

An algorithmic approach to maximal unions of chains in a partially ordered set

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Abstract. We exhibit a recursive procedure that enables us to construct a maximal union of k chains in a finite partially ordered set P for every positive integer k . As a consequence, we obtain an algorithmic proof of Greene's Duality Theorem on the relations between the cardinalities of maximal unions of chains and antichains in a finite poset.

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1 Introduction

As it is well known, Dilworth's Theorem, from 1950, asserts that the maximum cardinality of an antichain in a finite partially ordered set, or poset, P is equal to the minimum number of blocks in a partition of P into chains (see [5] for Dilworth's original paper, and [8] for a useful survey of works stemming from this result). For that matter, there is a *dual* theorem obtained by interchanging chains and antichains. It is natural to want to press further, and to study the cardinalities of maximal *unions* of chains and of antichains. This question was investigated in a series of papers [13, 14, 15, 16] by Greene and Kleitman in the mid-1970s, culminating in Greene's Duality Theorem which establishes the relations between the two cardinalities, and is recalled in our final section.

Greene originally deduced the Duality Theorem, in [15], as a corollary to other notable results he had obtained in collaboration with Kleitman, in [16], to which, indeed, [15] appeared as a sequel.

This topic has attracted an extensive attention, since, apart from its intrinsic interest, there are applications to scheduling problems and to VLSI design. Alternative proofs of the Greene and Kleitman's results were presented a few

years later by Fomin, in [9], and by Frank, in [11], who in the latter article exploits flows in networks. Moreover, such theorem has been extensively studied by other authors ([17], [24]) and generalized to directed graphs in ([1], [4], [19], [25]).

This paper enters that vein, approaching the question from an algorithmic perspective. We exhibit a recursive procedure that, starting from a union \mathcal{C} of $h - 1$ chains, produces a union \mathcal{D} of h chains, in such a way that, if \mathcal{C} has maximal cardinality among unions of $h - 1$ chains, then also \mathcal{D} has the maximal cardinality among unions of h chains. In our final Section, we show how our algorithmic approach yields an independent proof of the Duality Theorem. The key to our approach in this paper is an association between a finite labelled poset and a standard Young tableau in which the entries are related to particular chain families (k -matchings) of the poset. We established this association in an earlier work [2] without invoking Greene's Duality Theorem. The argumentations contained in the present paper only refer to concept which are intrinsic to poset theory and yield a constructive proof of the Duality Theorem. Moreover, MAINPROCEDURE gives a general answer to a problem that has been deeply investigated in some particular cases (see, for example, [6] for the case of planar point sets and [20] and [21] for the case of two and three chains).

2 Preliminaries

Let P be a poset on n vertices with a given linear extension (or labelling) λ , namely an order-preserving bijection

$$\lambda : P \rightarrow \{1, 2, \dots, n\}.$$

A k -matching in P is an array of labels

$$\begin{array}{cccc} a_{11} & a_{12} & \cdots & a_{1k} \\ a_{21} & a_{22} & \cdots & a_{2k} \\ \cdots & \cdots & \cdots & \cdots \\ a_{s1} & a_{s2} & \cdots & a_{sk} \end{array}$$

with $1 \leq a_{ij} \leq n$, such that

- a) $a_{ij} \neq a_{hj}$ for every i, j and h with $i \neq h$.
- b) the sequences $p_{i1} > p_{i2} > \cdots > p_{ik}$, $i = 1, 2, \dots, s$ are chains in P , setting $p_{ij} = \lambda^{-1}(a_{ij})$.

In other terms, the rows of the array correspond to chains in P of length k , with no repetition in any column.

Furthermore, we define the *source* of the k -matching to be the set $S = \{a_{11}, a_{21}, \dots, a_{s1}\}$. The integer s will be called the *size* of the source. A source S will be called *maximum sized* if it has the maximum cardinality among all possible sources of a k -matching in P .

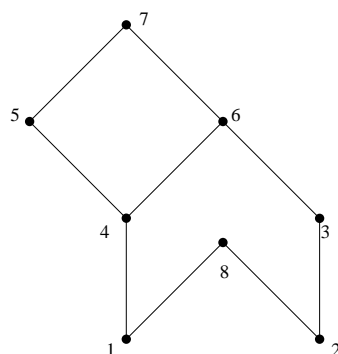


Figure 1: The labelled poset P .

Given a k -matching M in P , we will denote by $S(M)$ the source of M and, for every element $q \in S(M)$, we denote by $M(q)$ the chain of the matching starting from q . For example, consider the poset P shown in Figure 1. The arrays:

$$\begin{array}{ccc}
 7 & 6 & 3 \\
 6 & 3 & 2 \\
 5 & 4 & 1 \\
 (a)
 \end{array}
 \qquad
 \begin{array}{ccc}
 7 & 6 & 4 \\
 6 & 3 & 2 \\
 5 & 4 & 1 \\
 (b)
 \end{array}
 \qquad
 \begin{array}{ccc}
 7 & 5 & 4 \\
 5 & 4 & 1 \\
 6 & 3 & 2 \\
 (c)
 \end{array}$$

are 3-matchings of P sharing the source $S = \{5, 6, 7\}$.

