Pairwise Kidney Exchange over the Blood Group Barrier

Tommy Andersson
Jörgen Kratz

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Tommy Andersson† and Jörgen Kratz‡

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Abstract
Advances in medical technology have made kidney transplants over the blood group barrier feasible. This paper 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.

Keywords: market design; pairwise kidney exchange; blood group incompatibility; immunosuppressants; half-compatibility priority matchings.

JEL Classification: C78; D02; D63; D78.

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†Department of Economics, Lund University, P.O. Box 7082, SE–222 07 Lund, Sweden. E-mail: tommy.andersson@nek.lu.se.

‡Department of Economics, Lund University, P.O. Box 7082, SE–222 07 Lund, Sweden. E-mail: jorgen.kratz@nek.lu.se.
1 Introduction

Patients that suffer from end-stage renal disease need a kidney transplant to prolong their lives. A kidney can be transplanted from a deceased or living donor, but even when a patient has access to a living donor, a problem emerges if the patient is blood group or tissue type incompatible with the donor. This incompatibility can sometimes be overcome by exchanging kidneys with another incompatible patient-donor pair. This observation was instrumental to the establishment of the New England Program for Kidney Exchange which was launched in the United States more than a decade ago. It was the first centralized multi-hospital kidney exchange program based on optimization techniques and it was built on the work by Roth et al. (2004, 2005b). Only pairwise exchanges were allowed initially. After discussions with the medical community, development of new techniques and findings in simulation experiments, additional 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 added as well.\(^1\)

Despite the introduction of kidney exchange programs, there is a rapidly increasing shortage of kidneys. In the United 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). One 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 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 US doctors is to assume that two compatible living-donor kidneys essentially have the same survival rates (Delmonico, 2004; Gjertson and Cecka, 2000; Sönmez and Ünver, 2014). Nicoló and Rodríguez-Álvarez (2017) also focus 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

\(^1\) For an overview of the development of kidney exchange programs in the United States, see Anderson et al. (2015) or Sönmez and Ünver (2014). For a description of all 12 existing European kidney exchange programs, see Biró et al. (2017).
exchange programs as the patient may be assigned a different, strictly preferred donor. In similarity with Sönmez and Ünver (2014) and Nicoló and Rodríguez-Álvarez (2017), this paper 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. To explain how this is possible, a brief description of the ABO blood group classification system is provided below.

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) can not produce anti-A antibodies (anti-B antibodies) and will therefore only have anti-B antibodies (anti-A antibodies) in his 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. However, immunosuppressive protocols for removing anti-A and/or anti-B antibodies have been known since the 1970s (Alexander et al., 1987). These protocols make transplants over the blood group barrier feasible and they have been refined over the years. In 2001, the blood group antigen-specific filter GlycoSorb was introduced (Rydberg et al., 2005). This filter absorbs specific antibodies and the idea is to reduce the patient’s antibody level below a certain threshold in order to enable transplantation over the blood group barrier. The antibody level (antibody titer) 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 of a patient 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 to six months.\textsuperscript{2,3} GlycoSorb is now used in all Swedish transplant centers and at least 60 European centers spread across 17 countries. Between 2001–2012, 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). It can also be argued that there are no cost-benefit arguments for not using GlycoSorb. More precisely, 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.\textsuperscript{4} Hence, it only takes around three years to reach cost balance. 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). Even though the arguments above speak in favor 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 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 saved.

This paper studies the welfare consequences of introducing transplantation over the blood group barrier. The analysis is restricted to kidney exchange programs that only allow pairwise exchanges. A patient is said to be compatible with a donor if they are both blood group and tissue type compatible. If a patient and donor are tissue type compatible, blood group incompatible and

\textsuperscript{2}These numbers were communicated to one of the authors of this paper (Andersson) at a meeting in Stockholm (March, 2016) with immunologists and transplant surgeons from the four Swedish transplant centers (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., 2016).

\textsuperscript{3}The authors of this paper 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 of this paper (Andersson) in May 2016, that approximately 90 percent 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 titer 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 percent of all blood donors with blood group O had antibody titer values strictly below 1:128.

\textsuperscript{4}These figures are based on Swedish data and they can be found in Thydén et al. (2012) and Wennberg (2010). SEK 1 = USD 0.12 (December, 2017).
transplantation over the blood group barrier is feasible, then they are said to be half-compatible. That is, a patient can receive a kidney from a half-compatible donor only by crossing the blood group barrier. By the arguments above, it is natural to assume that patients with half-compatible donors strictly prefer compatible donors to their own blood group incompatible donors (e.g., to avoid additional medical treatments or to shorten the time to transplantation). The inclusion of such patient-donor pairs in a kidney exchange program would play a similar role as 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. 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 paper. They are called half-compatibility priority matchings and are guaranteed to be Pareto efficient. One innovation in this paper is to present a fast computational method for finding half-compatibility priority matchings.

The point of departure in the analysis is a Benchmark Model in which transplantation over the blood group barrier is unfeasible and kidney exchanges are selected in accordance with priority matchings (as in, e.g., Roth et al., 2005b). This paper attempts to answer the following question: given that the current situation corresponds to the Benchmark Model, how should the technology enabling transplantation over the blood group barrier be utilized? The answer is not immediately clear since there are multiple ways to implement the technology. To see this, consider the following two “models”. In the first model, referred to as Model (a), patients with half-compatible donors always receive transplants over the blood group barrier from their own donors. Patients with incompatible donors participate in the kidney exchange program and receive transplants in accordance with a half-compatibility priority matching. This is in line with current practice in, e.g., the French and Swedish kidney exchange programs, where patients that can feasibly receive kidneys from their own donors are not asked to participate in kidney exchange. In the second model, referred to as Model (b), all patients with either half-compatible or incompatible donors participate in the kidney exchange program and receive transplants in accordance with a half-compatibility priority matching. To ensure that patients with half-compatible donors have an incentive to participate in the exchange program, they are involved in kidney exchanges only if they receive compatible kidneys (since they are assumed to prefer their own donors to other half-compatible donors). Patients with half-compatible donors that not are involved in exchanges receive transplants over the blood group barrier from their own donors.

The theoretical findings in this paper 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 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). However, before making such a transition, it may be wise to investigate whether some patient groups would be proportionally disadvantaged by the transition, e.g., patients with incompatible donors or patients with blood group O.\footnote{It is well-known that blood group O patients are often proportionally disadvantaged in kidney exchange programs. See, e.g., Roth et al. (2007).}

To investigate this, it is first proved that if there is a transition from Model (a) to Model (b), all patients receiving a transplant in Model (a) will also receive a transplant in Model (b). What cannot be guaranteed is that all patients that are matched to compatible donors in Model (a) are also matched to compatible donors in Model (b). In other words, some patients may receive transplants over the blood group barrier in Model (b) even though they were matched to compatible donors in Model (a). However, the results from a simulation in this paper suggest that the prevalence of such situations is very low. In fact, it is more common that patients receive half-compatible kidneys in Model (a) and compatible kidneys in Model (b) than vice versa. The simulations also show that blood group O patients are on average less disadvantaged in Models (a) and (b) than they are in the Benchmark Model. Hence, transplantation over the blood group barrier will not only increase the number of transplants, it can also help disadvantaged patient groups. The simulation study, furthermore, reveal that the positive effect of transplantation over the blood group barrier on the number of transplants is significantly larger than the effect of including compatible patient-donors pairs or of allowing three-way exchanges.

A recent paper related to the model presented in this paper is Chun et al. (2015). They consider 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 percent.

Sönmez et al. (2016) analyze 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. (2016) 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 bio-
logically 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 titer level history for blood group O patients and a delay in the subtyping tests until incompatible pairs are transferred to the kidney exchange pool.

