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An $\frac{8}{5}$ -approximation algorithm for a hard variant of stable marriage

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Abstract. When ties and incomplete preference lists are permitted in the Stable Marriage problem, stable matchings can have different sizes. The problem of finding a maximum cardinality stable matching in this context is known to be NP-hard, even under very severe restrictions on the number, size and position of ties. In this paper, we describe a polynomial-time $\frac{8}{5}$ -approximation algorithm for a variant in which ties are on one side only and at the end of the preference lists. The particular variant is motivated by important applications in large scale centralized matching schemes.

1 Introduction

Background

An instance of the Stable Marriage problem with Ties and Incomplete Lists (SMTI) comprises a set of n_1 men m_1, \dots, m_{n_1} and a set of n_2 women w_1, \dots, w_{n_2} . Each person has a *preference list* consisting of a subset of the members of the opposite sex, his or her *acceptable partners*, listed in order of preference, with ties, consisting of two or more persons of equal preference, permitted. If man m and woman w appear on each other's preference list then (m, w) is called an *acceptable pair*. If w precedes w' on m 's list then m is said to *prefer* w to w' , while if w and w' appear together in a tie on m 's list then m is said to be *indifferent* between w and w' .

A *matching* is a set M of acceptable pairs so that each person appears in at most one pair of M . If M is a matching and $(m, w) \in M$ we write $w = M(m)$ and $m = M(w)$, and we say that m and w are *partners* in M . A pair (m, w) is a *blocking pair* for M , or *blocks* M , if m is either unmatched in M or prefers w to $M(m)$, and simultaneously w is either unmatched in M or prefers m to $M(w)$. A matching for which there is no blocking pair is said to be *stable*.

SMTI is an extension of the classical Stable Marriage problem (SM) introduced by Gale and Shapley [2]. In the classical case, the numbers of men and women are equal, all preference lists are complete, i.e., they contain all members of the opposite sex, and ties are not permitted, i.e., all preferences are strict. Gale and Shapley proved that, for every instance of SM, there is at least one

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stable matching, and they described an $O(n^2)$ time algorithm to find such a matching; this has come to be known as the *Gale-Shapley algorithm*.

This algorithm is easily extended to the case in which the numbers of men and women differ and preference lists are incomplete (SMI – Stable Marriage with Incomplete lists); it has complexity $O(a)$ in this case, where a is the number of acceptable pairs [4]. In the case of SMI, not everyone need be matched in a stable matching. In general, for a given instance of SMI, there may be many stable matchings – exponentially many in extreme cases – but all stable matchings have the same size and match exactly the same sets of men and women [15, 3].

The Gale-Shapley algorithm may be applied from either the men’s side or the women’s side, and in general these two applications will produce different stable matchings. When applied from the men’s side, the *man-optimal* stable matching is found; in this, every man has the best partner that he can have in any stable matching, and every woman the worst. When the algorithm is applied from the women’s side, the *woman-optimal* stable matching results, with analogous properties. Exceptionally, the man-optimal and woman-optimal stable matchings may coincide, in which case this is the unique stable matching, but in general there may be other stable matchings – possibly exponentially many – between these two extremes. However, for a given instance of SMI, all stable matchings have the same size and match exactly the same sets of men and women [15, 3].

The situation for SMTI is dramatically different. Again, at least one stable matching exists for every instance, and can be found in $O(a)$ time by breaking all ties in an arbitrary way to give an instance of SMI, and applying the Gale-Shapley algorithm to that instance. However, the ways in which ties are broken can significantly affect the outcome. In particular, not all stable matchings need be of the same size, and in the most extreme case, there may be two stable matchings M and M' with $|M| = 2|M'|$. Furthermore, the problem of finding a stable matching of maximum cardinality for an instance of SMTI – problem MAX-SMTI – is NP-hard [13]. This hardness result holds even under severe restrictions, for example, if the ties are on one side only, each list contains at most one tie, and that tie, if present, is at the end of the list.

