The Weighted Matching Approach to Maximum Cardinality Matching

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Abstract

Several papers have achieved time $O(\sqrt{nm})$ for cardinality matching, starting from first principles. This results in a long derivation. We simplify the task by employing well-known concepts for maximum weight matching. We use Edmonds’ algorithm to derive the structure of shortest augmenting paths. We extend this to a complete algorithm for maximum cardinality matching in time $O(\sqrt{nm})$.

1 Introduction

The most efficient known algorithms for cardinality matching on nondense graphs achieve time $O(\sqrt{nm})$. The best known of these algorithms are not readily accessible: Micali and Vazirani were first to present such an algorithm [9] but proving it correct has met difficulties [12, 13]. Gabow and Tarjan present a complete development but only at the end of a long paper with a different goal, a scaling algorithm for weighted matching [4]. Similarly Goldberg and Karzanov develop a new framework for flow and matching problems (“skew symmetric matchings”) and again the cardinality matching algorithm requires mastery of this framework. Each of these papers tackles a difficult subject from first principles.

This paper presents an accessible matching algorithm with time bound $O(\sqrt{nm})$. We simplify the task by taking advantage of the well-established theory for maximum weight matching. We include a review of Edmonds’ weighted matching algorithm [2] but still it is helpful to be familiar with the algorithm. Complete treatments are in various texts e.g., [1, 8, 10, 11].

At first glance maximum weight matching seems to offer little insight to the problem. However the dual variables for weighted matching reveal structure that can either be used directly or must be rederived in a presentation from first principles. More importantly we show that a judicious choice of edge weights maps a large piece of the puzzle into simple properties of weighted matching.

The use of weighted matching for cardinality matching was introduced by Gabow and Tarjan [4]. Their cardinality matching algorithm uses a relaxation of the linear program duals that is helpful for scaling. Our algorithm is based on the LP duals. In that respect it differs from [4] at the structural level.

However to make our presentation complete, at the data structure level we use the depth-first search procedure of [4], especially because of its simplicity. We also give a more detailed analysis of the procedure’s correctness than [4], in an appendix. An alternative for this part of the algorithm

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is the double depth-first search algorithm of Micali-Vazirani [9]. We use Edmonds’ algorithm to
deduce the key structure for this algorithm, in another appendix.

The paper presents our algorithm in a top-down fashion. Section 2 gives the overall approach,
using two Phases. Section 3 uses Edmonds’ algorithm to implement Phase 1. Section 4 restates
the Gabow-Tarjan algorithm for Phase 2 [4], with a complete correctness proof in Appendix A.
Section 5 gives details of the data structure that achieve our desired time bound. Appendix B uses
Edmonds’ algorithm to prove existence of the starting edge for the double depth-first search of the
Micali-Vazirani algorithm [9].

Terminology The given graph is always denoted as $G = (V, E)$. An edge in a minor of $G$ is
denoted as its preimage, i.e., $xy$ for $x, y \in V$. For a set of vertices $S \subseteq V$, $\gamma(S)$ denotes the set of
edges with both ends in $S$.

A matching $M$ on a graph is a set of vertex-disjoint edges. $M$ has maximum cardinality if it
has the greatest possible number of edges. Let each edge $e$ have a real-valued weight $w(e)$. For a set of edges $S$ define $w(S) = \sum_{e \in S} w(e)$. $M$ has maximum weight if $w(M)$ is maximum.

For an edge $xy \in M$ we say $x$ and $y$ are mates. A vertex is free if it is not on any matched edge.
An alternating path is a vertex-simple path whose edges are alternately matched and unmatched.
.Paths of 0 or 1 edges are considered alternating.) An augmenting path $P$ is an alternating path
joining two distinct free vertices. To augment the matching along $P$ means to enlarge the matching
$M$ to $M \oplus P$ (the symmetric difference of $M$ and $P$). This gives a matching with one more edge.

2 The approach

A shortest augmenting path, or sap, is an augmenting path of shortest length possible. Hopcroft
and Karp [6] and independently Karzanov [7] presented an efficient approach to finding a maximum
cardinality matching: Repeatedly find a maximal collection of vertex-disjoint saps and augment
the matching with them. This algorithm repeats only $O(\sqrt{n})$ times [6, 7]. Fig. 1 gives our imple-
mentation of this approach.

\[
M \leftarrow \emptyset \\
\text{loop} \\
\quad /* \text{Phase 1} */ \\
\quad \text{for every edge } e \text{ do } w(e) \leftarrow \begin{cases} 2 & \text{if } e \in M \\ 0 & \text{else} \end{cases} \\
\quad \text{execute a search of Edmonds’ weighted matching algorithm} \\
\quad \text{if no augmenting path is found then halt} /* M has maximum cardinality */ \\
\quad \text{form the graph } H \text{ of permissible edges} \\
\text{/* Phase 2 */} \\
\quad \mathcal{P} \leftarrow \text{a maximal set of vertex-disjoint augmenting paths in } H \\
\quad \text{augment } M \text{ by the paths of } \mathcal{P} \\
\]

Figure 1: The high-level cardinality matching algorithm.

We will show that Edmonds’ algorithm halts having found an sap (unless there is no augmenting
path). Furthermore it provides the information needed to construct the graph $H$, which has the
property that the saps of $G$ correspond 1-to-1 to the augmenting paths in $H$. We will complete the
algorithm using one of several known algorithms to find the maximal set of augmenting paths \( P \). Every iteration will use \( O(m) \) time so the entire algorithm uses \( O(\sqrt{nm}) \) time.

### 3 Phase 1 via Edmonds' algorithm

Section 3.1 states the simplified version of Edmonds' algorithm that we use. It also gives a brief review of blossoms. Section 3.2 characterizes the augmenting paths that are found. Section 3.3 gives the algorithm for Phase 1 and proves the graph \( H \) has the key property.

#### 3.1 Edmonds' weighted matching algorithm

Fig.2 gives pseudocode for a search of Edmonds' weighted matching algorithm [2]. The figure omits code that is never executed in the special case of Edmonds' algorithm that we use. Omissions are indicated by comments. (Basically they result from the fact that there are no blossoms at the start of a search.) We will explain the code of the figure and then give a precise statement of the assumptions that simplify the code (see (A) below). In the figure \( M \) denotes the matching, \( B_x \) is the blossom containing vertex \( x \), see below.

The algorithm is illustrated in Fig.3. Free vertices are square and matched edges are heavy. The dashed edges of Fig.3(f) form an augmenting path. The numbers in Fig.3 are defined below.

