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Department of Economics  
School of Economics and Management

# Pairwise Kidney Exchange with Blood-Group Incompatibility

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# Pairwise Kidney Exchange with Blood-Group Incompatibility<sup>☆</sup>

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## Abstract

Kidney transplants across the blood-group barrier are medically feasible even if blood-group compatibility is preferred from a medical point of view. However, these types of transplants are motivated by the fact that they help in increasing the number of kidney transplants with living donors. This paper investigates priority matchings in a pairwise kidney exchange problem where blood-group incompatibilities may be present. As a priority matching not necessarily is unique, it is from a medical point of view natural to select a priority matching where the number of blood-group compatible exchanges is maximized among all priority matchings. The main result demonstrates that this can be achieved by solving an appropriately defined maximum weight matching problem.

*Keywords:* pairwise kidney exchange, priority matchings, blood-group incompatibility.

*JEL Classification:* C78.

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## 1. Introduction

In a pairwise kidney exchange, two patients obtain living and compatible donors by swapping their own willing and living but incompatible donors. The key here is the notion of compatibility. This notion usually refers to two different compatibilities; blood-group (ABO) and tissue-type (HLA). Roth et al. (2005) discussed how to organize pairwise kidney exchanges based on a priority mechanism. In such mechanism, each patient is assigned a priority (e.g., based on “Panel Reactive Antibody” or “Match Probability”) and the basic idea is to maximize the number of kidney exchanges subject to the priority-order.

In a recent paper, Okumura (2014) revisited the priority mechanism and noted that the method introduced by Roth et al. (2005) is infeasible when the number of patient-donor pairs is “large” as all possible matchings must be listed and as there is no known method that achieves this task in polynomial time. To overcome this obstacle, Okumura (2014) provided a polynomial time method for identifying a priority matching. More explicitly, Okumura (2014) described the problem in terms of a graph where each vertex represents

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an incompatible patient-donor pair. Two vertices are connected in the graph if and only if a pairwise exchange is possible. Moreover, each edge is assigned a weight that equals the exact sum of the priorities of the two connected pairs. The situation is illustrated in Figure 1 for the case of five patient-donor pairs (numbered 1 to 5). For example, pairs 1 and 5 are connected which means that the donor of pair 1 (pair 5) is compatible with the patient of pair 5 (pair 1). Moreover, patient  $i$  (for  $i = 1, \dots, 5$ ) is assumed to have priority  $i$ , and, therefore, the weight attached to the edge connecting pairs 1 and 5 equals  $1 + 5 = 6$ , and so on. Given this graph structure, Okumura (2014) demonstrated that the problem of finding a priority matching is identical to solving the maximum weight matching problem associated to the graph. As any priority matching is Pareto efficient (Roth et al., 2005) and as any Pareto efficient matching is a maximum matching (Bogomolnaia and Moulin, 2004; Roth et al., 2005), the polynomial time method provided by Okumura (2014) thus generates a priority matching where, in addition, the maximum number of pairwise kidney exchanges can be performed. However, a priority matching need not be unique. In Figure 1, for example, there are two priority matchings;  $M = \{(1, 5), (2, 4)\}$  and  $M' = \{(1, 4), (2, 5)\}$ . Is there a good reason to select  $M$  or should  $M'$  be chosen? In this paper, we will argue that there are cases when one is better than the other.

It is well documented that blood-group incompatible kidney transplants are medically feasible (see, e.g., Shin and Kim, 2011). In Sweden, for example, the normal practice is to transplant kidneys across the blood-group barrier as long as there is no tissue-type incompatibility. From a medical point of view, however, blood-group compatibility is preferred, e.g., to avoid various medical treatments and procedures. However, if blood-group incompatible kidney transplants are performed, weakly more transplants will be conducted compared to the case when both types of compatibilities must be taken into consideration (this follows trivially as any transplant that is feasible when requiring blood-group and tissue-type compatibility also is feasible when only requiring tissue-type compatibility but not vice versa).<sup>1</sup> This is also the main argument for abandoning the requirement of blood-group compatibility in kidney transplants with living donors.

