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Pairwise Kidney Exchange over the Blood Group Barrier

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Advances in medical technology have made kidney transplants over the blood group barrier feasible. This article investigates how such technology should be implemented when designing pairwise kidney exchange programs. The possibility to receive a kidney transplant from a blood group incompatible donor motivates an extension of the preference domain, allowing patients to distinguish between compatible donors and half-compatible donors (*i.e.* blood group incompatible donors that only become compatible after undergoing an immunosuppressive treatment). It is demonstrated that the number of transplants can be substantially increased by providing an incentive for patients with half-compatible donors to participate in kidney exchange programs. The results also suggest that the technology is beneficial for patient groups that are traditionally disadvantaged in kidney exchange programs (*e.g.* blood group O patients). The positive effect of allowing transplants over the blood group barrier is larger than the corresponding effects of including altruistic patient–donor pairs or of allowing three-way exchanges in addition to pairwise exchanges.

Key words: Market design, Pairwise kidney exchange, Blood group incompatibility, Immunosuppressants, Half-compatibility priority matchings.

JEL Codes: C78, D02, D63, D78

1. INTRODUCTION

Since the pioneering work by Roth *et al.* (2004, 2005b) and the establishment of the first centralized multi-hospital kidney exchange program in New England in 2004, kidney exchange research has become an integral part of the market design literature. The research is motivated by the rapidly increasing shortage of kidneys[1] together with the key observation that even if

1. In the Unites States, for example, the number of patients on the waiting list for kidney transplantation increased from 22,063 to over 100,000 between 1992 and 2014 (Ellison, 2014).

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patients have access to living donors, they cannot always receive transplants due to medical incompatibilities. Kidney exchange programs facilitate transplantation for these patients by gathering them in exchange pools and by organizing centralized trades where incompatible patient–donor pairs exchange their kidneys with other pairs defined as medically compatible.[2]

The standard notion of medical compatibility in kidney exchange (adopted by, *e.g.*, Roth *et al.*, 2004, 2005a,b, 2007; Okumura, 2014; Saidman *et al.*, 2006; Sönmez and Ünver, 2014; Sönmez *et al.*, 2018) defines a patient and a donor as compatible if they are blood group and tissue type compatible. This article challenges this notion by considering a medical technology based on immunosuppressive protocols that enables kidney transplantation over the blood group barrier, *i.e.*, a technology that removes one of the two major sources for medical incompatibility. The extended compatibility notion allows patient–donor pairs to also be classified as half-compatible, meaning that a patient can receive a kidney from the donor only by crossing the blood group barrier. As demonstrated in this article, this seemingly small extension of the standard kidney exchange model will have large positive welfare effects for patients in need of transplantation if utilized correctly.

Following, *e.g.*, Roth *et al.* (2005b) and Sönmez and Ünver (2014), the analysis in this article is restricted to kidney exchange programs that only allow for pairwise exchanges. This was initially the case in the United States and it is the current practice in, for example, France, India, Italy, and Sweden.[3] The point of departure in the welfare analysis is a model, referred to as the Benchmark Model, in which transplantation over the blood group barrier is either *not allowed* or not an option considered by the transplant community. The Benchmark Model describes the standard kidney exchange model in the theoretical literature analysed in, *e.g.*, all of the above-cited papers. Note also that in, *e.g.*, Belgium, France, India, Italy, The Netherlands, Poland, and Portugal, transplantation over the blood group barrier is not allowed *within* their corresponding exchange programs. The article attempts to investigate how the availability of a medical technology that enables transplantation over the blood group barrier affects patient welfare in exchange programs. To investigate this, it is noted that the technology can be utilized in two different ways and these specific ways can be described and analysed in two different "models". Both these models *allow* for transplantation across the blood group barrier *within* the exchange program as in, *e.g.*, Austria, the Czech Republic, Spain, the United Kingdom, Sweden, and Switzerland.

In the first model, referred to as Model (a), patients with half-compatible donors receive kidneys from their own donors over the blood group barrier and are therefore not part of the kidney exchange program. Consequently, the kidney exchange pool consists exclusively of incompatible patient–donor pairs. Kidney exchanges over the blood group barrier are, however, allowed within the exchange program. This is in line with current practice in, *e.g.*, Sweden, where patients that can feasibly receive kidneys from their own donors over the blood group barrier are routinely referred to immunosuppressive treatments outside the kidney exchange program.[4] In fact, a recent paper by Biró *et al.* (2019) concludes that a key challenge reported by all European countries is immunosuppressive treatments outside of organized kidney exchange programs. It can therefore be argued that Model (a) is a fair description of the programs in Austria, the Czech Republic,

2. For an overview of the development of kidney exchange programs in the United States and Europe, see Anderson *et al.* (2015), Biró *et al.* (2017, 2018, 2019), and Sönmez and Ünver (2014).

3. All references to European kidney exchange programs in the remaining part of this section are from Biró *et al.* (2017, 2019). For the considered Indian program, see Jha *et al.* (2015).

4. Patients with half-compatible donors are strictly speaking not prohibited from participating in kidney exchange in Sweden but the option is routinely not presented to them. As far as we know, only one such pair participated in the Swedish program in the years 2017–8.

Spain, the United Kingdom, and Switzerland, where transplants over the blood group barrier are allowed within their corresponding exchange programs.[5]

In the second model, referred to as Model (b), all patients with either half-compatible or incompatible donors participate in the kidney exchange program. To the best of our knowledge, no such program currently exists in the world. As will be explained in more detail in Section 2, it is natural to assume that patients strictly prefer compatible donors to half-compatible donors, *e.g.*, to avoid additional medical treatments or to shorten the time to transplantation. Consequently, to ensure that patients with half-compatible donors have an incentive to participate in Model (b), it is reasonable to restrict the feasible exchanges for these patients to exchanges with compatible donors. Note also that patients with half-compatible donors that are included in the exchange pool, as in Model (b), but remain unmatched after the match run can always receive transplants over the blood group barrier from their own half-compatible donors. In this sense, patients with half-compatible donors are, in Model (b), always first given the possibility to receive a compatible kidney within the exchange framework. This possibility is never presented to patients in Model (a).

The theoretical findings in this article indicate that Model (b) always generates a weakly larger number of transplants than both the Benchmark Model and Model (a). Somewhat surprisingly, the theoretical results also reveal that the number of transplants need not be higher in Model (a) than in the Benchmark Model. In other words, if transplantation over the blood group barrier is implemented as in Model (a), it may actually reduce the number of transplants. These theoretical findings suggest that if the objective of a kidney exchange program is to maximize the number of transplants, then any program corresponding to the Benchmark Model or Model (a) should be redesigned in accordance with Model (b). The magnitudes of the theoretical findings are evaluated by means of a simulation study that, in addition, also investigates whether certain patient groups are proportionally disadvantaged by the technology enabling transplants over the blood group barrier, *e.g.*, patients with incompatible donors or patients with blood group O (it is well-known that blood group O patients are often proportionally disadvantaged in kidney exchange programs, see, *e.g.* Roth *et al.*, 2007). This exercise further strengthens the arguments in favour of Model (b). In particular, if the technology is utilized as in Model (b), there is a large spill over to patients with incompatible donors since they also receive transplants more frequently.

To put the medical technology enabling transplantation over the blood group barrier to the test, the simulation study also compares Models (a) and (b) to two other models that have design features that are known to substantially increase the number of transplants. These are the Altruistic Model (Roth *et al.*, 2005a; Sönmez and Ünver, 2014) in which compatible patient–donor pairs participate in the kidney exchange program, and the Cycle Model (Saidman *et al.*, 2006; Roth *et al.*, 2007) which allows for three-way exchanges in addition to pairwise exchanges. The simulation study reveals that the positive effect on the mean number of transplants is significantly larger for Models (a) and (b) than for the Altruistic Model and the Cycle Model. In addition, blood group O patients are on average less disadvantaged.

Even though the conclusions above suggest that a transition to Model (b) would improve patient welfare, it should be noted that when half-compatibility is introduced, the preference domain of the patients is extended from the dichotomous to the trichotomous domain. As can be expected from findings in the literature (*e.g.* Sönmez, 1999; Nicoló and Rodríguez-Álvarez, 2012), the domain extension makes it possible for some patients to manipulate any maximal matching mechanism to their advantage. Thus, half-compatibility introduces a trade-off between welfare improvements and incentives. However, the simulation results reveal that, depending on the pool size, between 6.2% and 15.9% of the patients can manipulate Model (a), but only between

5. Note, however, that some of these programs allow for larger cyclical exchanges.

1.9% and 8.5% of the patients can manipulate Model (b). Hence, Model (b) performs better than Model (a) in this respect as well. Here, it should also be noted that manipulation attempts are risky for patients because if they are unsuccessful, the patients will not receive any transplants at all. In this sense, an attempt to manipulate the outcome of the mechanism may ultimately come at the cost of the patient's own life.

1.1. *Related literature*

After the establishment of the kidney exchange program in New England 2004, new design features such as non-simultaneous extended altruistic donor chains (Roth *et al.*, 2006) and larger cyclic exchanges (Saidman *et al.*, 2006; Roth *et al.*, 2007) were suggested in the literature and added to existing exchange programs. One of the most important insights from the early literature is that a clever method for increasing the number of transplants in existing kidney exchange programs is to increase the number of participating patient–donor pairs. This can be achieved in a number of different ways. For example, Roth *et al.* (2005a) advocate the inclusion of patients with compatible donors, as this would generate "the largest patient welfare gains in comparison to a number of other design modifications" (Sönmez and Ünver, 2014, p. 108). Considering that the participation of compatible pairs is purely altruistic, one may wish to minimize the number of compatible pairs involved in exchanges. This is the idea in Sönmez and Ünver (2014), where a pairwise kidney exchange problem with both compatible and incompatible patient–donor pairs is investigated. They introduce Pareto efficient matchings that maximize the number of transplants while minimizing participation of compatible pairs.

A crucial assumption in Sönmez and Ünver (2014) is that patients are indifferent between compatible donors. This assumption can be supported by medical practice in the United States, as the general tendency among U.S. doctors is to assume that two compatible living donor kidneys essentially have the same survival rates (Gjertson and Cecka, 2000; Delmonico, 2004; Sönmez and Ünver, 2014). A recent paper by Nicoló and Rodríguez-Álvarez (2017) also focuses on the inclusion of compatible pairs in kidney exchange programs. Based on a number of medical studies (*e.g.* Gentry *et al.*, 2007; Øien *et al.*, 2007), they argue that the age and general health status of a donor impacts graft survival. Given this observation, patients in their model have strict preferences over compatible donors based on kidney age. This provides an incentive for compatible pairs to participate in exchange programs as the patient may be assigned a different, strictly preferred donor. As already explained above and in similarity with Sönmez and Ünver (2014) and Nicoló and Rodríguez-Álvarez (2017), this article also considers exchanges involving "compatible pairs". However, their participation is not motivated by altruism or the possibility to receive a preferred kidney in terms of age. Instead, the main argument rests, as in Chun *et al.* (2015), on recent developments in immunosuppressive protocols and, more specifically, on the possibility to transplant kidneys over the blood group barrier (see Section 2 for a description of the immunological conditions and the medical requirements for transplantation across the blood group barrier). This also motivates the extension of the compatibility concept to also include half-compatibility.

The inclusion of half-compatible patient–donor pairs in a kidney exchange program plays a similar role to the inclusion of compatible pairs, as the inclusion increases the size of the patient–donor pool. However, these patients have an incentive beyond altruism to participate since they may be assigned a compatible donor and thereby avoid transplantation over the blood group barrier. Due to the distinction between compatible and half-compatible donors, some standard results in the literature will not continue to hold. For example, Roth *et al.* (2005b) consider a pairwise kidney exchange problem with no transplantation over the blood group barrier and introduce a class of Pareto efficient matchings called priority matchings (see Appendix A.2).

However, priority matchings are no longer Pareto efficient in settings that distinguish between compatible and half-compatible donors. For this reason, a specific subset of priority matchings is introduced in this article. They are called half-compatibility priority matchings and are guaranteed to be Pareto efficient. The article also provides a computationally efficient method for identifying such matchings.

The two papers that are most closely related to this article are Chun *et al.* (2015) and Sönmez *et al.* (2018). The former of these papers considers a kidney exchange program where transplants can be carried out over immunological barriers (both blood group and tissue type). In their model, it is assumed that patients are indifferent between crossing the immunological barrier and not crossing it and that cyclic exchanges of arbitrary length are possible. To reflect that there is a limited availability of immunosuppressants in South Korea, Chun *et al.* (2015) assume that at most k patients are allowed to use immunosuppressants. For each kidney exchange problem, they first determine which patients are to receive immunosuppressants. Based on this selection and the compatibility structure, a matching is chosen. Their counterfactual analysis shows that the current use of immunosuppressants in South Korea can be reduced by 55%.

Sönmez *et al.* (2018) analyse a recent change in the United States where kidneys are transplanted over the blood group barrier using advanced blood subtyping. This new method allows a fraction of blood group A kidneys to be safely transplanted into a fraction of blood group B and O patients. Given their assumptions, Sönmez *et al.* (2018) demonstrate that the current implementation of this technology has some unintended consequences in the sense that it reduces the number of transplants from living donors, both in the overall population and for certain biologically disadvantaged groups. Their main results show that these unintended problems can be solved by making two small adjustments to the current practice. They suggest the establishment of an anti-A titre level history for blood group O patients and a delay in the subtyping tests until incompatible pairs are transferred to the kidney exchange pool.

1.2. *Outline of the article*

The remaining part of the article is outlined as follows: Section 2 provides a description of the immunological conditions and the medical requirements that enable transplantation across the blood group barrier. The formal kidney exchange framework is introduced in Section 3. Section 4 provides some properties of half-compatibility priority matchings and presents a computational method for finding them. Section 5 analyses the welfare implications of pairwise kidney exchange over the blood group barrier, both theoretically and by means of a simulation study. Section 6 concludes the article. Appendix A provides an equivalence between the set of priority matchings as defined in this article and the set of priority matchings as defined by Roth *et al.* (2005b), and some technical results relating to the matroid structure of pairwise kidney exchange problems. Appendix B contains the proofs of the theoretical results.

2. MEDICAL DETAILS OF BLOOD GROUP INCOMPATIBLE TRANSPLANTATION

This section provides a brief description of the ABO blood group classification system and a medical technology that enables transplantation across the blood group barrier. Throughout this section, the reader should keep in mind that transplantation across the blood group barrier is a medical reality not only in "regular" transplantation, but also within kidney exchange frameworks. As described in Section 1, European countries like Austria, the Czech Republic, Spain, the United Kingdom, Sweden, and Switzerland already use this technology within their exchange programs.

The central principle in the ABO blood group system is that antigens on red blood cells differ between individuals. Since there are two possible antigens (A and B), there are four possible

red blood cell types (or blood groups); O, A, B, and AB, where O is standard notation for the absence of antigen A and B. A patient who only has antigen A (antigen B) cannot produce anti-A antibodies (anti-B antibodies) and will therefore only have anti-B antibodies (anti-A antibodies) in her blood plasma. For a patient to be blood group compatible with a donor, the patient must not have anti-A or anti-B antibodies in the plasma that correspond to the A or B antigens in the donor's red blood cells. Consequently, a patient with red blood cell type A (type B) is only blood group compatible with donors that have red blood cell types A and O (types B and O). Patients with red blood cell type O have neither antigen A nor antigen B while carrying both antibodies, and patients with red blood cell type AB have both antigens while carrying neither antibody. Hence, red blood cell type O patients are only blood group compatible with donors that have red blood cell type O, whereas red blood cell type AB patients are blood group compatible with all donors independently of their red blood cell types.

The incompatibilities between some blood groups clearly impose restrictions on organ transplantation as the patient's immune system rejects kidneys from incompatible blood groups. However, immunosuppressive protocols for removing anti-A and/or anti-B antibodies, also known as desensitization, have been known since the 1970s (Alexander *et al.*, 1987). By removing antibodies, these protocols make transplants over the blood group barrier feasible. In 2001, the blood group antigen-specific filter GlycoSorb was introduced (Rydberg *et al.*, 2005). This filter absorbs specific antibodies with the purpose of reducing the patient's antibody level below a certain threshold in order to enable transplantation over the blood group barrier. The antibody level (antibody titre) is determined by a blood serum sample and is diluted in serial ratios (1:1, 1:2, 1:4, 1:8, 1:16, 1:32, …). Using an appropriate detection method, each dilution is tested for the presence of detectable levels of the antibody of interest. If the level of anti-A and/or anti-B antibodies in a patient's blood is below a threshold value after the filtering process and over a given period of time, a transplant over the blood group barrier is feasible. In Sweden, for example, the threshold is set to 1:32 and the time period is typically set between three and six months.[6,7] GlycoSorb is currently used in all Swedish transplant centres and at least 60 European centres spread across 17 countries. Between 2001 and 2012, more than 200 living donor kidney transplants over the blood group barrier were carried out in Sweden using this filter (Thydén *et al.*, 2012).

There are no medical reasons related to graft and/or patient survival for not using GlycoSorb to conduct transplants over the blood group barrier. In fact, the GlycoSorb filtering process is completely non-toxic (as opposed to non-specific plasma exchange). Moreover, the five-year graft survival rate and patient survival rate for living donor kidney transplants across the blood group barrier are identical to the corresponding five-year survival rates for "normal" blood group compatible living donor kidney transplants (Thydén *et al.*, 2007). Even though these arguments speak in favour of using this medical technology, there are also good reasons for not transplanting kidneys across the blood group barrier whenever alternative transplantation opportunities exist, *e.g.*, if patients have alternative compatible donors available or if it is possible

6. These numbers were communicated to one of the authors of this article (Andersson) at a meeting in Stockholm (March, 2016) with immunologists and transplant surgeons from the four Swedish transplant centres (Karolinska institutet, Akademiska sjukhuset, Sahlgrenska sjukhuset, and Skånes universitetssjukhus). In the United States, for example, a threshold of 1:8 must be maintained for six months before the transplant (Sönmez *et al.*, 2018).

7. The authors of this article are unaware of any studies that report the share of patients that can feasibly receive kidneys over the blood group barrier. Peter S. Björk at the "Immunotherapy Unit" at "Skånes universitetssjukhus" stated, in a telephone conversation with one of the authors (Andersson) in May 2016, that approximately 90% of patients can receive kidneys over the blood group barrier whenever the donor is tissue type compatible. Furthermore, Thydén *et al.* (2004) report that all patients in their sample with a titre value of at most 1:128 who were treated with GlycoSorb successfully received transplants over the blood group barrier and evidence in Dallaval *et al.* (2011) suggests that 86.9% of all blood donors with blood group O had antibody titre values strictly below 1:128.

to obtain kidneys from compatible donors by means of exchange. By taking advantage of such alternative transplantation opportunities, additional medical treatments before and after the transplant can be avoided, time to transplantation can be shortened and costs related to the purchase of immunosuppressants can be reduced.

Finally, we note that it can be argued that there are no cost–benefit reasons for not using GlycoSorb.[8] In Sweden, for example, the alternative to a transplant is to keep the patient on dialysis at an annual cost of SEK 650,000. The costs of the surgical procedure and the immunosuppressive protocol are SEK 2,000,000 and SEK 100,000, respectively. Hence, it only takes around three years to reach parity in expenses. In addition, sick leave costs are reduced as the patients no longer need to be on dialysis and patients often experience an increased quality of life after transplantation (Pinson *et al.*, 2000). Similar evidence can be found in, *e.g.*, the United States. In a recent debate article in the Washington Post, Cartwright and Roth (2018) concluded that a kidney transplant "pays for itself in less than two years".

3. THE MODEL

This section introduces the basic ingredients of the kidney exchange model together with a number of important concepts and definitions.

3.1. *Agents, preferences and priorities*

Let $N=\{1,\ldots,n\}$ be a finite set of *patients* participating in a kidney exchange program. Each patient $i\in N$ has a living *donor* d_i. Patient i is *compatible* with donor d_j if patient i can receive a kidney from donor d_j without crossing the blood group barrier. Patient i is *half-compatible* with donor d_j if patient i can receive a kidney from donor d_j only by crossing the blood group barrier. Patient i is *incompatible* with donor d_j if patient i cannot receive a kidney from donor d_j under any circumstances. No patient in N is compatible with her own donor since patients with compatible donors are assumed to receive kidneys from their own donors outside the kidney exchange program (except in Section 5.2). The patients in N are partitioned into two disjoint sets: N_H and N_I. A patient i belongs to N_H if and only if she is half-compatible with her own donor d_i. N_I thus contains all patients who are incompatible with their own donors. The *compatibility structure* C describes the compatibility between patient i and donor d_j for any patients $i,j\in N$.

For any patient $i\in N$, let $\succsim_i$ denote the patient's preferences over the set of donors. Let $\succ_i$ and $\sim_i$ denote the corresponding strict preference and indifference relations, respectively. Each patient in N strictly prefers any compatible donor to all half-compatible and incompatible donors, and any half-compatible donor to all incompatible donors. Each patient $i\in N$ is indifferent between two donors (not including d_i) whenever both are compatible or both are half-compatible with i. Patients in N_H also strictly prefer their own donors to all other half-compatible donors. Formally, for any $i,j\in N$ and any $k,l\in N\setminus\{i\}$:

- $d_k\sim_i d_l$ if d_k and d_l are either both compatible or both half-compatible with i,
- $d_k\succ_i d_j$ if i is compatible with d_k and half-compatible or incompatible with d_j,
- $d_k\succ_i d_j$ if i is half-compatible with d_k and incompatible with d_j,
- $d_i\succ_i d_k$ if $i\in N_H$ and i is half-compatible with d_k.

8. The figures in this paragraph are based on Swedish data and they can be found in Thydén *et al.* (2012) and Wennberg (2010). SEK 1 = USD 0.11 (February, 2019).