Practical applications

The practical importance of stable matching problems arises from their application in the assignment of applicants to positions in various job markets. The many-one version of the problem has come to be known as the Hospitals/Residents problem (HR) because of its widespread application in the medical employment domain [15, 9, 14, 1, 16]. In an instance of HR, each resident has a preference list of acceptable hospitals, while each hospital has a preference list of acceptable residents together with a quota of positions. A matching M is a set of acceptable resident-hospital pairs such that each resident is in at most one pair, and each hospital is in a number of pairs that is bounded by its quota. If pair (r, h) is in M , we write $h = M(r)$ and $r \in M(h)$, so that $M(h)$ is a *set* of residents for each hospital h . A matching is stable if it admits no blocking pair, i.e., an acceptable pair (r, h) such that r is either unmatched in M or prefers h

Men's preferences	Women's preferences
$m_1 : w_1 \ w_2$	$w_1 : (m_1 \ m_2)$
$m_2 : w_1$	$w_2 : m_1$

Fig. 1. An instance of SSMTI with stable matchings of sizes 1 and 2.

to $M(r)$, and simultaneously h is either under quota or prefers r to at least one member of $M(h)$.

As in the case of SMI, all stable matchings for an instance of HR have the same size, and so-called *resident-optimal* and *hospital-optimal* stable matchings can be found by applying an extended version of the Gale-Shapley algorithm from the residents' side or the hospitals' side respectively. But if ties are allowed in the preference lists - the Hospitals/Residents problem with Ties (HRT) - then as in the case of SMTI, stable matchings can have different sizes, and it is NP-hard to find a stable matching of maximum size, even under severe restrictions on the number, size, and position of ties.

Variants of the extended Gale-Shapley algorithm are routinely used in a number of countries, including the United States [14], Canada [1] and Scotland [16], to allocate graduating medical students to hospital posts, and in a variety of other countries and contexts. In large scale matching schemes of this kind, participants, particularly large popular hospitals, may not be able to provide a genuine strict preference order over what may be a very large number of applicants, so that HRT is a more appropriate model than HR. If artificial tie-breaking is carried out, either by the participant, because a strictly ordered list is required by the matching scheme, or by the administrators of the scheme, prior to running an algorithm that requires strict preferences, then the size of the resulting stable matching is likely to be affected. Breaking ties in different ways will typically yield stable matchings of different sizes; what would be ideal would be to find a way of breaking the ties that maximizes the size of the resulting stable matching, but the NP-hardness of this problem makes this an objective that is unlikely to be feasible.

A special case of HRT arises if residents are required to strictly rank their chosen hospitals but hospitals are asked to rank only as many of their applicants as they reasonably can, and then place the remainder in a single tie at the end. For example this variant has been employed in the Scottish Foundation Allocation Scheme (SFAS). The correspondingly restricted version of SMTI, where all men's lists are strict and women's lists may contain one tie at the end, is the special case in which all quotas are equal to one. We refer to these restricted versions of SMTI and HRT as *Special SMTI/HRT* (SSMTI/SHRT), and use the terms MAX-SSMTI and MAX-SHRT for the problems of finding maximum cardinality stable matchings in these cases, which remain NP-hard problems [13].

Figure 1 shows an example of SSMTI in which there are two stable matchings, $M_1 = \{(m_1, w_2), (m_2, w_1)\}$ of size 2 and $M_2 = \{(m_1, w_1)\}$ of size 1. A tie in the preference lists is indicated by parentheses.

Related results

It is trivial to establish that there can be at most a factor of two difference between the sizes of a minimum and maximum cardinality stable matching for an instance of SMTI, and as a consequence, breaking ties arbitrarily and applying the Gale-Shapley algorithm gives a 2-approximation algorithm for MAX-SMTI. A number of improved approximation algorithms for versions of SMTI have recently been proposed.

For the general case, Iwama et al [11] gave an algorithm with a performance guarantee of $(2 - c/\sqrt{n})$, (for the case of n men and n women), for a constant c . Very recently, Iwama et al [12] gave the first approximation algorithm for the general case with a constant performance guarantee better than 2, namely $\frac{15}{8}$. From the inapproximability point of view, Halldórsson et al showed the problem to be APX-complete [5], and gave a lower bound of $\frac{21}{19}$ on any polynomial-time approximation algorithm (assuming $P \neq NP$) [6]. This lower bound applies even to MAX-SSMTI.

As far as special cases are concerned, Halldórsson et al [6] gave a $(2/(1 + L^{-2}))$ -approximation algorithm for the case where all ties are on one side, and are of length at most L – so, for example, this gives a bound of $\frac{8}{5}$ when all ties are of length 2. If ties are on both sides and restricted to be of length 2, a bound of $\frac{13}{7}$ is shown in [6]. Halldórsson et al [7] also described a randomized algorithm with an expected performance guarantee of $\frac{10}{7}$ for the same special case under the additional restriction that there is at most one tie per list.