In [2] the authors proved that it is possible to associate with any finite poset P endowed with a linear extension a standard Young tableau $Y(P)$ with s rows such that, for each row index k , the set of entries in the rows $k, k + 1, \dots, s$ of $Y(P)$ is a maximum sized source of a k -matching in P . More precisely:

THEOREM 1 *Given a finite poset P endowed with a linear extension, consider the array $Y(P)$ with s rows such that, for every $1 \leq k \leq s$, the integers contained in the rows $k, k + 1, \dots, s$ form the maximum sized and lexicographically minimum source of a k -matching in P . Then $Y(P)$ is a standard Young tableau.*

For example, the Young tableau associated with the poset p in Figure 1 is:

$$\begin{array}{ccc}
 1 & 2 & 8 \\
 3 & 4 & \\
 5 & 6 & \\
 7 & &
 \end{array}$$

3 Construction of maximal chain families

First of all, we remark that it is possible to associate with a given family of mutually disjoint chains a specific k -matching as follows. Let $\mathcal{C} = \{C_1, \dots, C_s\}$

be a family of s disjoint chains of length c_1, \dots, c_s , respectively:

$$\begin{aligned} C_1 &= x_{1,1} > \cdots > x_{1,c_1}, \\ C_2 &= x_{2,1} > \cdots > x_{2,c_2}, \\ &\dots \\ C_s &= x_{s,1} > \cdots > x_{s,c_s}. \end{aligned}$$

Choose an integer $k \leq \min\{c_1, \dots, c_s\}$. The array

$$\begin{array}{ccccccc} x_{1,1} & & & > & \cdots & > & x_{1,k}, \\ x_{1,2} & & & > & \cdots & > & x_{1,k+1}, \\ & & & & \dots & & \\ x_{1,c_1-k+1} & & & > & \cdots & > & x_{1,c_1}, \\ & & & & \dots & & \\ x_{s,1} & & & > & \cdots & > & x_{s,k}, \\ x_{s,2} & & & > & \cdots & > & x_{s,k+1}, \\ & & & & \dots & & \\ x_{s,c_s-k+1} & & & > & \cdots & > & x_{s,c_s} \end{array}$$

is a k -matching of cardinality $c_1 + \cdots + c_s - ks + s$ that will be called the *standard k -matching* relative to \mathcal{C} . For example, the matchings (a) and (c) are standard 3-matchings of the poset in Figure 1 relative to the chain families $\{\{7, 6, 3, 2\}, \{5, 4, 1\}\}$ and $\{\{7, 5, 4, 1\}, \{6, 3, 2\}\}$, respectively, while there is no disjoint chain family \mathcal{D} in this poset such that (b) is the standard 3-matching relative to \mathcal{D} .

In the following we will be concerned with several different matchings sharing the same source of a given standard matching M' and we will need to analyze the behavior of the chains of such matchings. For this reason, we introduce the notion of distance between two matchings. Suppose that M' is the standard k -matching associated with a given union of chains $\mathcal{C} = \{C_1, \dots, C_s\}$, and M is a k -matching such that $S(M) = S(M')$. For every $p \in S(M)$, let C_j be the chain that contains p . Denote by $n(p)$ the number of points of the chain $M(p)$ not belonging to the chain C_j . The *distance* between M and M' is defined to be the integer:

$$\delta(M, M') = \sum_{p \in S(M)} n(p).$$

Consider now a family $\mathcal{C} = \{C_1, \dots, C_{h-1}\}$ of $h-1$ disjoint chains in P ($h \geq 2$), and an integer $k \leq \min\{|C_1|, \dots, |C_{h-1}|\}$ such that the source of the standard k -matching M' is not maximal. We describe a procedure that, starting from \mathcal{C} , produces a new family $\mathcal{D} = \{D_1, \dots, D_h\}$ of h chains in P .

Recall that the sources of k -matchings of a finite poset are the independent sets of a matroid (see Gansner [12]). Hence there exists an element $g \in P$ that can be added to $S(M')$ to obtain a larger source for a k -matching M . Now we distinguish two cases:

- i) the chain $M(g)$ is disjoint with the chains C_1, \dots, C_{h-1} . In this case we set $\mathcal{D} = \{C_1, \dots, C_{h-1}, M(g)\}$.

ii) Otherwise, we choose the matching M so that the distance between $M \setminus M(g)$ and the standard matching M' is minimal among all possible matchings N such that $S(N) = S(M')$. Note that in this case, the matching M is necessarily different from M' . In fact, the existence of an intersection between $M(g)$ and the union C of chains forces one chain $M(p)$ of the matching, with p in some C_j , to leave the chain C_j , namely, the chain $M(p)$ is not entirely contained in the chain C_j . We construct a family \mathcal{D} of h chains D_1, \dots, D_h obtained starting from the h chains $C_1, \dots, C_{h-1}, M(g)$ and modifying them by using the operation of deflection of a chain by another defined below.