The preferences of all patients in N are gathered in the list $\succsim := (\succsim_i)_{i\in N}$. Many existing kidney exchange programs give priority to patients that are highly HLA-sensitized (i.e, patients that are highly sensitized to Human Leukocyte Antigents), since it is particularly difficult to find compatible donors for such patients (see, *e.g.*, Biró *et al.*, 2017). As in Roth *et al.* (2005b), this is modelled by a *priority function* $\pi : N \to \mathbb{R}_{++}$ assigning each patient $i \in N$ a unique *priority* $\pi(i)$.[9] Patient i has *higher priority* than patient j whenever $\pi(i) > \pi(j)$. It is assumed that the priority $\pi(i)$ of each patient $i \in N$ is given by a fraction of the type $\pi(i) = \frac{p(i)}{q}$ for some $p(i) \in \{1, \ldots, p\}$ and some $p, q \in \mathbb{Z}_{++}$, where p and q are fixed and equal for all patients. The interpretation of this assumption is that all patients are assigned a priority that takes a value on a predetermined scale (based on, *e.g.*, Panel Reactive Antibody scores or some other measure of HLA-sensitization).[10] A kidney exchange *problem* is defined as a triple (N, C, π) and will, with a few exceptions, be held fixed throughout most of the article.

3.2. *Matchings and properties of matchings*

A *pairwise* kidney exchange between pairs (i, d_i) and (j, d_j) is *feasible* if and only if $d_j \succ_i d_i$ and $d_i \succ_j d_j$. That is, whenever both patients strictly benefit from the exchange. For a given problem (N, C, π), a matching M consists of (i) a set of mutually exclusive feasible pairwise exchanges and (ii) a set of patients in N_H that do not participate in any kidney exchanges. Informally, patients may either receive a transplant (i) through a kidney exchange or (ii) from their own half-compatible donors. A matching specifies which transplants to carry out. The set of all matchings for a given problem (N, C, π) is denoted by $\mathcal{M}$. For any matching M, patients that receive a transplant are said to be *matched* and patients that receive kidneys from their own half-compatible donors are said to be *self-matched*. A patient that does not receive a transplant is said to be *unmatched*. If patient i receives a kidney from donor d_j at a matching M, patient i is said to be *matched to* both j and d_j at M. All patients that are matched at a matching M are collected in the set $N^*(M)$. The number of transplants at a matching M is therefore given by the cardinality of $N^*(M)$, *i.e.*, by $|N^*(M)|$.

A matching $M \in \mathcal{M}$ is a *maximal matching* if $N^*(M)$ is not properly contained in the set $N^*(M')$ for any other matching $M' \in \mathcal{M}$, *i.e.*, if $N^*(M) \not\subset N^*(M')$ for all $M' \in \mathcal{M}$. A matching $M \in \mathcal{M}$ is a *maximum matching* if it maximizes the number of transplants over all matchings in $\mathcal{M}$, *i.e.*, if $|N^*(M)| \geq |N^*(M')|$ for all $M' \in \mathcal{M}$. For any matchings $M, M' \in \mathcal{M}$, matching M *Pareto dominates* matching M' if, according to the preferences $\succsim$, all patients in N weakly prefer the donors they are matched to at M to the donors they are matched to at M' with at least one strict preference. A matching in $\mathcal{M}$ is *Pareto efficient* if it is not Pareto dominated by any other matching in $\mathcal{M}$.

3.3. *Priority matchings and half-compatibility priority matchings*

There is a *planner* (or a market designer) with complete, transitive, and responsive *preferences* $\succsim_B$ over matchings in $\mathcal{M}$. Let $\succ_B$ and $\sim_B$ denote strict preference and indifference, respectively. A matching M is strictly preferred to a matching M' if all patients matched at M' are also matched at M and some patients not matched at M' are matched at M. Moreover, M is strictly preferred to M' if the set of patients matched at M can be obtained from the set of patients matched at M'

9. $\mathbb{R}_+$ and $\mathbb{R}_{++}$ denote the set of non-negative real numbers and the set of positive real numbers, respectively. The same convention applies to the set of integers, $\mathbb{Z}$.

10. This assumption on $\pi(i)$ is made without loss of generality to get a "non-messy" upper bound on the constant ε defined in Section 4.2. All results presented in the article hold for any $\pi(i) \in \mathbb{R}_{++}$ as long as the priorities are unique.

by replacing some patient matched at M' with some patient with higher priority matched at M. Finally, given that the planner distinguishes compatible donors from half-compatible donors, it is reasonable for the preference relation $\succsim_B$ to somehow separate the two notions of compatibility. For this purpose, let $B(M)$ denote the number of patients that are matched to compatible donors at matching M. Formally, a preference relation $\succsim_B$ belongs to a class of preferences called *half-compatibility priority preferences* if it is complete, transitive, and satisfies the following conditions:

$$M \succ_B M' \text{ if } \begin{cases} N^*(M') \subset N^*(M), \\ N^*(M) \setminus N^*(M') = \{i\}, N^*(M') \setminus N^*(M) = \{j\} \text{ and } \pi(i) > \pi(j), \\ N^*(M) = N^*(M') \text{ and } B(M) > B(M'), \end{cases} \tag{3.1}$$

$$M \sim_B M' \text{ if } N^*(M) = N^*(M') \text{ and } B(M) = B(M'). \tag{3.2}$$

Half-compatibility priority preferences are closely related to the *priority preferences* introduced by Roth *et al.* (2005b). In fact, a preference relation $\succsim_\pi$ is a priority preference relation if it satisfies all of the conditions above, given that (3.2) and the last line in (3.1) have been replaced by a requirement that the planner always be indifferent between M and M' whenever $N^*(M) = N^*(M')$.[11] The only difference between priority preferences and half-compatibility priority preferences is that whenever the same patients are matched at two different matchings, a planner with priority preferences is indifferent between the two matchings whereas a planner with half-compatibility priority preferences prefers the matching that minimizes the number of transplants over the blood group barrier. Note that $N^*(M) = N^*(M')$ implies that $B(M) = B(M')$ in models where transplantation over the blood group is either disallowed or not considered an option by the transplant community. Hence, the two classes of preferences coincide in such settings.

Consider some priority preferences $\succsim_\pi$ and some half-compatibility priority preferences $\succsim_B$. A matching M is called a *priority matching* if $M \succsim_\pi M'$ for every matching $M' \in \mathcal{M}$. For a given problem (N, C, π), all priority matchings are gathered in the set $\mathcal{M}^* \subseteq \mathcal{M}$. A matching M is called a *half-compatibility priority matching* if $M \succsim_B M'$ for every matching $M' \in \mathcal{M}$. For a given problem (N, C, π), all half-compatibility priority matchings are gathered in the set $\mathcal{M}^B$.

4. PROPERTIES OF HALF-COMPATIBILITY PRIORITY MATCHINGS

This section is divided into two parts. The first part discusses the properties of half-compatibility priority preferences and half-compatibility priority matchings. The second part provides a computational method based on graph theoretical techniques that can be used to find half-compatibility priority matchings.

4.1. *Properties*

A first observation is that the definition of half-compatibility priority preferences does not induce a unique preference relation. For a given problem, there may be multiple half-compatibility priority preference relations. A natural question is then whether the set of half-compatibility priority matchings $\mathcal{M}^B$ depends on the choice of preference relation $\succsim_B$. Fortunately, the following result reveals that $\mathcal{M}^B$ remains the same for any choice of half-compatibility priority preference relation $\succsim_B$.

11. See Appendix A.2 for a detailed discussion.

Proposition 1. For a given problem (N, C, π), all half-compatibility priority preference relations induce the same set of half-compatibility priority matchings.

Consider some matching mechanism that, for every problem (N, C, π), makes use of some half-compatibility priority preference relation to locate a half-compatibility priority matching M. Proposition 1 then guarantees that M is a half-compatibility priority matching for all half-compatibility priority preferences (such a mechanism is described in Section 4.2). Proposition 1 is closely related to the observation in Roth *et al.* (2005b, Corollary 1) that any priority matching (defined differently) is weakly preferred to every other matching by any priority preference relation. It is established in Appendix A.2 that the definition of priority matchings in this article is equivalent to the definition in Roth *et al.* (2005b) and that Corollary 1 in Roth *et al.* (2005b) can be extended to a biconditional statement both in settings with and without transplantation over the blood group barrier. Given the following result, it is not surprising that priority matchings and half-compatibility priority matchings share many properties.

Proposition 2. For a given problem (N, C, π), every half-compatibility priority matching is a priority matching.

Half-compatibility priority matchings can therefore be thought of as the subset of priority matchings that minimize the number of transplants over the blood group barrier. If patients do not distinguish between compatible and half-compatible matchings, then every maximal matching is Pareto efficient. Since priority matchings are maximal by construction, they are always Pareto efficient in such settings (Roth *et al.*, 2005b).[12] However, priority matchings are no longer necessarily Pareto efficient when transplantation over the blood group barrier is possible. The next result shows that, contrary to priority matchings, half-compatibility priority matchings are guaranteed to be Pareto efficient. Furthermore, half-compatibility priority matchings (and priority matchings) maximize the number of transplants.

Proposition 3. For a given problem (N, C, π), every half-compatibility priority matching is a Pareto efficient maximum matching.

Proposition 3 is silent about how the technology enabling transplantation over the blood group barrier is implemented. The result merely states that if a matching is a half-compatibility priority matching in a *given* problem, then it is Pareto efficient and a maximum matching in that *particular* problem. As will be discussed in Section 5, immunosuppressants can be introduced in a kidney exchange program by finding a half-compatibility priority matching for the patients in N_I and self-matching all the patients in N_H. Then the outcome may not be Pareto efficient or maximize the number of transplants when considering *all* patients in N (see Proposition 7). However, Proposition 3 still implies that the matching is a Pareto efficient maximum matching in the reduced problem containing only the patients in N_I.

Another implication of Proposition 3 is that all half-compatibility priority matchings result in the same number of transplants, *i.e.*, $|N^*(M)| = |N^*(M')|$ for all $M, M' \in \mathcal{M}^B$, since all maximum matchings necessarily match the same number of patients. In fact, Proposition 4 shows that all priority matchings (including all half-compatibility priority matchings) match exactly the same patients.

12. To see that priority matchings are maximal matchings, suppose that $M \in \mathcal{M}$ is a priority matching that is not maximal. Then there exists some other matching $M' \in \mathcal{M}$ such that $N^*(M) \subset N^*(M')$. This implies that $M' \succ_\pi M$ which contradicts the assumption that M is a priority matching (*i.e.* that $M \succsim_\pi M''$ for all $M'' \in \mathcal{M}$).

Proposition 4. For a given problem (N, C, π), $N^*(M) = N^*(M')$ for all $M, M' \in \mathcal{M}^*$.

This result no longer holds if priorities are not required to be unique as in, *e.g.*, Okumura (2014). To see this, imagine a situation with three patient–donor pairs; pairs 1, 2, and 3. There is a feasible kidney exchange between pair 1 and pair 2, a feasible exchange between pair 2 and pair 3, but no feasible exchange between pair 1 and pair 3. If pair 1 and pair 3 have the same priority, then each of the two feasible exchanges constitutes a priority matching. Only one of them can be selected by the planner and depending on this selection, different patients will be matched.

Many of the results in this section relate to the structure of pairwise kidney exchange problems in particular. One important aspect of pairwise kidney exchange problems is that the set of all patients N and a family $\mathcal{I}$ containing all sets of patients that can be matched simultaneously constitute a *matroid* $(N, \mathcal{I})$. Such a structure ensures that every maximal matching is a maximum matching and that the same number of patients receive a transplant at every Pareto efficient matching. Thanks to this structure, the opportunity cost of matching a particular patient (*e.g.* a high-priority patient) will never be more than one patient (with lower priority) who could otherwise have been matched. Roth *et al.* (2005b) showed that the pairwise kidney exchange problem has a matroid structure when the compatibility structure is binary (no transplantation over the blood group barrier). Proposition 11 in Appendix A.1 demonstrates that this result continues to hold in settings that distinguish between compatibility and half-compatibility. This is not immediately obvious since self-matches alter the structure of the sets of simultaneously matchable patients.

A final remark is that the findings in this section provide justification for half-compatibility priority preferences. As argued in Section 2, there are good reasons for minimizing the use of immunosuppressants. Furthermore, as described in Biró *et al.* (2017), maximizing the number of transplants is an objective in all existing European kidney exchange programs and all these programs (except in Austria and the Czech Republic) also prioritize patients in accordance with their HLA-sensitization levels. A planner with half-compatibility priority preferences selects a matching from the set of half-compatibility priority matchings. Consequently, the use of immunosuppressants is minimized, the number of transplants is maximized and patients receive priority based on, *e.g.*, the degree of HLA-sensitization. In addition, the planner is guaranteed that any choice of half-compatibility priority preferences will result in the same set of half-compatibility priority matchings and that the same set of patients will receive transplants. The last point implies that a planner need not worry about the specific choice of half-compatibility priority preference relation affecting various groups in a diverse patient population differently.

4.2. *Identification of half-compatibility priority matchings*

Given the desirable properties of half-compatibility priority matchings discussed in the previous section, the main purpose of this section is to investigate how these matchings can be computed. In contrast to the iterative method for identifying priority matchings introduced by Roth *et al.* (2005b), the method considered in this section takes a graph theoretical approach. More specifically, it is demonstrated that half-compatibility priority matchings can be identified in polynomial time by solving a maximum weight matching problem. This maximization technique is, in similarity with many algorithms like, *e.g.*, the deferred acceptance algorithm (Gale and Shapley, 1962) and the top trading cycles mechanism (Shapley and Scarf, 1974), frequently adopted in the market design literature to solve various matching problems. For example, solution methods based on maximum weight matching problems have previously been applied to problems related to school choice (Kesten and Ünver, 2015), delegate pairings at meetings (Vaggi *et al.*, 2014), kindergarten placements (Biró and Gudmundsson, 2017), and

kidney exchange (Biró *et al.*, 2009). To describe this computational method, some graph theoretical notation needs to be introduced.

For any compatibility structure C, there exists a corresponding *compatibility graph* $g=(N,E)$ comprising a set N of *vertices* and a set E of *edges*. It will sometimes be convenient to let $N(g)$ and $E(g)$ denote the vertex set and the edge set, respectively, of the compatibility graph g. Every vertex in a compatibility graph corresponds to a patient in N. There is an edge between two patients $i,j\in N$ if and only if a pairwise exchange between the pairs (i,d_i) and (j,d_j) is feasible, and there is a *loop* at vertex $i\in N$ if and only if patient i is half-compatible with her own donor d_i. Let ij denote an edge between patients i and j and let ii denote a loop at patient i. Formally, the edges in a compatibility graph $g=(N,E)$ have the following construction:

- if $i,j\in N$ and $i\neq j$, then $ij\in E$ if and only if $d_j\succ_i d_i$ and $d_i\succ_j d_j$,
- if $i\in N$, then $ii\in E$ if and only if $i\in N_H$.

For any compatibility graph $g=(N,E)$, a matching $M\subseteq E$ can be defined as a set of edges in the graph that are not incident to each other. That is, for any edge $ij\in M$, it must be the case that $ik\notin M$ and $jk\notin M$ for all $k\in N\setminus\{i,j\}$. There is an edge $ij\in M$ for some $i,j\in N$, $i\neq j$, whenever the pairs (i,d_i) and (j,d_j) are involved in a pairwise kidney exchange. Moreover, $ii\in M$ for some $i\in N_H$ whenever i receives a kidney from her own donor. The non-incidence requirement on the edges ensures that each patient receives at most one kidney and each donor donates at most one kidney. This definition of a matching is thus equivalent to the definition given in Section 3.2.

A *weighted graph* (g,w) consists of a graph g and a set of *edge weights* $w:=(w_{ij})_{ij\in E(g)}$ where w_{ij} is a weight assigned to edge $ij\in E(g)$. Let (g,w) be a weighted graph and let $S(M,w):=\sum_{ij\in M}w_{ij}$ be the sum of all edge weights at matching $M\in\mathcal{M}$. A matching M is a *maximum weight matching* in (g,w) if $S(M,w)\geq S(M',w)$ for all $M'\in\mathcal{M}$. Okumura (2014) demonstrated that priority matchings can be found by solving an appropriately defined maximum weight matching problem.

Lemma 1. (Okumura, 2014, Theorem 2). Consider a problem (N,C,π) with corresponding compatibility graph g. Suppose that transplantation over the blood group barrier is not possible.[13] If $w_{ij}=\pi(i)+\pi(j)$ for all $ij\in E(g)$, then M is a priority matching if and only if M is a maximum weight matching in (g,w).

The maximum weight matching problem described in Lemma 1 is not directly applicable in the setting considered in this article since the result is based on the assumptions that patients cannot receive kidneys from their own donors (*i.e.* no loops in the compatibility graph) and that there is no distinction between compatible and half-compatible donors. However, the following theorem shows that even if these assumptions are relaxed, priority matchings can be identified by solving an almost identical maximum weight problem (the only difference being the presence of loops in the graph).

Proposition 5. Consider a problem (N,C,π) with corresponding compatibility graph g. If $w_{ii}=\pi(i)$ for all $ii\in E(g)$ and $w_{ij}=\pi(i)+\pi(j)$ for all $ij\in E(g)$ whenever $i\neq j$, then M is a priority matching if and only if M is a maximum weight matching in (g,w).

13. Each patient $i\in N$ is incompatible with her own donor and either compatible or incompatible with donor d_j for all $j\in N$.

Recall that the set of half-compatibility priority matchings is the subset of priority matchings that minimize the number of transplants over the blood group barrier. Hence, solving the maximum weight matching problem defined in Proposition 5 will not necessarily identify a half-compatibility priority matching. To address this issue, a modified maximum weight matching problem is presented, the solution to which is guaranteed to be a half-compatibility priority matching. Consider a problem (N, C, π) with corresponding compatibility graph g. Let $0 < \varepsilon < \frac{1}{2nq}$ and let the weights $w^\varepsilon := (w^\varepsilon_{ij})_{ij \in E(g)}$ for each $i, j \in N$ be defined by:

$$w^\varepsilon_{ij} = \begin{cases} \pi(i) + \pi(j) + v(i,j) + v(j,i) \text{ if } i \neq j \\ \pi(i) \text{ if } i = j, \end{cases}$$

where

$$v(i,j) = \begin{cases} \varepsilon & \text{if patient } i \text{ is compatible with donor } d_j \\ 0 & \text{otherwise.} \end{cases}$$

Proposition 6. Consider a problem (N, C, π) with corresponding compatibility graph g. Then a matching is a half-compatibility priority matching if and only if it is a maximum weight matching in (g, w^ε).

A solution to the maximum weight matching problem in Proposition 6 can be found in polynomial time by adopting the techniques in Edmonds (1965).

5. WELFARE IMPLICATIONS OF KIDNEY EXCHANGE OVER THE BLOOD GROUP BARRIER

This section analyses the consequences of introducing transplantation over the blood group barrier in kidney exchange programs. Even though the existence of some welfare effects can be proven theoretically, a simulation study is necessary to estimate their magnitudes. The section ends with an extended discussion on the possibility to manipulate the matching mechanisms induced by Model (a) and Model (b).

As a benchmark in the analysis, we will use a model with pairwise exchanges, in which transplants over the blood group barrier are either not allowed or not an option considered by the medical community (as in, *e.g.* Roth *et al.*, 2005b). It is then assumed that the technology enabling transplants across the blood group barrier gets implemented within kidney exchange programs, *e.g.*, due to new legislation allowing such transplants, awareness, or changes in the attitude towards immunosuppressants in the transplant community. This will have the consequence that patient and planner preferences will distinguish between compatible and half-compatible donors and matchings. Two distinct "models" are introduced to represent two different ways in which the planner can implement this technology within kidney exchange frameworks. Both models can be thought of as extensions to the Benchmark Model. Let (N_I, C_I, π) denote a *reduced problem* containing only the patients in N_I, where C_I denotes the compatibility structure between patients in N_I and donors of patients in N_I.[14]

14. With the exception of Section 5.2, patients with compatible donors are assumed to receive kidneys from their own donors outside kidney exchange programs throughout the article. Patients with compatible donors are therefore not included in any of the models described below.

- **Benchmark Model.** Transplants over the blood group barrier are either disallowed or not considered an option by the medical community. A priority matching is found for the problem (N, C, π).
- **Model (a).** The technology enabling transplants over the blood group barrier is adopted by the medical community. Patients in N_H (*i.e.* patients with half-compatible donors) are self-matched and do not participate in the kidney exchange program. A half-compatibility priority matching is found for the reduced problem (N_I, C_I, π).
- **Model (b).** The technology enabling transplants over the blood group barrier is adopted by the medical community. A half-compatibility priority matching is found for the problem (N, C, π).

Even though there are variations in rules, regulations, techniques, etc., that differentiate kidney exchange programs from each other, many existing programs can, in general terms, be categorized within our framework. The Benchmark Model is the standard model in the theoretical kidney exchange literature and it has been analysed by, *e.g.*, Roth *et al.* (2004, 2005a,b, 2007), Okumura (2014), Saidman *et al.* (2006), Sönmez and Ünver (2014), and Sönmez *et al.* (2018). Note also that the initial program in the United States (Roth *et al.*, 2005b) and the current practice in, *e.g.*, France, India, and Italy (Jha *et al.*, 2015; Biró *et al.*, 2019), only considered/consider pairwise exchanges and transplants over the blood group barrier *within* the existing exchange programs were/are *not allowed* or not considered an option by the medical community. The same holds in, *e.g.*, Belgium, the Netherlands, Poland, and Portugal, even if larger cyclical exchanges are allowed in these countries (Biró *et al.*, 2017, 2019).

Transplantation across the blood group barrier is, however, allowed in Model (a). This model corresponds to the current program in, *e.g.*, Sweden, where only pairwise exchanges are considered and patients with half-compatible donors receive kidneys from their own donors outside the exchange system. Although larger cyclic exchanges are allowed in, *e.g.*, Austria, the Czech Republic, Spain, the United Kingdom, and Switzerland, it can be argued that the exchange programs in these countries correspond to Model (a). Patients in these countries are routinely referred to desensitization treatments outside their respective exchange programs, even though transplants over the blood group barrier are allowed within their corresponding exchange frameworks (Biró *et al.*, 2017, 2019).

Model (b) also allows for transplantation across the blood group barrier. To the best of our knowledge, no country in the world has adopted an exchange program that corresponds to Model (b), *i.e.*, a program that includes *all* incompatible and *all* half-compatible patient–donor pairs in a common exchange pool. The main difference between Model (b) and Model (a) is that the exchange program in the latter model does not include patients with half-compatible donors. These patients are, in Model (a), always self-matched with their own donors and will therefore never be part of an exchange.