The algorithm builds a “search structure” \( S \), a subgraph of \( G \). (Fig.3(b)–(e) show the various \( S \) structures.) It also maintains \( \overline{S} \), the subgraph \( S \) with various sets (called “blossoms”, defined

```markdown
make every free vertex the (outer) root of an \( \overline{S} \)-tree

/* general algorithm also makes free blossoms into roots */

loop
  if \( \exists \) tight edge \( e = xy \) with \( x \) outer, \( B_x \neq B_y \) then
    if \( y \not\in V(S) \) then /* grow step */
      add \( xy, yy' \) to \( S \), where \( yy' \in M \)
    /* general algorithm adds blossom \( B_y \) & its matched blossom */
  else if \( y \) is outer then
    if \( x \) and \( y \) are in the same search tree then /* blossom step */
      merge all blossoms in the fundamental cycle of \( e \) in \( \overline{S} \)
    else /* \( xy \) plus the \( \overline{S} \)-paths to \( x \) and \( y \) form an augmenting path */
      return /* general algorithm proceeds to augment the matching */
  else /* dual adjustment step */
    \( \delta = \min\{y(e) - w(e) : e = uv \text{ with } u \text{ outer, } v \not\in V(S)\} \cup \{y(e) - w(e)) / 2 : e = uv \text{ with } u, v \text{ in distinct outer blossoms}\} \)
    /* general algorithm includes set for duals of inner blossoms */
    if \( \delta = \infty \) then return /* \( M \) has maximum cardinality */
    for every vertex \( v \in V(S) \) do
      if \( v \) is inner then \( y(v) \leftarrow y(v) + \delta \) else \( y(v) \leftarrow y(v) - \delta \)
    /* general algorithm changes duals of blossoms. in particular */
    \( z(B) \leftarrow z(B) + 2\delta \) for every maximal outer blossom \( B \). */
```

Figure 2: Simplified search of Edmonds’ algorithm.
below) contracted. $\mathcal{S}$ is a forest. Its roots are the free vertices and contracted sets that each contain a free vertex. $\mathcal{S}$ is an “alternating forest” [2]: Any path from a node to the root of its tree is alternating. A node of $\mathcal{S}$ is inner (respectively outer) if its path starts with an unmatched (matched) edge. An inner node is always a vertex of $G$. An outer node can be a contracted set. Any vertex of $V$ in such a set is also called outer.

The algorithm adds new vertices and edges to $\mathcal{S}$ in a grow step, which adds an edge from an outer vertex to a new inner vertex $y$. It also adds the matched edge from $y$ to its mate, a new outer vertex. (Fig.3(b) shows the result of three grow steps.)

Suppose the algorithm discovers an edge $e$ joining two outer vertices. If $e$ joins two distinct trees of $\mathcal{S}$ it completes an augmenting path. An augment step enlarges the matching. (Fig.3(f) shows the algorithm’s augmenting path as dashed edges.)

If $e$ joins nodes in the same tree of $\mathcal{S}$ a blossom step is done: $e$ is added to $\mathcal{S}$, and the fundamental cycle $C$ of $e$ in forest $\mathcal{S}$ is contracted. The vertices of $V$ belonging to contracted nodes on $C$ form a blossom. (A blossom step is executed in each of Fig.3(c), (d), and (e).)

To describe the last step, recall that the algorithm is based on Edmonds’ formulation of weighted matching as a linear program [2]. Each vertex $v \in V$ has a dual value $y(v)$. Each blossom $B \subseteq V$
has a nonnegative dual value \( z(B) \). The duals dominate an edge \( uv \in E \) if
\[
y(u) + y(v) + \sum_{v,w \in B} z(B) \geq w(e).
\]
uv is tight if equality holds in this constraint. The algorithm maintains duals so that when \( z \) values are included, every edge is always dominated. Furthermore every matched edge is tight, and an edge triggering a grow, blossom or augment step must be tight. We use the common convention that for \( e = uv \in E \), \( y(e) \) denotes \( y(u) + y(v) \). Note that the test for tightness in Fig.2 has \( B_x \neq B_y \) and so does not require \( z \) values.

When no grow, blossom, or augment step can be done, the algorithm makes progress by executing a dual adjustment step. It modifies dual variables so one or more of the other steps can be performed. If this cannot be done the current matching has maximum cardinality. The modification maintains the invariant that every edge of \( S \) is tight.

In Fig.3 each matched (respectively unmatched) edge weighs 2 (0). Each vertex is labelled with its \( y \)-value. Each blossom is labelled with its \( z \)-value, even though these values are not recorded in our algorithm. The label is in the interior of the blossom, and only included when \( z \) is nonzero. For example the dual adjustment at the end of Fig.3(c) increases the \( z \)-value of the triangular blossom from 0 to 2. This dual increases to 4 after part (d), and does not change in the dual adjustment after part (e).

We conclude this section by stating the assumptions that allow our simplifications to the general weighted matching algorithm:

- The algorithm begins with a matching \( M \) and no blossoms.
- The algorithm begins with dual variables \( y(v), v \in V \) that dominate every edge and are tight on every matched edge (there are no \( z \) variables).
- The algorithm does not need to track \( z \) values of blossoms (since there will be no subsequent search).

**Blossoms** It is convenient to consider every vertex as a blossom. But these singleton vertices do not have a \( z \) dual. The notation \( B_x \) for \( x \in V \) denotes the maximal blossom containing \( x \).

Any blossom \( B \) has a base vertex: The base vertex of a singleton \( B = \{v\} \) is \( v \). The base vertex of a blossom constructed in the blossom step of Fig.2 is defined as follows: The fundamental cycle of \( e = xy \) in \( S \) contains a unique node of minimum depth – the nearest common ancestor \( a \) of \( x \) and \( y \). The base vertex of the new blossom is the base vertex of \( a \). (In Fig.3(b)–(f) the base of any blossom is the vertex closest to the root. For instance in part (e) the left subgraph is a blossom whose base vertex is the root.)

Note that the base vertex of an arbitrary blossom \( B \) is the unique vertex of \( B \) that is not matched to another vertex of \( B \). It may be free or matched to a vertex not in \( B \).