Let $A = a_1 > \dots > a_p$ and $B = b_1 > \dots > b_r$ be two chains with at least one common point. Let $a_i = b_j$ be the leftmost intersection. The *deflection* of A by B is the chain:

$$\text{defl}(A, B) = a_1, \dots, a_i, b_{j+1}, \dots, b_r$$

obtained following the first chain A till the common point a_i and then following B till its ending point b_r . A similar operation has been introduced in [17] for different purposes.

We introduce the following variables:

- for every $p \in S(M)$ the variable $\text{sc}(p)$ will denote the set containing the points $x \in S(M)$ such that $M'(p)$ (or $M(g)$ if $p = g$) and $M(x)$ have an intersection at the same relative level (the *level* of a point p relative to a chain C containing p is the cardinality of the saturated chain connecting p with the minimal point of the poset). In Figure 2 we show an example of two chains intersecting at the same relative level and of two chains intersecting at different relative levels. Roughly speaking, $\text{sc}(p)$ is the set of all points in $S(M)$ that force $M(p)$ to leave the chain C_j containing p . We initialize $\text{sc}(p)$ to be the empty set.
- for every $p \in S(M)$, the point $\text{force}(p)$ will be the second-last element inserted in $\text{sc}(p)$, or 0 if $\text{sc}(p)$ contains less than two elements.
- for every $q \in P$, we define $\text{ch}(q)$ to be either the chain C_j containing q if $q \in \bigcup C_i$, or the singleton $\{g\}$ if $q = g$, where g is the point that belongs to $S(M) \setminus S(M')$, or the empty set, otherwise.
- we initialize $D_i = C_i$ for every $i = 1, \dots, h - 1$, and $D_h = M(g)$.
- for every $p \in S(M)$, consider the chain $M(p) = \{p = a_1, a_2, \dots, a_k\}$. Let a_i be the leftmost point of $M(p)$ not belonging to the chain $\text{ch}(p)$. We define $\text{findpoint}(p)$ to be the leftmost point of $M(p)$ belonging to some chain C_j , with $\text{findpoint}(p) \leq a_i$. In other terms, the variable $\text{findpoint}(p)$ denotes the first intersection between $M(p)$ and one chain $C_j \in \mathcal{C}$ after the chain $M(p)$ leaves the chain $\text{ch}(p)$.

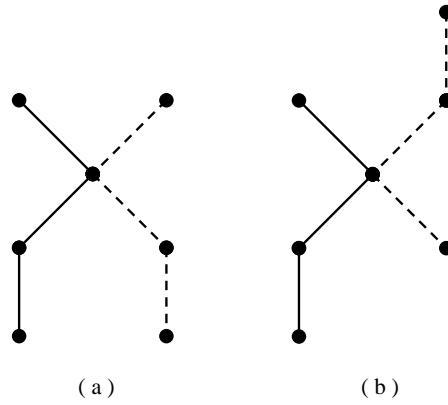


Figure 2: (a) chains intersecting at the same relative level
 (b) chains intersecting at different relative levels.

We describe the procedure in a pseudo code language. The input consist of the poset P , the matching M , the current chain family \mathcal{D} and the current point y (starting with $y = g$). The output is the final chain family \mathcal{D} .

```

MAINPROCEDURE( $y, M, \mathcal{D}, P$ )
 $f = |\text{sc}(y)|$ 
if  $f \geq 2$  then
  let  $\text{sc}(y) = \{a_1, \dots, a_f\}$ 
   $\text{force}(y) = a_{f-1}$ 
else
  FINDSTUFF ( $y, M, \mathcal{D}, P$ )
end if
if  $f \geq 2$  then
   $y \leftarrow \text{force}(y)$ 
  let  $D_s$  be the chain of the family  $\mathcal{D}$  containing  $y$ 
   $D_s \leftarrow \text{defl}(D_s, M(y))$ 
end if
if  $\text{findpoint} = 0$  then
  STOP
else
  let  $x_{m,r}$  be the point of  $C_m$ , say, such that  $\text{findpoint} = x_{m,r}$ 
   $D_s \leftarrow \text{defl}(D_s, C_m)$ 
  set  $l = |\{y > \dots > x_{m,r}\}|$ 
   $\text{sc}(x_{m,r-l+1})[f+1] = y$ 
end if
MAINPROCEDURE( $x_{m,r-l+1}, M, \mathcal{D}, P$ )
  
```

Now we describe the subroutine **FINDSTUFF** that computes the values of the

variable *findpoint*.

```

FINDSTUFF(z, M,  $\mathcal{D}$ , P)
if force(z) = 0 then
    let  $\beta$  be the lowest point in M(z) such that  $\{z > \dots > \beta\} \subseteq \text{ch}(z)$ 
else
    let  $\delta$  be the highest point of M(force(z)) such that  $\text{ch}(\delta) = \text{ch}(z)$ 
    let  $\beta$  be the lowest point in of M(force(z)) such that  $\{\delta > \dots > \beta\} \subseteq \text{ch}(z)$ 
    aux = force(z)
end if
search for the highest point  $\gamma \in M(\text{aux})$  strictly below  $\beta$  such that  $\text{ch}(\gamma) \neq \emptyset$ 
if such a  $\gamma$  exists then
    findpoint =  $\gamma$ 
else
    findpoint = 0
end if
    
```

Straightforward considerations show that MAINPROCEDURE works in polynomial time. In fact, in the worst case, its computational complexity is $O(n^4)$.