When transplantation over the blood group barrier is not a possibility, all priority matchings are half-compatibility priority matchings. This means that, by Proposition 3, the Benchmark model would always select Pareto efficient matchings. However, if blood group incompatible transplants are feasible, priority matchings are no longer necessarily half-compatibility priority matchings. In such settings, there are good reasons for a planner concerned with patient welfare to only select half-compatibility priority matchings, as in Model (a) and Model (b). The following example shows that priority matchings may be Pareto dominated by the matching half-compatibility matchings selected in Models (a) and (b).

Example 1. Suppose that $N = \{1, 2, 3, 4\}$, that each patient is incompatible with her own donor and that transplantation over the blood group barrier is permitted. Furthermore, suppose that

Patient 1 is compatible with donor d_2 and that no other patient is compatible with any other donor. A possible pairwise exchange between pairs (i, d_i) and (j, d_j) is denoted by ij and it is assumed that only the pairwise exchanges 12, 23, 34, and 14 are feasible.[15] In this case, matchings $M = \{12, 34\}$ and $M' = \{14, 23\}$ are both priority matchings since all patients receive transplants. However, only M is a half-compatibility priority matching since more patients are matched to compatible donors at M than at M'. Since Patient 1 strictly prefers donor d_2 to donor d_4 and all other patients are indifferent between M and M', it follows that M Pareto dominates M'. This demonstrates the importance of distinguishing between priority matchings and half-compatibility priority matchings and, as in Model (a) and Model (b), selecting matchings of the latter type. □

5.1. *Theoretical results*

A noteworthy difference between the Benchmark Model and Model (b) on the one hand and Model (a) on the other is that (half-compatibility) priority matchings are identified for the entire set of patients in the former two models, whereas Model (a) only selects a half-compatibility priority matching for the patients in N_I and self-matches the patients in N_H. Proposition 3 implies that the half-compatibility priority matching which patients in N_I are matched in accordance within Model (a) is a Pareto efficient maximum matching for the reduced problem (N_I, C_I, π). The matchings selected in the Benchmark Model and Model (b), on the other hand, are Pareto efficient maximum matchings for the problem (N, C, π) containing all patients in N (note that the matching selected in the Benchmark Model is only Pareto efficient under the constraint that transplantation over the blood group barrier is not possible).

By excluding the patients in N_H when identifying a half-compatibility priority matching in Model (a), the aggregate outcome, defined by the transplants outside the kidney exchange program and the transplants generated by exchanges within the exchange program, need not maximize the number of transplants or be Pareto efficient. Intuitively, this failure hinges on the use of immunosuppressants that enable patients with half-compatible donors to receive kidneys from their own donors outside the kidney exchange program. A planner implementing Model (a) not only denies patients with half-compatible donors the possibility to find a compatible donor within the exchange framework, but also shrinks the size of the patient–donor pool when self-matching all patients with half-compatible donors. This reduces the likelihood that patients with incompatible donors participate in pairwise exchanges since the set of patients they could be matched to is smaller.[16] The following result is proven with the help of an example that will also be useful later in this section.

Proposition 7. The matching selected in the Benchmark Model may Pareto dominate the matching selected in Model (a). In addition, the total number of transplants may be higher in the Benchmark Model than in Model (a).

Proof. Suppose that $N = \{1, 2\}$ where $N_I = \{1\}$ and $N_H = \{2\}$. Assume further that Patient 1 is compatible with donor d_2 and that Patient 2 is compatible with donor d_1. In Model (a), Patient 2 is self-matched as $2 \in N_H$. Since Patient 1 is incompatible with donor d_1, Patient 1 remains unmatched. In the Benchmark Model, no patients are self-matched. Patient 2 is therefore available for a mutually beneficial kidney exchange with Patient 1. Thus, both patients receive transplants in the Benchmark Model, whereas only Patient 2 receives a transplant in Model (a). Furthermore,

15. In the Benchmark model, no pairwise exchanges would be feasible.

16. It is well-known that larger patient–donor pools result in more transplants than smaller pools. See, *e.g.*, Roth *et al.* (2006).

Patient 2 is strictly better off in the Benchmark Model since Patient 2 is compatible with donor d_1 and only half-compatible with donor d_2. ‖

The above example shows that the introduction of transplantation over the blood group barrier could, in theory, reduce the number of transplants and make all patients worse off if implemented as in Model (a). In the simulation study in Section 5.2, the number of transplants was indeed lower in Model (a) than in the Benchmark Model in a small number cases for the smallest pool size. However, this problem vanished completely as the size of the patient–donor pool grew. Negative outcomes of this kind could never occur in Model (b) since it includes patients with half-compatible donors in the kidney exchange program and selects a Pareto efficient matching for all patients N in the problem (N, C, π). Given this observation, it is natural to ask whether Model (b) will generally result in a weakly larger number of transplants than the Benchmark Model and Model (a). According to the next result, it will.

Proposition 8. Consider a problem (N, C, π) and suppose that μ, μ', and μ'' contain all patients that receive transplants in the Benchmark Model, Model (a), and Model (b), respectively.[17] Then $|\mu''| \geq |\mu|$ and $|\mu''| \geq |\mu'|$.

The results above indicate that the manner in which medical technology enabling kidney transplants over the blood group barrier is used can have significant welfare implications. Even though one would suspect that this technology would increase the total number of kidney transplants, Proposition 7 reveals that this is not necessarily the case since a planner implementing Model (a) first maximizes the number of self-matches and only includes the remaining patient–donor pairs in the kidney exchange program. A planner implementing Model (b), on the other hand, regards self-matches as the last option for patients with half-compatible donors since these patients are first included in the exchange program in the hope of finding compatible donors for them. This inclusion means that a planner using Model (b) first aims to maximize the number of pairwise exchanges and, consequently, ensures that the number of patient–donor pairs participating in the kidney exchange program is maximized. As seen in Proposition 8, this strategy guarantees the total number of transplants to be (weakly) greater in Model (b) than it is in both the Benchmark Model and Model (a).

Recall that Model (a) corresponds to current practice in, *e.g.*, the Swedish kidney exchange program. Given the findings above, a natural question is then whether to transition from Model (a) to Model (b). The answer not only depends on the number of additional transplants that the transition would result in, it also depends on how it would affect patients with incompatible donors. To make this point clear, recall that patients with half-compatible donors can always receive kidneys over the blood group barrier from their own donors outside the exchange program. From a welfare perspective, it is then important to ensure that a patient with a half-compatible donor is not involved in an exchange at the expense of a patient with an incompatible donor as patients of the latter type cannot receive kidneys outside the exchange program. The next proposition ensures that such situations never occur. More precisely, Proposition 9 shows that all patients that would have received transplants in Model (a) will still receive transplants if there is a transition from Model (a) to Model (b).

Proposition 9. Consider a problem (N, C, π) and suppose that μ' and μ'' contain all patients that receive transplants in Model (a) and Model (b), respectively. Then $\mu' \subseteq \mu''$.

17. Note that $|\mu| = |N^*(M)|$ and $|\mu''| = |N^*(M'')|$ if matchings M and M'' are the outcomes of the Benchmark Model and Model (b), respectively.

From a welfare perspective, it is reassuring that a transition from Model (a) to Model (b) is guaranteed to weakly increase the number of transplants (Proposition 8) and that patients receiving transplants before the transition are guaranteed to still receive transplants after the transition (Proposition 9). This does, however, not say anything about what type of donors the patients will be matched to. It is clear that patients with half-compatible donors are made weakly better off by the transition since the worst possible outcome for them is to be paired with their own half-compatible donors, *i.e.*, the same outcome as in Model (a). The story for patients with incompatible donors is a bit different. and there is no general theoretical prediction. For some problems, there is no half-compatibility priority matching such that all patients with incompatible donors weakly gain by the transition from Model (a) to Model (b), and for some problems there is. A situation where all patients with incompatible donors are made better off by the transition is illustrated in the Proof of Proposition 7 above, since the outcomes in the Benchmark Model and Model (b) coincide. A situation where some patient is made worse off by the transition is illustrated in the following example.

Example 2. Suppose that $N=\{1,2,3,4\}$, $N_I=\{1,2,3\}$, $N_H=\{4\}$ and $\pi(1)>\pi(3)$. A feasible pairwise exchange between pairs (i,d_i) and (j,d_j) is denoted by ij and it is assumed that only the pairwise exchanges 12, 14, and 23 are feasible. Suppose further that Patient 1 is half-compatible with donor d_4 and that all patients in the other three feasible pairwise exchanges are compatible with the donors they participate in the exchanges with. In Model (a), Patient 4 is matched to her own half-compatible donor and the pairwise exchange 12 is conducted since $\pi(1)>\pi(3)$. In Model (b), the pairwise exchanges 14 and 23 are carried out. Even though Patient 1 receives a transplant in both models, Patient 1 is made worse off by a transition from Model (a) to Model (b) since the patient is compatible with donor d_2 and only half-compatible with donor d_4. □

5.2. *Simulation results*

This section aims to investigate the magnitudes of the theoretical findings presented in the previous section. It also attempts to shed light on some issues that are discussed extensively in the kidney exchange literature but have so far not been addressed in this article. For instance, this section will investigate how patients that are often proportionally disadvantaged in kidney exchange programs (specifically, blood group O patients) are affected by the introduction of transplantation over the blood group barrier.

In addition to the three models introduced earlier in this section, two additional models will be investigated. The first of these models is the Altruistic Model (Roth *et al.*, 2005a; Sönmez and Ünver, 2014) in which compatible patient–donor pairs participate in the kidney exchange program. It is called the Altruistic Model because patients with compatible donors do not benefit from participation in exchange programs, as they can already receive kidneys from their own donors (without crossing the blood group barrier). The compatible pairs ("altruistic pairs") participate to help other incompatible or half-compatible pairs. The second model, called the Cycle Model (Roth *et al.*, 2007), allows for three-way exchanges in addition to pairwise exchanges, *i.e.*, cyclic exchanges involving three patient–donor pairs.[18] The reason for including these models in the simulation study is that the design features of both models are known to (weakly) increase the number of transplants (see, *e.g.* Roth *et al.*, 2005a; Gentry *et al.*, 2007; Sönmez and Ünver, 2014). The outcomes in these two models are estimated under the assumption that transplants over the blood group barrier are either not allowed or not considered an option by the transplant

18. Cyclic exchanges involving four or more pairs are not considered in this section. This restriction can be supported by Roth *et al.* (2007) who demonstrated that allowing exchange cycles involving more than three pairs would only have a marginal impact on the number of transplants.

community, and compared to the outcomes in Models (a) and (b). This makes it possible to compare the effect of introducing medical technology enabling transplantation over the blood group barrier to the impact of other design features that are known to work well.

In order to analyse the Altruistic Model, a third type of patients must be added to the model, namely the patients with compatible donors. These patients are gathered in the set N_C and all patients in $N_C \cup N$ are included in the simulations, where $N_C \cap N = \emptyset$. The patients in N_C play no role in the Benchmark Model, Model (a), Model (b), or the Cycle Model since they are simply self-matched and unavailable for pairwise exchanges in all of these models. The patients in N_C do, however, play a significant role in the Altruistic Model. Let C_C be the compatibility structure between patients in $N_C \cup N$ and donors of patients in $N_C \cup N$. Furthermore, let $\pi_C : N_C \cup N \to \mathbb{R}_{++}$ be a priority function assigning each patient in $N_C \cup N$ a unique priority.

- **Altruistic Model.** Transplants over the blood group barrier are either disallowed or not considered an option by the medical community. A priority matching is found for the problem $(N_C \cup N, C_C, \pi_C)$.[19] Unmatched patients in N_C are then self-matched with their own compatible donors.
- **Cycle Model.** Transplants over the blood group barrier are either disallowed or not considered an option by the medical community. Three-way exchanges are permitted in addition to pairwise exchanges. A maximum matching[20] is found for the problem (N, C, π).

The reported results for the Cycle Model are taken from Roth *et al.* (2007), but these results are directly comparable to the other simulation results provided in this section (see footnotes 23 and 25 for details). For the other four models, a population of patient-donor pairs is generated using medical data (*e.g.* blood group distributions, PRA distributions (i.e., Panel Reactive Antibody distributions), crossmatch probabilities, etc.) identical to the data described in Roth *et al.* (2007) and Saidman *et al.* (2006).

Two pieces of information required for the simulations are missing in these articles; the share of patients that are female and have a spouse donor, and the share of patients for whom transplantation over the blood group barrier is feasible. The first of these numbers is based on Swedish medical data (Fehrman-Ekholm *et al.*, 2011) and is set to 10%. For the second number, it is assumed that transplantation over the blood group barrier is feasible for 75% of patients.[21] The priority $\pi(i)$ for each patient i is defined as in Keizer *et al.* (2005):

$$\pi(i) = \text{PRA}(i) \times (\text{share of donors in the pool that patient } i \text{ is incompatible with}) \tag{5.3}$$

The equation above captures the transplantation possibilities for patient i both outside and within the kidney exchange program. The higher the priority, the more difficult it is to find a suitable donor for the patient. Since both factors on the right hand side of equation (5.3) belong to the interval $[0, 1]$, patient priorities are guaranteed to take values between 0 and 1. Note also that the above

19. Since patients in N_C are assumed to be "altruistic" in the Altruistic Model, their preferences must be amended slightly. More precisely, patients in N_C are assumed to be indifferent between all compatible donors, including their own. Furthermore, it is sufficient that a patient $i \in N_C$ *weakly* gain in a pairwise exchange for the exchange to be feasible. Patients in N must, however, still *strictly* gain for an exchange to be feasible.

20. The reason the Cycle Model selects a maximum matching rather than a priority matching is that the matroid structure, discussed in Section 4.1 and Appendix A.1, is lost in the Cycle Model, giving rise to a trade-off between prioritization of HLA-sensitized patients and maximization of the number of transplants. See, *e.g.*, Kratz (2019) or Sönmez and Ünver (2014).

21. Recall from footnote 7 that this number is estimated to be around 90%. In the simulation study, however, a more conservative number is used to ensure that the results for Models (a) and (b) are not overestimated.

priorities are somewhat arbitrarily selected since priorities may be based on other methods and/or input variables. In the U.K. program, for example, priorities are based on previous unsuccessful matching runs, sensitization, HLA mismatch, and donor–donor age difference. For a technical overview of all European programs (including priority rules), see Biró *et al.* (2018).

The remainder of this section analyses a Monte Carlo simulation based on 1,000 populations randomly drawn from the medical distributions discussed above for population sizes of 25, 50, 100, 200, and 500 patient–donor pairs.[22] To put these population sizes in perspective, the kidney exchange program in the United Kingdom is the largest in Europe with 250 participating patient–donor pairs per matching run. The second largest European program is found in Spain with 110 participating pairs per run. In the simulations, around 50% of the patients already have compatible donors (see column "Self-match" in Table 1) and will, consequently, not be part of the patient–donor pool. This means that generated populations of 500 and 200 patient–donor pairs correspond to kidney exchange programs with 250 and 100 participating pairs, respectively, like the U.K. program and the Spanish program. Many European countries, including Austria, Belgium, France, Italy, Poland, Portugal, and Sweden, have much smaller programs captured by the population sizes 100, 50, and 25.

Table 1 displays the percentages of different types of transplants for each model and population size. In the table, "Exchange" only includes pairwise exchanges in all models except the Cycle Model, which includes three-way exchanges as well. Moreover, "ABOi" indicates that a patient receives a transplant over the blood group barrier. Note that such transplants, by assumption, are infeasible in the Benchmark Model, the Altruistic Model, and the Cycle Model. Furthermore, in all models except the Altruistic Model, patients with compatible donors receive kidneys from their own donors outside the kidney exchange program.

Recall Proposition 8, which states that Model (b) always generates a weakly larger number of transplants than both the Benchmark Model and Model (a). The exact magnitude of this difference can be seen in Table 1. For a population size of 50, an average of 34.2% of the patients in the Benchmark Model will not receive transplants.[23] The corresponding numbers for Models (a) and (b) are 11.1 % and 8.0 %, respectively. For a population size of 50, the simulation results also suggest that a transition from the Benchmark Model to Model (b) would on average result in 13.1 additional transplants (*i.e.* $34.2-8.0=26.2$ % of 50 patients). To achieve this, 11.5 patients (*i.e.* $14.6+8.4=23.0$ % of 50 patients) must on average receive transplants over the blood group barrier. An implied rule of thumb is that for every additional transplant achieved by a transition from the Benchmark Model to Model (b), one transplant must be carried out over the blood group barrier. This rule of thumb holds for all population sizes. Note also that the gain, measured in

22. The simulation makes use of Joris van Rantwijk's script for finding maximum weight matchings in graphs, ported to MATLAB by Daniel R. Saunders.

23. Roth *et al.* (2007) consider both the Benchmark Model and the Cycle Model. The patient–donor pool in their simulation study only contains patients with incompatible donors, whereas the patients in N_C are included in this section. Since roughly 50% of the pairs included in this simulation study have a compatible donor (see the "Self-match" column for the Benchmark Model in Table 1), the case when $n=50$ in this article roughly corresponds to the case when $n=25$ in Roth *et al.* (2007). Table 2 in Roth *et al.* (2007) shows that an average of 8.86 patients are involved in exchanges when $n=25$ and only pairwise exchanges are allowed. The corresponding number in this article is 8.6 patients (17.2% when $n=50$). Furthermore, Roth *et al.* (2007) find that an average of 21.8 patients are involved in pairwise exchanges when $n=50$. The corresponding number in this article is 21.5 (21.5% when $n=100$). In this sense, the results in this article confirm the findings in Roth *et al.* (2007). As a consequence, the results in Roth *et al.* (2007) for the Cycle Model can safely be used as an approximation of the corresponding results in this article.

TABLE 1
Distribution of different types of transplants for various models and population sizes

n	Model	No transplant	Self-match	ABOi self-match	Exchange	ABOi exchange	Total
25	Benchmark Model	38.5%	49.1%	0.0%	12.4%	0.0%	100.0%
	Model (a)	16.4%	49.1%	20.6%	9.5%	4.5%	100.0%
	Model (b)	13.1%	49.1%	15.4%	15.6%	6.8%	100.0%
	Altruistic Model	18.5%	25.9%	0.0%	55.6%	0.0%	100.0%
	Cycle Model[a]	N/A	N/A	N/A	N/A	N/A	N/A
50	Benchmark Model	34.2%	48.6%	0.0%	17.2%	0.0%	100.0%
	Model (a)	11.1%	48.6%	20.9%	13.2%	6.2%	100.0%
	Model (b)	8.0%	48.6%	14.6%	20.4%	8.4%	100.0%
	Altruistic Model	12.8%	22.0%	0.0%	65.2%	0.0%	100.0%
	Cycle Model[a]	28.9%	48.6%	0.0%	22.5%	0.0%	100.0%
100	Benchmark Model	29.9%	48.6%	0.0%	21.5%	0.0%	100.0%
	Model (a)	6.5%	48.6%	21.0%	16.5%	7.4%	100.0%
	Model (b)	4.1%	48.6%	13.5%	24.4%	9.4%	100.0%
	Altruistic Model	8.2%	19.9%	0.0%	71.9%	0.0%	100.0%
	Cycle Model[a]	24.1%	48.6%	0.0%	27.3%	0.0%	100.0%
200	Benchmark Model	27.3%	48.7%	0.0%	24.0%	0.0%	100.0%
	Model (a)	2.9%	48.7%	21.1%	19.1%	8.2%	100.0%
	Model (b)	1.7%	48.7%	12.9%	27.0%	9.7%	100.0%
	Altruistic Model	5.3%	19.0%	0.0%	75.7%	0.0%	100.0%
	Cycle Model[a]						
500	Benchmark Model	24.0%	48.8%	0.0%	27.2%	0.0%	100.0%
	Model (a)	0.4%	48.8%	20.9%	22.3%	7.6%	100.0%
	Model (b)	0.2%	48.8%	12.1%	29.7%	9.2%	100.0%
	Altruistic Model	3.0%	18.5%	0.0%	78.5%	0.0%	100.0%
	Cycle Model[a]	N/A	N/A	N/A	N/A	N/A	N/A

[a] Approximations from Roth *et al.* (2007). N/A, Not Available.

total number of transplants, from introducing transplants over the blood group barrier increases with pool size.[24]

It is also notable that not only do more patients receive transplants in Model (b) than in Model (a), the share of transplants over the blood group barrier is also lower. For a population size of 50, an average of 27.1 % (*i.e.* 20.9+6.2 %) of patients receive transplants over the blood group barrier in Model (a). The corresponding number in Model (b) is only 23.0 % (*i.e.* 14.6+8.4 %). This conclusion holds for all population sizes. The results in Table 1 also suggest that the impact on the number of transplants of introducing transplantation over the blood group barrier is larger than the impact of including altruistic donors or allowing three-way exchanges.[25] This conclusion holds for both Models (a) and (b).

24. This follows from the fact that both Models (a) and (b) select maximal matchings. More specifically, suppose that a set of patient–donor pairs are added to an existing exchange pool but that the number of transplants decreases. Then a contradiction is obtained immediately because the matching for the initial and smaller pool is feasible also for the larger pool and both Models (a) and (b) select maximal matchings. Consequently, the total number of transplants must increase with pool size (in fact, this conclusion holds for any matching mechanism that selects maximal matchings, including, *e.g.* the priority mechanism).

25. Note that the results in Table 1 for the Cycle Model are most likely marginally underestimated. This follows from the fact that the simulations in Roth *et al.* (2007) are based on population sizes of 25, 50 and 100, while the corresponding population sizes in this article are 25.7, 51.4, and 102.6 (see also footnote 23). Since Models (a) and (b) clearly outperform the Cycle Model in Table 1, the marginal difference in population sizes will not affect the general conclusions that can be drawn from the results.