Any blossom \( B \) has a natural representation as an ordered tree \( R_B \). The root is a node corresponding to \( B \). The leaves correspond to the vertices of \( V \) in \( B \). Any interior node corresponds to a blossom \( B' \) formed in the blossom step of Fig.2. Let the fundamental cycle \( C \) of that step consist of blossoms \( C_i, i = 0, \ldots, k \). Here \( C_0 \) contains the base vertex of \( B' \), and the indexing corresponds to the order of the blossoms in a traversal of \( C \) (in either direction). The children of \( B' \) correspond to \( C_i, i = 0, \ldots, k \), in that order. In addition \( R_B \) records the edge \( c_ic_{i+1} \) that joins each child \( C_i \) to the next child \( C_{i+1} \) (taking \( k + 1 \) to be 0). These edges are alternately unmatched and matched. Each matched edge has one of its ends a vertex of \( V \) (i.e., \( C_i = c_i \)). Each end is the base vertex of
its blossom. The base vertex of $B$ is also recorded in $R_B$, since it is not determined by a matched edge of $C$.

Note that the edges $c_i c_{i+1}$ of $R_B$ all belong to $E(S)$ and are tight. Also $R_B$ has $O(|B|)$ nodes. This follows since each $B'$ has $k+1$ children and $k/2$ matched edges. So the $k+1$ children can be associated with $2 \cdot k/2 = k$ vertices of $V$ in $B$ ($k \geq 2$).

Any vertex $v \in B$ has an even-length alternating path $P(v, b) \subseteq E(S)$ that starts with the matched edge at $v$ and ends at the base $b$. (The exception is $P(b, b)$, which has no edges.) $P(v, b)$ is specified recursively using $R_B$, as follows. Let $C_i, i = 0, \ldots, k$ be the children of the root $B$. Let $v$ belong to child $C_j$. The path $P(v, b)$ passes through $C_h$ for $h = j, j + 1, \ldots, k, 0$ if $c_j c_{j+1}$ is matched, else $h = j, j - 1, \ldots, 1, 0$ if $c_{j-1} c_j$ is matched. Applying this description recursively to the children $C_h$ gives the entire path $P(v, b)$. (Note that $P(v, b)$ traverses some recursive subpaths $P(v', b')$ in reverse order, from $b'$ to $v'$. But the algorithm does not require this order.)

As an example, the augmenting path of Fig.3(f) traverses the blossom of Fig.3(e) on the path $P(v, f)$ of length 10.

The paths $P(v, b)$ are used (in the complete version of Edmonds’ algorithm, as well as our algorithm in Phase 2) to augment the matching. Note that the order of edges in $P(v, b)$ is irrelevant for this operation, since we are simply changing matched edges to unmatched and vice versa. Also note that every edge of $P(v, b)$ is tight, since $P(v, b) \subseteq E(S)$. So augmenting keeps every matched edge tight.

### 3.2 Properties of Edmonds’ algorithm

Implicit in Edmonds’ algorithm is that it finds a maximum weight augmenting path. This section proves this and characterizes the structure of all maximum weight augmenting paths. We make this assumption on the initialization:

(A') The initial $y$ function is constant, with no unmatched edge tight.

A constant $y$ is the usual initialization of Edmonds’ algorithm. Having no unmatched tight means there is at least one dual adjustment – this assumption simplifies the notation.

As usual define the weight of a path $P$ to be

$$w(P) = w(P - M) - w(P \cap M).$$

**Lemma 3.1** At any point in Edmonds’ algorithm, any augmenting path $P$ and any free vertex $f$ have $w(P) \leq 2y(f)$.

**Proof:** An edge $rs$ is dominated if it is unmatched, i.e.,

$$w(rs) \leq y(r) + y(s) + \sum_{r, s \in V(B)} z(B),$$

and equality holds if $rs$ is matched. So replacing every term $w(rs)$ in the definition of $w(P)$ by the right-hand side of (3.1) gives an upper bound on $w(P)$. Any interior vertex of $P$, say $r$, has $y(r)$ appearing in both $w(P - M)$ and $w(P \cap M)$. Hence the $y$ terms in the upper bound sum to $2y(f)$. So it suffices to show the $z$ terms have nonpositive sum.

Let $B$ be any blossom and let $b$ be its base. Every vertex of $B$ except $b$ has its mate contained in $B$. $P$ is not contained in $\gamma(B)$ since $P$ contains two free vertices. Consider a maximal length subpath $S$ of $P \cap \gamma(B)$. $S$ is alternating. There are two cases:

6
Case \( S \) has \( b \) at one end: Following edges starting from \( b \) shows \( S \) ends at a matched edge of \( \gamma(B) \). So \( S \) has even length, and its edges make no net contribution of \( z(B) \) terms to the upper bound.

Case Neither end of \( S \) is \( b \): The first and last edges of \( S \) are matched. Thus \( S \) makes a net contribution of \( -z(B) \leq 0 \) to the upper bound.

We conclude the total contribution of \( z \) terms to the upper bound is \( \leq 0 \), as desired. \( \square \)

Call a blossom \( B \) positive if \( z(B) > 0 \). \( B \) is positive iff it was formed before the last dual adjustment.

The following corollary refers to the end of Edmonds’ search – tightness refers to the final duals, and blossoms are as defined over the entire algorithm.

**Corollary 3.2** An augmenting path \( P \) has maximum weight iff all its edges are tight and for every positive blossom \( B \), \( P \cap \gamma(B) \) is an even-length alternating path.

**Proof:** The if direction follows from the proof of the lemma. Specifically the proof implies that \( P \) achieves the upper bound of the lemma, i.e., \( w(P) = 2y(f) \), if every edge of \( P \) is tight and \( P \) traverses positive blossoms as specified in the lemma.

In particular the augmenting path \( A \) found in the search algorithm satisfies these sufficient conditions. (In fact \( A \) traverses every blossom as in the lemma.) Thus \( A \) is a maximum weight augmenting path.

This implies an augmenting path has maximum weight iff its weight is \( 2y(f) \). So the proof of the lemma implies the conditions of the corollary must hold for the final dual variables and the positive blossoms of the algorithm. \( \square \)

### 3.3 Phase 1

As in Fig.1 an edge weighs 2 if it is matched, else 0. We initialize Edmonds’ algorithm by setting every \( y \) value to 1. This makes every matched edge tight, every unmatched edge dominated but not tight, and \( y \) constant. Furthermore in every iteration of Fig.1 Edmonds’ algorithm starts afresh with no blossoms. So the assumptions of (A) and (A’) hold.

Assuming the matching is not maximum cardinality, Edmonds’ algorithm halts with a maximum weight augmenting path. Any augmenting path \( P \) of length \( |P| \) has

\[
(3.2) \quad |P| = -w(P) + 1.
\]

So an augmenting path has maximum weight iff it is an sap.