The contribution of this paper

In this paper, we focus on the problem MAX-SSMTI described above, and give a polynomial-time $\frac{8}{5}$ -approximation algorithm for this case. The algorithm is relatively easy to extend to MAX-HRT, and the same $\frac{8}{5}$ performance guarantee holds in this more general setting. We also show that this performance guarantee is the best that can be proved for the algorithm by providing an example for which this bound is realised.

2 The algorithm

In what follows, we assume that each man’s preference list is strict, and each woman’s preference list is strict except for a tie (of length ≥ 1) at the end. The algorithm consists of three phases. The first phase is a variant of the Gale-Shapley algorithm for the classical stable marriage problem, applied from the women’s side, but with women proposing only as far as the tie (if any) in their list. This results in a provisional matching involving precisely those men who received proposals. The second phase adds to this provisional matching a maximal set of acceptable pairs from among the remaining men and women. Finally, in Phase 3 all ties are broken, favouring unmatched men over matched men, and the standard Gale-Shapley algorithm is run to completion on the resulting instance of SMI.

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assign each person to be free;
while (some woman  $w$  is free) and ( $w$  has a non-empty list)
  and ( $w$  has an untied man  $m$  at the head of her list) {
     $w$  proposes, and becomes engaged to  $m$ ;
    for each successor  $w'$  of  $w$  on  $m$ 's list {
      if  $w'$  is engaged to  $m$ 
        break the engagement, so that  $w'$  becomes free;
      delete the pair  $(m, w')$  from the preference lists;
    }
  }

```

Fig. 2. Phase 1 of Algorithm SSMTI-APPROX

Phase 1 of Algorithm SSMTI-APPROX

The first phase of the algorithm is a variant of the Gale-Shapley algorithm for the classical stable marriage problem, applied from the women's side. During this phase, zero or more deletions are made from the preference lists – by the deletion of the pair (m, w) , we mean the removal of w from m 's list and the removal of m from that of w . Initially, everyone is free. During execution of the algorithm, a woman may alternate between being free and being engaged, but once a man becomes engaged, he remains in that state, though the identity of his partner may change over time. A free woman w who still has an untied man on her current list proposes to the first such man and becomes (at least temporarily) engaged to that man. When a man m receives a proposal from woman w , he rejects his current partner (if any), setting her free, and all pairs (m, w') such that m prefers w to w' are deleted. This phase of the algorithm is summarised in Figure 2.

When Phase 1 of the algorithm terminates on a given instance I , a woman w 's preference list must be in one of three possible states – it may be empty, it may consist of a single tie, or it may have a unique untied man m at its head. In the latter case, it is clear that m cannot be the unique man at the head of any other woman's list, and that w is the last entry in m 's list.

Lemma 1. *On termination of Phase 1 of Algorithm SSMTI-APPROX,*

- (i) *no deleted pair can belong to a stable matching;*
- (ii) *if man m is the unique man at the head of some woman's list then m is matched in every stable matching.*

Proof. (i) Suppose that (m, w) is a deleted pair that belongs to a stable matching M , and that (m, w) was the first such pair to be deleted in an execution of Phase 1 of the algorithm. This must have happened because m received a proposal from some woman w' whom he prefers to w . Woman w' is either unmatched in M or prefers m to $M(w)$, because any pair (m', w') such that w' prefers m' to m must have been previously deleted, and by our assumption, this pair cannot be in a stable matching. Hence (m, w') blocks M , a contradiction.

$V = Y_1 \cup Q_1$;
 $E = \{(m, w) \in Y_1 \times Q_1 : (m, w) \text{ is a Phase 1 acceptable pair}\}$;
 construct the bipartite graph $G = (V, E)$;
 $K =$ a maximum cardinality matching in G ;
 for each pair $(m, w) \in K$
 promote m from the tie to the head of w 's list;
 re-activate the proposal sequence of Phase 1;

Fig. 3. Phase 2 of Algorithm SSMTI-APPROX

(ii) Suppose that m is the unique man at the head of woman w 's list, and that M is a stable matching in which m is unmatched. Then, by part (i), w is either unmatched in M or prefers m to $M(w)$, so that (m, w) blocks M , a contradiction. \square

We refer to the men who appear untied at the head of some woman's list after Phase 1 of the algorithm as the *Phase 1 X-men* and the other men as the *Phase 1 Y-men*, and we denote these sets by X_1 and Y_1 respectively. Likewise, the women who have an untied man at the head of their list are the *Phase 1 P-women* and the others are the *Phase 1 Q-women*, denoted by P_1 and Q_1 . So the engaged pairs at the end of Phase 1 constitute a perfect matching between X_1 and P_1 , and the essence of Lemma 1(ii) is that each member of X_1 is matched in every stable matching. We call the preference lists that remain after Phase 1 the *Phase 1 lists*, and if man m and woman w are in each other's Phase 1 lists, we say that (m, w) is a *Phase 1 acceptable pair*.