The remaining part of the paper is outlined as follows. Section 2 introduces the model. Section 3 provides some properties of half-compatibility priority matchings and presents a computational method for finding them. Section 4 analyzes the welfare implications of pairwise kidney exchange over the blood group barrier, both theoretically and by means of a simulation study. Section 5 concludes the paper. Appendix A provides an equivalence between the set of priority matchings as defined in this paper and the set of priority matchings as defined by Roth et al. (2005b). Appendix B contains the proofs of the theoretical results.

2 Model

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

2.1 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 $i$ can not receive a kidney from donor $d_j$ under any circumstances. No patient in $N$ is compatible with his own donor since patients with compatible donors are assumed to receive kidneys from their own donors outside the kidney exchange program (except in Section 4.2). The patients in $N$ are partitioned into two disjoint sets: $N_H$ and $N_I$. Patient $i$ belongs to $N_H$ if and only if patient $i$ is half-compatible with his own donor $d_i$. 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 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 \( d_k \).

The preferences of all patients in \( N \) are gathered in the list \( \succeq := (\succeq_i)_{i \in N} \). Many existing kidney exchange programs give priority to patients that are highly sensitized 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 modeled by a priority function \( \pi : N \rightarrow \mathbb{R}_{++} \) assigning each patient \( i \in N \) a unique priority \( \pi(i) \). 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). Throughout the paper (with the exception of some results in Section 5 related to incentives), a kidney exchange problem is fixed and defined as a triple \((N, C, \pi)\).

### 2.2 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 \((N, C, \pi)\), 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 \((N, C, \pi)\) 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 \( N^*(M) \nsubseteq N^*(M') \) for all \( M' \in \mathcal{M} \). A

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\( \mathbb{R}_{++} \) 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, \( \mathbb{Z} \).

This assumption on \( \pi(i) \) is made without loss of generality to get a “non-messy” upper bound on the constant \( \varepsilon \) defined in Section 3.2. All results presented in the paper hold for any \( \pi(i) \in \mathbb{R}_{++} \) as long as the priorities are unique.
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 $\succeq$, 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 $\mathcal{M}$.

### 2.3 Priority Matchings and Half-Compatibility Priority Matchings

There is a planner (or a market designer) with complete, transitive and responsive preferences $\succeq_B$ 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 $M'$ 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 $\succeq_B$ 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 $\succeq_B$ belongs to a class of preferences called half-compatibility priority preferences if it is complete, transitive and satisfies the following conditions:

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

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

Half-compatibility priority preferences are closely related to the priority preferences introduced by Roth et al. (2005b). In fact, a preference relation $\succeq_\pi$ is a priority preference relation if it satisfies all of the conditions above, given that (2) and the last line in (1) have been replaced by a requirement that the planner always be indifferent between $M$ and $M'$ whenever $N^*(M) = N^*(M')$. 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 barrier is not feasible. Hence, the two classes of preferences coincide in such settings.

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8See Appendix A for a detailed discussion.
Consider some priority preferences $\succeq_\pi$ and some half-compatibility priority preferences $\succeq_B$. A matching $M$ is called a priority matching if $M \succeq_\pi M'$ for every matching $M' \in \mathcal{M}$. For a given problem $(N, C, \pi)$, all priority matchings are gathered in the set $\mathcal{M}^* \subseteq \mathcal{M}$. A matching $M$ is called a half-compatibility priority matching if $M \succeq_B M'$ for every matching $M' \in \mathcal{M}$. For a given problem $(N, C, \pi)$, all half-compatibility priority matchings are gathered in the set $\mathcal{M}^B$.

3 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.

3.1 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 $\succeq_B$. Fortunately, the following result reveals that $\mathcal{M}^B$ remains the same for any choice of half-compatibility priority preference relation $\succeq_B$.

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

Consider some matching mechanism that, for every problem $(N, C, \pi)$, makes use of some half-compatibility priority preference relation to locate a half-compatibility priority matching $M$. Theorem 1 then guarantees that $M$ is a half-compatibility priority matching for all half-compatibility priority preferences. Such a mechanism is described in Section 3.2. Theorem 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 that the definition of priority matchings in this paper 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 1. For a given problem $(N, C, \pi)$, 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). However, priority matchings are no longer necessarily Pareto efficient when transplantation over the blood group barrier is feasible. 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 2.** For a given problem \((N, C, \pi)\), every half-compatibility priority matching is a Pareto efficient maximum matching.

Proposition 2 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 4, 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 6). However, Proposition 2 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 2 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 3 shows that all priority matchings (including all half-compatibility priority matchings) match exactly the same patients.

**Proposition 3.** For a given problem \((N, C, \pi)\), \(N^*(M) = N^*(M')\) 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; pair 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

---

9To 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 \(M \succeq_{\pi} M''\) for all \(M'' \in \mathcal{M}\)).
all patients $N$ and a family $\mathcal{I}$ containing all sets of patients that can be matched simultaneously constitute a matroid\(^{10}\) $(N, \mathcal{I})$. This was shown by Roth et al. (2005b) for settings with a binary compatibility structure (no transplantation over the blood group barrier). Proposition 4 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.

**Proposition 4.** 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.

This structure ensures that every maximal matching is a maximum matching. If cyclic exchanges involving three or more patient-donor pairs are feasible, then Proposition 4 no longer holds, giving rise to a trade-off between prioritizing patients and maximizing the number of transplants. See, e.g., Kratz (2017) and Sönmez and Ünver (2014) for more detailed discussions.

A final remark is that the findings in this section provide justification for half-compatibility priority preferences. As argued in the introduction, there are good reasons for minimizing the use of immunosuppressants. Furthermore, as described in Biró et al. (2017), maximal number of transplants is a criterion 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.

### 3.2 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. One advantage of this method is that it is computationally efficient in the sense that it can find half-compatibility priority matchings in polynomial time. In order to describe this computational method, some graph theoretical notation must 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

\(^{10}\)A formal definition of matroids is given in Appendix A (Definition 1).
\(N(g)\) and \(E(g)\) denote the vertex set and the edge set of the compatibility graph \(g\), respectively. 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 his 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 \(k \in N \setminus \{i, j\}\). Then \(ij \in M\) 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 his own donor. The non-incidence requirement on the edges ensures that each patient is assigned 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 2.2.

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.

\textbf{Lemma 1.} (Okumura, 2014, Theorem 2). Consider a problem \((N, C, \pi)\) with corresponding compatibility graph \(g\). Suppose that transplantation over the blood group barrier is not possible. 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 paper 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).

\footnote{Each patient \(i \in N\) is incompatible with his own donor and either compatible or incompatible with donor \(d_j\) for all \(j \in N\).}
Proposition 5. Consider a problem \((N, C, \pi)\) 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 \((g, w)\).

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 \((N, C, \pi)\) with corresponding compatibility graph \(g\). Let \(0 < \varepsilon < \frac{1}{2nu}\) 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:

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

Theorem 2. Consider a problem \((N, C, \pi)\) 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 \((g, w^\varepsilon)\).

A solution to the maximum weight matching problem in Theorem 2 can be found in polynomial time by adopting the Hungarian method of Kuhn (1955) and Munkres (1957).

4 Welfare Implications of Kidney Exchange over the Blood Group Barrier

This section analyses the consequences of introducing a medical technology enabling transplants over the blood group barrier. Even though the existence of some welfare effects can be proven, a simulation study is necessary to estimate their magnitudes. For this reason, this section contains both theoretical results and simulation results.

A model with pairwise exchanges and no transplantation over the blood group barrier (as in, e.g., Roth et al., 2005b) is used as a benchmark. When a medical technology which makes transplants over the blood-group barrier feasible is available, patient and planner preferences will distinguish between compatible and half-compatible donors and matchings, respectively. Two distinct “models” are introduced to represent two different ways in which the planner can implement this technology. Both models can be thought of as extensions to the Benchmark Model. Let \((N_I, C_I, \pi)\) 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 \(N_I\).
- **Benchmark Model.** Transplants over the blood group barrier are not feasible. A priority matching is found for the problem \((N,C,\pi)\).