The last step of Phase 1 constructs \( H \), the graph whose augmenting paths correspond to the saps of \( G \). \( H \) is formed from \( G \) by contracting every positive blossom, and keeping only the tight edges that join distinct vertices. As usual each edge of \( H \) records its preimage in \( E \), allowing an augmenting path in \( H \) to be converted to its preimage in \( G \).

Phase 1 requires that the augmenting paths in \( H \) are precisely the images of the saps of \( G \). We will show this using Corollary 3.2.

Case \( P \) is an sap in \( G \): Consider any positive blossom \( B \) with \( P \cap \gamma(B) \neq \emptyset \). The corollary implies \( P \cap \gamma(B) \) is a path that starts with a matched edge and ends with an unmatched edge incident to the base vertex \( b \) of \( B \). So \( P \) either contains exactly 1 edge incident to \( B \) (if \( b \) is free), or 2 edges

\footnote{Edmonds’ search may end before exploring some tight edges. This does not affect the definition of \( H \).}
procedure find_ap_set
initialize $S$ to an empty graph and $P$ to an empty set
for each vertex $v \in V$ do $b(v) \leftarrow v$ /* $b(v)$ maintains the base vertex of $B_v$ */
for each free vertex $f$ do
  if $f \notin V(P)$ then
    add $f$ to $S$ as the root of a new search tree
    find_ap($f$)
procedure find_ap($x$) /* $x$ is an outer vertex */
1 for each edge $xy \notin M$ do /* scan $xy$ from $x$ */
  if $y \notin V(S)$ then
    if $y$ is free then /* $y$ completes an augmenting path */
      add $xy$ to $S$ and add path $yP(x)$ to $P$
      terminate every currently executing recursive call to find_ap
  else /* grow step */
    add $xy$, $yy'$ to $S$, where $yy' \in M$
    find_ap($y'$)
2 else if $b(y)$ is an outer proper descendant of $b(x)$ in $S^-$ then /* blossom step */
  /* equivalent test: $b(y)$ became outer strictly after $b(x)$ */
  let $u_i$, $i = 1, \ldots, k$ be the inner vertices in $P(y, b(x))$, ordered so $u_i$ precedes $u_{i-1}$
  for $i \leftarrow 1$ to $k$ do
    for every vertex $v$ with $b(v) \in \{u_i, u'_i\}$, where $u_iu'_i \in M$ do $b(v) \leftarrow b(x)$
    /* this executes the blossom step for $xy$. each $u_i$ is now outer */
  for $i \leftarrow 1$ to $k$ do find_ap($u_i$)
3 else return

Figure 4: Path-preserving depth-first search.

incident to $B$, one being the matched edge incident to $b$. In both cases the image of $P$ in $H$ is an
alternating path. This makes $P$ an augmenting path in $H$.

Case $P$ is augmenting in $H$: Consider any blossom node $B$ on $P$. $P$ contains an unmatched edge
incident to some vertex $v \in B$. Letting $b$ be the base vertex of $B$, either $b$ is free or $P$ contains the
matched edge incident to $b$. In both cases we can add the $P(v, b)$ path through $B$. Doing this for
every $B$ on $P$ yields a path in $G$, with all edges tight. The corollary shows $P$ is an sap.

4 Phase 2

We can find a maximal set of augmenting paths in $H$ using the double depth-first search of Micali
and Vazirani [9], or the algorithm of Goldberg and Karzanov [5], or the depth-first search of Gabow
and Tarjan [4]. To make this paper complete Fig[4] restates the algorithm of [4]. The find_ap
algorithm is illustrated in Fig[5]. This section discusses the idea of the algorithm and gives the
high-level analysis, for both correctness and the linear time bound $O(m)$. Appendix [A] completes
the analysis. The development is similar to [4] but includes more details.

Note that the search of Micali-Vazirani [9] requires an additional property of $H$, which is proved
in Appendix [B].
We first introduce a variant of previous notation that is used in the rest of the paper: $\mathcal{S}^{-}$ denotes the subgraph of $\mathcal{S}$ consisting of the edges added in grow steps. Clearly $\mathcal{S}^{-}$ consists of trees that span $\mathcal{S}$. Also $\overline{\mathcal{S}}$ is a contraction of $\mathcal{S}^{-}$. We use $\mathcal{S}^{-}$ to state ancestry relationships (e.g., line 3 of Fig.4). These relations essentially hold in $\overline{\mathcal{S}}$ but $\mathcal{S}^{-}$ has the advantage of being more stable. Note that $\mathcal{S}^{-}$ is not alternating. (For instance in Fig.5(a) add a matched edge $aa'$ with an unmatched edge from 11 to a.)

Next we review Fig. 4. $\text{find}_{\text{ap}}$ implements a search of Edmonds’ cardinality matching algorithm (the algorithm of Fig.2 with no dual variables, every edge is tight). In line 2 $P(x)$ is the naturally defined alternating path in $H$ from $x$ to $f$. Specifically $P(x)$ is formed from the $\overline{\mathcal{S}}$-path from $B_x$ to $B_f$, by traversing every blossom of $\text{find}_{\text{ap}}$ using the appropriate $P(v,b)$ path. In line 4 $P(y,b(x))$ can be traversed by simply using the $\overline{\mathcal{S}}$-path from $B_y$ to $B_x$. Note this simple property of the base vertex function $b$: $b(v)$ is always an $\mathcal{S}^{-}$-ancestor of $v$.

The idea for $\text{find}_{\text{ap}}$ is to search for an augmenting path depth-first, making sure that all vertices currently being explored remain on the current search path. This is an obvious property of ordinary depth-first search. It is also desirable for finding disjoint augmenting paths: When we find an augmenting path and delete it from further consideration, no problems are created by partially explored vertices remaining in the graph – these vertices all get deleted.

To achieve this property blossom steps must be scheduled carefully. Fig.4 does this by delaying blossom steps. (In Fig.5 $\text{mate}(2)$ is the 10th vertex to become outer, not the third.) Also the blossom step explores the new outer vertices $u_i$ in order of decreasing $P(u_i)$ length. (Vertex 7 is explored before vertex 8.)

It is easy to see that $\text{find}_{\text{ap}}$ correctly implements the grow and blossom steps of Edmonds’ cardinality matching algorithm. Specifically $\mathcal{S}, \overline{\mathcal{S}}, b(x)$, and $P(x)$ correspond to their definitions. However it is not immediately clear that $\text{find}_{\text{ap}}$ does every possible blossom step. This is proved in Appendix A (Lemma A.4).