We now show that the procedure described above is well defined, providing that, whenever the set $\text{sc}(x) = \{a_1, \dots, a_f\}$ has cardinality at least 2, we have $\text{findpoint}(a_1) > \text{findpoint}(a_2) > \dots > \text{findpoint}(a_f)$. The following Lemma 2 ensures that this condition holds.

LEMMA 2 *Let $p, q \in \text{sc}(x_{i,j})$ such that q has been inserted after p in $\text{sc}(x_{i,j})$ by MAINPROCEDURE. Then:*

$$\text{findpoint}(p) > \text{findpoint}(q).$$

Proof. The two points $\text{findpoint}(p)$ and $\text{findpoint}(q)$ can not coincide by the definition of k -matching. Suppose now that $\text{findpoint}(p) < \text{findpoint}(q)$. It is easy to verify that, in this case, we can obtain a new matching \widehat{M} such that $\delta(\widehat{M} \setminus \widehat{M}(g), M') < \delta(M \setminus M(g), M')$ by replacing the chain $M(x_{i,j})$ with the chain $\text{defl}(M'(x_{i,j}), M(q))$, contradicting our initial hypothesis. \square

In other terms, the statement of Lemma 2 claims that the configuration shown in Figure 3 is forbidden. In that figure, we used the convention to represent a chain $C \in \mathcal{C}$ with a vertical line, while a chain belonging to the matching M is drawn oblique.

Note that MAINPROCEDURE must have a stop: in fact, at each step we consider either a new point or a point y that has been already processed. In this latter case, we simply move $\text{findpoint}(y)$ in a lower position in the chain $M(y)$.

The presented procedure constructs the chains D_1, \dots, D_h by deflecting the family $C_1, \dots, C_h - 1$ by the chains $M(x_{i,j})$ not contained in C_i . The chains $\{D_1, \dots, D_h\}$ are in general far from being pairwise disjoint. However, if we choose an initial family \mathcal{C} whose cardinality is maximal among all possible families of $h-1$ chains, then the chains D_1, \dots, D_h are actually pairwise disjoint.

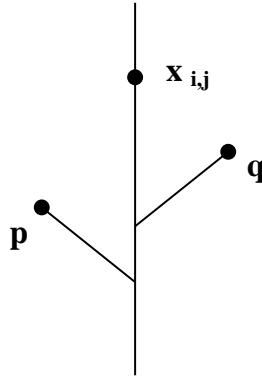


Figure 3: A first forbidden configuration.

We firstly show that the chains D_s have no intersection along the initial chains C_t . We need the following preliminary result:

LEMMA 3 *Let $x_{i,s}, x_{i,t} \in C_i$ ($s < t$) be two distinct points of P belonging to the source of the matching M , such that the chains $M(x_{i,s})$ and $M(x_{i,t})$ are not contained in the chain C_i . Set $y = \text{force}(x_{i,t})$, and let α (resp. β) the minimum point of the chain $M(x_{i,s})$ (resp. $M(x_{i,t})$) such that $\{x_{i,s}, \dots, \alpha\} \subseteq C_i$ (resp. $\{x_{i,t}, \dots, \beta\} \subseteq C_i$). Then:*

$$y' = \text{findpoint}(y) \in \{\alpha, \dots, \beta\}.$$

Proof. Suppose that $y' = \text{findpoint}(y)$ lies strictly below β . In this case we are allowed to replace the chain $M(x_{i,s})$ by the chain consisting of the first l_h points in $\text{defl}(M'(x_{i,s}), M(x_{i,t}))$, finding a new matching \widehat{M} with $\delta(\widehat{M} \setminus \widehat{M}(g), M') < \delta(M \setminus M(g), M')$, contradicting the minimality of $\delta(M \setminus M(g), M')$. \square

Lemma 3 states that, if the chosen matching M is such that $\delta(M \setminus M(g), M')$ is minimal, the configuration reproduced in Figure 4 can not be found in P .

PROPOSITION 4 *For every $1 \leq i < j \leq h$ and for every $1 \leq l < h$,*

$$D_i \cap D_j \cap C_l = \emptyset.$$

Proof. Suppose that there exist two points y and z such that $M(y)$ and $M(z)$ intersect the same chain C_i , with $y \in \text{sc}(x_{i,s})$ and $z \in \text{sc}(x_{i,t})$, $s < t$. Let β be the lowest point in $M(x_{i,t})$ such that $\{x_{i,t}, \dots, \beta\} \subseteq C_i$. It follows from Lemma 3 that β must belong to the interval

$$\{\text{findpoint}(y), \dots, \text{findpoint}(z)\}.$$

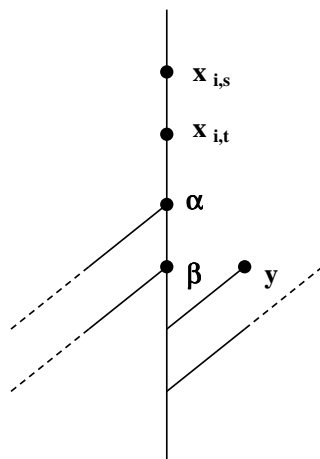


Figure 4: A second forbidden configuration.