- **Model (a).** Transplants over the blood group barrier are feasible. 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 \((N_{I}, C_{I}, \pi)\).

- **Model (b).** Transplants over the blood group barrier are feasible. A half-compatibility priority matching is found for the problem \((N,C,\pi)\).

The difference between Model (a) and Model (b) is that the former model does not include patients with half-compatible donors in the kidney exchange program. Such patients are always self-matched and never participate in kidney exchanges. Model (a) corresponds to some small and recently established European kidney exchange programs (e.g., the French and Swedish programs), which only allow for pairwise exchanges and patients with half-compatible donors receive kidneys over the blood group barrier from their own donors outside the exchange systems (see Biró et al., 2017). With the exception of Section 4.2, patients with compatible donors are also assumed to receive kidneys from their own donors outside kidney exchange programs throughout the paper. Patients with compatible donors are therefore not included in any of the models described above.

An important distinction between the Benchmark Model and the other two models is that the matching selected in the Benchmark Model may not be a half-compatibility priority matching. There are good reasons for a planner concerned with patient welfare to select half-compatibility priority matchings, which are known to be Pareto efficient, in Models (a) and (b). The following example shows that priority matchings may be Pareto dominated by the matchings selected in Models (a) and (b).

**Example 1.** Suppose that \(N = \{1, 2, 3, 4\}\) and that each patient is incompatible with his own 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. Suppose further that patient 1 is compatible with donor \(d_2\) and that no other patient is compatible with any other donor. 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 \(M'\). This means that both \(M\) and \(M'\) could be selected in the Benchmark Model, but only \(M\) can be selected in Models (a) and (b). 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 \(M'\). □
4.1 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 2 implies that the half-compatibility priority matching patients in $N_I$ are matched in accordance with in Model (a) is a Pareto efficient maximum matching for the reduced problem $(N_I, C_I, \pi)$. The matchings selected in the Benchmark Model and Model (b), on the other hand, are Pareto efficient maximum matchings for the problem $(N, C, \pi)$ 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 feasible). 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.\(^\text{12}\) The following result is proven with the help of an example that will also be useful later in this section.

**Proposition 6.** 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, 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 $d_2$. \(\qed\)

The example above 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.

\(^\text{12}\)It is well-known that larger patient-donor pools result in more transplants than smaller pools. See, e.g., Roth et al. (2006)
as in Model (a). This is not the case 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 $(N, C, \pi)$. 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 7.** Consider a problem $(N, C, \pi)$ and suppose that $\mu$, $\mu'$ and $\mu''$ contain all patients that receive transplants in the Benchmark Model, Model (a) and Model (b), respectively.\(^{13}\) 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 6 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 7, 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 the French and Swedish kidney exchange programs. 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 8 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 8.** Consider a problem $(N, C, \pi)$ and suppose that $\mu'$ and $\mu''$ contain all patients that receive transplants in Model (a) and Model (b), respectively. Then $\mu' \subseteq \mu''$.

\(^{13}\)Note that $|\mu| = |N^*(M)|$ and $|\mu''| = |N^*(M'')|$ if matchings $M$ and $M''$ are the outcomes of the Benchmark Model and 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 7) and that patients receiving transplants before the transition are guaranteed to still receive transplants after the transition (Proposition 8). 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 6 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 his 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 $d_4$.

4.2 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 paper. 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 more 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”) partic-
ipate 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. 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., Gentry et al., 2007; Roth et al., 2005a; Sönmez and Ünver, 2014). The outcomes in these two models are estimated under the assumption that transplants over the blood group barrier are not allowed 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 analyze 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 $\pi_C : N_C \cup N \rightarrow \mathbb{R}_{++}$ be a priority function assigning each patient in $N_C \cup N$ a unique priority.

- **Altruistic Model.** Transplants over the blood group barrier are not possible. A priority matching is found for the problem $(N_C \cup N, C_C, \pi_C)$. Unmatched patients in $N_C$ are self-matched with their own compatible donors.

- **Cycle Model.** Transplants over the blood group barrier are not possible. Three-way exchanges are permitted in addition to pairwise exchanges. A maximum matching is found for the problem $(N, C, \pi)$.

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 19 and 20 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, crossmatch probabilities, etc.) identical to the data described in Roth et al. (2007) and Saidman et al. (2006).

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14Cyclic 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.

15Since 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.

16The reason the Cycle Model selects a maximum matching rather than a priority matching is that the matroid structure discussed in Section 3 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 (2017) and Sönmez and Ünver (2014).
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 percent. For the second number, it is assumed that transplantation over the blood group barrier is feasible for 75 percent of patients. The priority $\pi(i)$ for each patient $i$ is defined as in Keizer et al. (2005):

$$\pi(i) = \text{PRA}(i) \times \text{(share of donors in the pool that patient } i \text{ is incompatible with)} \quad (3)$$

The equation above captures the transplantation possibilities of patient $i$ both outside and within the kidney exchange program. The higher priority, the more difficult it is to find a suitable donor for the patient. Since both factors on the right hand side of equation (3) belong to the interval $[0, 1]$, patient priorities are guaranteed to take values between 0 and 1. The remainder of this section analyses a Monte Carlo simulation based on 1000 populations randomly drawn from the medical distributions discussed above for population sizes of 25, 50, 100, 200 and 500 patient-donor pairs. 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. Around 50 percent of patients already have compatible donors and consequently do not participate in kidney exchange programs. This means that a generated population of 500 patient-donor pairs corresponds to a kidney exchange program with 250 participating pairs. Many European countries, including Austria, Belgium, France, Poland, Portugal and Sweden, have much smaller programs in which fewer than 20 exchanges have been conducted (Biró et al., 2017).

Table 1 describes the percentage 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 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 7, 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 34.1 percent of the patients in the Benchmark Model will not receive transplants. The corresponding numbers for

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17 Recall from footnote 3 that this number is estimated to be around 90 percent. In the simulation study, however, a more conservative number is used to ensure that the results for Models (a) and (b) are not overestimated.

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

19 Roth et al. (2007) consider both the Benchmark Model and the Cycle Model. The patient-donor pool in their
Models (a) and (b) are 11.0 percent and 7.9 percent, 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., $34.1 - 7.9 = 26.2$ percent of 50 patients). To achieve this, 11.6 patients (i.e., $14.6 + 8.5 = 23.1$ percent of 50 patients) must receive transplants over the blood group barrier on average. 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).

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 27.3 percent (i.e., $21.0 + 6.3$ percent) of patients receive transplants over the blood group barrier in Model (a). The corresponding number in Model (b) is only 23.1 percent (i.e., $14.6 + 8.5$ percent). 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. This conclusion holds for both Models (a) and (b).

Proposition 6 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 2 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 0.2 percent of the cases. In fact, in nearly 100 percent of all cases, Model (a) generates a strictly larger number of transplants than the Benchmark Model. Hence, the theoretical finding in Proposition 6 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 should worry about.

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 paper is 8.7 patients (17.3 percent 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 paper is 20.8 (20.8 percent when $n = 100$). In this sense, the results in this paper 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 paper.

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 paper are 25.7, 51.2 and 102.8 (see footnote 19). 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 1: Percentage of different types of transplants for various models and population sizes.

<table>
<thead>
<tr>
<th>n</th>
<th>Model</th>
<th>No transplant</th>
<th>Self-match</th>
<th>ABOi self-match</th>
<th>Exchange</th>
<th>ABOi exchange</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>25</td>
<td>Benchmark Model</td>
<td>38.5%</td>
<td>48.8%</td>
<td>0.0%</td>
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<tr>
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<td>Model (a)</td>
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<td>Model (b)</td>
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</tr>
<tr>
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<td>Model (a)</td>
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<td>100.0%</td>
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<td>N/A</td>
<td>N/A</td>
<td>N/A</td>
<td>N/A</td>
</tr>
</tbody>
</table>

* Approximations from Roth et al. (2007). N/A = Not Available.