TABLE 2
Distribution of transplant types for Model (a) when different proportions of patients accept ABOi transplants

n	Model (a)	No transplant (%)	Self-match (%)	ABOi self-match (%)	Exchange (%)	ABOi exchange (%)	Total (%)
25	0 % accept	38.5%	49.1%	0.0%	12.4%	0.0%	100.0%
	25 % accept	32.3%	49.1%	5.1%	11.9%	1.6%	100.0%
	50 % accept	26.8%	49.1%	10.1%	11.2%	2.8%	100.0%
	75 % accept	21.0%	49.1%	15.3%	10.7%	3.9%	100.0%
	100 % accept	16.4%	49.1%	20.6%	9.5%	4.5%	100.0%
50	0 % accept	34.2%	48.6%	0.0%	17.2%	0.0%	100.0%
	25 % accept	27.6%	48.6%	5.2%	16.6%	2.0%	100.0%
	50 % accept	21.5%	48.6%	10.4%	15.7%	3.8%	100.0%
	75 % accept	15.9%	48.6%	15.6%	14.7%	5.2%	100.0%
	100 % accept	11.1%	48.6%	20.9%	13.2%	6.2%	100.0%
100	0 % accept	29.9%	48.6%	0.0%	21.5%	0.0%	100.0%
	25 % accept	23.3%	48.6%	5.3%	20.5%	2.3%	100.0%
	50 % accept	17.0%	48.6%	10.5%	19.4%	4.5%	100.0%
	75 % accept	11.0%	48.6%	15.8%	18.2%	6.4%	100.0%
	100 % accept	6.5%	48.6%	21.0%	16.5%	7.4%	100.0%
200	0 % accept	27.3%	48.7%	0.0%	24.0%	0.0%	100.0%
	25 % accept	20.4%	48.7%	5.2%	23.0%	2.7%	100.0%
	50 % accept	13.6%	48.7%	10.5%	21.9%	5.3%	100.0%
	75 % accept	7.5%	48.7%	15.8%	20.7%	7.3%	100.0%
	100 % accept	2.9%	48.7%	21.1%	19.1%	8.2%	100.0%
500	0 % accept	24.0%	48.8%	0.0%	27.2%	0.0%	100.0%
	25 % accept	16.9%	48.8%	5.2%	26.1%	3.0%	100.0%
	50 % accept	10.0%	48.8%	10.5%	25.2%	5.5%	100.0%
	75 % accept	4.1%	48.8%	15.7%	24.1%	7.3%	100.0%
	100 % accept	0.4%	48.8%	20.9%	22.3%	7.6%	100.0%

The results for Models (a) and (b) in Table 1 are based on the assumption that all patients would accept receiving a kidney from *any* half-compatible donor.[26] Even though this is a reasonable assumption since most patients would prefer receiving a half-compatible kidney to not receiving any transplant at all[27], a sensitivity analysis is provided in Tables 2 and 3. These tables provide the recalculated results for Model (a) and Model (b) under the assumption that 0, 25, 50, 75, or 100 % of all patients are willing to receive kidneys from all half-compatible donors.

Note first that the results for 0% and 100% in Table 2, by definition, represent the Benchmark Model and Model (a) as presented in Table 1, respectively. Similarly, the results for 0% and 100% in Table 3 represent the Benchmark Model and Model (b) as presented in Table 1, respectively. As can be seen in Tables 2 and 3, for every additional 25% of patients that are willing to receive kidneys from half-compatible donors, between 3% and 7% more of the patients in the pool will receive transplants. This conclusion holds for both Model (a) and Model (b) independently of pool size. Furthermore, it suffices that at least 25% of the patients are willing to receive kidneys from half-compatible donors for Model (a) and Model (b) to perform better than the Cycle Model in terms of the number of transplants. However, more than 75% of the patients must be willing to

26. This assumption will be discussed further in Section 5.3 in relation to manipulability. Note also that even if all patients are assumed to be willing to receive kidneys from all half-compatible donors, not all patients are able to receive kidneys from all half-compatible donors as explained earlier (see footnote 7).

27. This assumption has also been informally confirmed by the Swedish transplant doctors and immunologists we have spoken to based on the observation that patients follow the recommendations made by their medical doctors in almost all cases and the fact that Sweden has had a well-functioning program for kidney transplantation across the blood group barrier for more than 10 years (see Fehrman-Ekholm *et al.*, 2011). Unfortunately, we have been unable to confirm this informal statement with official statistics.

TABLE 3
Distribution of transplant types for Model (b) when different proportions of patients accept ABOi transplants

n	Model (b)	No transplant	Self-match	ABOi self-match	Exchange	ABOi exchange	Total
25	0 % accept	38.5%	49.1%	0.0%	12.4%	0.0%	100.0%
	25 % accept	31.7%	49.1%	4.4%	13.2%	1.6%	100.0%
	50 % accept	25.3%	49.1%	8.3%	14.0%	3.3%	100.0%
	75 % accept	18.8%	49.1%	12.2%	14.8%	5.1%	100.0%
	100 % accept	13.1%	49.1%	15.4%	15.6%	6.8%	100.0%
50	0 % accept	34.2%	48.6%	0.0%	17.2%	0.0%	100.0%
	25 % accept	27.0%	48.6%	4.4%	17.9%	2.1%	100.0%
	50 % accept	20.0%	48.6%	8.4%	18.7%	4.3%	100.0%
	75 % accept	13.5%	48.6%	12.1%	19.4%	6.4%	100.0%
	100 % accept	8.0%	48.6%	14.6%	20.4%	8.4%	100.0%
100	0 % accept	29.9%	48.6%	0.0%	21.5%	0.0%	100.0%
	25 % accept	22.6%	48.6%	4.3%	22.1%	2.4%	100.0%
	50 % accept	15.5%	48.6%	8.3%	22.7%	4.9%	100.0%
	75 % accept	8.9%	48.6%	11.7%	23.5%	7.3%	100.0%
	100 % accept	4.1%	48.6%	13.5%	24.4%	9.4%	100.0%
200	0 % accept	27.3%	48.7%	0.0%	24.0%	0.0%	100.0%
	25 % accept	19.7%	48.7%	4.3%	24.5%	2.8%	100.0%
	50 % accept	12.5%	48.7%	8.2%	25.1%	5.5%	100.0%
	75 % accept	6.1%	48.7%	11.5%	25.9%	7.8%	100.0%
	100 % accept	1.7%	48.7%	12.9%	27.0%	9.7%	100.0%
500	0 % accept	24.0%	48.8%	0.0%	27.2%	0.0%	100.0%
	25 % accept	16.3%	48.8%	4.3%	27.6%	3.0%	100.0%
	50 % accept	9.5%	48.8%	7.9%	28.3%	5.5%	100.0%
	75 % accept	3.6%	48.8%	11.1%	29.1%	7.4%	100.0%
	100 % accept	0.2%	48.8%	12.1%	29.7%	9.2%	100.0%

TABLE 4
Frequency of cases in which fewer, equally many and more patients receive transplants in Model (a) than in the Benchmark Model for different population sizes

Patient-donor pool size	25	50	100	200	500
Fewer transplants in Model (a) than in the Benchmark Model	0.3%	0.0%	0.0%	0.0%	0.0%
Equally many transplants in Model (a) and the Benchmark Model	0.9%	0.0%	0.0%	0.0%	0.0%
More transplants in Model (a) than in the Benchmark Model	98.8%	100.0%	100.0%	100.0%	100.0%
Total	100.0%	100.0%	100.0%	100.0%	100.0%

receive kidneys from any half-compatible donors for Model (a) and Model (b) to perform better than the Altruistic Model. The two latter conclusions also hold independently of pool size.

Proposition 7 showed that the Benchmark Model may generate a larger number of transplants than Model (a). The simulation results in Table 1 suggest that this is not the average case. Table 4 provides more details for the different population sizes. For population sizes 50, 100, 200, and 500, the Benchmark Model never generates more transplants than Model (a). For a population size of 25, the Benchmark Model only generates more transplants than Model (a) in 0.3% of the cases. In fact, in nearly 100% of all cases, Model (a) generates a strictly larger number of transplants than the Benchmark Model. Hence, the theoretical finding in Proposition 7 that fewer patients may receive transplants in Model (a) than in the Benchmark model appears to mostly be a theoretical possibility and not something a planner needs to worry about.

Proposition 9 showed that if there is a transition from Model (a) to Model (b), then all patients receiving transplants in the former model will still receive transplants in the latter. However, Example 2 revealed that some patients that would have been matched to compatible donors in Model (a) may only be matched to half-compatible donors in Model (b). For this reason, it is

TABLE 5
Shares of patients receiving transplants in Model (a) that are matched to better, equally compatible and worse donors in Model (b) in terms of blood group compatibility

Patient-donor pool size	25	50	100	200	500
Compatible donor in Model (a) and half-compatible donor in Model (b)	1.2%	1.6%	2.0%	2.2%	2.4%
Equally compatible donors in Models (a) and (b)	92.4%	90.8%	89.2%	88.4%	87.9%
Half-compatible donor in Model (a) and compatible donor in Model (b)	6.4%	7.6%	8.8%	9.5%	9.7%
Total	100.0%	100.0%	100.0%	100.0%	100.0%

important to investigate how many patients are made better off and how many patients are made worse off by such a transition. Table 5 shows that, on average, between 1.2% and 2.4% of the patients (depending on the population size) who were matched to compatible donors in Model (a) were matched to half-compatible donors in Model (b). By comparison, an average of between 6.4 and 9.7 % of the patients (again, depending on the population size) who were matched to half-compatible donors in Model (a) were matched to compatible donors in Model (b). In this sense, a transition from Model (a) to Model (b) would improve the average "kidney quality" for patients receiving transplants in Model (a). Another indication of this result can be found in Table 1 where, for a population size of 50, an average of 27.1% of patients receive kidneys over the blood group barrier in Model (a), whereas the corresponding number for Model (b) is 23.0%.

So far, there has been no discussion of the patients who remain unmatched after a matching has been selected. It is, for example, well-known that patients with blood group O are often proportionally disadvantaged in kidney exchange programs (Roth *et al.*, 2007; Sönmez and Ünver, 2013; Sönmez *et al.*, 2018). The underlying reason for this is that there are typically more blood group O patients than there are blood group O donors in kidney exchange pools when transplants over the blood group barrier are infeasible. A blood group O patient is less likely to be involved in a kidney exchange than a patient with a different blood group since she can only receive kidneys from blood group O donors (see Section 2 for a description of the ABO blood group classification system). Hence, not only are blood group O patients expected to be over-represented in the kidney exchange pool, the proportion of blood group O patients is also expected to increase after the exchanges have been carried out.

Table 6 sheds some light on the impact that the introduction of transplantation over the blood group barrier would have on this biological unbalance. In the table, the "Ex Ante" distribution is the blood group distribution in the kidney exchange pool, whereas the "Ex Post" distribution is the blood group distribution of the patients that remain in the pool after the matched patients have been removed.

As in Roth *et al.* (2007) and Saidman *et al.* (2006), the simulations are based on a blood group distribution where 48, 34, 14, and 4% of the patients have blood group O, A, B, and AB, respectively. The biological unbalance described above is confirmed for the Benchmark Model where between 58.5% and 59.5% (depending on population size) of patients included in the kidney exchange pool have blood group O. These numbers are even higher in the ex post distribution and range between 69.0% and 86.3. In fact, the proportion of all blood groups except blood group O is lower in the ex post distribution than in the ex ante distribution in the Benchmark Model. Hence, not only are blood group O patients over-represented in the ex ante distribution, they are even more over-represented in the ex post distribution. The ex ante blood group distribution in the Altruistic Model is expected to be close to the assumed underlying blood group distribution since all patients are included in the ex ante distribution, independently of whether they can receive kidneys from their own donors. However, blood group O patients are still clearly disadvantaged in the ex post distribution in the Altruistic Model as well. Again, this finding hinges on the fact

TABLE 6
Average ex ante and ex post distributions of blood groups in the patient–donor pool for various models and population sizes

Model	n	Distribution	O	A	B	AB	Total
Benchmark Model	25	Ex Ante	59.5% *(7.56)*	24.2% *(3.08)*	14.5% *(1.85)*	1.8% *(0.23)*	100.0% *(12.73)*
		Ex Post	69.0% *(6.64)*	18.9% *(1.82)*	11.2% *(1.08)*	0.9% *(0.09)*	100.0% *(9.63)*
Benchmark Model	50	Ex Ante	58.8% *(15.12)*	24.6% *(6.33)*	14.7% *(3.78)*	1.9% *(0.49)*	100.0% *(25.75)*
		Ex Post	72.5% *(12.41)*	16.7% *(2.86)*	10.1% *(1.73)*	0.7% *(0.12)*	100.0% *(17.12)*
Benchmark Model	100	Ex Ante	58.5% *(30.07)*	25.0% *(12.85)*	14.6% *(7.51)*	1.9% *(0.98)*	100.0% *(51.41)*
		Ex Post	76.9% *(23.02)*	14.3% *(4.28)*	8.2% *(2.45)*	0.6% *(0.18)*	100.0% *(29.93)*
Benchmark Model	200	Ex Ante	59.0% *(60.53)*	25.0% *(25.65)*	14.3% *(14.67)*	1.7% *(1.74)*	100.0% *(102.59)*
		Ex Post	80.8% *(44.04)*	12.1% *(6.60)*	6.8% *(3.71)*	0.3% *(0.16)*	100.0% *(54.51)*
Benchmark Model	500	Ex Ante	59.2% *(151.56)*	24.7% *(63.11)*	14.3% *(36.67)*	1.8% *(4.66)*	100.0% *(256.00)*
		Ex Post	86.3% *(103.54)*	8.5% *(10.23)*	5.1% *(6.07)*	0.1% *(0.17)*	100.0% *(120.01)*
Model (a)	25	Ex Ante	53.7% *(4.07)*	29.0% *(2.20)*	14.3% *(1.08)*	3.0% *(0.23)*	100.0% *(7.58)*
		Ex Post	57.5% *(2.36)*	26.1% *(1.07)*	13.7% *(0.56)*	2.7% *(0.11)*	100.0% *(4.10)*
Model (a)	50	Ex Ante	52.4% *(8.00)*	30.1% *(4.60)*	14.4% *(2.20)*	3.1% *(0.47)*	100.0% *(15.27)*
		Ex Post	59.1% *(3.29)*	26.0% *(1.45)*	12.4% *(0.69)*	2.5% *(0.14)*	100.0% *(5.57)*
Model (a)	100	Ex Ante	51.9% *(15.77)*	30.6% *(9.30)*	14.2% *(4.32)*	3.3% *(1.00)*	100.0% *(30.39)*
		Ex Post	61.3% *(4.00)*	23.4% *(1.53)*	12.7% *(0.83)*	2.6% *(0.17)*	100.0% *(6.53)*
Model (a)	200	Ex Ante	52.4% *(31.67)*	30.4% *(18.38)*	14.3% *(8.64)*	2.9% *(1.75)*	100.0% *(60.44)*
		Ex Post	67.1% *(3.95)*	20.0% *(1.18)*	11.2% *(0.66)*	1.7% *(0.1)*	100.0% *(5.89)*
Model (a)	500	Ex Ante	52.8% *(80.02)*	30.1% *(45.56)*	14.0% *(21.21)*	3.1% *(4.66)*	100.0% *(151.45)*
		Ex Post	69.9% *(1.43)*	16.7% *(0.34)*	11.0% *(0.22)*	2.4% *(0.05)*	100.0% *(2.04)*
Model (b)	25	Ex Ante	59.5% *(7.67)*	24.2% *(3.08)*	14.5% *(1.85)*	1.8% *(0.23)*	100.0% *(12.73)*
		Ex Post	61.1% *(2.00)*	24.0% *(0.79)*	12.6% *(0.41)*	2.3% *(0.08)*	100.0% *(3.28)*
Model (b)	50	Ex Ante	58.8% *(15.12)*	24.6% *(6.33)*	14.7% *(3.78)*	1.9% *(0.49)*	100.0% *(25.72)*
		Ex Post	65.4% *(2.63)*	21.7% *(0.87)*	10.5% *(0.42)*	2.4% *(0.10)*	100.0% *(4.02)*
Model (b)	100	Ex Ante	58.5% *(30.07)*	25.0% *(12.85)*	14.6% *(7.51)*	1.9% *(0.98)*	100.0% *(51.31)*
		Ex Post	69.0% *(2.82)*	19.5% *(0.80)*	9.2% *(0.38)*	2.3% *(0.09)*	100.0% *(4.09)*
Model (b)	200	Ex Ante	59.0% *(60.53)*	25.0% *(25.65)*	14.3% *(14.67)*	1.7% *(1.74)*	100.0% *(102.59)*
		Ex Post	76.1% *(2.58)*	15.4% *(0.52)*	7.2% *(0.24)*	1.3% *(0.04)*	100.0% *(3.38)*
Model (b)	500	Ex Ante	59.2% *(151.56)*	24.7% *(63.11)*	14.3% *(36.67)*	1.8% *(4.66)*	100.0% *(256.00)*
		Ex Post	85.7% *(0.96)*	9.1% *(0.10)*	5.0% *(0.06)*	0.2% *(0.00)*	100.0% *(1.12)*
Altruistic Model	25	Ex Ante	48.0% *(12.00)*	33.8% *(8.45)*	14.1% *(3.52)*	4.1% *(1.03)*	100.0% *(25.00)*
		Ex Post	68.1% *(3.16)*	19.2% *(0.89)*	11.7% *(0.54)*	1.0% *(0.05)*	100.0% *(4.64)*
Altruistic Model	50	Ex Ante	48.0% *(24.00)*	33.9% *(16.95)*	14.1% *(7.05)*	4.0% *(2.00)*	100.0% *(50.00)*
		Ex Post	70.5% *(4.52)*	17.3% *(1.11)*	11.5% *(0.74)*	0.7% *(0.04)*	100.0% *(6.41)*
Altruistic Model	100	Ex Ante	47.5% *(47.50)*	34.2% *(34.20)*	14.1% *(14.10)*	4.2% *(4.20)*	100.0% *(100.00)*
		Ex Post	71.8% *(5.90)*	16.2% *(1.33)*	11.5% *(0.94)*	0.5% *(0.04)*	100.0% *(8.21)*
Altruistic Model	200	Ex Ante	47.8% *(95.60)*	34.3% *(68.60)*	13.9% *(27.80)*	4.0% *(8.00)*	100.0% *(200.00)*
		Ex Post	72.4% *(7.73)*	16.2% *(1.73)*	11.1% *(1.18)*	0.3% *(0.03)*	100.0% *(10.67)*
Altruistic Model	500	Ex Ante	47.8% *(239.19)*	34.2% *(170.84)*	14.0% *(70.00)*	4.0% *(19.97)*	100.0% *(500.00)*
		Ex Post	74.4% *(11.16)*	15.0% *(2.24)*	10.5% *(1.57)*	0.1% *(0.02)*	100.0% *(14.99)*

Notes: The absolute number of patients is displayed inside parenthesis.

that it is more difficult for blood group O patients to find donors within the kidney exchange pool compared to patients with other blood groups.

When the medical technology that enables transplantation over the blood group barrier is introduced, blood group O patients become less disadvantaged than they were in the Benchmark Model and the Altruistic model, although they are still disadvantaged. The ex post proportion of blood group O patients in Models (a) and (b) for a population size of 50 is 59.1% and 65.4%, respectively. This can be compared to the corresponding numbers for the Benchmark Model and the Altruistic Model, which are 72.5% and 70.5%, respectively. This means that transplantation over the blood group barrier both increases the number of transplants and makes blood group O patients less disadvantaged. This conclusion holds for almost all population sizes. The only exception is for $n=200$ and $n=500$, in which the proportion of blood group O patients in the ex post distribution is 76.1% and 85.7%, respectively, in Model (b) and 72.4% and 74.4%,

TABLE 7
Average improvement over the Benchmark model in the number of blood group O patients receiving transplants

n	Model (a)		Model (b)		Altruistic Model	
25	4.28	(35.7%)	4.64	(38.6%)	3.48	(29.0%)
50	9.12	(38.0%)	9.78	(40.7%)	7.90	(33.0%)
100	19.02	(40.0%)	20.21	(42.5%)	17.12	(36.1%)
200	40.09	(42.0%)	41.46	(43.4%)	36.31	(38.0%)
500	102.11	(42.7%)	102.58	(42.9%)	92.39	(38.6%)

Notes: The improvement as a percentage of the total number of blood group O patients is displayed inside parenthesis.

respectively, in the Altruistic Model. However, note that Table 6 also reports the average (absolute) number of patients for each blood group (in parenthesis). It can be seen that the higher percentages in Model (b) are a direct consequence of the fact that only an average of 3.38 and 1.12 patients remain unmatched in Model (b) for $n = 200$ and $n = 500$, respectively. That is, it hinges on the fact that the proportion of unmatched patients with a specific blood group in the ex post distributions is defined relative to the proportion of unmatched patients with other blood groups.

Furthermore, a quick look at Table 6 may give the impression that blood group O patients are less disadvantaged in Model (a) than in Model (b) since the proportion of blood group O patients in the ex post distribution in Model (a) is lower than the corresponding proportion in Model (b) for all population sizes. However, Model (b) generates significantly more transplants than Model (a) and the patients that remain unmatched tend to be those that are the most difficult to find suitable donors for, *e.g.*, blood group O patients. By consulting the absolute values (in parenthesis) in Table 6, it is clear that the skewed ex post distributions for Model (b) is a direct consequence of the fact that almost all patients receive transplants. The average number of blood group O patients that remain unmatched is lower in Model (b) than in all other models for all population sizes. To make this point clearer, Table 7 shows the average improvement in the number of blood group O patients receiving transplants compared to the Benchmark model. For example, with a pool size of 100, transitioning from the Benchmark model to Model (b) would on average help 20 additional blood group O patients receive transplants, which is 42.5% of all blood group O patients. Note that Model (b) helps a larger number of blood group O patients receive transplants than the other two Models for every pool size.

If a planner in a "small" program (*e.g.* the programs in Austria, Belgium, France, Poland, Portugal, and Sweden) is concerned about the outcome for blood group O patients in Models (a) and (b), the edge weights in the maximum weight matching problem (previously defined in Section 4.2) can be adjusted slightly, by adding a "sufficiently small" constant for blood group O patients to increase their likelihood of receiving transplants.