When kidney exchanges across the blood-group barrier are conducted, it also becomes important to distinguish between different priority matchings. More explicitly, suppose that the aim of a pairwise kidney exchange program is to find a priority matching given some priority-order. In this case, the method provided by Okumura (2014) can be adopted. However, if there are several priority matchings, as in the above example, it is from a medical point of view reasonable to select a priority matching where the number of blood-group compatible exchanges is maximized among all priority matchings. Suppose, for example, that only pairs 1 and 5 are blood-group compatible in the above example. It is then natural to select the priority matching  $M$  over matching  $M'$ . This paper provides a modification of the maximum weight matching problem proposed by Okumura (2014),

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<sup>1</sup>If, for example, the compatibilities in Figure 1 only reflect tissue-type compatibility, we know from the above that two pairwise exchanges can be performed, but if, for example, only pairs 1 and 5 are blood-group compatible, and blood-group compatibility is a requirement, only one pairwise exchange can be carried out.

and demonstrates that this modification always generates a priority matching where the number of blood-group compatible exchanges is maximized among all priority matchings.

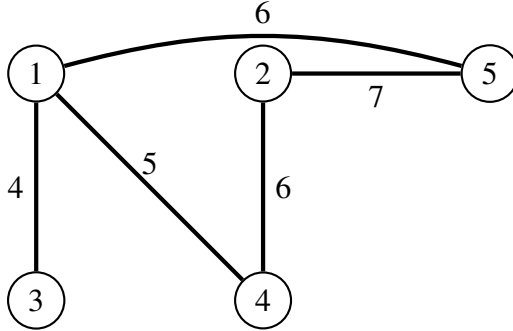


Figure 1: An example of a graph in a maximum weight matching problem.

## 2. The Model and Results

Let  $N = \{1, \dots, n\}$  be a finite set of *patients*. Each patient  $i \in N$  has a living but incompatible donor  $d_i$ . A donor  $d_j$  is *acceptable* for patient  $i$  if and only if donor  $d_j$  and patient  $i$  are tissue-type compatible (HLA), i.e., we are initially not interested in blood-group (ABO) compatibility. For any two patient-donor pairs,  $(i, d_i)$  and  $(j, d_j)$ , patients  $i$  and  $j$  are *compatible* if and only if donor  $d_j$  is acceptable for patient  $i$  and donor  $d_i$  is acceptable for patient  $j$ . As, e.g., Okumura (2014), we will present the problem as a *graph*  $g = (N, E)$  comprising a set  $N$  of *vertices* together with a set  $E$  of *edges*. An edge  $ij$  belongs to the graph  $g$  if and only if patients  $i$  and  $j$  are compatible. A subset of  $g$  is called a *subgraph*. A *matching*  $M$  is a subgraph of  $g$  such that for all  $i, j \in N$ , if  $ij \in M$ , then  $ik \notin M$  and  $jk \notin M$  for all  $k \in N \setminus \{i, j\}$ . Patient  $i$  is *matched* (*unmatched*) at matching  $M$  if  $ij \in M$  (if  $ij \notin M$ ) for exactly one  $j \in N$  (for all  $j \in N$ ). All matched patients at matching  $M$  are collected in the set  $N^*(M) \subseteq N$ . The set of all possible matchings is denoted by  $\mathcal{M}$ . A matching  $M$  is a *maximum matching* if  $|M| \geq |M'|$  for any matching  $M' \in \mathcal{M}$ .