Table 2: 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.

<table>
<thead>
<tr>
<th>Patient-donor pool size</th>
<th>25</th>
<th>50</th>
<th>100</th>
<th>200</th>
<th>500</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fewer transplants in Model (a) than in the Benchmark Model</td>
<td>0.2%</td>
<td>0.0%</td>
<td>0.0%</td>
<td>0.0%</td>
<td>0.0%</td>
</tr>
<tr>
<td>Equally many transplants in the Benchmark Model and Model (a)</td>
<td>1.3%</td>
<td>0.0%</td>
<td>0.0%</td>
<td>0.0%</td>
<td>0.0%</td>
</tr>
<tr>
<td>More transplants in Model (a) than in the Benchmark Model</td>
<td>98.5%</td>
<td>100.0%</td>
<td>100.0%</td>
<td>100.0%</td>
<td>100.0%</td>
</tr>
</tbody>
</table>

Total | 100.0% | 100.0% | 100.0% | 100.0% | 100.0% |

Proposition 8 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 important to investigate how many patients are made better off and how many patients are made worse off by such a transition. Table 3 shows that, on average, between 1.0 and 2.5 percent 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 6.7 and 9.7 percent 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.
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 27.3 percent of patients receive kidneys over the blood group barrier in Model (a), whereas the corresponding number for Model (b) is 23.1 percent.

Table 3: Shares of patients receiving transplants in Model (a) that are matched to better, equally good and worse donors in Model (b) in terms of blood group compatibility.

<table>
<thead>
<tr>
<th>Patient-donor pool size</th>
<th>25</th>
<th>50</th>
<th>100</th>
<th>200</th>
<th>500</th>
</tr>
</thead>
<tbody>
<tr>
<td>Compatible donor in Model (a) and half-compatible donor in Model (b)</td>
<td>1.0%</td>
<td>1.6%</td>
<td>1.9%</td>
<td>2.2%</td>
<td>2.5%</td>
</tr>
<tr>
<td>Equally good donors in Models (a) and (b)</td>
<td>92.3%</td>
<td>90.8%</td>
<td>89.5%</td>
<td>88.4%</td>
<td>87.8%</td>
</tr>
<tr>
<td>Half-compatible donor in Model (a) and compatible donor in Model (b)</td>
<td>6.7%</td>
<td>7.6%</td>
<td>8.6%</td>
<td>9.4%</td>
<td>9.7%</td>
</tr>
<tr>
<td>Total</td>
<td>100.0%</td>
<td>100.0%</td>
<td>100.0%</td>
<td>100.0%</td>
<td>100.0%</td>
</tr>
</tbody>
</table>

So far, there has been no discussion on 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 et al., 2016). 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 (Sönmez and Ünver, 2013). This means that blood group O patients will generally be involved in fewer exchanges than patients with other blood groups since they can only receive kidneys from blood group O donors (see the Introduction 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 4 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 percent, 34 percent, 14 percent and 4 percent 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 59.1 and 59.5 percent (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 68.9 and 85.9 percent. 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 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.

Table 4: Ex ante and ex post distributions of blood groups in the patient-donor pool for various models and population sizes.

<table>
<thead>
<tr>
<th>Model</th>
<th>n</th>
<th>Distribution</th>
<th>O</th>
<th>A</th>
<th>B</th>
<th>AB</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Benchmark Model</td>
<td>25</td>
<td>Ex Ante</td>
<td>59.3%</td>
<td>25.2%</td>
<td>13.8%</td>
<td>1.7%</td>
<td>100.0%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Ex Post</td>
<td>68.9%</td>
<td>19.8%</td>
<td>10.4%</td>
<td>0.9%</td>
<td>100.0%</td>
</tr>
<tr>
<td>Benchmark Model</td>
<td>50</td>
<td>Ex Ante</td>
<td>59.5%</td>
<td>24.7%</td>
<td>13.9%</td>
<td>1.9%</td>
<td>100.0%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Ex Post</td>
<td>73.7%</td>
<td>16.7%</td>
<td>8.8%</td>
<td>0.8%</td>
<td>100.0%</td>
</tr>
<tr>
<td>Benchmark Model</td>
<td>100</td>
<td>Ex Ante</td>
<td>59.1%</td>
<td>24.7%</td>
<td>14.4%</td>
<td>1.8%</td>
<td>100.0%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Ex Post</td>
<td>77.1%</td>
<td>14.4%</td>
<td>8.0%</td>
<td>0.5%</td>
<td>100.0%</td>
</tr>
<tr>
<td>Benchmark Model</td>
<td>200</td>
<td>Ex Ante</td>
<td>59.1%</td>
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<td>1.8%</td>
<td>100.0%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Ex Post</td>
<td>81.0%</td>
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<tr>
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<td>Ex Ante</td>
<td>59.3%</td>
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<td>1.8%</td>
<td>100.0%</td>
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<tr>
<td></td>
<td></td>
<td>Ex Post</td>
<td>85.9%</td>
<td>8.7%</td>
<td>5.3%</td>
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<tr>
<td>Model (a)</td>
<td>25</td>
<td>Ex Ante</td>
<td>52.9%</td>
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<td>2.9%</td>
<td>100.0%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Ex Post</td>
<td>57.2%</td>
<td>27.7%</td>
<td>12.7%</td>
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<td>Model (a)</td>
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<tr>
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<td>2.6%</td>
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<td>Model (a)</td>
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<tr>
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<td>Altruistic Model</td>
<td>500</td>
<td>Ex Ante</td>
<td>48.0%</td>
<td>34.0%</td>
<td>14.0%</td>
<td>4.0%</td>
<td>100.0%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Ex Post</td>
<td>72.0%</td>
<td>15.4%</td>
<td>12.4%</td>
<td>0.2%</td>
<td>100.0%</td>
</tr>
</tbody>
</table>

21 For large $n$, these two distributions are expected to coincide. This is also the case when $n = 200$ and $n = 500$ (see Table 4).
When medical technology enabling 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 59.4 and 65.6 percent, respectively. This can be compared to the corresponding numbers for the Benchmark Model and the Altruistic Model, which are 73.7 and 72.1 percent, 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 all population sizes.\textsuperscript{22}

The simulation study suggests that Model (a) is less blood group O discriminatory than 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. The intuition behind this is that 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. Since blood group O patients belong to this group, it is not surprising that the ex post proportion of blood group O patients is larger in Model (b) than in Model (a).

5 Conclusions

This paper has investigated a pairwise kidney exchange program where a new medical technology makes transplantation over the blood group barrier feasible. In particular, the focus has been on the set of half-compatibility priority matchings and how the new technology is best utilized. If a planner is interested in maximizing the number of transplants and, in addition, designing a program that is less discriminatory against the biologically disadvantaged blood group O patients, the findings in this paper suggest the following policy recommendations. First, if technology enabling transplantation over the blood group barrier is available, any existing kidney exchange program should be amended to make use of it. In the language of this paper, a transition from the Benchmark Model to Model (b) is recommended. This would generate a significantly larger number of transplants. However, the planner should be aware that for each additional transplant this transition generates, roughly one transplant must be carried out over the blood group barrier. Second, if this technology exists but is mainly used to obtain self-matches outside a kidney exchange program as in, e.g., France, Sweden, the Netherlands and the United Kingdom (see Biró et al., 2017), a transition to a system where the technology is used within the program is recommended. In the language of this paper, a transition from Model (a) to Model (b) is recommended. This would generate more transplants and patients would on average receive kidneys from donors that are more preferred in terms of blood group compatibility. The only argument

\textsuperscript{22}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 76.9 and 87.1 percent, respectively, in Model (b) and 72.4 percent and 72.0 percent, respectively, in the Altruistic Model. Note, however, that only 1.7 percent and 0.2 percent of patients remain unmatched in Model (b) for population size $n = 200$ and $n = 500$, respectively, making this finding fairly inconsequential.
speaking against such a transition would be if the planner has a very strong concern for blood
group O patients, who are less disadvantaged in Model (a) than in Model (b).