This means that the chain D_l containing y can not contain the last part $\{\text{find-point}(z), \dots, x_{i,l_i}\}$ of the chain C_i , since it is the result of an operation of deflection involving $M(x_{i,t})$. This implies that the two chains D_l and D_m containing respectively y and z cannot have any intersection along the chain C_i . \square

If we assume that the family \mathcal{C} has maximal cardinality among all possible unions of $h - 1$ chains, we can give some more detailed information about the chains D_j :

THEOREM 5 *If the family of chains $\mathcal{C} = \{C_1, \dots, C_{h-1}\}$ has maximal cardinality among all possible unions of $h - 1$ chains, the chains D_1, \dots, D_h computed in MAINPROCEDURE are pairwise disjoint.*

Proof. Firstly, remark that the statement of Proposition 4 ensures that two different chains D_i and D_j can not contain the same point $x_{i,j}$. Henceforth, it is enough to prove that the chains $\{D_1, \dots, D_h\}$ have no intersections in the set $P - \bigcup C_i, i = 1, \dots, h - 1$. Let $p, p' \in S(M)$ be the first two points processed by MAINPROCEDURE such that $M(p) \cap M(p')$ consists of at least one point of $P - \bigcup C_i, i = 1, \dots, h - 1$. Let y be the maximum point in such intersection. Suppose that p has been processed by MAINPROCEDURE for the first time before p' has been processed for the first time. Set:

$$\begin{aligned} M(p) &= p_1, \dots, p_{l_h}, \\ M(p') &= p'_1, \dots, p'_{l_h}. \end{aligned}$$

Then, $y = p_j = p'_i$ for some $i, j = 2, \dots, l_h$. Remark that, by definition of l_h -matching, the indices i and j must be different. We consider the sequence

q_1, \dots, q_s such that

$$\begin{aligned} \text{force}(q_1) &= p, \\ \text{force}(q_i) &= q_{i-1}, \quad i = 2, \dots, s, \\ \text{force}(p') &= q_s. \end{aligned}$$

We distinguish two cases:

- 1) Firstly, suppose $i > j$. In this case we can find a new union of $h-1$ chains in P whose cardinality exceeds $|C_1| + \dots + |C_{h-1}|$. More precisely, we construct a new chain \tilde{D} deflecting the chain D_j that contains p' by $M(p)$ and then deflecting the obtained chain by D_l , with $p \in D_l$. We obtain the desired union by considering the chain \tilde{D} and the chains C_t such that $q_i \notin C_t$, $t \neq h$, together with the chains D_j such that $q_i \in D_j$ for some i .
- 2) Suppose now that $i < j$. In this case, it is possible to rearrange the chains of the matching M in order to get a new matching \widehat{M} with $\delta(\widehat{M} \setminus \widehat{M}(g), M') < \delta(M \setminus M(g), M')$. Since we supposed this last quantity to be minimal, we get a contradiction. To be more explicit, suppose that

$$\begin{aligned} M(p) &= p_1, \dots, y, p_{j+1}, \dots, p_{l_h}, \\ M(p') &= p'_1, \dots, y, p_{i+1}, \dots, p'_{l_h}. \end{aligned}$$

We set

$$\widehat{M}(p) = p_1, \dots, y, p'_{j+1}, \dots, p'_{l_h}.$$

In order to get the desired matching \widehat{M} , set $Q = \{q_1, \dots, q_s, p'\}$. For every $x \in Q$ such that $|\text{sc}(x)| = 1$ we set $\widehat{M}(x) = M'(x)$. For every $x \in Q$ with $|\text{sc}(x)| > 1$ we define $\widehat{M}(x)$ to be the deflection of the chain $M'(x)$ by the chain $M(q_r)$, where r is the maximal integer such that $q_r \in \text{sc}(x)$ (the correctness of this last construction is ensured by Lemma 2). Finally, for every $x \in P \setminus (Q \cup \{p\})$ we set $\widehat{M}(x) = M(x)$. \square

The next lemma proves that, if the family \mathcal{C} has maximal cardinality, our procedure never stops after having processed a point p with $\text{findpoint}(p) \neq 0$.