We close this section with a simple proof that $\text{find}_{\text{ap}} \text{-set}$ is correct, assuming Lemma A.4. Correctness means that $\text{find}_{\text{ap}} \text{-set}$ halts with $\mathcal{P}$ a maximal set of vertex-disjoint augmenting paths.

Figure 5: (a) Example graph for $\text{find}_{\text{ap}}$. Vertices are numbered in the order they become outer. (b)–(e) $\overline{\mathcal{S}}$ after each of the four blossom steps of $\text{find}_{\text{ap}}$. Dashed edges are not in $\overline{\mathcal{S}}$. $[i..j]$ denotes the set of consecutive integers $\{i, \ldots, j\}$. 
The above remarks imply that each path of \( P \) is augmenting. So the issue is to prove maximality -- no augmenting path of \( H \) is vertex-disjoint from \( P \).

At any point in the execution of \texttt{find\_ap\_set} call an outer vertex \( x \) completely scanned if \texttt{find\_ap\_set}(x) has returned in line 5. The other possibility for an outer \( x - x \) is not completely scanned -- holds when either \texttt{find\_ap\_set}(x) has not been called, or it is currently executing, or it was terminated because an augmenting path was discovered.

The important invariant is

\[(I) \quad \text{Whenever line 1 of } \texttt{find\_ap\_set}(x) \text{ scans an edge, } P(x) \text{ contains every outer vertex that has not been completely scanned.}\]

For instance when vertex 8 scans edge 8,6, vertex 7 is not in \( P(8) \) but it has been completely scanned. It is easy to see invariant (I) is preserved when a recursive call is made: In the grow step \( P(y') \) contains \( P(x) \); in the blossom step \( P(u_i) \) contains \( P(u_j), i < j \leq k \), and also \( P(x) \). So (I) holds on entry to \texttt{find\_ap\_set}(x). Any vertex that becomes outer after this is completely scanned whenever control returns to \texttt{find\_ap\_set}(x). So (I) holds throughout the execution of \texttt{find\_ap\_set}(x), and throughout the entire algorithm.

(I) implies that any augmenting path added to \( P \) contains every outer vertex that has not been completely scanned. Put the other way, when \texttt{find\_ap\_set} halts every outer vertex not on a path of \( P \) has been completely scanned. We conclude the following properties when \texttt{find\_ap\_set} halts:

\[(i) \quad \text{Any free vertex } u \notin V(P) \text{ is outer.}\]
\[(ii) \quad \text{Any edge } uv \text{ with } u \text{ outer and } u,v \notin V(P) \text{ has } v \text{ inner or } B_u = B_v.\]

Note that (ii) depends on Lemma A.4.

Now consider any alternating path \( P \) that is disjoint from \( V(P) \) and starts at a free vertex \( f \). We claim that every vertex of \( P \) is inner or outer. Furthermore for any outer blossom \( B \) with \( B \cap V(P) \neq \emptyset \), the first vertex of \( P \) in \( B \) is the base of \( B \), which is either \( f \) or the mate of an inner vertex.

To prove the claim we argue by induction on the length of \( P \). The claim holds if \( P \) is just the starting vertex \( f \), by (i). Inductively assume \( P \) has reached an outer vertex \( x \), having already reached \( b(x) \). If the next vertex \( y \) is outer (ii) shows \( b(y) = b(x) \). If \( y \) is not outer (ii) shows it is inner. Furthermore \( y \) is followed by \texttt{mate}(y), which is the base of its blossom \( B_{\text{mate}(y)} \).

Now observe that \( P \) does not contain a free vertex \( f' \neq f \). In proof, \( f' \) is outer. The claim shows \( P \) must enter \( B_{f'} \) on its base \( b \) and \( b \neq f' \). But \( f' \) is the base of any blossom containing it. Hence \( f' \notin P \). We have shown that no augmenting path is disjoint from \( V(P) \), as desired.

We close this section with two high-level properties of \texttt{find\_ap\_set} that lead to its linear time bound.

First, any edge is scanned at most twice, once from each end. In proof observe the call \texttt{find\_ap\_set}(x) occurs when \( x \) becomes a new outer vertex. Thus \texttt{find\_ap\_set} is called at most once for any given vertex \( x \in V \).

Second, the test of line 3 is convenient to prove correctness of the algorithm, but is not straightforward to implement. The test of the comment is easily implemented. Appendix A shows the two tests are equivalent.

5 The data structure

This section gives the data structures that show Phases 1 and 2 both use time \( O(m) \). Thus the entire algorithm runs in time \( O(\sqrt{nm}) \).
The matching is represented using an array \textit{mate}, where any vertex \( v \) on matched edge \( vv' \) has \( \text{mate}(v) = v' \). The forest \( S^- \) is represented using a pointer \( \ell(v) \) for every outer vertex \( v \in V \). Specifically a grow step adds \( y \) and \( y' \) to \( S^- \) by setting \( \ell(y') = x \).

We now discuss each step of our algorithm in turn, presenting the data structure for it and verifying that linear time is achieved. We begin with Phase 1. Grow steps are trivial.

**Blossom steps** We find the fundamental cycle \( C \) of edge \( xy \) in time \( O(|C|) \) by climbing the paths from \( B_x \) and \( B_y \) to the root in parallel. This is accomplished using \textit{mate} and \( \ell \) pointers, and a data structure to find the base of a blossom \( B_x \) given an arbitrary vertex \( x \).

The data structure is the incremental-tree set-merging algorithm of Gabow and Tarjan [3]. The operation \textit{find}(\( x \)) returns the base vertex of \( B_x \). \textit{union} operations are used to contract \( C \). The incremental-tree version of [3] works on a tree that grows by addition of leaves, so it works correctly on \( S^- \). The time for \( O(m) \) \textit{finds} and \( O(n) \) \textit{unions} is \( O(m + n) \) and the space is \( O(n) \).

**Dual adjustment steps** It is well-known how to implement dual adjustment steps efficiently using (a) the parameter \( \Delta \), defined as the current sum of all dual adjustment quantities \( \delta \) so far; and (b) an appropriate priority queue.