The patients in  $N$  are ordered by a *priority-order*  $\pi$ . Patient  $i \in N$  have higher priority than patient  $j \in N$  if  $\pi(i) > \pi(j)$ . Throughout the paper, it is assumed that the priority  $\pi(i)$  for patient  $i \in N$  is given by a fraction of type  $\pi(i) = \frac{p(i)}{q}$  for some  $p(i) \in \{0, 1, \dots, p\}$  and some  $p, q \in \mathbb{N}_{++}$ . The interpretation is that all patients are assigned a priority that must take a value on a predetermined scale (note that  $p$  and  $q$  are fixed and equal for all patients).<sup>2</sup>

The (responsive) *priority preferences* are denoted by  $\succsim$  and are represented by a complete and transitive binary relation on the set of matchings  $\mathcal{M}$ . The corresponding strict

<sup>2</sup>All results are valid for any  $\pi(i) \in \mathbb{R}_{++}$  so the assumption on  $\pi(i)$  is made without loss of generality to get a “non-messy” upper bound on  $\varepsilon$  that is defined later in this section. A real-life example is when the priority is based on the PRA of the patients as PRA always is a fraction  $x/100$  for some  $x \in \{0, 1, 2, \dots, 100\}$ .

and indifference relations are denoted by  $\succ$  and  $\sim$ , respectively. More precisely,  $M \succ M'$  if  $N^*(M')$  is a strict subset of  $N^*(M)$  or:

$$N^*(M) = (N^*(M') \cup \{i\}) \setminus \{j\} \text{ and } \pi(i) > \pi(j). \quad (1)$$

Moreover,  $M \sim M'$  if condition (1) holds for  $\pi(i) = \pi(j)$ . A matching  $M$  is a *priority matching* if  $M \succeq M'$  for any matching  $M' \in \mathcal{M}$ . For a given graph  $g$ , all priority matchings are gathered in the set  $\mathcal{M}^*(g) \subseteq \mathcal{M}$ .<sup>3</sup>

Let  $w_{ij}$  be a *weight* assigned to each  $ij \in g$  and  $w = (w_{ij})_{ij \in g}$ , and define, for each matching  $M \in \mathcal{M}$ , the function:  $\lambda_{ij}(M) = 1$  if  $ij \in M$  and  $\lambda_{ij} = 0$  if  $ij \notin M$ . Let now  $S(M, w) = \sum_{ij \in g} w_{ij} \lambda_{ij}$ . Then, for any given  $(g, w)$ , a matching  $M$  is a *maximum weight matching* if and only if  $S(M, w) \geq S(M', w)$  for any matching  $M' \in \mathcal{M}$ .

**Theorem 1.** (Okumura, 2014, Theorem 2) Let  $w_{ij} = \pi(i) + \pi(j)$  for all  $ij \in g$ . Then, for any  $g$  and any  $\pi$ ,  $M$  is a priority matching if and only if  $M$  is a maximum weight matching in  $(g, w)$ .

Recall now that only tissue-type compatibility was included in the definition of compatibility. However, as explained in Section 1, if the aim of a pairwise kidney exchange program is to find a priority matching given some priority-order, it is natural from a medical point of view to pick a priority matching where the number of blood-group compatible exchanges is maximized. For this reason, define  $B(M)$  to be the number of pairwise blood-group compatible edges at matching  $M$ . It is clear that  $B(M) \subseteq M$ . Further, let  $M \in \mathcal{M}^B(g)$  if  $M \in \mathcal{M}^*(g)$  and if  $B(M) \geq B(M')$  for all  $M' \in \mathcal{M}^*(g)$ . Hence,  $\mathcal{M}^B(g)$  is the set of priority matchings where the number of blood-group compatible exchanges are maximized among all priority matchings. Our main result demonstrates how the weights  $w_{ij} = \pi(i) + \pi(j)$  can be modified to identify a matching in the set  $\mathcal{M}^B(g)$ . This modification will be based on the edge weights and not on the priorities as the priorities are patient specific (i.e., vertex specific) whereas the notion of blood-group (in)compatibility reveals something about the relation between two patient-donor pairs (i.e., two vertices) in a pairwise exchange, i.e., blood-group (in)compatibility is edge related. Let now  $\Delta \equiv \frac{1}{q}$  and  $0 < \varepsilon < \Delta/n$ . Define:

$$w_{ij}^\varepsilon = \begin{cases} \pi(i) + \pi(j) & \text{if patients } i \text{ and } j \text{ are blood-group incompatible} \\ \pi(i) + \pi(j) + \varepsilon & \text{if patients } i \text{ and } j \text{ are blood-group compatible,} \end{cases}$$

and  $w^\varepsilon = (w_{ij}^\varepsilon)_{ij \in g}$ . The following theorem states the result of this paper, i.e., by using the weights  $w^\varepsilon$  in the maximum weight matching problem, the outcome will always result in a priority matching where the number of blood-group compatible exchanges is maximized among all priority matchings. We also note that this outcome is a maximum matching.