5.3. *On manipulability*

An important problem in all market design applications is whether or not agents can manipulate the outcome of the matching mechanism by misrepresenting their preferences over donors. When only pairwise exchanges are allowed and patient preferences are dichotomous, as in, *e.g.*, the Benchmark Model, it is well-known that it always is in the best interest of the patients to truthfully report their preferences (Roth *et al.*, 2005b). However, when expanding the preference domain from the dichotomous to the trichotomous domain, as in, *e.g.*, Model (a) and Model (b), the positive findings relating to non-manipulability no longer hold. Specifically, if the planner insists on always selecting maximum matchings that minimize the use of immunosuppressants (such as half-compatibility priority matchings), it may be possible for patients to benefit by misrepresenting their preferences as illustrated in the following example.

Example 3. Suppose that $N=\{1,2,3,4\}$ and that each patient is incompatible with her own donor. A possible pairwise exchange between the pairs (i,d_i) and (j,d_j) is denoted by ij and it is assumed that only the pairwise exchanges 12, 14, and 23 are feasible. Assume that Patient 1 is compatible with donor d_2 but only half-compatible with donor d_4, *i.e.*, that Patient 1 strictly prefers a pairwise exchange with the pair $(2,d_2)$ over a pairwise exchange with the pair $(4,d_4)$. Next, suppose that Patient 2 and Patient 3 are half-compatible with donor d_3 and donor d_2, respectively. In this case, the unique maximum matching that minimizes the use of immunosuppressants is described by the pairwise exchanges 14 and 23. However, Patient 1 can manipulate the outcome by declaring herself incompatible with donor d_4. In this case, the unique maximum matching that minimizes the use of immunosuppressants is described by the pairwise exchange 12. □

The findings in Example 3 should come as no surprise as it is well-known that non-manipulability is incompatible with individual rationality and Pareto efficiency (or maximality) on preference domains more general than the dichotomous (Sönmez, 1999).[28] Note also that no priority function is needed to obtain the negative conclusion in Example 3., *i.e.*, it is maximality in combination with minimal use of immunosuppressants that drives the result. Moreover, while Example 3 demonstrates that Model (b) can be manipulated, it is easy to construct an example showing that Model (a) can be manipulated as well. In fact, as will be demonstrated below, it is "easier" for patients to manipulate Model (a) than Model (b). Before evaluating which patients that can manipulate Models (a) and (b), we state a few general remarks regarding the above type of manipulation in kidney exchange.

It is by no means obvious that patients are allowed to or even should be allowed to declare themselves incompatible with specific donors. Such decisions are more likely to be made by their immunologists and medical doctors based on observable and verifiable medical data. This conclusion was recently stated by two of the researches that have pioneered kidney exchange research:

> "…manipulations of this sort [preference manipulation] do not play a significant role, since compatibility information is usually obtained from observable and verifiable medical data." (Sönmez and Ünver, 2014, p. 114)

If preferences are solely based on medical information, the manipulation strategy adopted by patient 1 in Example 3 will no longer work.[29] However, even though the use of immunosuppressants can increase the number of transplants, it may also introduce new opportunities for manipulation. Whether or not a patient finds kidney transplants over the blood group barrier acceptable is the patient's *private information* (recall the discussion relating to Tables 2 and 3). Then, if patients are allowed to object to the use of immunosuppressive treatments, they may use this option to manipulate the matching mechanism. That is, even if a patient accepts half-compatible donors, she may claim that she does not as part of a strategy to be matched to a more preferred donor, exactly like Patient 1 did in Example 3. A similar discussion can, for example, be found in liver exchange frameworks (Ergin *et al.*, 2018) where it is private information for living donors whether or not they are willing to donate the right lobe of their livers. This kind of strategy may then be adopted in an attempt to avoid donating the right lobe of the liver as

28. This conclusion has previously been reached in a kidney exchange framework by Nicoló and Rodríguez-Álvarez (2012). For similar results in other matching frameworks, see, *e.g.*, Alcalde and Barberà (1994), Roth (1982), or Schummer (1999).

29. Unless patients are assisted by their immunologists and/or medical doctors in manipulating the matching mechanism.

the mortality rate is 4–5 times higher for right lobe donors than for left lobe donors. As already argued in Section 2, no such medical risks are associated with kidney transplantation over the blood group barrier, but whether or not patients consider these types of transplants to be acceptable is nevertheless private information. Here, it should also be noted that this type of manipulation attempt is very risky. If it is unsuccessful, the patient will not receive a transplant at all. In this sense, an attempt to manipulate the outcome of the matching mechanism may ultimately come at the cost of the patient's own life.

Given the insight that patients may successfully manipulate matching mechanisms by declaring half-compatible donors unacceptable, it is next investigated under what circumstances patients can gain by such manipulation strategies. Since Roth *et al.* (2005b) and Sönmez and Ünver (2014) have already proved that the Benchmark Model and the Altruistic Model, respectively, cannot be manipulated, the analysis is restricted to Model (a) and Model (b). To make the analysis tractable, it will be based on two assumptions, namely that (i) all medical information is observable and can be verified, and that (ii) no patient $i \in N$ can affect the priority function π by declaring certain donors (such as half-compatible donors) unacceptable. The first assumption can be justified by the arguments above. The second assumption is also standard in the literature, where priorities are assumed to be exogenously given (see *e.g.* Roth *et al.* (2005b) and Okumura (2014)).[30] The second assumption implies that patients cannot affect the edge weights in the maximum weight matching problem described in Section 4.2. Patients can, however, remove some edges from the graph by declaring half-compatible donors unacceptable. If some patient i declares half-compatible donors unacceptable, all edges between patient i and patients whose donors are half-compatible with i would be removed. Proposition 10 states that only patients matched to half-compatible donors have the potential to manipulate Model (a) and Model (b) in this way.

Proposition 10. Consider a problem (N, C, π) and a matching M selected in Model (b) (Model (a)). Suppose that a patient $i \in N$ is either unmatched or matched to a compatible donor at M. Then, in Model (b) (Model (a)), patient i cannot benefit by declaring half-compatible donors unacceptable.

Note that Proposition 10 provides a necessary, but not sufficient, condition for this type of manipulation. Any patients that could potentially manipulate the matching mechanism in this way are either (a) incompatible with their own donors and receive half-compatible donors through exchange or (b) matched to their own half-compatible donors. This means that a failed manipulation attempt would always result in the patient not receiving any transplant.

A simulation study is conducted to evaluate how "difficult" it is for patients matched to half-compatible donors to gain by strategic misrepresentation of preferences, *i.e.*, to gain by declaring half-compatible donors unacceptable. The simulation study is based on each of the $1{,}000 \times 5 = 5{,}000$ populations considered in Section 5.2. The following method is adopted for each population. First, all patients matched to half-compatible donors are identified. The proportion of these patients is stated in the column "Potential manipulation" in Table 8. For example, for Model (a) and population size 50, this group represents, on average, 27.1% of the patients (this can also be

30. If a patient can improve her priority by declaring certain donors unacceptable, it is easy to find problems in which the priority mechanism in Roth *et al.* (2005b) can be manipulated (see Appendix A.2 for a formal description of the priority mechanism). For instance, suppose that some unmatched patient i is compatible with some donor d_j, but the patient matched to d_j has higher priority than i when i reports truthfully. Clearly, if i could raise her priority above j's priority by declaring some donors (other than d_j) unacceptable, the priority mechanism would match i to donor d_j, which she prefers to being unmatched.

TABLE 8
Mean percentage of patients that can successfully manipulate Models (a) and (b)

n	Model	Potential manipulation	Success among potential	Success in pool
25	Model (a)	25.1%	24.8%	6.2%
	Model (b)	22.2%	8.3%	1.9%
50	Model (a)	27.1%	30.2%	8.2%
	Model (b)	23.0%	14.7%	3.4%
100	Model (a)	28.4%	37.2%	10.6%
	Model (b)	22.9%	22.9%	5.2%
200	Model (a)	29.3%	44.3%	13.0%
	Model (b)	22.6%	31.0%	7.0%
500	Model (a)	28.5%	56.0%	15.9%
	Model (b)	21.3%	39.9%	8.5%

seen in Table 1 where $20.9+6.2=27.1$ % of the 50 patients in the pool are matched to half-compatible donors on average). Second, each of these patients will then, one by one, declare all half-compatible donors unacceptable. For each such unilateral declaration, the maximum weight matching problem is solved for the modified graph and the matching for the patient that declared all half-compatible donors unacceptable is compared to the original matching.[31] If the patient is matched to a compatible donor when declaring all half-compatible donors unacceptable, the manipulation is said to be *successful*. Note also that successful manipulation always comes at the cost of fewer transplants in total.

The mean success rate among the patients that could potentially manipulate the matching mechanism is stated in the column "Success among potential" in Table 8. As can be seen in the table, patients in Model (a) are on average more successful than patients in Model (b) and the success rate increases monotonically with pool size. The success rates for the different pool sizes are between 24.8% and 56.0% in Model (a), and between 8.3% and 39.9% in Model (b). That it is more difficult to manipulate in Model (b) follows from the fact that patients with half-compatible donors are always given the opportunity to be matched to a fully compatible donor as they are always, by construction, included in the kidney exchange pool even when not declaring half-compatible donors unacceptable. Patients with half-compatible donors in Model (a), however, are never given this opportunity as they are always, by construction, matched to their own half-compatible donors. That it is easier to manipulate in larger pools follows from the fact that there are more transplantation opportunities (*i.e.* more edges in the graph) in larger pools and patients are therefore more likely to receive transplants even if they remove edges from the graph by declaring half-compatible donors unacceptable. The column "Success in pool" in Table 8 reports the mean percentage of *all* patients in the pool that can successfully manipulate the matching mechanism. Given the conclusions above, this number is also expected to be lower in Model (b) compared to Model (a) but increasing in pool size. This is confirmed in Table 8 where it is shown that the success rate among *all* patients in the pool is between 6.2% and 15.9% in Model (a), but only between 1.9% and 8.5% in Model (b).

31. For, *e.g.*, Model (b) and pool size 500, this means that 106,500 additional maximum weight matching problems had to be solved. This follows since, for each of the 1,000 populations, an average of 106.5 patients (*i.e.* $12.1+9.2=21.3$ % of 500 the patients in the pool) were matched to half-compatible donors.

6. CONCLUSIONS

This article has investigated pairwise kidney exchange programs using a medical technology for transplanting kidneys over the blood group barrier. In particular, the focus has been on the set of half-compatibility priority matchings and how the technology is best utilized. If a planner is only interested in maximizing the number of transplants, minimizing the number of transplants over the blood group barrier and, in addition, designing a program that is less biased against the biologically disadvantaged blood group O patients, the theoretical results and the findings in the simulation study suggest the following policy recommendations.

First, if the technology enabling transplantation over the blood group barrier not is allowed *within* the existing kidney exchange framework, like in, *e.g.*, Belgium, France, India, Italy, the Netherlands, Poland, and Portugal, and there is a change in the legal framework or in the attitude towards immunosuppressants in the transplant community allowing for transplantation over the blood group barrier *within* the exchange program, then any existing kidney exchange program should be amended to make use of it. In the language of this article, a transition to Model (b) is recommended. This would generate a significantly larger number of transplants and, in addition, help the biologically disadvantaged blood group O patients.

Second, if the technology enabling transplantation over the blood group barrier is allowed but mainly used to obtain self-matches over the blood group barrier outside a kidney exchange program as in, *e.g.*, Austria, the Czech Republic, Spain, Sweden, Switzerland, and the United Kingdom, a transition to a system where patients with half-compatible donors are first added to the exchange pool in search of a compatible donor is recommended. In the language of this article, a transition from Model (a) to Model (b) is recommended. This would generate more transplants in total and reduce the proportion of patients receiving transplants over the blood group barrier.

The conclusions above are only valid if the social planner can accept that some patients may be able to manipulate the outcome of the matching mechanism. More precisely, the introduction of the technology enabling transplants over the blood group barrier naturally extends the preference domain from the dichotomous to the trichotomous domain and, therefore, also opens up for manipulation possibilities. However, fewer patients can manipulate Model (b) than Model (a), so the former model performs better than the latter in this respect as well. Since less than 10 % of all patients can successfully manipulate Model (b) even in very large exchange pools (and they attempt to do so with their own lives at stake), the main take away message is that if the social planner can accept that a small fraction of all patients may be able manipulate the matching mechanism, then a transition to Model (b) is recommended independently of what the current exchange framework is.

It should be noted that Model (a) is an exact description of the exchange program currently used in Sweden. This program was initiated and designed by one of the authors of this article (Andersson) and will be expanded to also include Norway and Denmark in the spring of 2019 at the latest.[32] Patients with half-compatible donors are not routinely asked to join the Swedish exchange program, although there is a discussion within the transplant community about designing a protocol for investigating their interest in participating. The findings in this article strongly support any such initiative.

The theoretical results and the simulation results presented in this article are valid for kidney exchange programs where only pairwise exchanges are allowed. Considering the findings in this article, it is important that future research investigates how transplantation over the blood group barrier can be integrated into more sophisticated kidney exchange programs allowing for, *e.g.*, non-simultaneous extended altruistic donor chains and larger cyclic exchanges. Such features

32. For more details on the Swedish/Scandinavian program (STEP), see Biró *et al.* (2018, 2019).

will with certainty lead to even more transplants. In general, new medical technology and more potent immunosuppressants will most likely continue to affect kidney exchange programs in the future, making more research in this direction important. Apart from the results presented in this article, future research may also build on, *e.g.*, Chun *et al.* (2015), Nicoló and Rodríguez-Álvarez (2017), and Sönmez *et al.* (2018).

A. PRIORITY MATCHINGS AND MATROIDS

This Appendix is divided in two parts. The first shows that pairwise kidney exchange problems have a matroid structure, even in settings with immunosuppressants. The second demonstrates that the set of priority matchings defined in this article is equivalent to the set of priority matchings defined by Roth *et al.* (2005b). The graph theoretical definition of matchings will be adopted throughout both Appendices A and B. That is, for any problem (N,C,π) with corresponding compatibility graph g, a matching $M \subseteq E(g)$ is defined as a set of edges in g that are not incident to each other (see Section 4.2).

A.1. *Matroids*

Many of the results in Section 4.1 relate to the structure of *pairwise* kidney exchange problems in particular. One important aspect of pairwise kidney exchange problems is that the set of all patients N and a family $\mathcal{I}$ containing all sets of patients that can be matched simultaneously constitute a matroid $(N,\mathcal{I})$. This was shown by Roth *et al.* (2005b) for settings with a binary compatibility structure (no transplantation over the blood group barrier). Proposition 11 below states that the matroid result in Roth *et al.* (2005b) continues to hold in settings that distinguish between compatibility and half-compatibility. This is not immediately obvious since self-matches alter the structure of the sets of simultaneously matchable patients.

Definition 1. A pair $(X,\mathcal{I})$ where X is a finite set (called the *ground set*) and $\mathcal{I}$ is a family of subsets of X (called the *independent sets*) is a *matroid* if it has the following two properties.

- If $I \in \mathcal{I}$ and $J \subset I$, then $J \in \mathcal{I}$ (*the hereditary property*).
- If $I,J \in \mathcal{I}$, and $|J| < |I|$, then there exists some $i \in I \setminus J$ such that $J \cup \{i\} \in \mathcal{I}$ (*the augmentation property*).

The matroid structure ensures that every maximal matching is a maximum matching. Before stating the matroid result formally, note that if cyclic exchanges involving three or more patient–donor pairs are feasible, the matroid result no longer holds, giving rise to a trade-off between prioritizing patients and maximizing the number of transplants, see, *e.g.*, Kratz (2019) or Sönmez and Ünver (2014) for detailed discussions.

Proposition 11. Let $\mathcal{I}$ be the sets of simultaneously matchable patients, *i.e.*, $\mathcal{I} := \{I \subseteq N \mid I \subseteq N^*(M) \text{ for some } M \in \mathcal{M}\}$. Then $(N,\mathcal{I})$ is a matroid.

Proof. The hereditary property holds trivially. The rest of this proof will focus on elements in $\mathcal{I}$, each of which containing *all* patients matched at some matching. By the hereditary property, this is without loss of generality. Let M and M' be two matchings such that $|N^*(M)| < |N^*(M')|$. To reach a contradiction, suppose that the augmentation property does not hold. Then there exists no patient $i \in N^*(M') \setminus N^*(M)$ such that $N^*(M) \cup \{i\} \in \mathcal{I}$. By the hereditary property, this can only be true if $N^*(M) \setminus N^*(M') \neq \emptyset$. This conclusion together with $|N^*(M)| < |N^*(M')|$ implies that $|N^*(M) \setminus N^*(M')| < |N^*(M') \setminus N^*(M)|$. Hence, $N^*(M') \setminus N^*(M) \neq \emptyset$.

Now consider an arbitrary patient $i \in N^*(M') \setminus N^*(M)$. First note that it must be the case that $ij \in M'$ for some $j \in N^*(M)$. To see why, note that if both $i,j \in N^*(M') \setminus N^*(M)$, then $M \cup \{ij\} \in \mathcal{M}$. Furthermore, if $ii \in M'$, then $M \cup \{ii\} \in \mathcal{M}$. Both cases contradict the non-existence of some $i \in N^*(M') \setminus N^*(M)$ such that $N^*(M) \cup \{i\} \in \mathcal{I}$.

Next, note that it must be the case that $jk \in M$ for some $k \in N^*(M) \setminus \{j\}$. Otherwise, $jj \in M$ and $(M \setminus \{jj\}) \cup \{ij\} \in \mathcal{M}$, which again is a contradiction.

Finally, note that it cannot be the case that $kl \in M'$ for some $l \in N^*(M') \setminus N^*(M)$, because then $(M \setminus \{jk\}) \cup \{ij,kl\} \in \mathcal{M}$, which again contradicts the non-existence of some $i \in N^*(M') \setminus N^*(M)$ such that $N^*(M) \cup \{i\} \in \mathcal{I}$. Hence, (a) $k \in N^*(M) \setminus N^*(M')$, or (b) $kl \in M'$ for some $l \in N^*(M)$. In case (b), both $ll \in M$ and $ll' \in M'$ for some $l' \in N^*(M') \setminus N^*(M)$ result in the same contradiction. This "chain" continues until reaching some patient $j' \in N^*(M) \setminus N^*(M')$.

Thus, both in case (a) and case (b), there exists exactly one "corresponding" patient in $N^*(M) \setminus N^*(M')$ for every patient $i \in N^*(M') \setminus N^*(M)$. This contradicts the assumption that $|N^*(M)| < |N^*(M')|$. Hence, the augmentation property holds and $(N,\mathcal{I})$ is a matroid. ‖

Henceforth, for any problem (N,C,π), $\mathcal{I}$ will always denote the sets of simultaneously matchable patients, *i.e.*, $\mathcal{I}:=\{I\subseteq N\,|\,I\subseteq N^*(M)$ for some $M\in\mathcal{M}\}$.

A.2. *Priority matchings*

This section finds an equivalence between the set of priority matchings defined in this article and the set of priority matchings defined by Roth *et al.* (2005b). To achieve this, Proposition 11 is used to derive a number of new lemmas. These lemmas will not only prove to be important in showing the equivalence mentioned above, they will also be useful in proving some of the results in Appendix B.

Let $\Gamma:N\to\{1,\ldots,n\}$ be a permutation of N such that $\Gamma(i)=j$ if i is the patient with the jth highest priority. That is, $\Gamma^{-1}(1)$ is the top priority patient and $\Gamma^{-1}(n)$ is the patient with lowest priority. Roth *et al.* (2005b) define priority matchings in terms of the following *priority mechanism*:

- Let $\mathcal{E}_0=\mathcal{M}$.
- For $k\in\{1,\ldots,n\}$, let $\mathcal{E}_k\subseteq\mathcal{E}_{k-1}$ be defined by

$$\mathcal{E}_k=\begin{cases}\{M\in\mathcal{E}_{k-1}\,|\,\Gamma^{-1}(k)\in N^*(M)\}\text{ if non-empty,}\\ \mathcal{E}_{k-1}\text{ otherwise.}\end{cases}$$

The set $\mathcal{E}_n$ is the set of priority matchings in Roth *et al.* (2005b). Note that $\mathcal{E}_n$ is defined without reference to any preferences. To avoid confusion between the two definitions of priority matchings before they have been shown to be equivalent, $\mathcal{E}_n$ will be used whenever discussing priority matchings as defined by Roth *et al.* (2005b).

A first observation is that all priority matchings are maximal matchings by construction. One implication of Proposition 11 is then that all priority matchings are also maximum matchings.

Lemma 2. For a given problem (N,C,π), each priority matching is a maximum matching.

Proof. Consider any priority matching $M\in\mathcal{E}_n$. M is maximal by construction. Suppose that M is not a maximum matching. Then there exists some $M'\in\mathcal{M}$ such that $|N^*(M)|<|N^*(M')|$. Note that $N^*(M),N^*(M')\in\mathcal{I}$ by definition of $\mathcal{I}$. Since $(N,\mathcal{I})$ is a matroid, by Proposition 11, there exists some $i\in N^*(M')\setminus N^*(M)$ such that $N^*(M)\cup\{i\}\in\mathcal{I}$ by the augmentation property. Consequently, there is some matching $M''\in\mathcal{M}$ such that $N^*(M)\cup\{i\}\subseteq N^*(M'')$. Hence, M is not a maximal matching. This contradicts the assumption that $M\in\mathcal{E}_n$, since all priority matchings are maximal. ‖

Priority preference relations were defined informally in Section 3. Formally, a preference relation $\succsim_\pi$ is called a priority preference relation if it is complete, transitive, and satisfies the following conditions:

$$M\succ_\pi M'\text{ if }\begin{cases}N^*(M')\subset N^*(M),\\ N^*(M)\setminus N^*(M')=\{i\},N^*(M')\setminus N^*(M)=\{j\}\text{ and }\pi(i)>\pi(j),\end{cases}$$

$$M\sim_\pi M'\text{ if }N^*(M)=N^*(M').$$

The proof of the result that any priority matching is preferred to any other matching by any priority preference relation (Lemma 3) is included alongside the proof of the converse statement (Lemma 5) for completeness. Lemmas 3 and 5 imply that the set of priority matchings as defined in this article is identical to the set of priority matchings as defined by Roth *et al.* (2005b), *i.e.*, that $\mathcal{M}^*=\mathcal{E}_n$.

Lemma 3. (Roth *et al.*, 2005b). For any priority preference relation $\succsim_\pi$ and any $M\in\mathcal{E}_n$, $M\succsim_\pi M'$ for all $M'\in\mathcal{M}$.