Phase 2 of Algorithm SSMTI-APPROX

In Phase 2 of the algorithm, we seek to increase the number of men who are guaranteed to be matched. To this end, we find a maximum cardinality matching K of Y_1 to Q_1 , where a pair (m, w) can be in this matching only if $m \in Y_1$, $w \in Q_1$, and (m, w) is a Phase 1 acceptable pair. For each pair (m, w) in K , we break the tie in w 's Phase-1 list by promoting m to the head of that list (and leaving the rest of the tie intact). We then re-activate the proposal sequence of Phase 1, which will lead to a single proposal corresponding to each pair in K , and which may result in some further deletions from the preference lists, but no rejections and no other proposals. This produces an instance I' of SSMTI that is a refinement of the original instance I – or more properly, a refinement of the variant of I that results from application of Phase 1; clearly any matching that is stable for I' is also stable for I , but not necessarily vice-versa. Phase 2 of the algorithm is summarised in Figure 3.

Lemma 2. *Every man who is untied at the head of some woman's list on termination of Phase 2 of Algorithm SSMTI-APPROX is matched in every stable matching for I' .*

Proof. The proof is completely analogous to that of Lemma 1(ii). \square

Note that, while Lemma 2 can be expected, in many cases, to give a stronger lower bound on the size of a stable matching than is given by Lemma 1, this need not be the case. It is perfectly possible that the Phase 1 Q -women have only Phase 1 X -men in their preference lists, and that, as a consequence, K is the empty matching. However, we now extend the set of X -men and P -women to include those who became engaged during Phase 2. Henceforth, we use the term X -men to refer to those men who appear untied at the head of some woman's list, and the P -women are the women who have an X -man at the head of their list, after Phase 2 of the algorithm. Let x be the number of X -men and P -women, and suppose that these sets are $X = \{m_1, \dots, m_x\}$ and $P = \{w_1, \dots, w_x\}$ respectively. We also define $Y = \{m_{x+1}, \dots, m_{n_1}\}$ and $Q = \{w_{x+1}, \dots, w_{n_2}\}$, and refer to these sets as the Y -men and Q -women respectively.

Lemma 3. *Let A be a matching that is stable for I' , and let M be a maximum cardinality stable matching for I . Then*

- (i) *A Y -man who is matched in M must be matched in M with a P -woman.*
- (ii) $|M| \leq |A| + x$;
- (iii) $|M| \leq 2x$.

Proof. (i) Suppose that m is a Y -man and that $(m, w) \in M$. Then if w were a Q -woman, she must be a Phase 1 Q -woman who failed to be matched during Phase 2, and therefore the matching found in Phase 2 could have been extended by adding the pair (m, w) , contradicting its maximality.

(ii) By Lemma 2, all of the X -men are matched in A . So the only men who can be matched in M but not in A are Y -men. By (i), such a man must be matched in M with a P -woman. The inequality follows, as there are just x P -women.

(iii) Men matched in M are either X -men, and there are x of these, or Y -men matched with P -women (by (i)), and there are x of the latter, hence at most $2x$ such men in total. \square

Phase 3 of Algorithm SSMTI-APPROX

Phase 3 of the algorithm involves completely breaking the remaining ties and then applying to the resulting instance of SMI the standard Gale-Shapley algorithm (or at least the extended version of that algorithm that deletes redundant entries from the preference lists - see [4]). The algorithm may be applied from either the men's or women's side; as is well known, the size of the resulting matching will be the same in each case. Tie-breaking is carried out according to just one restriction, namely, for each tie, the Y -men are given priority over the X -men. In other words, each tie is resolved by listing the Y -men that it contains, in arbitrary order, followed by the X -men that it contains, again in arbitrary order. It is immediate that the algorithm produces a matching that is stable for the original instance of SMTI. For an instance I of SMTI, we denote by I'' an instance of SMI obtained by application of Phases 1 and 2 of Algorithm SSMTI-APPROX, followed by tie-breaking according to this rule. Again it is immediate that a matching that is stable for I'' is also stable for I . Phase 3 of the algorithm is summarised in Figure 4.


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for each woman  $w$ 
    break the tie (if any) in  $w$ 's list, placing the  $Y$ -men ahead of the  $X$ -men;
/* Now apply the standard Gale-Shapley algorithm */
assign each person to be free;
while (some man  $m$  is free) and ( $m$  has a non-empty list) {
     $w =$  the first woman on  $m$ 's list;
     $m$  proposes, and becomes engaged to  $w$ ;
    for each successor  $m'$  of  $m$  on  $w$ 's list {
        if  $m'$  is engaged to  $w$ 
            break the engagement, so that  $m'$  becomes free;
        delete the pair  $(m', w)$  from the preference lists;
    }
}
return the set  $A$  of engaged pairs;