Our choice for (b) depends on the fact that \( \Delta \) is always an integer \( \leq n/2 \). We first prove the upper bound. At any point in the algorithm let \( P \) be any augmenting path. Lemma 3.1 shows \( w(P) \leq 2y(f) \). Then using (3.2) gives

\[
\Delta \geq \sum_{\delta} y(v) - w(e) = -w(P) + 1 \geq -2y(f) + 1.
\]

Rearranging gives \( y(f) \geq 1 - n/2 \). Since \( y \) values are initially 1, this implies \( \Delta \leq n/2 \).

To prove integrality we claim that all the \( y(v) \) values, \( v \in V(S) \), are always integers of the same parity. (Since a free vertex \( f \) has \( y(f) = 1 - \Delta \) this implies \( \Delta \) is integral.) The claim holds initially by (A'). In the definition of \( \delta \) in Fig.2, any edge \( e \) has \( y(e) - w(e) = y(e) \) an even integer. So the set defining \( \delta \) consists of integers, and \( \delta \) is integral. The adjustment of \( y \) values in Fig.2 keeps all values \( y(v), v \in V(S) \) integers of the same parity.

Now we sketch the algorithm and data structure. The priority queue consists of a collection of lists \( L(d) \), each containing the edges that become tight when \( \Delta \) has increased to \( d \). To get the next edge for the search lists \( L(\Delta') \) are examined, for \( \Delta' = \Delta, \Delta + 1, \ldots \), until an edge that triggers a grow, blossom, or augment step is found. This also gives the next value of \( \Delta \).

Suppose a grow or blossom step makes vertex \( u \in V \) outer. Every unmatched edge \( e = uv \) is scanned. \( e \) is added to list \( L(\Delta + d) \) where \( d \) is \( y(e) \) if \( v \notin V(S) \) or \( y(e)/2 \) if \( v \) is outer.

The next two steps are implemented using the representation \( R_B \) for every maximal blossom \( B \). In the data structure for \( R_B \), the children of any node \( B' \) form a doubly linked ring. Each link also records the edge \( xy \in E \) that joins the two subblossoms.

**Constructing graph \( H \)** The first task is to identify the blossoms that become vertices of \( H \), i.e., the blossoms that are maximal immediately before the last dual adjustment. During Edmonds' search each blossom is marked with the value of \( \Delta \) when it is formed. When the search ends each representation \( R_B \) is traversed top-down, and blossoms with the final value of \( \Delta \) are discarded. The remaining roots of \( R_B \) representations are the maximal positive blossoms that become vertices of \( V(H) \).

To construct \( E(H) \), we continue the top-down traversal and label every vertex of \( V \) with the \( V(H) \) vertex containing it. Then every edge \( e \in E \) is scanned and added to \( E(H) \) if it is tight and
joins distinct $V(H)$ vertices, at least one being outer. ($z$ values are not needed for these edges.) $H$ is represented as an adjacency structure, and the vertex labels are used to add $e$ to the two appropriate adjacency lists. $e$ also records its preimage in $G$, so augments can be performed in $G$.

Turning to Phase 2, the blossom base function $b$ is maintained as in Phase 1 using incremental-tree set-merging.

**Computing $P(x)$ in find_ap** First observe that an $R_B$ data structure allows a path $P(v,b)$ to be computed in time $O(|B|)$ by following the recursive procedure sketched in Section 3.1. This suffices for our applications, since an augmenting path passes through a maximal blossom at most once. (In Phase 2 if an augmenting path passes through a blossom $B$, the vertices of $B$ never get re-explored.) A more careful approach computes $P(v,b)$ in time linear in its length. The idea is not to start at the root of $R_B$ (as in Section 3.1) but rather start at the node whose child contains the matched edge incident to $v$.

find_ap builds $R_B$ representations for the blossoms it creates. They are used to compute the augmenting paths $yP(x)$. These paths are then converted to paths in $G$ by adding in $P(v,b)$ paths that traverse blossom-vertices of $H$. This is done using the $R_B$ representations from Phase 1.

Combining our correctness proof and the above data structures giving linear time, our goal is achieved:

**Theorem 5.1** A maximum cardinality matching can be found in time $O(\sqrt{nm})$ and space $O(m)$.

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A Analysis of find_ap_set

We will consider $S^-$ to be an ordered tree, where grow steps add the children of an outer vertex in left-to-right order. We also assume $\overline{S}$ inherits this order. (Thus in Fig.5(b) vertex 3 became outer after vertex 2.)

Lemma A.1 Any outer vertex $r$ that is not completely scanned has $b(r)$ on the rightmost path of $S^-$. 

Example: The blossom step of Fig.5(b) makes vertex 8 outer but not completely scanned. 8 is not on the rightmost path of $S^-$ but $b(r) = 3$ is.

Proof: A simple induction shows that when a vertex $x$ is made outer, every vertex $s \in P(x)$ has $b(s)$ on the rightmost path of $S^-$. Recall invariant (I) says whenever find_ap($x$) scans an edge, $P(x)$ contains every outer vertex $r$ that has not been completely scanned. So $b(r)$ is on the rightmost path of $S^-$. □

Lemma A.2 At any point in the algorithm, consider an edge $rs$ where $r$ is outer and $s \in V(S)$. Either $s$ is inner and left of $r$ in $S^-$, or $b(r)$ and $b(s)$ are related in $S^-$. 

Example: Consider edge 8,6 immediately after the blossom step forming Fig.5(b). $b(8) = 3$ is related to $b(6) = 6$ in $S^-$. But 8 itself is not related to 6 in $S^-$. Neither is 5, the mate of 8.

Proof: We will show that every grow and blossom step preserves the lemma. We start with this preliminary observation: Once an outer vertex $r$ has been completely scanned, any adjacent vertex $s$ is in $S$.

Consider a grow step. It adds new vertices $y, y'$, with $b(y) = y, b(y') = y'$. 

Subcase $r \neq y'$: If $r$ is not completely scanned, Lemma A.1 implies $b(r)$ is related to both $b(y)$ and $b(y')$. If $r$ is completely scanned the preliminary observation shows $s$ was in $S$ before the grow step. So $s \neq y, y'$. We conclude the lemma is preserved.

Subcase $r = y'$: Since $r$ is the rightmost vertex of $S^-$, any vertex is either related to $r$ or to the left of $r$. So the lemma holds if $s$ is inner. If $s$ is outer it cannot be left of $r$, since then the preliminary observation shows $r$ was in $S$ before the grow step.

Now consider a blossom step. We consider the possibilities for $r$.