Proof. Consider some priority preference relation $\succsim_\pi$ and some $M\in\mathcal{E}_n$. To reach a contradiction, suppose that there exists some $M'\in\mathcal{M}$ such that $M'\succ_\pi M$. Note that matchings in $\mathcal{E}_n$ are maximal by construction. Furthermore, since $(N,\mathcal{I})$ is a matroid by Proposition 11, every maximal matching is a maximum matching by the augmentation property. Since $M'\succ_\pi M$, it must be the case that $N^*(M)\neq N^*(M')$ since if $N^*(M)=N^*(M')$, then $M\sim_\pi M'$ by the definition of $\succsim_\pi$.[33]

Let $N^*(M)\triangle N^*(M')$ be the symmetric difference between $N^*(M)$ and $N^*(M')$, *i.e.*, the set of patients that are matched at M or M' but not both. In the case that M' is not a maximum matching, there exists some maximum matching $M_1\in\mathcal{M}$

33. It should be noted that this requirement on priority preferences is only imposed implicitly in Roth *et al.* (2005b), but is nevertheless necessary for Lemma 3 to hold.

such that $N^*(M') \subset N^*(M_1)$ by the augmentation property. Then $M_1 \succ_\pi M$ by transitivity, since $M_1 \succ_\pi M' \succ_\pi M$. Let M_1 denote some maximum matching such that $M_1 \succ_\pi M$. Note that $N^*(M) \triangle N^*(M_1)$ contains the same number of patients from $N^*(M)$ and $N^*(M_1)$ and that its cardinality is at least 2, since $N^*(M) \neq N^*(M_1)$ by $M_1 \succ_\pi M$.

First, suppose that $|N^*(M) \triangle N^*(M_1)| = 2$. Then $N^*(M_1) \setminus N^*(M) = \{j\}$ and $N^*(M) \setminus N^*(M_1) = \{j'\}$ for some $j, j' \in N$. Since $M_1 \succ_\pi M$, it must be the case that $\pi(j) > \pi(j')$ by the definition of priority preferences. Let $\Gamma(j) = t$. It then follows from $M \in \mathcal{E}_n$ that $M \in \mathcal{E}_{t-1}$. Furthermore, since $N^*(M) \triangle N^*(M_1)$ contains only j and j' and since $\Gamma(j') > t$ by $\pi(j) > \pi(j')$, it follows that $i \in N^*(M_1)$ for all $i \in N^*(M)$ such that $\Gamma(i) < t$. Hence, $M_1 \in \mathcal{E}_{t-1}$ as well. Due to the fact that $\Gamma^{-1}(t) = j$, $M_1 \in \mathcal{E}_{t-1}$ and $j \in N^*(M_1) \setminus N^*(M)$, it follows from the definition of $\mathcal{E}_t$ that $M \notin \mathcal{E}_t$. Since $\mathcal{E}_n \subseteq \mathcal{E}_t$, this contradicts $M \in \mathcal{E}_n$. Thus, $|N^*(M) \triangle N^*(M_1)| > 2$.

Let j be the patient with the highest priority in $N^*(M) \triangle N^*(M_1)$. Such patient must exist since each patient have a unique priority and $|N^*(M) \triangle N^*(M_1)| > 2$. By definition of the set $N^*(M) \triangle N^*(M_1)$, it must be the case that $j \in N^*(M_1)$ or $j \in N^*(M)$. To reach the desired contradiction, it will be demonstrated that (a) $j \notin N^*(M_1)$ and (b) $j \notin N^*(M)$.

(a) Suppose that $j \in N^*(M_1)$. Let $A = N^*(M) \cap N^*(M_1)$ be the set of patients matched at both M and M_1. Since $A \cup \{j\} \subset N^*(M_1)$ and $N^*(M_1) \in \mathcal{I}, A \cup \{j\} \in \mathcal{I}$ by the hereditary property. Furthermore, because $|A \cup \{j\}| < |N^*(M)|$, there exists some patient $j' \in N^*(M) \setminus (A \cup \{j\})$ such that $A \cup \{j, j'\} \in \mathcal{I}$ by the augmentation property. Patients can continue to be added in this way until the union between A and the added patients have the same cardinality as $N^*(M)$. That is, there exists some $A' \subset N^*(M) \setminus (A \cup \{j\})$ such that $A \cup A' \cup \{j\} \in \mathcal{I}$ and $|A \cup A' \cup \{j\}| = |N^*(M)|$. Since $A \cup A' \cup \{j\} \in \mathcal{I}$, there exists some $M_2 \in \mathcal{M}$ such that $A \cup A' \cup \{j\} \subseteq N^*(M_2)$ by the definition of $\mathcal{I}$. Since M is a maximum matching, $A \cup A' \cup \{j\} = N^*(M_2)$. Note that $N^*(M_2) \setminus N^*(M) = \{j\}$ and $N^*(M) \setminus N^*(M_2) = \{j''\}$ for some $j'' \in N^*(M) \triangle N^*(M_1)$. Since M_2 is a maximum matching such that $M_2 \succ_\pi M$ (as $\pi(j) > \pi(j'')$) and $|N^*(M) \triangle N^*(M_2)| = 2$, this is identical to the case discussed above and, consequently, results in the same contradiction. Thus, $j \notin N^*(M_1)$.

(b) Suppose that $j \in N^*(M)$. As before, let $A = N^*(M) \cap N^*(M_1)$ and note that $A \cup \{j\} \in \mathcal{I}$. By the same logic as in case (a), there exists some $A' \subset N^*(M_1) \setminus N^*(M)$ such that $A \cup A' \cup \{j\} \in \mathcal{I}$ by (possibly repeated application of) the augmentation property. Moreover, there exists some $M_2 \in \mathcal{M}$ such that $N^*(M_2) = A \cup A' \cup \{j\}$. Since $\pi(j) > \pi(i)$ for the unique patient $i \in N^*(M_1) \setminus (A \cup A' \cup \{j\})$, it follows that $M_2 \succ_\pi M_1$. Note that $|N^*(M) \triangle N^*(M_2)| = |N^*(M) \triangle N^*(M_1)| - 2$, since j is matched at M and M_2 but not at M_1 and, furthermore, since i is matched at M_1 but not at M or M_2. Now, $|N^*(M) \triangle N^*(M_1)| > 2$ and $|N^*(M) \triangle N^*(M_2)| > 0$ imply that $N^*(M) \neq N^*(M_2)$. Suppose that the highest priority patient j' in $|N^*(M) \triangle N^*(M_2)|$ (which does not contain j) belongs to $N^*(M)$. Then a matching $M_3 \in \mathcal{M}$ containing j' can be constructed in the same way as above such that $M_3 \succ_\pi M_2 \succ_\pi M_1$ and $|N^*(M) \triangle N^*(M_3)| = |N^*(M) \triangle N^*(M_3)| - 2$. This process can continue until some M_t (possibly identical to M_3) is found such that either $|N^*(M) \triangle N^*(M_t)| = 0$ or the highest priority patient in $N^*(M) \triangle N^*(M_t)$ belongs to $N^*(M_t)$. If $|N^*(M) \triangle N^*(M_t)| = 0$, then $N^*(M) = N^*(M_t)$, implying that $M \sim_\pi M_t$. Since $M \sim_\pi M_t \succ_\pi \cdots \succ_\pi M_1$, it follows that $M \succ_\pi M_1$ by transitivity. This contradicts $M_1 \succ_\pi M$. The process can thus continue until some $M_t \in \mathcal{M}$ is found such that $|N^*(M) \triangle N^*(M_t)| > 0$ and the patient with highest priority in $N^*(M) \triangle N^*(M_t)$ belongs to $N^*(M_t)$. Then, either $|N^*(M) \triangle N^*(M_t)| = 2$ or $|N^*(M) \triangle N^*(M_t)| > 2$. Since M_t is a maximum matching such that $M_t \succ_\pi M$ and the highest priority patient in $N^*(M) \triangle N^*(M_t)$ belongs to $N^*(M_t)$, both cases have already been shown to result in contradictions. Hence, $j \notin N^*(M)$.

As explained above, cases (a) and (b) provide the desired contradiction. Consequently, there exists no $M' \in \mathcal{M}$ and no priority preference relation $\succsim_\pi$ such that $M' \succ_\pi M$. ‖

Lemma 4. Consider any priority preference relation $\succsim_\pi$ and any matching $M \in \mathcal{M}$ such that $M \succsim_\pi M'$ for all $M' \in \mathcal{M}$. Then $N^*(M) = N^*(M')$ for any $M' \in \mathcal{E}_n$.

Proof. Consider some priority preference relation $\succsim_\pi$ and some $M_1 \in \mathcal{M}$ such that $M_1 \succsim_\pi M'$ for all $M' \in \mathcal{M}$. First note that $\mathcal{E}_n \neq \emptyset$ as $\mathcal{M} \neq \emptyset$. Since $\succsim_\pi$ is a priority preference relation, Lemma 3 implies that $M \succsim_\pi M'$ for all $M \in \mathcal{E}_n$ and all $M' \in \mathcal{M}$. This implies that $M_1 \sim_\pi M'$ for all $M' \in \mathcal{E}_n$. This, in turn, requires that $|N^*(M_1)| = |N^*(M')|$ for all $M' \in \mathcal{E}_n$. To see why, first note that since priority matchings are maximal by construction and since $(N, \mathcal{I})$ is a matroid by Proposition 11, every priority matching is a maximum matching by the augmentation property. Hence, $|N^*(M_1)| \leq |N^*(M')|$ for all $M' \in \mathcal{E}_n$. To reach a contradiction, suppose that $|N^*(M_1)| < |N^*(M)|$ for some $M \in \mathcal{E}_n$. Since $N^*(M_1), N^*(M) \in \mathcal{I}$ and since $(N, \mathcal{I})$ is a matroid by Proposition 11, there exists some patient $i \in N^*(M) \setminus N^*(M_1)$ such that $N^*(M_1) \cup \{i\} \in \mathcal{I}$ by the augmentation property. Thus, there exists a feasible matching M_2 such that $N^*(M_1) \cup \{i\} \subseteq N^*(M_2)$. Then, $M_2 \succ_\pi M_1$ since $N^*(M_1) \subset N^*(M_2)$. Therefore, $M_2 \succ_\pi M_1 \sim_\pi M$ which implies that $M_2 \succ_\pi M$ by transitivity. This contradicts $M \in \mathcal{E}_n$, since $M \succsim_\pi M'$ for all $M' \in \mathcal{M}$ (including M_2) by Lemma 3. Hence, $|N^*(M_1)| = |N^*(M')|$ for all $M' \in \mathcal{E}_n$.

Next, it will be shown that $N^*(M_1) = N^*(M')$ for all $M' \in \mathcal{E}_n$. Assume that $N^*(M_1) \neq N^*(M)$ for some $M \in \mathcal{E}_n$ to reach a contradiction. Note that $|N^*(M_1)| = |N^*(M)|$ implies that $|N^*(M_1) \setminus N^*(M)| = |N^*(M) \setminus N^*(M_1)|$. As before, let $N^*(M_1) \triangle N^*(M)$ be the symmetric difference between $N^*(M_1)$ and $N^*(M)$. That is, the set of patients matched at either

M_1 or M, but not both. Again, note that the symmetric difference always contains the same number of patients from $N^*(M_1)$ and $N^*(M)$ and that its cardinality is at least 2, since $N^*(M_1) \neq N^*(M)$ by assumption.

First, suppose that $|N^*(M_1) \triangle N^*(M)| = 2$. Then there exist $j, j' \in N$ such that $N^*(M_1) \setminus N^*(M) = \{j\}$ and $N^*(M) \setminus N^*(M_1) = \{j'\}$. Since $\succsim_\pi$ is a priority preference relation, $M_1 \succ_\pi M$ if $\pi(j) > \pi(j')$, and $M \succ_\pi M_1$ if $\pi(j') > \pi(j)$. Both cases contradict $M_1 \sim_\pi M$. Hence, $|N^*(M_1) \triangle N^*(M)| > 2$.

Let j be the patient in $N^*(M_1) \triangle N^*(M)$ with highest priority. Without loss of generality, suppose that $j \in N^*(M_1)$. Let $A = N^*(M_1) \cap N^*(M)$ be the (possibly empty) set of patients matched at both M_1 and M. Since $A \cup \{j\} \subset N^*(M_1)$ and $N^*(M_1) \in \mathcal{I}$, $A \cup \{j\} \in \mathcal{I}$ by the hereditary property. As $|N^*(M_1) \triangle N^*(M)| > 2$, it follows that $|A \cup \{j\}| < |N^*(M)|$. Hence, there exists some $j' \in N^*(M) \setminus (A \cup \{j\})$ such that $A \cup \{j, j'\} \in \mathcal{I}$ by the augmentation property. Patients can continue to be added like this until the union between A and the added patients has the same cardinality as $N^*(M)$. That is, there exists some $A' \subset N^*(M) \setminus (A \cup \{j\})$ such that $A \cup A' \cup \{j\} \in \mathcal{I}$ and $|A \cup A' \cup \{j\}| = |N^*(M)|$. Since $A \cup A' \cup \{j\} \in \mathcal{I}$, there exists some $M_2 \in \mathcal{M}$ such that $A \cup A' \cup \{j\} \subseteq N^*(M_2)$. Furthermore, since $|A \cup A' \cup \{j\}| = |N^*(M)|$ and M is a maximum matching by $M \in \mathcal{E}_n$, it follows that $A \cup A' \cup \{j\} = N^*(M_2)$. Note that $N^*(M) \setminus (A \cup A') = \{j'\}$ for some $j' \in N^*(M)$ and $N^*(M_2) \setminus (A \cup A') = \{j\}$. Then, since $A \cup A'$ is a subset of both $N^*(M_2)$ and $N^*(M)$, $N^*(M_2) \setminus N^*(M) = \{j\}$ and $N^*(M) \setminus N^*(M_2) = \{j'\}$. As $j' \in N^*(M_1) \triangle N^*(M)$ and j is the patient in $N^*(M_1) \triangle N^*(M)$ with the highest priority, it follows that $\pi(j) > \pi(j')$. Hence, $M_2 \succ_\pi M$. This violates the assumption that $M \succsim_\pi M'$ for all $M' \in \mathcal{M}$. Thus, $N^*(M_1) = N^*(M)$. Since M is an arbitrary priority matching, $N^*(M_1) = N^*(M)$ for any $M \in \mathcal{E}_n$. ‖

Lemma 5. For any priority preference relation $\succsim_\pi$ and any $M \in \mathcal{M}$, if $M \succsim_\pi M'$ for all $M' \in \mathcal{M}$, then $M \in \mathcal{E}_n$.

Proof. Consider some $M \in \mathcal{M}$ such that $M \succsim_\pi M'$ for all $M' \in \mathcal{M}$. If $M' \in \mathcal{E}_n$ and $N^*(M) = N^*(M')$, then $M \in \mathcal{E}_n$ by the definition of $\mathcal{E}_n$. To see this, note that whether or not a matching $M \in \mathcal{M}$ belongs to $\mathcal{E}_n$ is exclusively determined by the patients matched at M, *i.e.*, the patients in $N^*(M)$. By Lemma 4, $N^*(M) = N^*(M')$ for all $M' \in \mathcal{E}_n$. Hence, $M \in \mathcal{E}_n$. ‖

B. PROOFS OF THE THEORETICAL RESULTS

This Appendix contains the proofs of all theoretical results except Propositions 11 and 7. The Proof of Proposition 11 is found in Appendix A.1 and the Proof of Proposition 7 is found in Section 5.1. Many proofs make use of results from other lemmas and propositions. For this reason, the proofs are not necessarily presented in the same order as their corresponding results in the main text. To make it easier for the reader to find the proofs, this Appendix is divided into four parts that are named after the specific sections where the results are presented in the main text. As in Appendix A, the graph theoretical definition of matchings will be adopted in this Appendix as well (see Section 4.2).

B.1. *Proofs of the results in Section 4.1*

Proposition 2. For a given problem (N, C, π), every half-compatibility priority matching is a priority matching.

Proof. Consider some priority matching $M \in \mathcal{M}^*$. Then $M \succsim_\pi M'$ for all $M' \in \mathcal{M}$ and all priority preference relations $\succsim_\pi$ by Lemma 3. Note that if $M \succ_\pi M'$ for some $M' \in \mathcal{M}$ and all priority preferences $\succsim_\pi$, then $M \succ_B M'$ for all half-compatibility priority preferences $\succsim_B$. To see this, first note that if M is preferred to M' by *all* priority preference relations, then this preference does not depend on the choice of priority preference relation. Thus, the preference is induced by the properties of priority preferences, *i.e.*, the restrictions imposed on priority preference relations. Note that the same restrictions are imposed on both priority preference relations and half-compatibility priority preference relations when considering matchings $M, M' \in \mathcal{M}$ for which $N^*(M) \neq N^*(M')$. Since $M \not\sim_\pi M'$, it follows that $N^*(M) \neq N^*(M')$. The restrictions imposed on half-compatibility priority preference relations will therefore induce the same preferences over M and M'. Then, because $M \succ_\pi M'$ for all $M \in \mathcal{M}^*$, all $M' \in \mathcal{M} \setminus \mathcal{M}^*$ and all priority preference relations $\succsim_\pi$, it follows that $M \succ_B M'$ for all $M \in \mathcal{M}^*$, all $M' \in \mathcal{M} \setminus \mathcal{M}^*$ and all half-compatibility priority preference relations $\succsim_B$. That is, half-compatibility priority preference relations prefer all priority matchings to all non-priority matchings. Consequently, $\mathcal{M}^B \subseteq \mathcal{M}^*$, *i.e.*, every half-compatibility priority matching is a priority matching. ‖

Proposition 3. For a given problem (N, C, π), every half-compatibility priority matching is a Pareto efficient maximum matching.

Proof. Consider any $M \in \mathcal{M}^B$. It follows immediately from Lemma 2 and Proposition 2 that M is a maximum matching. Suppose that M is not Pareto efficient to reach a contradiction. Then there exists some $M' \in \mathcal{M}$ that Pareto dominates M. First, suppose that $N^*(M) \neq N^*(M')$. Note that $N^*(M) \not\subset N^*(M')$ since M is a maximum matching. Hence, there exists some $i \in N^*(M) \setminus N^*(M')$, which implies that $M \succ_i M'$. This contradicts the assumption that M' Pareto dominates M. It

must therefore be the case that $N^*(M)=N^*(M')$. Furthermore, since $N^*(M)=N^*(M')$ and since M' Pareto dominates M, it must be the case that $B(M')>B(M)$. To see this, note that each patient must weakly prefer the kidney she receives at M' to the kidney she receives at M with strict preference for some patients. Since $M\in\mathcal{M}^B$, it follows by the construction of $\mathcal{M}^B$ that $B(M)\geq B(M')$. This contradicts $B(M')>B(M)$. Hence, every half-compatibility priority matching is a Pareto efficient maximum matching. ‖

Proposition 4. For a given problem (N,C,π), $N^*(M)=N^*(M')$ for all $M,M'\in\mathcal{M}^*$.

Proof. The proof follows directly from Lemma 4 and the fact that the set of priority matchings defined in this article is equivalent to the set of priority matchings defined by Roth *et al.* (2005b). ‖

Proposition 1. For a given problem (N,C,π), all half-compatibility priority preference relations induce the same set of half-compatibility priority matchings.

Proof. Consider any half-compatibility priority preference relation $\succsim_B$. Note that for any $M,M'\in\mathcal{M}$, either $B(M)>B(M'),B(M)<B(M')$ or $B(M)=B(M')$. Since $N^*(M)=N^*(M')$ for all $M,M'\in\mathcal{M}^*$, by Proposition 4, all half-compatibility priority preference relations will rank all priority matchings in the same way. That is, for any $M,M'\in\mathcal{M}^*$, $M\succsim_B M'$ for some half-compatibility priority preference relation $\succsim_B$ if and only if $M\succsim'_B M'$ for all half-compatibility priority preference relations $\succsim'_B$. By Proposition 2, $\mathcal{M}^B\subseteq\mathcal{M}^*$. This implies that $N^*(M)=N^*(M')$ for all $M,M'\in\mathcal{M}^B$ as well. Hence all half-compatibility priority preferences induce the same set of half-compatibility priority matchings. ‖

B.2. *Proof of Proposition 5*

The Proof of Proposition 5 is divided into two main parts. In the first part (Lemmas 7–10), a *specific problem*, denoted by $(N,\hat{C},\pi_M)$, plays an important role. More specifically, a number of equivalences are derived between an arbitrary problem (N,C,π) and a specific problem $(N,\hat{C},\pi_M)$, which has a *simple* corresponding compatibility graph $\hat{g}$. For any problem (N,C,π), the corresponding compatibility graph g is a simple graph whenever it contains no loops, *i.e.*, whenever $N_H=\emptyset$. While Lemma 1 is only applicable in problems with corresponding compatibility graphs that are simple graphs, this is not a sufficient requirement. It also requires that no transplantation over the blood group barrier be possible, *i.e.*, that the compatibility structure is binary in the sense that any patient i and donor d_j are either incompatible or compatible. The main idea in the second part of the proof (Lemma 11 to the end of Appendix B.2) is therefore to use the findings from the first part of the proof to demonstrate that an arbitrary problem (N,C,π) can be translated into an equivalent specific problem $(N,\check{C},\pi)$ with a corresponding simple graph, where $\check{C}$ is a compatibility structure at which *no* patients are half-compatible with *any* donors. Once this has been established, the proof of Proposition 5 follows from Lemma 1 and the findings in this Appendix. Note that this section (Appendix B.2) involves multiple compatibility structures (*e.g.* C, $\hat{C}$, $\check{C}$), each of which may induce a different set of matchings $\mathcal{M}$. For this reason, the notation $\mathcal{M}(C)$ will be used throughout the section to denote the set of all matchings for a given compatibility structure C. The sets $\mathcal{M}^*(C)$ and $\mathcal{M}^B(C)$ are defined analogously.

Before introducing the problem $(N,\hat{C},\pi_M)$, it is first proved that all patients in N_H are matched at any maximal matching and, by extension, at any maximum weight matching or priority matching.

Lemma 6. Consider a problem (N,C,π) with corresponding compatibility graph g, where $N_H\neq\emptyset$. Then each patient in N_H is matched at each maximal matching.