LEMMA 6 *Assume that the family \mathcal{C} has maximal cardinality among all possible unions of $h-1$ chains. Then, for every $p \in P$, if $\text{findpoint}(p) \neq 0$, then there exists $q \in P$ such that $p \in \text{sc}(q)$.*

Proof. Set $\text{findpoint}(p) = x_{i,j}$. Suppose that $p \notin \text{sc}(q)$ for every $q \in P$, meaning that the length of the chain $\{p > \dots > x_{i,j}\}$ is strictly greater than j . In this case, the set

$$D = \bigcup_{m \neq j} D_m$$

is a union of $h-1$ chains whose cardinality exceeds the cardinality of $C_1 \cup \dots \cup C_{h-1}$, that was assumed to have maximal cardinality. \square

A further property of MAINPROCEDURE is that, at the end, it produces a family of chains D_1, \dots, D_h whose sum of cardinalities equals the integer $|C_1| + \dots + |C_{h-1}| + k$. This result holds only if the family $\mathcal{C} = \{C_1, \dots, C_{h-1}\}$ has maximal cardinality among all possible unions of $h - 1$ chains in P . More precisely:

PROPOSITION 7 *Assume that the chain family \mathcal{C} has maximal cardinality among all possible unions of $h - 1$ chains in P . Then, at the end of MAINPROCEDURE, we have:*

$$|D_1| + \dots + |D_h| = |C_1| + \dots + |C_{h-1}| + k.$$

Proof. For every point $q \in S(M)$ processed during MAINPROCEDURE, consider the points $p = \text{force}(q)$ and $f = \text{findpoint}(p)$. While processing the point q , we replace the chain $\{q, \dots, f\}$ by $\{p, \dots, f\}$. The two chains have the same cardinality by construction, hence this replacement leaves the cardinality of the union of chains unchanged. The statement of Lemma 6 ensures that, at the last step, we add a new chain of cardinality k to the union of yielded chains. \square

We are now in position to state our main result:

THEOREM 8 *Given a finite labelled poset P , denote by l_1, l_2, \dots, l_t the lengths of the first, second, \dots , t -th column of the standard Young tableau $Y(P)$ associated with P . Then, for every integer $h = 1, 2, \dots, t$, the maximal cardinality of the union of h chains in P equals $l_1 + \dots + l_h$.*

Proof. We proceed by complete induction on h . If $h = 1$, the assertion is trivially true, since the length of the first column equals the maximal integer j for which a j -matching exists in P . Suppose now the statement true for each $h' \leq h - 1$.

First of all, we remark that, given any maximal union of $h - 1$ chains in P , C_1, \dots, C_{h-1} , ordered by decreasing length, the length of each of these chains is at least equal to the integer l_{h-1} . In order to prove this assertion, denote by c_i the cardinality of the chain C_i . By the inductive hypothesis, we have

$$c_1 + \dots + c_{h-1} = l_1 + \dots + l_{h-1}.$$

Suppose that $c_{h-1} < l_{h-1}$. Then we have:

$$c_1 + \dots + c_{h-2} > l_1 + \dots + l_{h-2},$$

namely, the union of the first $h - 2$ chains has a cardinality greater than the sum of the lengths of the first $h - 2$ columns of $Y(P)$, hence contradicting the induction hypothesis. This implies that $c_{h-1} \geq l_{h-1}$.

As a consequence, since $l_h \leq l_{h-1}$, we can consider the standard l_h -matching M' related to the family $\mathcal{C} = \{C_1, \dots, C_{h-1}\}$. Note that the source of such matching has cardinality $l_1 + \dots + l_{h-1} - (h - 1)l_h + (h - 1)$. Denote by

$$S(M') = \{x_{1,1}, x_{1,2}, \dots, x_{2,1}, x_{2,2}, \dots, x_{h-1,1}, x_{h-1,2}\}$$

the source of the matching, where $x_{i,j} \in C_i$. By previous considerations, the matching M' is not maximal.

Now set $k = l_h$ and apply MAINPROCEDURE. The chains D_1, \dots, D_h obtained at the end of the procedure have the following properties:

- i) the chains D_1, \dots, D_h are pairwise disjoint;
- ii) $|D_1| + \dots + |D_h| = |C_1| + \dots + |C_{h-1}| + l_h = l_1 + \dots + l_h$.

These two remarks show that the union $D_1 \cup \dots \cup D_h$ has the desired cardinality. It remains to prove that this cardinality is maximal. In fact, suppose that there exists a family of disjoint chains $\mathcal{D}' = \{D'_1, \dots, D'_h\}$ such that

$$\sum_{i=1}^h |D'_i| > l_1 + \dots + l_h.$$

In this case, by previous remarks, each chain D'_i must satisfy the condition $|D'_i| \geq l_h$, so we can consider the standard $(l_h + 1)$ -matching N on \mathcal{D}' . Straightforward computations show that the size of the source $S(N)$ is strictly greater than the number of boxes contained in the rows below the $(l_h + 1)$ -th, yielding a contradiction. \square

As an example, consider the poset P in Figure 5.