```

Fig. 4. Phase 3 of Algorithm SSMTI-APPROX

The performance guarantee

Let A be a matching produced by application of Algorithm SSMTI-APPROX, and let M be a maximum cardinality stable matching for the original instance I of SSMTI. As previously established, all of the X -men are matched in A . Suppose that exactly r of the Y -men, say m_{x+1}, \dots, m_{x+r} , are matched in M but not in A . Let us call these men the *extra men* (for M), and their partners in M the *extra women*.

Lemma 4. (i) *Each extra woman is matched in A .*
(ii) *An extra woman is either matched in A to a Y -man or strictly prefers her A -partner to her M -partner.*

Proof. Let w be an extra woman, and let m be her partner in M . Recall that M is stable for the original instance I , while A is stable for the refined instance I'' (of SMI), and therefore also for the instances I' and I (of SSMTI).

(i) By definition, m is an extra man and therefore is not matched in A , so that if w is not matched in A it is immediate that the pair (m, w) blocks A .

(ii) Let a be w 's A -partner. If w strictly prefers m to a then, since m is unmatched in A , the pair (m, w) blocks A in I , a contradiction. If m and a are tied in w 's list, and a is an X -man then, when that tie was broken to form I'' , m , being a Y -man, must have preceded a in the resulting strict preference list. Hence, again since m is unmatched in A , the pair (m, w) blocks A in I'' , a contradiction. \square

We partition M 's extra men into two sets U and V ; those in U have an M -partner who is matched in A to an X -man, and those in V have an M -partner who is matched in A to a Y -man. Suppose, without loss of generality, that $U = \{m_{x+1}, \dots, m_{x+s}\}$ and $V = \{m_{x+s+1}, \dots, m_{x+r}\}$, i.e., $|U| = s$, $|V| = r - s$. Let $M(U)$ denote the set of women who are matched in M to a man in U .

Suppose that, among the men who are matched in A with women in $M(U)$, exactly t ($\leq s$) are unmatched in M . (These are all X -men, by definition of U , but some X -men – those who became so during Phase 2 of the algorithm, need not be matched in M .)

Our next lemma gives us certain inequalities involving the sizes of matchings M and A that will enable us to establish the claimed performance guarantee for Algorithm SSMTI-APPROX.

Lemma 5. (i) $|M| \leq |A| + r - t$.

(ii) $|A| \geq x + r - s$.

(iii) $|A| \geq r + s - t$.

Proof. (i) All the X -men are matched in A , but at least t of them are not matched in M , and the Y -men who are matched in M but not in A number exactly r .

(ii) Consider the set V . Each woman w who is the partner in M of a man in V is matched in A to a Y -man, and there are $r - s$ such women w . This gives us $r - s$ of the Y -men who are matched in A , and together with all x of the X -men who, by Lemma 1(ii), are all matched in A , we have a total of $x + r - s$ distinct men who are matched in A .

(iii) Consider the set U , and suppose that (m_{x+j}, w_{i_j}) is in M for $j = 1, \dots, s$. By definition of U , each w_{i_j} has an X -man as her partner in A ; without loss of generality, suppose that (m_j, w_{i_j}) is in A , for $j = 1, \dots, s$. By Lemma 4, w_{i_j} strictly prefers her A -partner m_j to her M -partner m_{x+j} . Each m_j is an X -man and $s - t$ is the number of these men who are matched in M ; suppose, without loss of generality, that (m_j, w_{k_j}) is in M , for $j = 1, \dots, s - t$. Then none of these w_{k_j} can be an extra woman, for the M -partners of the latter are Y -men. Also, each of the men m_j prefers w_{k_j} to w_{i_j} , for otherwise (m_j, w_{i_j}) would block M . Furthermore, each w_{k_j} must be matched in A . For if not, the pair (m_j, w_{k_j}) would block A . It follows that we have a total of $r + s - t$ women who must be matched in A , namely the r extra women, by Lemma 4, and the $s - t$ women $w_{k_1}, \dots, w_{k_{s-t}}$. \square

We are now in a position to establish our main theorem.