Proof. By construction, $ii\in E(g)$ for all $i\in N_H$. To obtain a contradiction, suppose that there exists some patient $i\in N_H$ who is unmatched at some maximal matching M. Then $M':=M\cup\{ii\}\in\mathcal{M}(C)$ since $i\in N_H$. This contradicts the assumption that M is a maximal matching. Hence, each patient in N_H is matched at each maximal matching. ‖

Consider a problem (N,C,π) with corresponding compatibility graph g and let $M\in\mathcal{M}(C)$. As mentioned above, the construction of the problem $(N,\hat{C},\pi_M)$ is key in the first part of the proof of Proposition 5. For any compatibility structure C', let $N_H(C')$ denote the set of patients that are half-compatible with their own donors at C' and define $N_I(C')$ analogously, *i.e.*, $N_I(C')=N\setminus N_H(C')$. The priority function π_M is defined by:

$$\pi_M(i) = \pi(i) \text{ for all } i\in N_I(C), \tag{B.1}$$

$$\sum\nolimits_{i\in N_H(C)}\pi_M(i) < \min\{\pi_M(j)\,|\,j\in N_I(C)\}, \tag{B.2}$$

$$\sum\nolimits_{i\in\Phi_M}\pi_M(i) < \min\{\pi_M(j)\,|\,j\in N_H(C)\setminus\Phi_M\}, \tag{B.3}$$

where Φ_M is the set containing each patient in $N_H(C)$ not matched to any patient in $N_I(C)$ at matching M. Moreover, the compatibility structure $\hat{C}$ is defined by the following two conditions:

- For any $i,j \in N_H(C)$, i and j are incompatible at $\hat{C}$. This includes the cases when $i=j$.
- Consider two patients $i,j \in N$ such that $i \notin N_H(C)$ or $j \notin N_H(C)$. Then i and j are compatible (half-compatible) at $\hat{C}$ if and only if they are compatible (half-compatible) at C.

Note that the first condition removes all the loops at patients in N_H. Consequently, the resulting compatibility graph $\hat{g}$ is a simple graph. Furthermore, for each matching in $\mathcal{M}(\hat{C})$, a patient in $N_H(C)$ is either unmatched or matched to a patient in $N_I(C)$. Let $L(g) := \{ij \in E(g) \mid i,j \in N_H(C)\}$ be the set of edges between patients in $N_H(C)$, including all loops. Then $E(\hat{g})$ and $L(g)$ constitute a partitioning of $E(g)$, *i.e.*, $E(g) = E(\hat{g}) \cup L(g)$ and $E(\hat{g}) \cap L(g) = \emptyset$. A final observation is that if $N_H(C) = \emptyset$, then $C = \hat{C}$ and $\pi = \pi_M$. In that case, the proofs of Lemmas 7–10, below, follow immediately. Hence, in the proofs of these four lemmas, it is assumed that $N_H(C) \neq \emptyset$. Let $w(\pi)$ be defined by $w_{ii}(\pi) = \pi(i)$ for all $i \in N$ and $w_{ij}(\pi) = \pi(i) + \pi(j)$ for all $i,j \in N$ such that $i \neq j$.

Lemma 7. Consider two problems (N,C,π) and (N,C,π_M) with corresponding compatibility graph g and let $M \in \mathcal{M}(C)$. Then M is a maximum weight matching in $(g, w(\pi))$ if and only if M is a maximum weight matching in $(g, w(\pi_M))$.

Proof. Consider some patient $i \in N_H(C)$ such that M is a maximum weight matching in $(g, w(\pi))$. By definition, M is a maximum weight matching in $(g, w(\pi))$ whenever $S(M, w(\pi)) - S(M', w(\pi)) \geq 0$ for all $M' \in \mathcal{M}(C)$. Since each maximum weight matching is a maximal matching, patient i is matched at M by Lemma 6. Consider an arbitrary matching M' where, without loss of generality, patient i is matched. Then the term $\pi(i)$ is found in both the sum $S(M, w(\pi))$ and the sum $S(M', w(\pi))$. Thus, $\pi(i)$ cancels out in the difference $S(M, w(\pi)) - S(M', w(\pi))$. Consequently, $S(M, w(\pi)) - S(M', w(\pi)) \geq 0$ for all $M' \in \mathcal{M}(C)$ and all values of $\pi(i)$. That is, M is a maximum weight matching in $(g, w(\pi))$ for all values of $\pi(i)$. Since this argument can be repeated for all $i \in N_H$ and since $\pi(j) = \pi_M(j)$ for all $j \in N_I$, it follows that M is a maximum weight matching in $(g, w(\pi_M))$ as well. The same argument can be used in reverse to show that if M is a maximum weight matching in $(g, w(\pi_M))$, then it is a maximum weight matching in $(g, w(\pi))$. ‖

Lemma 8. Consider two problems (N,C,π) and (N,C,π_M) with corresponding compatibility graph g and let $M \in \mathcal{M}(C)$. Then M is a priority matching at (N,C,π) if and only if it is a priority matching at (N,C,π_M).

Proof. Since almost identical arguments can be used in both directions of the proof, it is only shown that if M is a priority matching at (N,C,π), then it is a priority matching at (N,C,π_M). To reach a contradiction, suppose that M is a priority matching at (N,C,π) but not at (N,C,π_M). As M is a priority matching at (N,C,π), it is a maximum matching by Proposition 3. Furthermore, since the priority function does not impact whether a matching is a maximum matching, M is a maximum matching at (N,C,π_M) as well. Then there exists some pair of patients $i,j \in N$ and some maximum matching M' such that $N^*(M) \setminus N^*(M') = \{i\}$, $N^*(M') \setminus N^*(M) = \{j\}$ and $\pi_M(j) > \pi_M(i)$. First, suppose that $i \in N_H$. This means that i can feasibly be self-matched. Hence, $M' \cup \{ii\} \in \mathcal{M}(C)$. $N^*(M) \subset N^*(M' \cup \{ii\})$ contradicts the observation that M is a maximum matching. Hence, $i \in N_I$. Since $\pi_M(j) > \pi_M(i)$, condition (B.2) in the definition of π_M implies that $j \in N_I$ as well. As $\pi_M(i) = \pi(i)$ and $\pi_M(j) = \pi(j)$, this contradicts the assumption that M is a priority matching at (N,C,π). Consequently, if M is a priority matching at (N,C,π), then it is a priority matching at (N,C,π_M). ‖

Now recall that $L(g) := \{ij \in E(g) \mid i,j \in N_H(C)\}$ is defined to be the set of edges between patients in $N_H(C)$, including all loops.

Lemma 9. Consider two problems (N,C,π_M) and $(N,\hat{C},\pi_M)$ with corresponding compatibility graphs g and $\hat{g}$, respectively. Let $M \in \mathcal{M}(C)$ be a maximal matching. Then M is a maximum weight matching in $(g, w(\pi_M))$ if and only if $M' := M \setminus L(g)$ is a maximum weight matching in $(\hat{g}, w(\pi_M))$.

Proof. It will first be shown that M is a maximum weight matching in $(g, w(\pi_M))$ *only if* $M' := M \setminus L(g)$ is a maximum weight matching in $(\hat{g}, w(\pi_M))$. Suppose that M is a maximum weight matching in $(g, w(\pi_M))$. Since $M \subseteq E(g)$ and $E(g) \setminus L(g) = E(\hat{g})$, by construction, it follows that $M' \in \mathcal{M}(\hat{C})$. As $L(g)$ only contains edges between patients in $N_H(C)$, it is clear that $N^*(M) \cap N_I(C) = N^*(M') \cap N_I(C)$. Now, to reach a contradiction, suppose that M' is not a maximum weight matching in $(\hat{g}, w(\pi_M))$. By definition of π_M, it must be the case that $\pi_M(j) > \sum_{i \in N_H(C)} \pi_M(i)$ for any $j \in N_I(C)$. Consequently, any maximum weight matching at (N,C,π_M) or $(N,\hat{C},\pi_M)$ must match all patients in $N^*(M) \cap N_I(C)$ since M is a maximum weight matching at (N,C,π_M) and all patients in $N(M) \cap N_I(C)$ are simultaneously matchable at $(N,\hat{C},\pi_M)$ by $N^*(M) \cap N_I(C) = N^*(M') \cap N_I(C)$ and $M' \in \mathcal{M}(\hat{C})$.

If M' is not a maximum weight matching at $(N,\hat{C},\pi_M)$, then there must exist some maximum matching $\hat{M} \in \mathcal{M}(\hat{C})$ such that $N^*(M) \cap N_I(C) = N^*(\hat{M}) \cap N_I(C)$ and some $i \in (N^*(M') \cap N_H(C)) \setminus N^*(\hat{M})$ such that $\pi(i) <$

$\sum_{j\in(N^*(\hat{M})\cap N_H(C))\setminus N^*(M')}\pi(j)$. Next, note that $i\in N_H(C)\setminus\Phi_M$ for all $i\in(N^*(M')\cap N_H(C))\setminus N^*(\hat{M})$, since all patients in Φ_M are unmatched at M' by construction. Moreover, every patient in $N_H(C)$ matched to a patient in $N_I(C)$ at M is still matched to the same patient at M' and every patient in $N_H(C)$ that is matched at M' or $\hat{M}$ is matched to some patient in $N_I(C)$ since $\hat{g}$ contains no loops or edges between patients in $N_H(C)$. Thus, $j\in\Phi_M$ for all $j\in(N^*(\hat{M})\cap N_H(C))\setminus N^*(M')$. This contradicts condition (B.3). Hence, M is a maximum weight matching in $(g,w(\pi_M))$ only if M' is a maximum weight matching in $(\hat{g},w(\pi_M))$.

It is next proved that M is a maximum weight matching in $(g,w(\pi_M))$ **if** M' is a maximum weight matching in $(\hat{g},w(\pi_M))$. Suppose that M' is a maximum weight matching in $(\hat{g},w(\pi_M))$. Then condition (B.2) implies that there exists no $\hat{M}\in\mathcal{M}(\hat{C})$ such that $\sum_{i\in N^*(\hat{M})\cap N_I(C)}\pi(i)>\sum_{i\in N^*(M')\cap N_I(C)}\pi(i)$. Recall that $N^*(M)\cap N_I(C)=N^*(M')\cap N_I(C)$. These two findings together with the observation that $L(g)$ only contains loops and edges between patients in $N_H(C)$ imply that there exists no $\tilde{M}\in\mathcal{M}(C)$ such that $\sum_{i\in N^*(\tilde{M})\cap N_I(C)}\pi(i)>\sum_{i\in N^*(M)\cap N_I(C)}\pi(i)$. To reach a contradiction, suppose that M is not a maximum weight matching in $(g,w(\pi_M))$. Then there exists some $\tilde{M}\in\mathcal{M}(C)$ such that $S(\tilde{M},w(\pi_M))>S(M,w(\pi_M))$. Considering that $\sum_{i\in N^*(\tilde{M})\cap N_I(C)}\pi(i)\leq\sum_{i\in N^*(M)\cap N_I(C)}\pi(i)$, it must be the case that $\sum_{i\in N^*(\tilde{M})\cap N_H(C)}\pi(i)>\sum_{i\in N^*(M)\cap N_H(C)}\pi(i)$. However, this is a contradiction as all patients in $N_H(C)$ are matched at M by Lemma 6. Hence, M is a maximum weight matching in $(g,w(\pi_M))$ if M' is a maximum weight matching in $(\hat{g},w(\pi_M))$. ‖

Some definitions related to paths are helpful in some of the coming proofs.

Definition 2. An ordered list of (not necessarily unique) patients $(i_1,\ldots,i_t)$ is a *path of length* t in a graph g if:

- $i_ji_{j+1}\in E(g)$ for all $j\in\{1,\ldots,t-1\}$,
- $i_ji_{j+1}\neq i_{j'}i_{j'+1}$ for all distinct $j,j'\in\{1,\ldots,t-1\}$.[34]

A path is a *maximal path* if it is not contained in a longer path.

Lemma 10. Consider a problem (N,C,π_M) with corresponding compatibility graph g and let $M\in\mathcal{M}(C)$ be a maximal matching. Then M is a priority matching at (N,C,π_M) if and only if $M':=M\setminus L(g)$ is a priority matching at $(N,\hat{C},\pi_M)$.

Proof. It will first be shown that M is a priority matching at (N,C,π_M) *only if* M' is a priority matching at $(N,\hat{C},\pi_M)$. Suppose that M is a priority matching at (N,C,π_M). Since $M\subseteq E(g)$ and $E(g)\setminus L(g)=E(\hat{g})$, by construction, it follows that $M'\in\mathcal{M}(\hat{C})$. To reach a contradiction, suppose that M' is not a priority matching at $(N,\hat{C},\pi_M)$. Then there exists some $\hat{M}\in\mathcal{M}(\hat{C})$ such that $\hat{M}\succ_{\pi_M}M'$. Furthermore, since M' is a maximal matching, there must exist some matching $\hat{M}\in\mathcal{M}(\hat{C})$ such that $N^*(\hat{M})\setminus N^*(M')=\{i\}$ and $N^*(M')\setminus N^*(\hat{M})=\{j\}$ for some $i,j\in N$, where $\pi_M(i)>\pi_M(j)$. By the definitions of $N_I(C)$ and $N_H(C)$ and by the existence of patient i, it must be the case that $i\in N_I(C)$ or $i\in N_H(C)$. Two different cases must be considered to reach the desired contradiction:

(i) Suppose that $i\in N_I(C)$. Since $N^*(M)\cap N_I(C)=N^*(M')\cap N_I(C)$, it must then be the case that $i\notin N^*(M)$ and $j\in N^*(M)$. Let $\tilde{M}:=\hat{M}\cup\{kk\,|\,k\in N_H(C)\setminus N^*(\hat{M})\}$ be an amended version of $\hat{M}$, where all patients in $N_H(C)$ that are unmatched at $\hat{M}$ are self-matched at $\tilde{M}$. Note that $\tilde{M}\in\mathcal{M}(C)$. If $j\in N_H(C)$, then $N^*(M)\subset N^*(\tilde{M})$. If $j\in N_I(C)$, then $N^*(M)\setminus N^*(\tilde{M})=\{j\}$ and $N^*(\tilde{M})\setminus N^*(M)=\{i\}$, where $\pi_M(i)>\pi_M(j)$. However, this in implies that $\tilde{M}\succ_{\pi_M}M$ in both cases, which contradicts the assumption that M is a priority matching at (N,C,π_M). Hence, $i\notin N_I(C)$.

(ii) Suppose that $i\in N_H(C)$. Then condition (B.2) implies that $j\in N_H(C)$ as well. Furthermore, $i\in\Phi_M$ and $j\in N_H(C)\setminus\Phi_M$ by construction. This is a contradiction, since $\pi_M(i)<\pi_M(j)$ by condition (B.3). Hence, $i\notin N_H(C)$.

In conclusion, $i\notin N_I(C)$ and $i\notin N_H(C)$, which contradict the existence of patient i. Thus, M is a priority matching at (N,C,π_M) only if M' is a priority matching at $(N,\hat{C},\pi_M)$.

Finally, it will be shown that M is a priority matching at (N,C,π_M) *if* M' is a priority matching at $(N,\hat{C},\pi_M)$. To reach a contradiction, suppose that M' is a priority matching at $(N,\hat{C},\pi_M)$ and that M is not a priority matching at (N,C,π_M). Then there exists some $\hat{M}\in\mathcal{M}(C)$ such that $\hat{M}\succ_{\pi_M}M$. Furthermore, since all patients in $N_H(C)$ are matched at all maximal matchings given the priority structure C, there exists some $\hat{M}\in\mathcal{M}(C)$ such that $N^*(\hat{M})\setminus N^*(M)=\{i\}$ and $N^*(M)\setminus N^*(\hat{M})=\{j\}$ for some $i,j\in N_I(C)$ such that $\pi(i)>\pi(j)$. Note that $\tilde{M}:=\hat{M}\setminus L(g)\in\mathcal{M}(\hat{C})$ and that $(N^*(\tilde{M})\cap N_I)\setminus(N^*(M')\cap N_I)=\{i\}$ and $(N^*(M')\cap N_I)\setminus(N^*(\tilde{M})\cap N_I)=\{j\}$.

Let $i:=i_1$ and note that there must exist a maximal path $(i_1,\ldots,i_t)$ in $(N,\tilde{M}\cup M')$, where $i_1\neq i_t$. Hence, $t\geq2$. To establish the contradiction, it will next be demonstrated that it cannot be the case that $t\geq2$.

34. In the case when $ii\in E(g)$ for some $i\in N$, the list (i_1,i_2) is a path of length 2 where $i_1=i_2$, *i.e.*, every path has a length of at least 2.

(i) Suppose that $t=2$. Since i_t is matched at M while i is not, this implies that $i_t i_t \in M$ and consequently that $i_t \in \Phi_M$. Then $\breve{M} := M' \cup \{i_1 i_t\} \in \mathcal{M}(\hat{C})$. Since $N^*(M') \subset N^*(\breve{M})$, this contradicts the assumption that M' is a priority matching at $(N, \hat{C}, \pi_M)$.

(ii) Suppose that $t=3$. Then either $i_t \in N_I(C) \setminus N^*(\tilde{M})$ and $i_t = j$, or $i_t \in N_H(C)$. Note that $\breve{M} := (M' \setminus \{i_2 i_t\}) \cup \{i_1 i_2\} \in \mathcal{M}(\hat{C})$. Furthermore, by $\pi(i) > \pi(j)$ and condition (B.2), $\pi(i_1) > \pi(i_t)$ both in the case when $i_t = j$ and the case when $i_t \in N_H(C)$. This implies that $\breve{M} \succ_{\pi_M} M'$, which contradicts the assumption that M' is a priority matching at $(N, \hat{C}, \pi_M)$.

(iii) Suppose that $t \geq 4$. Recall that there are no edges between patients in $N_H(C)$ or loops in M' or $\tilde{M}$. Two different cases arise:

- If t is even, then $i_t \in \Phi_M$. Define $\gamma := \{i_k i_{k+1} \mid k \in \{2, \ldots, t-2\} \subset 2\mathbb{N}\}$ and $\gamma' := \{i_k i_{k+1} \mid k \in \{1, \ldots, t-1\} \subset \mathbb{N} \setminus 2\mathbb{N}\}$. Note that $\breve{M} := (M' \setminus \gamma) \cup \gamma' \in \mathcal{M}(\hat{C})$. Since $N^*(M') \subset N^*(\breve{M})$, $\breve{M} \succ_{\pi_M} M'$. This contradicts the assumption that M' is a priority matching at $(N, \hat{C}, \pi_M)$.
- If t is odd, then either $i_t \in N_I(C) \setminus N^*(\tilde{M})$ and $i_t = j$, or $i_t \in N_H(C) \setminus \Phi_M$. Define $\gamma := \{i_k i_{k+1} \mid k \in \{2, \ldots, t-1\} \subset 2\mathbb{N}\}$ and $\gamma' := \{i_k i_{k+1} \mid k \in \{1, \ldots, t-2\} \subset \mathbb{N} \setminus 2\mathbb{N}\}$. Note that $\breve{M} := (M' \setminus \gamma) \cup \gamma' \in \mathcal{M}(\hat{C})$. Furthermore, $N^*(\breve{M}) \setminus N^*(M') = \{i_t\}$ and $N^*(M') \setminus N^*(\breve{M}) = \{i\}$. By $\pi(i) > \pi(j)$ and condition (B.2), it follows that $\pi(i_1) > \pi(i_t)$ both in the case when $i_t = j$ and the case when $i_t \in N_H(C) \setminus \Phi_M$. This implies that $\breve{M} \succ_{\pi_M} M'$, which contradicts the assumption that M' is a priority matching at $(N, \hat{C}, \pi_M)$.

Hence, M is a priority matching at (N, C, π_M) if M' is a priority matching at $(N, \hat{C}, \pi_M)$. ‖

The next result (Lemma 11) finds an equivalence between priority matchings and maximum weight matchings for any given problem (N, C, π). The problem $(N, \hat{C}, \pi_M)$ has a corresponding simple compatibility graph $\hat{g}$, since all the loops have been removed. However, while no patients are half-compatible with their own donors at $\hat{C}$, they may still be half-compatible with other donors. Therefore, the key idea in the proof of Proposition 5 will be to demonstrate that for any problem (N, C, π), there exists an equivalent problem $(N, \breve{C}, \pi)$ with a corresponding simple graph $\breve{g}$, in which *no* patients are half-compatible with *any* donors. That is, $\breve{C}$ is binary, in the sense that any pair of patients and donors is either compatible or incompatible at $\breve{C}$. Gather all compatibility structures at which no patients are half-compatible with any donors in the set $\mathcal{C}_{02}$. Note that the compatibility structures considered by Okumura (2014) belong to $\mathcal{C}_{02}$. Lemma 1 is only applicable in problems with compatibility structures belonging to $\mathcal{C}_{02}$. To understand Lemma 11, note that the problem (N, C, π) need not correspond to the conditions in Lemma 1 by Okumura (2014). Any problem (N, C, π) in which $N_H = \emptyset$ has a corresponding simple compatibility graph. However, $N_H = \emptyset$ does not guarantee the requirement in Lemma 1 that no patients and donors are half-compatible to be satisfied. Lemma 11 is therefore not implied by Lemma 1, since there are compatibility structures not belonging to $\mathcal{C}_{02}$ with corresponding compatibility graphs that are simple graphs.

Lemma 11. For any problem (N, C, π) with corresponding simple compatibility graph g, a matching M is a priority matching at (N, C, π) if and only if M is a maximum weight matching in $(g, w(\pi))$.

Proof. It will first be demonstrated that for any problem (N, C, π) with corresponding simple compatibility graph g, there exists a compatibility structure $\breve{C}$ such that no patients and donors are half-compatible, a matching M is a priority matching at (N, C, π) if and only if it is a priority matching at $(N, \breve{C}, \pi)$ and $\mathcal{M}^*(C) = \mathcal{M}^*(\breve{C})$. The corresponding compatibility graph of $\breve{C}$ is denoted by $\breve{g}$.