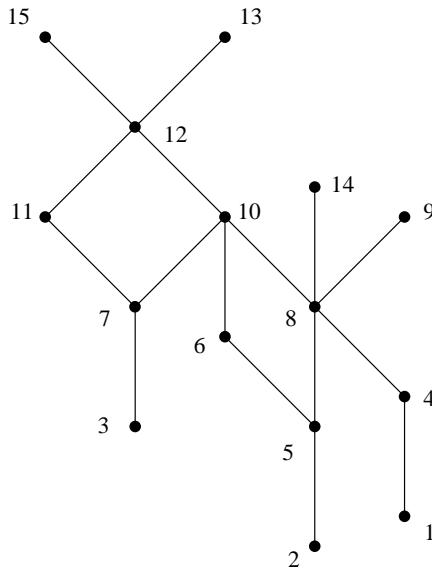


Figure 5: A First example.

The algorithm described in [2] associates to P the following standard Young tableau:

1	2	3	14
4	5	7	
6	8	11	
9	10	15	
12			
13			

Now we use MAINPROCEDURE to find a union of two chains of cardinality $10 = 6 + 4$ in P , starting with the chain $H = \{13, 12, 10, 8, 4, 1\}$ of maximal length. Consider the standard 4-matching M' related to H , whose source is $S(M') = \{13, 12, 10\}$. The point labelled 9 can be added to $S(M')$ in order to get the source of a new matching. There is no chain of length 4 disjoint from H whose starting point is 9, hence we search for a 4-matching M such that $\delta(M', M \setminus M(g))$ is minimal. The desired matching is:

13	12	10	8
12	10	8	4
10	6	5	2
9	8	4	1

Now we apply the procedure starting with $D_1 = C_1 = H$ and $D_2 = C_2 = M(9)$. The first step yields $D_2 = \{9, 8, 4, 1\}$. Now the set $sc(10)$ contains the element 9. Hence we process the chain D_1 containing the point 10. This second step yields $D_1 = \{13, 12, 10, 6, 5, 2\}$. This new chain has no further intersection with the other chain D_2 , so the procedure stops and the produced chains are disjoint.

Now we can use the chain family $\mathcal{C} = \{D_1, D_2\}$ as a starting point for a further application of MAINPROCEDURE. The third column of the tableau $Y(P)$ has length 4, so we consider the standard 4-matching L' relative to the chain family \mathcal{C} :

13	12	10	6
12	10	6	5
10	6	5	2
9	8	4	1

The source $S(L')$ is not maximum sized: the point labelled 15 can be added to $S(L')$ in order to have the source of a new matching L . Since there exists a chain $L(15) = \{15, 11, 7, 3\}$ of length 4 disjoint from \mathcal{C} , we can simply add this chain to the standard matching. The procedure immediately stops, yielding the chain family $\mathcal{D} = \{D_1, D_2, L(15)\}$ shown in Figure 6.

Consider now the poset Q in Figure 7.

The associated tableau is:

1	4	5	8
2	6	7	
3	9	10	

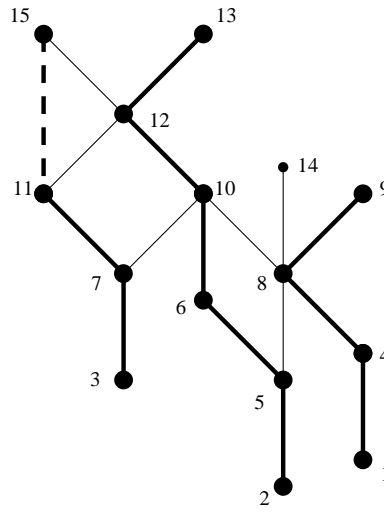


Figure 6: The chains D_1 , D_2 and D_3 obtained at the end of the procedure.

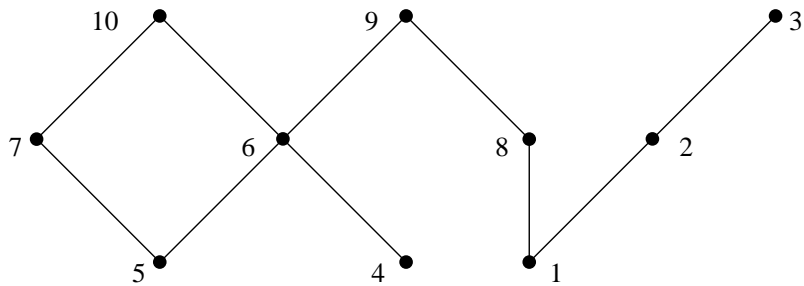


Figure 7: A second example.

We use MAINPROCEDURE to find a union of three chains of cardinality $9 = 3 + 3 + 3$ in Q , starting with the chain family $\mathcal{C} = \{\{9, 8, 1\}, \{10, 6, 5\}\}$. Consider the standard 3-matching M' related to \mathcal{C} , whose source is $S(M') = \{9, 10\}$. The point labelled 3 can be added to $S(M')$ in order to get the source of a new matching. There is no chain of length 3 disjoint from \mathcal{C} whose starting point is 3, hence we search for a 3-matching M such that $\delta(M', M \setminus M(g))$ is minimal. The desired matching is:

$$\begin{matrix} 3 & 2 & 1 \\ 9 & 6 & 4 \\ 10 & 7 & 5 \end{matrix}$$

Now we apply the procedure starting with $D_1 = \{9, 8, 1\}$, $D_2 = \{10, 7, 5\}$ and