Theorem 1. For a given instance of SSMTI, let M be a maximum cardinality stable matching and let A be a stable matching returned by Algorithm SSMTI-APPROX. Then $|M| \leq 8|A|/5$.

Proof. By Lemma 5 we have $|A| \geq \max(x + r - s, r + s - t) \geq \frac{1}{2}((x + r - s) + (r + s - t)) = x/2 + r - t/2$. So, by Lemma 3(iii), $|A| \geq |M|/4 + r - t/2$. Hence, by Lemma 5(i), $|A| \geq |M|/4 + |M| - |A| + t - t/2$, and so $2|A| \geq 5|M|/4 + t/2$, from which the claimed bound follows. \square

Complexity of the algorithm

The worst-case complexity of Algorithm SSMTI-APPROX is dominated by the

maximum cardinality matching step in Phase 2. Using the Hopcroft-Karp algorithm [8], this can be achieved in $O(\sqrt{na})$ time, where n is the total number of men and women, and a is the sum of the lengths of the preference lists. However, there is a variant of the algorithm that achieves the same performance guarantee but with $O(a)$ complexity. This is obtained by observing that, in Phase 2, it suffices to find a *maximal* matching – i.e., a matching that cannot be extended to a larger matching by adding further pairs – rather than a maximum cardinality matching, of men in Y_1 to women in Q_1 . The only place in the subsequent argument where the relevant property of this matching is needed is in the proof of Lemma 3(i), and it is indeed merely maximality that is required. A maximal matching can be found in $O(a)$ time, and all other parts of the algorithm are merely variants of the Gale-Shapley algorithm. It is not hard to show that these can also be implemented to run in $O(a)$ time (see [4]).

Tightness of the approximation guarantee

This is the tightest bound that can be established for Algorithm SSMTI-APPROX. Figure 5 shows an example where the ratio of $|M|$ to $|A|$ is $\frac{8}{5}$. The matching $M = \{(m_1, w_5), (m_2, w_6), (m_3, w_7), (m_4, w_8), (m_5, w_1), (m_6, w_2), (m_7, w_3), (m_8, w_4)\}$ is a maximum cardinality stable matching of size 8, whereas if ties are broken simply by removing the parentheses, the algorithm returns matching $A = \{(m_1, w_2), (m_2, w_3), (m_3, w_5), (m_4, w_6), (m_8, w_1)\}$, of size 5. By duplicating this pattern, we can obtain arbitrarily large instances realising the $\frac{8}{5}$ ratio.

Men's preferences	Women's preferences
$m_1 : w_5 \ w_2$	$w_1 : m_3 \ (m_8 \ m_5)$
$m_2 : w_6 \ w_3$	$w_2 : m_1 \ m_6$
$m_3 : w_5 \ w_7 \ w_8 \ w_1$	$w_3 : m_2 \ m_7$
$m_4 : w_6 \ w_8 \ w_7 \ w_4$	$w_4 : m_4 \ m_8$
$m_5 : w_1$	$w_5 : (m_3 \ m_1)$
$m_6 : w_2$	$w_6 : (m_4 \ m_2)$
$m_7 : w_3$	$w_7 : (m_4 \ m_3)$
$m_8 : w_1 \ w_4$	$w_8 : (m_3 \ m_4)$

Fig. 5. An instance of SSMTI with ratio $\frac{8}{5}$

Extension to Special HRT

In view of the fact that our study was motivated by practical applications of the HRT problem, it is important to note that we can obtain exactly the same $\frac{8}{5}$ performance guarantee for an analogous algorithm for the special case of HRT in which each hospital's preference list has a tie of length ≥ 1 at the end. Full details of the extended algorithm and a correctness proof can be found in [10].

3 Summary and Open Problems

We have described a polynomial-time approximation algorithm with a performance guarantee of $\frac{8}{5}$ for a maximum cardinality stable matching in NP-hard variants of the Stable Marriage and Hospitals/Residents problems that are of significant practical interest. We have also shown that this performance guarantee is the best that can be proved for the algorithm.

The most obvious open question to pursue is whether this or a similar approach can yield useful performance guarantees for more general versions of SMTI and HRT, for example when there can be a single tie at the end of the lists on both sides, or when the lists on one side can contain arbitrary ties.

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