
            add (f(e), e) to the list S_y
17
18
        /* update elements of S_x to L */
19
        for each (f(e), e) \in S_x where e = (x, a) do
20
            b \leftarrow \mathsf{cal}\varphi(L, d, \pi^{-1}(a))
21
            if b > 0 and L_b.len < f(e) then
22
                 L_b \leftarrow (f(e), e, 0)
23
24
        /* update L and d before L passes coordinate i = x * /
25
        L_{\pi^{-1}(x)}.swept \leftarrow 1
26
        if \pi^{-1}(x) > 1 and L_{\pi^{-1}(x)-1}.swept = 1 then
27
            union(d, \pi^{-1}(x) - 1, \pi^{-1}(x))
28
        if \pi^{-1}(x) < n and L_{\pi^{-1}(x)+1}.swept = 1 then
29
            union(d, \pi^{-1}(x), \pi^{-1}(x) + 1)
30
        b \leftarrow \mathsf{cal}\varphi(L, d, \pi^{-1}(x))
31
        if b > 0 and L_b.len < L_{\pi^{-1}(x)}.len then
32
            L_b \leftarrow (L_{\pi^{-1}(x)}.len, L_{\pi^{-1}(x)}.trace, 0)
33
34
35 return (f, link)
```

## Appendix D.

```
Procedure 9: buildAllMatches(\tau)
   Description: Step 1: Construct all matches on SPACE(\tau) and store them as adjacent lists.
1 /* initiallize */
2 Create linked list LL of n nodes numbered from 1 to 2n, where LL.head = 2n, and
    i.next = i - 1 for all 1 < i \le 2n (the next node of node numbered 1 is NULL)
3 for each A \in \tau do
      revMatch(A) \leftarrow \emptyset // A's reversed match list with duplicable elements
4
5
       Match(A) \leftarrow \emptyset
                                                                          // Match list of A
6
7 /* build reversed match lists with possibly duplicate elements */
8 for y \leftarrow 2n down to 1 do
9
      p' \leftarrow \text{NULL}
                                                                              // previous node
      p \leftarrow \texttt{LL}.head
10
                                                                               // current node
      suppose that y = R.y_1 or y = R.y_2 for some R \in \tau
11
       while true do
12
          suppose that p = A.x_1 or p = A.x_2 for some A \in \tau
13
          if A = R then
14
              if (p = R.x_1 and y = R.y_2) or (p = R.x_2 and y = R.y_1) then
15
                  break
16
          else if A.x_2 < R.x_2 then
17
              add R to revMatch(A)
18
          else
19
              add A to revMatch(R)
20
          p' \leftarrow p, p \leftarrow p.next
21
       /* remove node p */
22
      if p' \neq \text{NULL} then
23
          p'.next \leftarrow p.next
24
      else
25
          LL.head \leftarrow p.next
26
27
28 /* build Match lists from revMatch lists */
  for y \leftarrow 2n down to 1 do
29
      if y = A.y_2 for some A \in \tau then
30
31
          for each B \in revMatch(A) do
              if A is not added to Match(B) then
32
                  add A to Match(B)
33
34
35 return \{Match(A) \mid A \in \tau\}
```

## Appendix E.

**Procedure 10:** calculateFAndLink $(\tau, Match)$ 

```
Description: Step 2: Calculate 2 functions f and link for all matches e.
1 /* initiallize S, L and d */
2 d \leftarrow \{\{1\}, \{2\}, ..., \{2n\}\}
3 for x \leftarrow 1 to 2n do
       S_x \leftarrow \emptyset
4
       if x = A.y_2 for some A \in \tau then L_x \leftarrow (0, \text{NULL}, 0)
5
       else
6
            L_x \leftarrow (0, \text{NULL}, 1)
7
            if x > 1 and L_{x-1}. swept = 1 then union(d, x - 1, x)
8
9
10 /* calculate functions f and link */
11 for x \leftarrow 2n down to 1 do
       if x = A.x_2 for some A \in \tau then
12
            /* calculate f and link for matches (*, A), pointer z decreasing
13
                from \varphi(2n+1) */
            z \leftarrow \mathsf{cal}\varphi(L, d, 2n+1), maxLen \leftarrow 0, trace \leftarrow \mathsf{NULL}
14
            for B \leftarrow Match(A).begin to Match(A).end do
15
                while z \ge \max(A.y_2, B.y_2) do
16
                    if L_z.len > maxLen then maxLen \leftarrow L_z.len, trace \leftarrow L_z.trace
17
                    z \leftarrow \mathsf{cal}\varphi(L,d,z)
18
19
                e \leftarrow (B, A)
                f(e) \leftarrow maxLen + 1, link(e) \leftarrow trace
20
                add (f(e), e) to the list S_{\min(A,x_1,B,x_1)}
21
22
            /* update L and d before L passes coordinate i = x * /
23
            L_{A,u_2}.swept \leftarrow 1
24
            if A.y_2 > 1 and L_{A.y_2-1}.swept = 1 then union(d, A.y_2 - 1, A.y_2)
25
            if A.y_2 < 2n and L_{A.y_2+1}.swept = 1 then union(d, A.y_2, A.y_2 + 1)
26
            z \leftarrow \mathsf{cal}\varphi(L, d, A.y_2)
27
            if z > 0 and L_z.len < L_{A.y_2}.len then L_z \leftarrow (L_{A.y_2}.len, L_{A.y_2}.trace, 0)
28
                                                                         // x = A.x_1 for some A \in \tau
       else
29
            /* update elements in S_x to L */
30
            for each (f(e), e) \in S_x where e = (A, B) do
31
                z \leftarrow \mathsf{cal}\varphi(L, d, \min(A.y1, B.y1))
32
                if z > 0 and L_z.len < f(e) then
33
                    L_z \leftarrow (f(e), e, 0)
34
35
36 return (f, link)
```