Subcase $r$ is a vertex whose $b$-value is changed to $b(x)$: (These are the vertices that enter $B_x$.) Any vertex $s$ has $b(s)$ either related to $b(x)$ or left of $b(x)$ ($b(x)$ is on the rightmost path by Lemma A.1). So we can assume $b(s)$ is left of $b(x)$. This implies $s$ is also left of $b(x)$. $s$ cannot be outer (as before, $s$ is completely scanned, so $r$ would be in $S$ before it becomes a descendant of $b(x)$). So $s$ is inner as desired.

Subcase $r$ is outer and $b(r)$ is not changed to $b(x)$: We can assume $s$ is a vertex that enters $B_x$. We can further assume $b(r)$ is not related to $b(s) = b(x)$. Thus $b(r)$ is to the left of $b(x)$. As before $r$ is completely scanned, making $s$ in $S$ before it becomes a descendant of $b(x)$. □
Lemma A.3 At any point in the algorithm let \( t \) be an inner vertex, whose outer mate \( t' \) is completely scanned, and \( s \) an inner \( S^- \)-descendant of \( t \). A blossom step that makes \( s \) outer makes \( b(s) = b(t) \).

**Proof:** Let \( P \) be the \( S^- \)-path from \( t \) to \( s \). We prove the lemma by induction on \(|P|\).

Among all the inner vertices on \( P \), let \( u \) be the first to become outer in a blossom step. (If there is more than one choice take \( u \) as deep as possible.) Let that blossom step be triggered by edge \( xy \) where \( b(x) \) is an ancestor of \( b(y) \). \( u \) is an \( S^- \)-ancestor of \( b(y) \) and \( b(x) \) is an ancestor of \( u \).

Every outer vertex \( r \) on \( P \) is completely scanned, since \( t' \) is. (This follows since \( r \) became outer while \( \text{find}_\text{ap}(t') \) was executing.) So \( b(x) \) is not on \( P \). Thus \( b(x) \) is a proper ancestor of \( t \). Letting \( u' \) be the mate of \( u \), the blossom step sets

\[
(A.1) \quad b(t) = b(u) = b(u').
\]

If \( u = s \) we are done. Otherwise let \( v \) be the inner vertex that follows \( u \) on \( P \). Let \( v' \) be its mate. As already mentioned, \( v' \) is completely scanned. So the inductive assertion holds for \( v \) and \( s \). Consider the blossom step that makes \( s \) outer. Let \( b_1 \) denote the \( b \) function at the end of this step. The inductive assertion shows

\[
b_1(v) = b_1(s).
\]

Since \( v \) was inner, we also have \( b_1(v) = b_1(u') \). \((A.1)\) implies \( b_1(t) = b_1(u') \). Combining equations gives \( b_1(t) = b_1(s) \). This completes the induction. \( \square \)

Lemma A.4 At any point in the algorithm, let \( rs \) be an edge that has been scanned from both its ends. Then \( b(r) = b(s) \).

**Proof:** Whenever \( r \) and \( s \) are both outer, \( b(r) \) and \( b(s) \) are related in \( S^- \) (Lemma A.2). Let \( b(r) \) be an ancestor of \( b(s) \) the first time both are outer. Although \( b(r) \) and \( b(s) \) may change over time, \( b(r) \) will always be an ancestor of \( b(s) \).

Consider the three possibilities for \( s \) when \( rs \) is scanned from \( r \).

**Case s is not in the search forest:** A grow step makes \( s \) an inner child of \( r \). Eventually \( s \) becomes outer in a blossom step. The new blossom has an outer base vertex, so the blossom includes \( r \), i.e., \( b(r) = b(s) \).

**Case s is outer:** Clearly a blossom step is executed, making \( b(r) = b(s) \).

**Case s is inner:** When \( rs \) is scanned from \( r \) let \( t \) be first inner vertex on the \( S^- \)-path from \( b(r) \) to \( s \). When \( r \) scans \( rs \), \( t' = \text{mate}(t) \) is completely scanned. Now apply Lemma A.3 to \( t \) and \( s \). The blossom step that makes \( s \) outer makes \( b_1(t) = b_1(s) \). Since \( t \) has become outer \( b_1(t) = b_1(r) \). Thus \( b_1(s) = b_1(r) \) as desired. \( \square \)

To implement the algorithm efficiently we change the test for a blossom step, line 3, to the test of the comment. We will show the two tests are equivalent, i.e.,

\[ b(y) \text{ is an outer proper descendant of } b(x) \text{ in } S^- \text{ iff } b(y) \text{ became outer strictly after } b(x). \]

To prove the if direction assume \( b(x) \) and \( b(y) \) are both outer. As blossom bases they both became outer when they were added to \( S \). Edge \( xy \) makes \( b(x) \) and \( b(y) \) related (Lemma A.2). So if \( b(y) \) was made outer strictly after \( b(x) \) it was added to \( S \) after \( b(x) \), i.e., it descends from \( b(x) \). Thus the condition of line 3 holds.

The only if direction is obvious, since any vertex is added to \( S^- \) after its ancestors.
B Searching from the middle

The algorithm of Micali and Vazirani [9] is based on a “double depth-first search”: This search begins at an edge $e = uv$. It attempts to complete an augmenting path using disjoint paths from each of $u$ and $v$ to a free vertex. This is done with two coordinated depth-first searches, one starting at $u$, the other at $v$.

The key fact for this approach is a characterization of the starting edge $e$. We will begin by describing the conditions satisfied by $e$, using our terminology. Then we prove that any augmenting path contains such an edge $e$. Then we discuss the implications of this structure, including how the DDFS of [9] can be used for our Phase 2.

We start with terminology based on the state of the search immediately before the last dual adjustment. Let $T'$ be the set of edges of $G$ that are tight at that time. Let $D_1 \cup D_2$ be the set of edges that become tight in the last dual adjustment, where $D_1$ refers to a grow step and $D_2$ is for a blossom step. So $e \in D_1$ has $y'(e) = \delta$ with one end of $e$ outer and the other not in $S$. $e \in D_2$ has $y'(e) = 2\delta$ with both ends of $e$ outer. (Recall $w(e) = 0$.) Here $y'$ is the dual function right before the last dual adjustment, and “outer” and $S$ also refer to that time.

Lemma B.1 Any maximum weight augmenting path can be written as

$$P_1, Q, P_2$$

where

- each $P_i$ is an even length alternating path from a free vertex to an outer vertex, $P_i \subseteq T'$,
- $Q$ has the form $(e)$ with $e \in D_2$, or $(g_1, e, g_2)$ with $g_1, g_2 \in D_1$.