$D_3 = M(3)$. The first step yields $D_3 = \{3, 2, 1\}$. Now the set $sc(9)$ contains the element 3. Hence we process the chain D_1 containing the point 9. This second step yields $D_1 = \{9, 6, 5\}$. This new chain intersects chain D_2 in the point labelled 6, and the set $sc(10)$ contains the element 9. This implies that, at the end of the next step, we get $D_2 = \{10, 7, 5\}$. Moreover, the set $sc(10)$ contains the further point 10. Since $|sc(10)| \geq 2$, we must go back to the chain D_1 and look for $findpoint(9) = 6$. Thus, we modify the chain D_1 getting $D_1 = \{9, 6, 4\}$. Since this chain is disjoint from D_2 and D_3 , the procedure stops, yielding the chain family $\mathcal{D} = \{D_1, D_2, D_3\}$ shown in Figure 8.

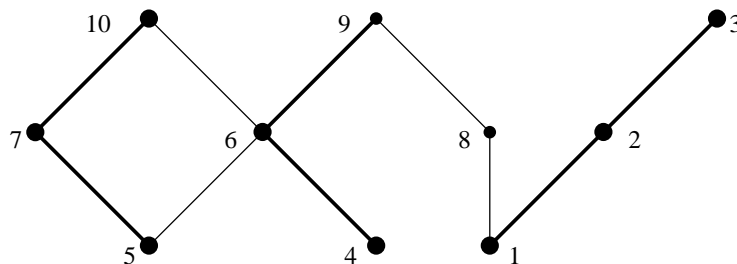


Figure 8: The chains D_1, D_2 and D_3 obtained at the end of the procedure.

4 The Duality Theorem

Given a finite poset P , denote by $d_k(P)$ (resp. $\hat{d}_k(P)$) the maximal cardinality of a union of k antichains (resp. chains) in P . Let $\lambda_k = d_k(P) - d_{k-1}(P)$ and $\hat{\lambda}_k = \hat{d}_k - \hat{d}_{k-1}$ for every $k \geq 1$.

THEOREM 9 (GREEN'S DUALITY THEOREM) *For any finite poset P , the sequences $\lambda = (\lambda_1, \lambda_2, \dots)$ and $\hat{\lambda} = (\hat{\lambda}_1, \hat{\lambda}_2, \dots)$ are weakly decreasing and form conjugate partitions of the integer $|P|$.*

A notable fallout of Theorem 8 is an independent proof of the Duality Theorem. In fact, it implies that, given a finite poset P and an integer k , the number of boxes contained in the first k columns of $Y(P)$ equals the maximal cardinality of the union of k chains in P , $\hat{d}_k(P)$. Moreover, exploiting a remark of Greene in [14], we can prove the following result:

THEOREM 10 *The number of boxes contained in the first k rows of the tableau $Y(P)$ is equal to the maximal cardinality of the union of k antichains in P .*

Proof. For every positive integer k , we define a *graded multipartite graph* $\Gamma_k(P)$ as follows. Let P_1, P_2, \dots, P_{k+1} be $k + 1$ disjoint copies of the poset P . Then $\Gamma_k(P)$ is obtained from these copies together with a source s and a sink t by (i)

connecting s to every vertex in P_1 ; (ii) for each i , with $1 \leq i \leq k$, connecting a vertex x in P_i to a vertex y in P_{i+1} if $x < y$ in P ; (iii) connecting every vertex in P_{k+1} to t .

A k -matching of P can be seen as a partial matching of $\Gamma_k(P)$ connecting the source to the sink. By Menger's Theorem, a minimal separating set of $\Gamma_{k+1}(P)$ has the same cardinality as the source of a maximal $(k+1)$ -matching. Remark that finding a separating set Q in $\Gamma_{k+1}(P)$ means breaking all possible chains of length at least $k+1$, implying that the set $P \setminus Q$ is the union of at most k antichains. The only thing to be proved is that Q does not contain two different representatives of the same point $p \in P$. First of all, suppose Q to be minimal, implying that, for every $x \in Q$, there exists at least a path C of the multipartite graph such that $C \cap Q = \{x\}$. Suppose that Q contains two different copies p_i and p_j of the same element $p \in P$, and consider two paths C_i and C_j , $i < j$, such that $C_i \cap Q = \{p_i\}$ and $C_j \cap Q = \{p_j\}$. Set $r_i = C_j \cap P_i$ and $s_{i+1} = C_i \cap P_{i+1}$. Since C_j contains both r_i and p_j , we have $r < p$. Similarly, we have $p < s$, meaning that the multipartite graph contains an edge connecting r_i and s_{i+1} . We can construct the path \tilde{C} following C_j from the source to r_i , then the edge (r_i, s_{i+1}) and finally C_i until the sink. Since C_j and C_i do not contain any point of Q other than p_i and p_j , we get $\tilde{C} \cap Q = \emptyset$, that is a contradiction. \square

Remark that the statement of Theorem 9 easily follows from the two results contained in Theorems 8 and 10.

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