**Theorem 2.** Let  $w_{ij} = \pi(i) + \pi(j)$  for all  $ij \in g$ , and let  $w^\varepsilon$  be defined as in the above. Then for any  $g$ ,  $M$  belongs to the set  $\mathcal{M}^B(g)$  if it is a maximum weight matching in  $(g, w^\varepsilon)$ .

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<sup>3</sup>This set may contain several matchings for a given  $g$ . This can be seen in the example in Section 1.

*Proof.* Suppose that  $M$  is a maximum weight matching in  $(g, w^\varepsilon)$ . We first demonstrate that  $M$  is a maximum weight matching in  $(g, w)$ . To obtain a contradiction, suppose that  $M$  is not a maximum weight matching in  $(g, w)$ . This means that there is some other matching  $M' \in \mathcal{M}$ , with  $\lambda'_{ij}$  defined accordingly, where  $S(M', w) > S(M, w)$ . By the construction of  $w$ , it is clear that:

$$S(M', w) - S(M, w) \geq \Delta. \quad (2)$$

We next note that  $w_{ij}^\varepsilon - w_{ij} \in \{0, \varepsilon\}$  for all  $ij \in g$  by construction of  $w$  and  $w^\varepsilon$ . Hence:

$$S(M, w^\varepsilon) - S(M, w) < \Delta. \quad (3)$$

$$S(M', w^\varepsilon) - S(M', w) \geq 0. \quad (4)$$

Adding conditions (2)–(4) yield:

$$S(M, w^\varepsilon) - S(M', w^\varepsilon) < 0,$$

which contradicts that  $M$  is a maximum weight matching in  $(g, w^\varepsilon)$ , i.e., that  $S(M, w^\varepsilon) \geq S(M', w^\varepsilon)$ . Hence,  $M$  is a maximum weight matching in  $(g, w)$  and, consequently, a priority matching by Theorem 1. Hence,  $M \in \mathcal{M}^*(g)$ .

It remains to prove that  $M \in \mathcal{M}^B(g)$ . To obtain a contradiction, suppose that  $M \notin \mathcal{M}^B(g)$ . Consider now a matching  $M'$  that belongs to  $\mathcal{M}^B(g)$ . As  $M' \in \mathcal{M}^B(g)$  and  $\mathcal{M}^B(g) \subseteq \mathcal{M}^*(g)$ ,  $M'$  is a maximum weight matching in  $(g, w)$  by Theorem 1. However, as demonstrated in the above,  $M$  is also a maximum weight matching in  $(g, w)$ . Hence,  $S(M, w) = S(M', w)$ . Because,  $M' \in \mathcal{M}^B(g)$  and  $M \notin \mathcal{M}^B(g)$ , by assumption, it is then clear from the construction of  $w^\varepsilon$  that  $S(M, w^\varepsilon) < S(M', w^\varepsilon)$  which contradicts the assumption that  $M$  is a maximum weight matching in  $(g, w^\varepsilon)$ . Hence,  $M \in \mathcal{M}^B(g)$ .  $\square$

**Corollary 1.** Let  $w_{ij} = \pi(i) + \pi(j)$  for all  $ij \in g$ , and let  $w^\varepsilon$  be defined as in the above. Then for any  $g$ ,  $M$  is a maximum matching if it is a maximum weight matching in  $(g, w^\varepsilon)$ .

*Proof.* From the proof of Theorem 2, we know that  $M$  is a maximum weight matching in  $(g, w)$ . Consequently,  $M$  is a priority matching by Theorem 1, and, therefore, a maximum matching by the results in Bogomolnaia and Moulin (2004) and Roth et al. (2005).  $\square$

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