An important problem in all market design applications that has so far not been discussed in
this paper is whether or not the agents can manipulate the outcome of the matching mechanism
by misrepresenting their preferences. When only pairwise exchanges are allowed and when pa-
tient preferences are dichotomous, 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 introducing
immunosuppressants in a kidney exchange program and expanding the preference domain from
dichotomous to trichotomous preferences, the positive results 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 (see Example 3, below).
This should come as no surprise since it is well-known that non-manipulability is incompati-
ble with individual rationality and Pareto efficiency on preference domains more general than
the dichotomous (Sönmez, 1999). 23 Hence, while introducing immunosuppressants can increase
number of transplants, it may also create manipulation possibilities for the patients. Is this an
acceptable trade-off? It is generally difficult to give an answer to this question, but through their
contacts with the medical community, Sönmez and Ünver (2014, p.114) have concluded that
“manipulations of this sort [preference manipulation] do not play a significant role, since com-
patibility information is usually obtained from observable and verifiable medical data.” While
the example below demonstrates that Model (b) can be manipulated, it is easy to construct an
example showing that Model (a) can be manipulated as well.

Example 3. Suppose that $N = \{1, 2, 3, 4\}$ and that each patient is incompatible with his own
donor. A possible pairwise exchange between pairs $(i, d_i)$ and $(j, d_j)$ is denoted by $ij$ and it is as-
sumed that only the pairwise exchanges 12, 14, and 23 are feasible. Assume that patient 1 is com-
patible 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 himself 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. Note,
finally, that no priority function is needed to obtain this conclusion. That is, it is maximality in
combination with minimal use of immunosuppressants that drives the result.

The theoretical results and the simulation results presented in this paper are valid for kidney

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23 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) and Schummer (1999).
exchange programs where only pairwise exchanges are allowed. Considering the findings in this paper, 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. 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 paper, future research may also build on, e.g., Chun et al. (2015), Nicoló and Rodríguez-Álvarez (2017) and Sönmez et al. (2016).

A Priority Matchings and Matroids

This Appendix demonstrates that the set of priority matchings defined in this paper is equivalent to the set of priority matchings defined by Roth et al. (2005b). To prove this, it is convenient to use Proposition 4 to derive a number of new lemmas. These lemmas will not only be important in showing the equivalence described above, they will also be useful in proving some of the results in Appendix B. Note that the graph theoretical definition of matchings will be adopted in this Appendix. That is, for any problem \((N, C, \pi)\) 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 3.2).

Let \(\Gamma : N \rightarrow \{1, \ldots, n\}\) be a permutation of \(N\) such that \(\Gamma(i) = j\) if \(i\) is the patient with the \(j\)th 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 \(E_0 = \mathcal{M}\).
- For \(k \in \{1, \ldots, n\}\), let \(E_k \subseteq E_{k-1}\) be defined by

\[
E_k = \begin{cases} 
\{M \in E_{k-1} \mid \Gamma^{-1}(k) \in N^*(M)\} & \text{if non-empty}, \\
E_{k-1} & \text{otherwise}.
\end{cases}
\]

The set \(E_n\) is the set of priority matchings in Roth et al. (2005b). Note that \(E_n\) 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, \(E_n\) will be used whenever discussing priority matchings as defined by Roth et al. (2005b).

Roth et al. (2005b) showed that any matching in \(E_n\) is preferred to all other matchings by any priority preference relation. Furthermore, Roth et al. (2005b) pointed out that \(N\) and the sets of simultaneously matchable patients constitute a matroid in settings with binary compatibility structure.
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).

Proposition 4 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.

Proposition 4. 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 \(M, M'\) 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 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 can not 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 \((N, C, \pi)\), \(\mathcal{I}\) will always denote the sets of simultaneously matchable patients, i.e., \(\mathcal{I} := \{I \subseteq N \mid I \subseteq N^*(M)\text{ for some } M \in \mathcal{M}\}\). All priority matchings are maximal matchings by construction. One implication of Proposition 4 is that all priority matchings are also maximum matchings.
Lemma 2. For a given problem \((N, C, \pi)\), 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 4, 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 2. Formally, a preference relation \(\succeq_\pi\) is called a priority preference relation if it is complete, transitive and satisfies the following conditions:

\[
M \succeq_\pi M' \text{ if } \begin{cases} N^*(M') \subseteq N^*(M), \\ N^*(M) \setminus N^*(M') = \{i\}, N^*(M') \setminus N^*(M) = \{j\} \text{ and } \pi(i) > \pi(j), \\ \end{cases}
\]

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

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 paper 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 \(\succeq_\pi\) and any \(M \in \mathcal{E}_n\), \(M \succeq_\pi M'\) for all \(M' \in \mathcal{M}\).

Proof. Consider some priority preference relation \(\succeq_\pi\) 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 4, 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 \(\succeq_\pi\).

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 \(M_1 \in \mathcal{M}\) 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

\(^{24}\)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.
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 $M_1 \succeq_\pi M$.

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 $M_1 \succeq_\pi M$, 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 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 $A \cup A' \cup \{j\} \subset N^*(M_2)$ 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
Consider any priority preference relation $\succsim$ that induction implies that each patient prefers augmentation property. Hence, by Lemma 3, cases (a) and (b) provide the desired contradiction. Consequently, there exists no $M' \in \mathcal{M}$ and no priority preference relation $\succsim$ such that $M' \succsim M$.  

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

Proof. Consider some priority preference relation $\succsim$ and some $M_1 \in \mathcal{M}$ such that $M_1 \succsim M'$ for all $M' \in \mathcal{M}$. First note that $\mathcal{E}_n \neq \emptyset$ as $\mathcal{M} \neq \emptyset$. Since $\succsim$ is a priority preference relation, Lemma 3 implies that $M \succsim M'$ for all $M \in \mathcal{E}_n$ and all $M' \in \mathcal{M}$. This implies that $M_1 \sim \succsim M'$ 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 4, every priority matching is a maximum matching by the augmentation property. Hence, $|N^*(M)| \leq |N^*(M')|$ 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 4, 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, $M_2 \succsim M_1$ since $N^*(M_1) \subset N^*(M_2)$. Therefore, $M_2 \succsim M_1 \sim \succsim M$ which implies that $M_2 \succsim M$ by transitivity. This contradicts $M \in \mathcal{E}_n$, since $M \succsim M'$ 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 $\succsim$ 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 \(M \sim_{\pi} M\). 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 \(M \gtrless_{\pi} M'\) 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 \(M \in \mathcal{E}_n\).

\[\square\]

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

**Proof.** Consider some \(M \in \mathcal{M}\) such that \(M \gtrless_{\pi} M'\) 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, \(M \in \mathcal{E}_n\).

\[\square\]

**B Proofs of the Theoretical Results**

This Appendix contains the proofs of all theoretical results except Proposition 4 and Proposition 6. The proof of Proposition 4 is found in Appendix A and the proof of Proposition 6 is found in Section 4.1. 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 3.2).
B.1 Proofs of the Results in Section 3.1

**Proposition 1.** For a given problem \((N, C, \pi)\), every half-compatibility priority matching is a priority matching.