Remark: Clearly $e$ is unmatched in the first form and matched in the second. Neither end of $e$ is in $S$ in the matched form.

Proof: Let $y$ be the final dual function. The dual adjustment step shows that any free vertex $f$ has $y(f) = y'(f) - \delta$. As mentioned in the proof of Corollary 3.2 an augmenting path $P$ has maximum weight iff $w(P) = 2y(f)$. Thus

$$w(P) = 2y'(f) - 2\delta.$$

Furthermore the corollary shows that for any positive blossom $B$, $P \cap \gamma(B)$ is an even length alternating path, so $z(B)$ makes no net contribution to $w(P)$. Thus $P$ contains edges that are not tight in $y'$, in fact these edges belong to $D_1 \cup D_2$ and have total slack $2\delta$.

Suppose $P$ contains an edge $e \in D_2$. Since $y'(e) = 2\delta$, $P$ contains exactly 1 such edge. The properties of the lemma for both $P_1$ and $Q$ follow easily.

The other possibility is that $P$ contains exactly two edges $g_1, g_2 \in D_1$. Each $g_i$ is unmatched and has an end $v_i \notin S$. $P$ must contain a $v_1v_2$-subpath of edges in $T'$. It must consist of just one edge $v_1v_2 \in M$, since unmatched edges with no end in $S$ are not tight. The properties of the lemma for both $P_1$ and $Q$ follow.

It may not be clear how $findAp$ succeeds in ignorance of this structure. So we take a more detailed look. We start with a simple fact:

Proposition B.2 No edge $uv \in T'$ joins 2 inner vertices.

Proof: A grow step that makes $u$ inner has $y(u) = 1$. Every subsequent dual adjustment increases $y(u)$. So the search ends with $y(u) \geq 1$. If $u$ and $v$ are inner then $uv \notin M$, and
\( y(u) + y(v) \geq 2 > w(uv) = 0. \)

We now present a more detailed proof of the lemma. Consider the search graph \( \mathcal{S} \) immediately before the last dual adjustment. \( \mathcal{S} \) is a subgraph of \( H \). Define a path form similar to the lemma, as

\[
P, Q, P'
\]

where

- \( P \) is an even length alternating path from a free vertex to an outer vertex of \( \mathcal{S} \), \( P \subseteq T' \);
- \( Q \) has the form of the lemma;
- \( P' \) is an odd alternating path whose last edge is matched and last vertex is inner in \( \mathcal{S} \), \( P' \subseteq T' \).

Let \( A \) be an alternating even-length path in \( H \) that starts at a free vertex. We claim that \( A \) is a prefix of the above form. Clearly the claim forces \( \text{find}_{ap} \) to find a path with the structure of the lemma.

We prove the claim inductively. Suppose an even length prefix \( A' \) of \( A \) ends at vertex \( u \), and the next two edges of \( A \) are \( uv, vv' \) with \( uv \notin M \ni vv' \).

If \( A' \) has length 0 then \( u \) is free. \( A' \) has the form \( P \).

Suppose \( A' \) has form \( P \). There are three possibilities:

**Subcase \( v \) is inner in \( \mathcal{S} \):** Its mate \( v' \) is outer, so form \( P \) holds for the longer prefix.

**Subcase \( v \) is outer in \( \mathcal{S} \):** \( uv \) joins two outer vertices of \( \mathcal{S} \). Thus \( uv \in D_2 \). The matched edge \( vv' \) joins an outer vertex with an inner, so \( v' \) is inner. So the new prefix of \( A \) has form \( P, Q, P' \) for \( P' = (vv') \).

**Subcase \( v \notin \mathcal{S} \):** This makes \( uv \in D_1 \). The new prefix has the form \( P, g_1, e \) with \( g_1, e \) as in \( Q \).

Now suppose \( A' \) has form \( P, g_1, e \) with \( g_1, e \) as in \( Q \). Since \( e \notin \mathcal{S} \) and \( uv \) is tight, \( uv \in D_2 \). So \( v \) is outer. Thus \( v' \) is inner. The new prefix has form \( P, Q, P' \) (\( P' = (vv') \)).

Finally suppose \( A' \) has form \( P, Q, P' \). No end of an edge of \( D_1 \cup D_2 \) is inner. Since \( u \) is inner this makes \( uv \in T' \). Also \( u \) inner makes \( v \) outer (Proposition B.2). The new prefix ends with edge \( vv' \in M \) and \( v' \) inner. Thus it has form \( P, Q, P' \). The induction is complete.

The lemma opens up the possibility of having a Phase 2 search start from an edge \( e \) of type \( Q \). DDFS uses this strategy.

The Micali-Vazirani algorithm uses DDFS in Phase 1 as well. This depends on the fact that blossoms have a starting edge \( e \) similar to the lemma. (More precisely suppose a blossom step creates a blossom \( B \) with base \( b \), with \( v \in B \) a new outer vertex. Then \( P(v, b) \) contains a unique subpath of form \( Q \) of the lemma. This is easily proved as above, e.g., use the second argument, traversing the path \( P(v, b) \) starting from \( b \).)

Using DDFS in both Phases 1 and 2 makes the Micali-Vazirani algorithm elegant and avoids any overhead in transitioning to Phase 2.

The proof of [13] that DDFS is correct is involved. Possibly it could be simplified using the lemmas we have presented, as well as other structural properties that weighted matching makes clear. The following aspects of the finer structure of \( H \) are not needed for our development but are used in [13].

[13] defines \( evenlevel(x) \) as the length of a shortest even alternating path from a free vertex to \( x \). The proof of Lemma 3.1 shows any even alternating \( fx \)-path has length \( \geq y(x) - y(f) \). Furthermore it shows that an outer vertex \( x \) has \( evenlength(x) = y(x) - y(f) = |P(x)| \).
oddlevel($x$), the length of a shortest odd alternating path from a free vertex to $x$, has a similar characterization, e.g., any odd alternating $fx$-path has length $\geq 1 - y(x) - y(f) + \sum z(B)$, where the sum extends over blossoms $B$ with base vertex $b$ and $x \in B - b$.

Finally [L3] divides the edges of $H$ into bridges and props. This is due to the fact that an edge $e$ of form $Q$ can trigger an initial blossom step, which can be followed by blossom steps triggered by unmatched edges of $T'$. $e$ is a bridge and the other triggers are props. (In the precise blossom structure stated above, $e$ is the $Q$ edge and the prop triggers are in $T'$.)