Let $\overline{C}$ be a compatibility structure for which each patient is incompatible with her own donor and compatible with every other donor. Then $\overline{C} \in \mathcal{C}_{02}$ and the corresponding compatibility graph, $\overline{g}$, is a complete graph. Consider some arbitrary set of edges $E' \subseteq E(\overline{g})$. Let $\hat{C}'$ be a compatibility structure for which each patient $i \in N$ is compatible with some donor d_j if and only if $id_j \in E(\overline{g}) \setminus E'$ and let $\hat{g}'$ be its corresponding compatibility graph. Then $\hat{C}' \in \mathcal{C}_{02}$, $E(\hat{g}') \subset E(\overline{g})$ and $E(\overline{g}) \setminus E(\hat{g}') = E'$. Since $\overline{C} \in \mathcal{C}_{02}$, $\overline{g}$ is a complete graph and E' is an arbitrary set of edges, there exists some $C' \in \mathcal{C}_{02}$ with corresponding compatibility graph $g' = (N, E)$ for any $E \subseteq E(\overline{g})$. Hence, for any compatibility structure $C \notin \mathcal{C}_{02}$ with corresponding simple compatibility graph g, there exists some $\breve{C} \in \mathcal{C}_{02}$ with corresponding simple compatibility graph $\breve{g}$ such that $\breve{g} = g$. If $\breve{g} = g$, then $\mathcal{M}^*(C) = \mathcal{M}^*(\breve{C})$ since the set of priority matchings for a given compatibility structure only depends the priority function, which is fixed, and on information contained in its corresponding compatibility graph. Hence, for any problem (N, C, π) with corresponding simple compatibility graph g, there exists some $\breve{C} \in \mathcal{C}_{02}$ such that a matching M is a priority matching at (N, C, π) if and only if it is a priority matching at $(N, \breve{C}, \pi)$.

To conclude the proof, note that since $\breve{C} \in \mathcal{C}_{02}$, Lemma 1 implies that M is a priority matching at $(N, \breve{C}, \pi)$ if and only if it is a maximum weight matching in $(\breve{g}, w)$. Since $\breve{g} = g$, M is a maximum weight matching in $(\breve{g}, w)$ if and only if it is

a maximum weight matching in (g,w). Hence, for any problem (N,C,π) with corresponding simple compatibility graph g, M is a priority matching if and only if M is a maximum weight matching in (g,w). ‖

Proposition 5. Consider a problem (N,C,π) with corresponding compatibility graph g. If $w_{ii}=\pi(i)$ for all $ii\in E(g)$ and $w_{ij}=\pi(i)+\pi(j)$ for all $ij\in E(g)$ whenever $i\neq j$, then M is a priority matching if and only if M is a maximum weight matching in (g,w).

Proof. Let (N,C,π) be a problem with corresponding, not necessarily simple, compatibility graph g and suppose that M is a maximum weight matching in (g,w). Since M is a maximal matching in g, Lemmas 7 and 9 imply that there exists a compatibility matrix $\hat{C}$ with corresponding simple compatibility graph $\hat{g}$ such that M is a maximum weight matching in (g,w) if and only if $M':=M\setminus L(g)$ is a maximum weight matching in $(\hat{g},w(\pi_M))$. Since $\hat{g}$ is a simple compatibility graph, it follows from Lemma 11 that $M':=M\setminus L(g)$ is a priority matching at $(N,\hat{C},\pi_M)$ if and only if it is a maximum weight matching in $(\hat{g},w(\pi_M))$. This implies that M is a maximum weight matching in (g,w) if and only if $M':=M\setminus L(g)$ is a priority matching at $(N,\hat{C},\pi_M)$. This conclusion together with Lemmas 8 and 10 implies that for any problem (N,C,π), M is a maximum weight matching in (g,w) if and only if M is a priority matching. ‖

B.3. *Proof of Proposition 6*

Proposition 6. Consider a problem (N,C,π) with corresponding compatibility graph g. Then a matching is a half-compatibility priority matching if and only if it is a maximum weight matching in (g,w^ε).

Proof. ($\Rightarrow$) It is first proved that any maximum weight matching in (g,w^ε) is a half-compatibility priority matching, *i.e.*, if a matching M is a maximum weight matching in (g,w^ε), then $M\in\mathcal{M}^B$. Let M be a maximum weight matching in (g,w^ε). The first step in this part of the proof is to show that M is also a maximum weight matching in (g,w), where w is defined as in Proposition 5. To obtain a contradiction, suppose that M is not a maximum weight matching in (g,w). This means that there is some other matching $M'\in\mathcal{M}$ such that $S(M',w)>S(M,w)$. By the construction of w, it is clear that:

$$S(M',w)-S(M,w)\geq\frac{1}{q}$$

$$\iff\quad S(M',w)\geq S(M,w)+\frac{1}{q}. \tag{B.4}$$

Next, note that $w^\varepsilon_{ij}-w_{ij}\in[0,2\varepsilon]$ for all $ij\in E(g)$ by the construction of w and w^ε. Hence:

$$S(M,w^\varepsilon)-S(M,w)\ \leq\ |N^*(M)|\varepsilon\leq n\varepsilon<\frac{n}{2qn}=\frac{1}{2q}<\frac{1}{q}$$

$$\iff S(M,w^\varepsilon)\ <\ S(M,w)+\frac{1}{q}. \tag{B.5}$$

Inequalities (B.4) and (B.5) imply that:

$$S(M',w)>S(M,w^\varepsilon). \tag{B.6}$$

Since $w^\varepsilon_{ij}-w_{ij}\in[0,2\varepsilon]$ for all $ij\in E(g)$, it follows that:

$$S(M',w^\varepsilon)\geq S(M',w). \tag{B.7}$$

Inequalities (B.6) and (B.7) then imply that $S(M',w^\varepsilon)>S(M,w^\varepsilon)$. But this contradicts the assumption that M is a maximum weight matching in (g,w^ε), *i.e.*, that $S(M,w^\varepsilon)\geq S(M',w^\varepsilon)$ for all $M'\in\mathcal{M}$. Hence, M is a maximum weight matching in (g,w) and, consequently, a priority matching by Proposition 5.

To complete this part of the proof, it will next be shown that $M\in\mathcal{M}^B$. To obtain a contradiction, suppose that $M\notin\mathcal{M}^B$. Consider a matching M' that belongs to $\mathcal{M}^B$. As $\mathcal{M}^B\subseteq\mathcal{M}^*$, M' is a maximum weight matching in (g,w) by Proposition 5. However, as demonstrated above, M is also a maximum weight matching in (g,w). Hence, $S(M,w)=S(M',w)$. Furthermore, note that:

$$S(M',w^\varepsilon)-S(M',w)=\varepsilon B(M') \tag{B.8}$$

$$S(M,w^\varepsilon)-S(M,w)=\varepsilon B(M). \tag{B.9}$$

Since $M\in\mathcal{M}^*\setminus\mathcal{M}^B$ and $M'\in\mathcal{M}^B$, it must be that $B(M')>B(M)$. This implies that $\varepsilon B(M')>\varepsilon B(M)$, as $\varepsilon>0$. It then follows from the conclusion that $S(M,w)=S(M',w)$ and from equations (B.8) and (B.9) that:

$$S(M',w^\varepsilon)-S(M',w)>S(M,w^\varepsilon)-S(M,w)\iff S(M',w^\varepsilon)>S(M,w^\varepsilon).$$

This contradicts the assumption that M is a maximum weight matching in (g,w^ε). Hence, $M\in\mathcal{M}^B$.

($\Leftarrow$) It will now be proved that any $M \in \mathcal{M}^B$ is a maximum weight matching in (g, w^ε). To obtain a contradiction, consider a matching $M \in \mathcal{M}^B$ and assume that M is not a maximum weight matching in (g, w^ε). Then there exists some other matching $M' \in \mathcal{M}$ such that:

$$S(M', w^\varepsilon) > S(M, w^\varepsilon). \tag{B.10}$$

From Proposition 5, it follows that $S(M', w) \leq S(M, w)$ since $M \in \mathcal{M}^*$. It is next demonstrated that $S(M', w) = S(M, w)$. To reach a contradiction, suppose that $S(M', w) < S(M, w)$. Then:

$$\begin{aligned} & S(M, w) - S(M', w) \geq \frac{1}{q} \\ \iff \quad & S(M, w) \geq S(M', w) + \frac{1}{q} \\ \implies \quad & S(M, w^\varepsilon) \geq S(M', w) + \frac{1}{q}. \end{aligned} \tag{B.11}$$

As before, $w^\varepsilon_{ij} - w_{ij} \in [0, 2\varepsilon]$ for all $ij \in E(g)$ ensures that:

$$\begin{aligned} & S(M', w^\varepsilon) - S(M', w) < \frac{1}{q} \\ \iff \quad & S(M', w) + \frac{1}{q} > S(M', w^\varepsilon). \end{aligned} \tag{B.12}$$

Inequalities (B.11) and (B.12) imply that $S(M, w^\varepsilon) > S(M', w^\varepsilon)$, which contradicts inequality (B.10). Hence, $S(M', w) = S(M, w)$.

Next, note that M is a maximum weight matching in (g, w) by Proposition 5 since $M \in \mathcal{M}^*$. But then, M' is also a maximum weight matching in (g, w) because $S(M', w) = S(M, w)$ by the conclusion above. Hence, $M' \in \mathcal{M}^*$ by Proposition 5. Recall that:

$$S(M', w^\varepsilon) - S(M', w) = \varepsilon B(M'), \tag{B.13}$$

$$S(M, w^\varepsilon) - S(M, w) = \varepsilon B(M). \tag{B.14}$$

Now, the conclusion that $S(M', w) = S(M, w)$ together with inequality (B.10) and equations (B.13) and (B.14) imply that:

$$\varepsilon(B(M') - B(M)) = S(M', w^\varepsilon) - S(M, w^\varepsilon) > 0. \tag{B.15}$$

Condition (B.15) and $\varepsilon > 0$ imply that $B(M') > B(M)$. But this contradicts the assumption that $M \in \mathcal{M}^B$ as $M' \in \mathcal{M}^*$. That is, M cannot be an element in $\mathcal{M}^B$ if there exists another priority matching M' at which the number of patients receiving a compatible kidney is larger. Hence, M is a maximum weight matching in (g, w^ε). ‖

B.4. *Proofs of the results in Section 5.1*

Proposition 9. Consider a problem (N, C, π) and suppose that μ' and μ'' contain all patients that receive transplants in Model (a) and Model (b), respectively. Then $\mu' \subseteq \mu''$.

Proof. Consider a problem (N, C, π) with corresponding compatibility graph g and let $\tilde{g}$ be the compatibility graph corresponding to the reduced problem (N_I, C_I, π). That is, let $\tilde{g} = (N_I, E(\tilde{g}))$ where $ij \in E(\tilde{g})$ for all $i, j \in N_I$ such that $ij \in E(g)$. Suppose that M is a maximum weight matching in (g, w^ε) and $\tilde{M}$ is a maximum weight matching in $(\tilde{g}, w^\varepsilon)$. By Proposition 6, M corresponds to a matching selected in Model (b) and $\tilde{M}$ corresponds to a matching selected in Model (a). Moreover, $\mu'' = N^*(M)$ and $\mu' = N^*(\tilde{M}) \cup N_H$. Note that while Model (a) and Model (b) only select a single matching each from a set of half-compatibility priority matchings in their corresponding problems, the selection is inconsequential since any half-compatibility priority matching is a maximum weight matching in the corresponding weighted compatibility graphs.

To prove the result, it will be demonstrated that any patient contained in a maximal path (see Definition 2) in the graph $(N, M \cup \tilde{M})$ belongs to $N^*(M)$.[35] The result mentioned above is first proved for maximal paths of length $t = 2$, *i.e.*, paths of the type (i_1, i_2) in $(N, M \cup \tilde{M})$.

35. Recall that a matching is defined as a set of non-incident edges in a compatibility graph g (or $\tilde{g}$). $M \cup \tilde{M} \subseteq E(g)$ is therefore a subset of the edges in the compatibility graph g, constituting the edge set in the graph $(N, M \cup \tilde{M})$. Maximal paths in $(N, M \cup \tilde{M})$ are of interest since any patient corresponding to an *interior* element (non-end point) in such a maximal path will be matched at both M and $\tilde{M}$. Thus, attention can be restricted to the end points of such maximal paths.

Now consider a maximal path of the type (i_1, i_2) and suppose first that $i_1 = i_2$. Since i_1 belongs to a path in $(N, M \cup \tilde{M})$, i_1 must be matched at either M or $\tilde{M}$. Furthermore, since $i_1 = i_2$ and (i_1, i_2) is a maximal path in $(N, M \cup \tilde{M})$, i_1 must be self-matched at M or $\tilde{M}$. This implies that $i_1 \in N_H$ and consequently that that i_1 is matched at M, as all patients in N_H are matched at M. Hence, $i_1 \in N^*(M)$. Suppose next that $i_1 \neq i_2$ and that i_1 is matched to i_2 at $\tilde{M}$ but that both i_1 and i_2 are unmatched at M. Then $M' := M \cup \{i_1 i_2\} \in \mathcal{M}$, which contradicts the assumption that M is a maximum weight matching in (g, w^ε). Hence, $i_1, i_2 \in N^*(M)$. In summary, any patient contained in a maximal path of length $t = 2$ in $(N, M \cup \tilde{M})$ belongs to $N^*(M)$.

In the remaining part of the proof, maximal paths of length $t \geq 3$ are considered, *i.e.*, paths of the type $(i_1, \ldots, i_t)$ in $(N, M \cup \tilde{M})$. Suppose first that $i_1 = i_t$. Then all patients in $\{i_1, \ldots, i_t\}$ are matched at both M and $\tilde{M}$. Hence, $i \in N^*(M)$ for all $i \in \{i_1, \ldots, i_t\}$. The more difficult case is when $i_1 \neq i_t$.[36] Now consider all interior elements in the path, *i.e.*, each $i \in \{i_2, \ldots, i_{t-1}\}$. To be an interior element in a maximal path, i must be matched at both M and $\tilde{M}$. This implies that $i \in N_I$ and $i \in N^*(M)$ for all $i \in \{i_2, \ldots, i_{t-1}\}$. Hence, for any patient $i \in N_H$, $i \in (i_1, \ldots, i_t)$ only if $i \in \{i_1, i_t\}$. That is, if a patient in N_H is an element in a maximal path, then the patient is a starting point or an end point of that path. Now define:

$$\begin{aligned}
\gamma &:= \{i_k i_{k+1} \,|\, k \in \{2, \ldots, t-2\} \subset 2\mathbb{N}\},\\
\gamma' &:= \{i_k i_{k+1} \,|\, k \in \{1, \ldots, t-1\} \subset \mathbb{N} \setminus 2\mathbb{N}\},\\
\hat{\gamma} &:= \{i_k i_{k+1} \,|\, k \in \{2, \ldots, t-1\} \subset 2\mathbb{N}\},\\
\hat{\gamma}' &:= \{i_k i_{k+1} \,|\, k \in \{1, \ldots, t-2\} \subset \mathbb{N} \setminus 2\mathbb{N}\}.
\end{aligned}$$

To complete the proof, three distinct cases, called (a)–(c), are considered. These cases are also divided into a number of subcases.

(a) Suppose that $i_1, i_t \in N_I$. The following three subcases illustrate that this always results in a contradiction.

(a.1) Suppose that $t = 3$, $i_1 \in N^*(M) \setminus N^*(\tilde{M})$, and $i_t \in N^*(\tilde{M}) \setminus N^*(M)$. Since $M' := (M \setminus \{i_1 i_2\}) \cup \{i_2 i_t\}$ is a feasible matching in $\tilde{g}$ and since $\tilde{M}$ is a maximum weight matching in $(\tilde{g}, w^\varepsilon)$, it must be the case that $\pi(i_1) < \pi(i_t)$. Next, because $M'' := (\tilde{M} \setminus \{i_t i_t\}) \cup \{i_1 i_2\}$ is a feasible matching in g and since M is a maximum weight matching in (g, w^ε), it must be the case that $\pi(i_1) > \pi(i_t)$. This is a contradiction.

(a.2) Suppose that $t \geq 4$ and that t is even. Then i_1 and i_t are either both unmatched at M or both unmatched at $\tilde{M}$. Suppose that both are unmatched at $\tilde{M}$. Then $M' := (\tilde{M} \setminus \gamma) \cup \gamma'$ is a feasible matching in $\tilde{g}$. Since $N^*(\tilde{M}) \subset N^*(M')$, this contradicts the assumption that $\tilde{M}$ is a maximum weight matching in $(\tilde{g}, w^\varepsilon)$.

(a.3) Suppose that $t \geq 4$, that t is odd, that $i_1 \in N^*(M) \setminus N^*(\tilde{M})$ and that $i_t \in N^*(\tilde{M}) \setminus N^*(M)$. Then $M' := (\tilde{M} \setminus \hat{\gamma}) \cup \hat{\gamma}'$ is a feasible matching in $\tilde{g}$, which implies that $\pi(i_1) < \pi(i_t)$. Furthermore, $M'' := (M \setminus \hat{\gamma}') \cup \hat{\gamma}$ is a feasible matching in g, which implies that $\pi(i_1) > \pi(i_t)$. This is a contradiction.

(b) Suppose that $i_1 \in N_H$ and $i_t \in N_I$. Since $i_1 \notin N(\tilde{g})$ and $i_1 \in N^*(M) \setminus N^*(\tilde{M})$, it follows that $i_t \in N^*(\tilde{M}) \setminus N^*(M)$ whenever t is odd and $i_t \in N^*(M) \setminus N^*(\tilde{M})$ whenever t is even.

(b.1) Suppose that $t = 3$. Then $M' := (M \setminus \{i_1 i_2\}) \cup \{i_2 i_t, i_1 i_1\}$ is a feasible matching in g. This contradicts the assumption that M is a maximum weight matching in (g, w^ε). Hence $t \geq 4$.

(b.2) Suppose that $t \geq 4$ and that t is odd. Then $M' := (M \setminus \hat{\gamma}') \cup \hat{\gamma} \cup \{i_1 i_1\}$ is a feasible matching in g where $N^*(M) \subset N^*(M')$. This contradicts the assumption that M is a maximum weight matching in (g, w^ε). Hence, t is even.

(b.3) Suppose that $t \geq 4$ and that t is even. Then $i \in N^*(M)$ for all $i \in \{i_1, \ldots, i_t\}$.

(c) Suppose that $i_1, i_t \in N_H$. Then $i_1, i_t \in N^*(M) \setminus N^*(\tilde{M})$. Hence, $i \in N^*(M)$ for all $i \in \{i_1, \ldots, i_t\}$.

From cases (a)–(c), it can be concluded that any patient contained in a maximal path of length $t \geq 3$ in $(N, M \cup \tilde{M})$ belongs to $N^*(M)$.

It has thus been shown that every patient contained in a maximal path of any length is matched at M. Since every patient in N_I who is matched at $\tilde{M}$ is contained in some maximal path, it must be the case that $N^*(\tilde{M}) \subseteq N^*(M)$. Recall that $\mu'' = N^*(M)$, $\mu' = N^*(\tilde{M}) \cup N_H$ and note that $N_H \subseteq \mu''$ by Lemma 6 and the maximality of M. Hence, $\mu' \subseteq \mu''$. ‖

36. No maximal paths $(N, M \cup \tilde{M})$ of lengths strictly greater than 2 may contain loops. A loop $ii \in M \cup \tilde{M}$ implies that $i \in N_H$ and that i is self-matched at M. Since $i \notin N_I$, there exists no $j \in N$ such that $ij \in \tilde{M}$.

Proposition 8. Consider a problem (N, C, π) and suppose that μ, μ', and μ'' contain all patients that receive transplants in the Benchmark Model, Model (a), and Model (b), respectively. Then $|\mu''| \geq |\mu|$ and $|\mu''| \geq |\mu'|$.

Proof. Consider some problem (N, C, π). Let M, M', and M'' be the matchings selected in the Benchmark Model, Model (a), and Model (b), respectively. By Proposition 3, $|N^*(M'')| \geq |N^*(\hat{M})|$ for all $\hat{M} \in \mathcal{M}$. Since $M \in \mathcal{M}$, it follows that $|N^*(M'')| \geq |N^*(M)|$. That is, $|\mu| \leq |\mu''|$. By Proposition 9, $|\mu'| \leq |\mu''|$. ‖

Proposition 10. Consider a problem (N, C, π) and a matching M selected in Model (b) (Model (a)). Suppose that a patient $i \in N$ is either unmatched or matched to a compatible donor at M. Then, in Model (b) (Model (a)), patient i cannot benefit by declaring half-compatible donors unacceptable.

Proof. Consider a problem (N, C, π) with corresponding weighted compatibility graph (g, w^ε). First note that no patient can affect the weights by declaring half-compatible donors unacceptable by Assumption (ii). This means that a patient i may only influence the outcome of the maximum weight matching problem by removing edges incident to i in g. Let M be a maximum weight matching in (g, w^ε) and consider a patient $i \in N$. Furthermore, let $\hat{C}$ be the resulting compatibility structure when i removes some edges incident to i and let $(\hat{g}, \hat{w}^\varepsilon)$ be the corresponding weighted compatibility graph. Note that, given $\hat{w}^\varepsilon$, all edges in $\hat{g}$ are assigned the same weights as in (g, w^ε).

First, if i is unmatched at M, then there are no edges incident to i in M. Thus, M is still a feasible matching at $\hat{C}$. Since $\hat{g}$ is a subgraph of g (*i.e.* it contains the same vertices and a subset of the edges) and both $\hat{w}^\varepsilon$ and w^ε assign the same weights to the edges in $\hat{g}$, if M is a maximum weight matching in in (g, w^ε), it must also be a maximum weight matching in $(\hat{g}, \hat{w}^\varepsilon)$. Thus, by Propositions 4 and 6, exactly the same patients are matched at both (N, C, π) and $(N, \hat{C}, \pi)$ in Model (b) and i remains unmatched. Since (N, C, π) is an arbitrary problem, the same arguments apply to the reduced problem considered in Model (a) as well.

Finally, suppose that i is matched to a compatible donor d_j at M. Then there exists no donor in the exchange pool that i strictly prefers to d_j. Consequently, i can only be made weakly worse off by declaring half-compatible donors unacceptable. ‖

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Supplementary Data

Supplementary data are available at *Review of Economic Studies* online.

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