*Proof.* Consider some priority matching \(M \in \mathcal{M}^*\). Then \(M \succeq_{\pi} M'\) for all \(M' \in \mathcal{M}\) and all priority preference relations \(\succeq_{\pi}\) by Lemma 3. Note that if \(M \succeq_{\pi} M'\) for some \(M' \in \mathcal{M}\) and all priority preferences \(\succeq_{\pi}\), then \(M \succ_B M'\) for all half-compatibility priority preferences \(\succeq_B\). 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 \(M \nless_{\pi} M'\), 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 \(M \succeq_{\pi} M'\) for all \(M \in \mathcal{M}^*\), all \(M' \in \mathcal{M} \setminus \mathcal{M}^*\) and all priority preference relations \(\succeq_{\pi}\), 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 \(\succeq_B\). 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. \(\square\)

**Proposition 2.** For a given problem \((N, C, \pi)\), 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 1 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 \(N^*(M) \nsubseteq N^*(M')\) 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 \(B(M') \geq B(M)\). To see this, note that each patient must weakly prefer the kidney he receives at \(M'\) to the kidney he 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. \(\square\)

**Proposition 3.** For a given problem \((N, C, \pi)\), \(N^*(M) = N^*(M')\) 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 paper is equivalent to the set of priority matchings defined by Roth et al. (2005b). \(\square\)
Theorem 1. For a given problem \((N, C, \pi)\), all half-compatibility priority preference relations induce the same set of half-compatibility priority matchings.

Proof. Consider any half-compatibility priority preference relation \(\succeq_B\). 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 3, all half-compatibility priority preference relations will rank all priority matchings in the same way. That is, for any \(M, M' \in \mathcal{M}^*\), \(M \succeq_B M'\) for some half-compatibility priority preference relation \(\succeq_B\) if and only if \(M \succeq_B M'\) for all half-compatibility priority preference relations \(\succeq_B\). By Proposition 1, \(\mathcal{M}^B \subseteq \mathcal{M}^*\). 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 between an arbitrary problem \((N, C, \pi)\) and a specific problem \((N, \hat{C}, \pi_M)\) are derived. For any problem \((N, C, \pi)\), the corresponding compatibility graph \(g\) is not a simple graph whenever it contains loops, i.e., whenever \(N_H \neq \emptyset\). The main idea in the second part of the proof (Lemma 11 to the end of Appendix B.2) is to use the findings from the first part of the proof to demonstrate that an arbitrary problem \((N, C, \pi)\) can be translated into an equivalent specific problem \((N, \hat{C}, \hat{\pi})\) with a corresponding simple graph, where \(\hat{C}\) is a compatibility structure in 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.

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 \((N, C, \pi)\) 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, \(i\hat{ii} \in E(g)\) 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 \(M' := M \cup \{i\hat{ii}\} \in \mathcal{M}(C)\) 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 \((N, C, \pi)\) 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., \(N_I(C') = \ldots\)
Consider two problems

\[ M \text{ is a maximum weight matching in graph } g \]

assumed that of Lemmas 7–10, below, follow immediately. Hence, in the proofs of these four lemmas, it is

Proof. Consider some patient \( i \) such that \( \hat{M} \) without loss of generality, patient \( i \) is matched at \( \hat{M} \) and let \( i \) be the set of edges between patients in \( N \) and \( C \) if and only if they are compatible at \( H \). That is, \( M \) is a maximum weight matching in \( g \). For any \( i,j \) in \( N \) such that \( i \neq N_H(C) \) or \( j \neq N_H(C) \). Then \( i \) and \( j \) are compatible at \( H \) if and only if they are compatible at \( H \).

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 \( M(\hat{C}) \), a patient in \( N_H(C) \) is either unmatched or matched to a patient in \( N_I(C) \). Let \( L(g) := \{ij \in E(g) | i,j \in N_H(C) \} \) 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 \( i \neq j \).

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

\textbf{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 \( S(M,w(\pi)) - \pi_M(w(\pi)) \geq 0 \) for all \( M' \in M(C) \). 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 \( M' \in M(C) \) 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 \((N, C, \pi)\) and \((N, C, \pi_M)\) with corresponding compatibility graph \(g\) and let \(M \in \mathcal{M}(C)\). Then \(M\) is a priority matching at \((N, C, \pi)\) if and only if it is a priority matching at \((N, C, \pi_M)\).

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 \((N, C, \pi)\), then it is a priority matching at \((N, C, \pi_M)\). To reach a contradiction, suppose that \(M\) is a priority matching at \((N, C, \pi)\) but not at \((N, C, \pi_M)\). As \(M\) is a priority matching at \((N, C, \pi)\), it is a maximum matching by Proposition 2. Furthermore, since the priority function does not impact whether a matching is a maximum matching, \(M\) is a maximum matching at \((N, C, \pi_M)\) 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 (5) in the definition of \(\pi_M\) 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 \((N, C, \pi)\). Consequently, if \(M\) is a priority matching at \((N, C, \pi)\), then it is a priority matching at \((N, C, \pi_M)\). \(\square\)

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 \((N, C, \pi_M)\) and \((\hat{N}, \hat{C}, \pi_M)\) 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 \(\pi_M\), 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 \((N, C, \pi_M)\) or \((\hat{N}, \hat{C}, \pi_M)\) must match all patients in \(N^*(M) \cap N_I(C)\) since \(M\) is a maximum weight matching at \((N, C, \pi_M)\) 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 \(i \in (N^*(M') \cap N_H(C)) \setminus N^*(M)\) such that \(\pi(i) < \sum_{j \in (N^*(M') \cap N_H(C)) \setminus N^*(\hat{M})} \pi(j)\). Next, note that \(i \in N_H(C) \cap \Phi_M\) for all \(i \in (N^*(M') \cap N_H(C)) \setminus N^*(\hat{M})\), since all patients in \(\Phi_M\) 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 $j \in (\hat{N}^{*}(\hat{M}) \cap N_H(C)) \setminus N^{*}(M')$. This contradicts condition (6). 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 (5) implies that there exists no $\hat{M} \in \mathcal{M}(\hat{C})$ such that $\sum_{i \in \hat{N}^{*}(\hat{M}) \cap N_I(C)} \pi(i) > \sum_{i \in N^{*}(M') \cap N_I(C)} \pi(i)$. 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 $\hat{M} \in \mathcal{M}(C)$ such that $\sum_{i \in \hat{N}^{*}(\hat{M}) \cap N_I(C)} \pi(i) > \sum_{i \in N^{*}(M) \cap N_I(C)} \pi(i)$. To reach a contradiction, suppose that $M$ is not a maximum weight matching in $(g, w(\pi_M))$. Then there exists some $\hat{M} \in \mathcal{M}(C)$ such that $S(\hat{M}, w(\pi_M)) > S(M, w(\pi_M))$. Considering that $\sum_{i \in N^{*}(M) \cap N_I(C)} \pi(i) \leq \sum_{i \in N^{*}(M') \cap N_I(C)} \pi(i)$, it must be the case that $\sum_{i \in \hat{N}^{*}(\hat{M}) \cap N_I(C)} \pi(i) > \sum_{i \in N^{*}(M) \cap N_H(C)} \pi(i)$. 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:

- $i_j i_{j+1} \in E(g)$ for all $j \in \{1, \ldots, t-1\}$,
- $i_j i_{j+1} \neq i_{j'} i_{j'+1}$ for all distinct $j, j' \in \{1, \ldots, t-1\}$.\(^{25}\)

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

**Lemma 10.** Consider a problem $(N, C, \pi_M)$ with corresponding compatibility graph $g$ and let $M \in \mathcal{M}(C)$ be a maximal matching. Then $M$ is a priority matching at $(N, C, \pi_M)$ 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 $(N, C, \pi_M)$ only if $M'$ is a priority matching at $(N, \hat{C}, \pi_M)$. Suppose that $M$ is a priority matching at $(N, C, \pi_M)$. Since $M \subseteq E(g)$ and $E(g) \setminus L(g) = E(\hat{g})$, by construction, it follows that $M' \in \mathcal{M}(\hat{C})$. 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 $N^{*}(M) \setminus N^{*}(M') = \{i\}$ and $N^{*}(M') \setminus N^{*}(\hat{M}) = \{j\}$ for

\(^{25}\)In the case when $i i \in E(g)$ 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.
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 agent $i$, 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 $\hat{M} := \hat{M} \cup \{kk \mid k \in N_H(C) \setminus N^*(\hat{M})\}$ be an amended version of $\hat{M}$, where all patients in $N_H(C)$ that are unmatched at $\hat{M}$ are self-matched at $\hat{M}$. Note that $\hat{M} \in \mathcal{M}(C)$. If $j \in N_H(C)$, then $N^*(M) \subset N^*(\hat{M})$. If $j \in N_I(C)$, then $N^*(M) \cap N^*(\hat{M}) = \{j\}$ and $N^*(\hat{M}) \cap N^*(M) = \{i\}$, where $\pi_M(i) > \pi_M(j)$. However, this in implies that $\hat{M} \succ_{\pi_M} M$ in both cases, which contradicts the assumption that $M$ is a priority matching at $(N, C, \pi_M)$. Hence, $i \notin N_I(C)$.

(ii) Suppose that $i \in N_H(C)$. Then condition (5) implies that $j \in N_H(C)$ as well. Furthermore, $i \notin \Phi_M$ and $j \notin N_H(C) \setminus \Phi_M$ by construction. This is a contradiction, since $\pi_M(i) < \pi_M(j)$ by condition (6). Hence, $i \notin N_H(C)$.

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

Finally, it will be shown that $\hat{M}$ is a priority matching at $(N, \hat{C}, \pi_M)$ 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 $\hat{M}$ is not a priority matching at $(N, C, \pi_M)$. 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 $\hat{M} := \hat{M} \setminus L(g) \in \mathcal{M}(\hat{C})$ and that $(N^*(\hat{M}) \cap N_I) \setminus (N^*(M') \cap N_I) = \{i\}$ and $(N^*(M') \cap N_I) \setminus (N^*(\hat{M}) \cap N_I) = \{j\}$.

Let $i := i_1$ and note that there must exist a maximal path $(i_1, \ldots, i_t)$ in $(N, \hat{M} \cup M')$, where $i_1 \neq i_t$. Hence, $t \geq 2$. To establish the contradiction, it will next be demonstrated that it can not be the case that $t \geq 2$.

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

(ii) Suppose that $t = 3$. Then either $i_t \in N_I(C) \setminus N^*(\hat{M})$ and $i_t = j$, or $i_t \in N_H(C)$. Note that $\hat{M} := (M' \setminus \{i_2 i_t\}) \cup \{i_1 i_2\} \in \mathcal{M}(\hat{C})$. Furthermore, by $\pi(i) > \pi(j)$ and condition (5), $\pi(i_1) > \pi(i_t)$ both in the case when $i_t = j$ and the case when $i_t \in N_H(C)$. This implies that $\hat{M} \succ_{\pi_M} M'$, 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 $\hat{M}$. 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 $\hat{M} := (M' \setminus \gamma) \cup \gamma' \in \mathcal{M}(\hat{C})$. Since $N^*(M') \subset N^*(\hat{M}), \hat{M} \succ_{\pi_M} M'$. This contradicts the assumption that $M'$ is a priority matching at $(N, \hat{C}, \pi_M)$.

- If $t$ is odd, then either $i_t \in N_I(C) \setminus N^*(\hat{M})$ 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 $\hat{M} := (M' \setminus \gamma) \cup \gamma' \in \mathcal{M}(\hat{C})$. Furthermore, $N^*(\hat{M}) \setminus N^*(M') = \{i_t\}$ and $N^*(M') \setminus N^*(\hat{M}) = \{i\}$. By $\pi(i) > \pi(j)$ and condition (5), it follows that $\pi(i_t) > \pi(i_t)$ both in the case when $i_t = j$ and the case when $i_t \in N_H(C) \setminus \Phi_M$.

This implies that $\hat{M} \succ_{\pi_M} M'$, which contradicts the assumption that $M'$ is a priority matching at $(N, \hat{C}, \pi_M)$.

Hence, $M$ is a priority matching at $(N, C, \pi_M)$ 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 $(N, C, \pi)$. The key idea in the proof of Proposition 5 will be to demonstrate that for any problem $(N, C, \pi)$, there exists an equivalent problem $(N, \hat{C}, \hat{\pi})$ with a corresponding simple graph $\hat{g}$, in which no patients are half-compatible with any donors. That is, any pair of patients and donors is either compatible or incompatible at $\hat{C}$. Gather all compatibility structures at which no patients are half-compatible with any donors in the set $C_{02}$. Note that the compatibility structures considered by Okumura (2014) belong to $C_{02}$. Lemma 1 is only applicable in problems with compatibility structures belonging to $C_{02}$. To understand Lemma 11, note that the problem $(N, C, \pi)$ need not correspond to the conditions in Lemma 1 by Okumura (2014). For any problem $(N, C, \pi)$ 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 $C_{02}$ with corresponding compatibility graphs that are simple graphs.

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

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

Let $\overline{C}$ be a compatibility structure for which each patient is incompatible with his own donor and compatible with every other donor. Then $\overline{C} \in C_{02}$ and the corresponding compatibility
graph, $\bar{g}$, is a complete graph. Consider some arbitrary set of edges $E' \subseteq E(\bar{g})$. 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 $id_j \in E(\bar{g}) \setminus E'$ and let $\hat{g}'$ be its corresponding compatibility graph. Then $\hat{C}' \subseteq C_{02}, E(\hat{g}') \subseteq E(\bar{g})$ and $E(\bar{g}) \setminus E(\hat{g}') = E'$. Since $\bar{C} \subseteq C_{02}, \bar{g}$ is a complete graph and $E'$ is an arbitrary set of edges, there exists some $C' \subseteq C_{02}$ with corresponding compatibility graph $g' = (N, E')$ for any $E \subseteq E(\bar{g})$. Hence, for any compatibility structure $C \notin C_{02}$ with corresponding simple compatibility graph $g$, there exists some $\hat{C} \subseteq C_{02}$ with corresponding simple compatibility graph $\hat{g}$ such that $\hat{g} = g$. If $\hat{g} = g$, then $M^*(C) = M^*(\hat{C})$ 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 $(N, C, \pi)$ with corresponding simple compatibility graph $g$, there exists some $\hat{C} \subseteq C_{02}$ such that a matching $M$ is a priority matching at $(N, C, \pi)$ if and only if it is a priority matching at $(N, \hat{C}, \pi)$.

To conclude the proof, note that since $\hat{C} \subseteq C_{02}$, Lemma 1 implies that $M$ is a priority matching at $(N, \hat{C}, \pi)$ if and only if it is a maximum weight matching in $(\hat{g}, w)$. Since $\hat{g} = g$, $M$ is a maximum weight matching in $(\hat{g}, w)$ if and only if it is a maximum weight matching in $(g, w)$. Hence, for any problem $(N, C, \pi)$ with corresponding simple compatibility graph $g$, $M$ is a priority matching if and only if $M$ is a maximum weight matching in $(g, w)$. \hfill \Box

**Proposition 5.** Consider a problem $(N, C, \pi)$ with corresponding compatibility graph $g$. If $w_{ii} = \pi(i)$ for all $i \in E(g)$ 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 $(N, C, \pi)$ 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 $(\hat{g}, w)$ 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 $(N, C', \pi_M)$ 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 Lemma 8 and Lemma 10 implies that for any problem $(N, C, \pi)$, $M$ is a maximum weight matching in $(g, w)$ if and only if $M$ is a priority matching. \hfill \Box

### B.3 Proof of Theorem 2

**Theorem 2.** Consider a problem $(N, C, \pi)$ 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 $(g, w^*)$. 
\textbf{Proof.} \((\Rightarrow)\) It is first proved that any maximum weight matching in \((g, w^\varepsilon)\) is a half-compatibility priority matching, i.e., if a matching \(M\) is a maximum weight matching in \((g, w^\varepsilon)\), then \(M \in \mathcal{M}^B(C)\). Let \(M\) be a maximum weight matching in \((g, w^\varepsilon)\). 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 \(M' \in \mathcal{M}(C)\) such that \(S(M', w) > S(M, w)\). By the construction of \(w\), it is clear that:

\[
S(M', w) - S(M, w) \geq \frac{1}{q} \iff S(M', w) \geq S(M, w) + \frac{1}{q}. \quad (7)
\]

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

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

\[
\iff S(M, w^\varepsilon) < S(M, w) + \frac{1}{q}. \quad (8)
\]

Inequalities (7) and (8) imply that:

\[
S(M', w) > S(M, w^\varepsilon). \quad (9)
\]

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

\[
S(M', w^\varepsilon) \geq S(M', w). \quad (10)
\]

Inequalities (9) and (10) then imply that \(S(M', w^\varepsilon) > S(M, w^\varepsilon)\). But this contradicts the assumption that \(M\) is a maximum weight matching in \((g, w^\varepsilon)\), i.e., that \(S(M, w^\varepsilon) \geq S(M', w^\varepsilon)\) for all \(M' \in \mathcal{M}(C)\). 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 \(M \in \mathcal{M}^B(C)\). To obtain a contradiction, suppose that \(M \notin \mathcal{M}^B(C)\). Consider a matching \(M'\) that belongs to \(\mathcal{M}^B(C)\). As \(\mathcal{M}^B(C) \subseteq \mathcal{M}^*(C)\), \(M'\) 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:

\[
S(M', w^\varepsilon) - S(M', w) = \varepsilon B(M') \quad (11)
\]

\[
S(M, w^\varepsilon) - S(M, w) = \varepsilon B(M). \quad (12)
\]

Since \(M \in \mathcal{M}^*(C) \setminus \mathcal{M}^B(C)\) and \(M' \in \mathcal{M}^B(C)\), 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 (11) and (12) 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 \( (g, w^\varepsilon) \). Hence, \( M \in \mathcal{M}^B(C) \).

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

\[
S(M', w^\varepsilon) > S(M, w^\varepsilon). \tag{13}
\]

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

\[
S(M, w) - S(M', w) \geq \frac{1}{q} \iff S(M, w) \geq S(M', w) + \frac{1}{q} \implies S(M, w^\varepsilon) \geq S(M', w) + \frac{1}{q}. \tag{14}
\]

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

\[
S(M', w^\varepsilon) - S(M', w) < \frac{1}{q} \iff S(M', w) + \frac{1}{q} > S(M', w^\varepsilon). \tag{15}
\]

Inequalities (14) and (15) imply that \( S(M, w^\varepsilon) > S(M', w^\varepsilon) \), which contradicts inequality (13). Hence, \( S(M', w) = S(M, w) \).

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

\[
S(M', w^\varepsilon) - S(M', w) = \varepsilon B(M'), \tag{16}
\]

\[
S(M, w^\varepsilon) - S(M, w) = \varepsilon B(M). \tag{17}
\]

Now, the conclusion that \( S(M', w) = S(M, w) \) together with inequality (13) and equations (16) and (17) imply that:

\[
\varepsilon (B(M') - B(M)) = S(M', w^\varepsilon) - S(M, w^\varepsilon) > 0. \tag{18}
\]

Condition (18) and \( \varepsilon > 0 \) imply that \( B(M') > B(M) \). But this contradicts the assumption that \( M \in \mathcal{M}^B(C) \) as \( M' \in \mathcal{M}^*(C) \). That is, \( M \) can not be an element in \( \mathcal{M}^B(C) \) 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 \( (g, w^\varepsilon) \).
B.4 Proofs of the Results in Section 4.1

Proposition 8. Consider a problem \((N, C, \pi)\) and suppose that \(\mu'\) and \(\mu''\) contain all patients that receive transplants in Model (a) and Model (b), respectively. Then \(\mu' \subseteq \mu''\).

Proof. Consider a problem \((N, C, \pi)\) with corresponding compatibility graph \(g\) and let \(\tilde{g}\) be the compatibility graph corresponding to the reduced problem \((N_I, C_I, \pi)\). 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 \((g, w^\epsilon)\) and \(\tilde{M}\) is a maximum weight matching in \((\tilde{g}, w^\epsilon)\). By Theorem 2, \(M\) 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 \((N, M \cup \tilde{M})\) belongs to \(N^*(M)\). This result is first proved for maximal paths of length \(t = 2\), i.e., paths of the type \((i_1, i_2)\) in \((N, M \cup \tilde{M})\).

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 \(M' := M \cup \{i_1i_2\} \in M(C)\), which contradicts the assumption that \(M\) is a maximum weight matching in \((g, w^\epsilon)\). Hence, \(i_1, i_2 \in N^*(M)\). In summary, any patient contained in a maximal path of length \(t = 2\) in \((N, E(M) \cup E(\tilde{M}))\) 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 \(i_1 \neq i_t\). 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 unmatched in both \(M\) and \(\tilde{M}\).

\(^{26}\)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 \(ij \in \tilde{M}\).
a starting point or an end point of that path. Now define:
\[
\begin{align*}
\gamma &:= \{i_ki_{k+1} \mid k \in \{2, \ldots, t - 2\} \subset 2\mathbb{N}\}, \\
\gamma' &:= \{i_ki_{k+1} \mid k \in \{1, \ldots, t - 1\} \subset \mathbb{N} \setminus 2\mathbb{N}\}, \\
\hat{\gamma} &:= \{i_ki_{k+1} \mid k \in \{2, \ldots, t - 1\} \subset 2\mathbb{N}\}, \\
\hat{\gamma}' &:= \{i_ki_{k+1} \mid k \in \{1, \ldots, t - 2\} \subset \mathbb{N} \setminus 2\mathbb{N}\}.
\end{align*}
\]

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 \(i_1, i_t \in \tilde{N}_t\). 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 \(M' := (M \setminus \{i_1i_2\}) \cup \{i_2i_t\}\) 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 \(M'' := (\tilde{M} \setminus \{i_1i_t\}) \cup \{i_1i_2\}\) is a feasible matching in \(g\) and since \(M\) is a maximum weight matching in \((g, w^\varepsilon)\), 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 \(N^*(M) \subset N^*(M')\), 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 \(M' := (M \setminus \{i_1i_2\}) \cup \{i_2i_t, i_1i_1\}\) is a feasible matching in \(g\). This contradicts the assumption that \(M\) is a maximum weight matching in \((g, w^\varepsilon)\). Hence \(t \geq 4\).

(b.2) Suppose that \(t \geq 4\) and that \(t\) is odd. Then \(M' := (M \setminus \hat{\gamma}') \cup \hat{\gamma} \cup \{i_1i_1\}\) is a feasible matching in \(g\) where \(N^*(M) \subset N^*(M')\). This contradicts the assumption that \(M\) is a maximum weight matching in \((g, w^\varepsilon)\). 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, $\mu' \subseteq \mu''$. □

**Proposition 7.** Consider a problem $(N, C, \pi)$ and suppose that $\mu$, $\mu'$ and $\mu''$ 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 $(N, C, \pi)$. Let $M$, $M'$ and $M''$ be the matchings selected in the Benchmark Model, Model (a) and Model (b), respectively. By Proposition 2, $|N^*(M'')| \geq |N^*(\tilde{M})|$ for all $\tilde{M} \in \mathcal{M}(C)$. Since $M \in \mathcal{M}(C)$, it follows that $|N^*(M'')| \geq |N^*(M)|$. That is, $|\mu| \leq |\mu''|$. By Proposition 8, $|\mu'| \leq |\mu''|$. □

**References**


