Unpaired Kidney Exchange: Overcoming Double Coincidence of Wants without Money*

Mohammad Akbarpour† Julien Combe‡ Yinghua He§ Victor Hiller¶
Robert Shimer‖ Olivier Tercieux**

August 1, 2019
Preliminary Draft

Abstract

We propose a new matching algorithm—*Unpaired* kidney exchange—to tackle the problem of double coincidence of wants without using money. The fundamental idea is that "memory" can serve as a medium of exchange. In a dynamic matching model with heterogeneous agents, we prove that average waiting time under the Unpaired algorithm is close-to optimal, and substantially less than the standard pairwise and chain exchange algorithms. We evaluate this algorithm using a rich dataset of the kidney patients in France. Counterfactual simulations show that the Unpaired algorithm can match nearly 57% of the patients, with an average waiting time of 424 days (state-of-the-art algorithms match about 31% with an average waiting time of 675 days or more). The optimal algorithm performs only slightly better: it matches 58% of the patients and leads to an average waiting time of 410 days. The Unpaired algorithm confronts two incentive-related practical challenges. We address those challenges via a practical version of the Unpaired algorithm that employs kidneys from the deceased donors waiting list. The practical version can match nearly 87% of patient-donor pairs, while reducing the average waiting time to about 141 days.

Keywords: Kidney exchange, medium of exchange, dynamic matching.

JEL classification codes: D47, C78, E00

*We thank Itai Ashlagi, Alvin Roth, Paul Milgrom, and several seminar participants for valuable comments. All errors remain our own.

†Graduate School of Business, Stanford University. Email: mohamwad@stanford.edu
‡Department of Economics, University College London. Email: j.combe@ucl.ac.uk
§Rice University and Toulouse School of Economics. Email: yinghua.he@rice.edu
¶Université Paris 2. Email: victor.hiller@u-paris2.fr
‖Department of Economics, University of Chicago. Email: rshimer@uchicago.edu
**CNRS and Paris School of Economics. Email: tercieux@pse.ens.fr

1 Introduction

Transplantation is the treatment of choice for kidney failure. Yet, all around the world, many people must struggle with dialysis while enduring long waits for transplantation and imposing substantial healthcare costs on society,[1] with many thousands of patients dying each year, all due to the shortage of compatible organs. *Kidney exchange* is a recent innovation addressing this issue. Kidney exchange arises when an individual, who is willing to donate a kidney to a kidney patient in need of transplant, is unable to do so since she is biologically incompatible with her intended patient. In such cases, if the donor of each pair is compatible with the patient of the other, an incompatible patient-donor pair can exchange kidneys with another pair. While ingenious, this leads to the well-known "double coincidence of wants" problem—you not only have to have the kidney that I want, but also have to want the kidney I have (Jevons, 1885).

Economists have proposed a solution to the double coincidence problem, legalizing a market where kidneys can be exchanged for money (Becker and Elias, 2007). A market for kidneys addresses two issues simultaneously. First, it breaks the double coincidence of wants problem by allowing a kidney donor to sell her kidney to an unrelated patient at one point in time, and then permitting her related patient to buy back a kidney at a later date from an unrelated donor. Second, a market for kidneys has the potential to increase the supply.[2]

While a market for kidneys is appealing to many economists, many other people find such a market repugnant. Roth (2007) lists three reasons why a kidney market might be repugnant. First, giving a kidney to a loved one is intrinsically good, while giving one for money may be morally wrong because it objectifies the human body. Second, it is likely that disproportionately many poor people would sell a kidney, and this may be viewed as coercive. Third, a market for kidneys may be a slippery slope into more ethically dubious arrangements, for example, those in which debtors could be forced to give a kidney in bankruptcy proceedings. We do not take a stance on whether a market for kidneys is repugnant, but simply note that it is illegal everywhere in the world except Iran today, and that changing the law is probably not politically feasible in most countries.

Instead, we propose a new matching algorithm—*Unpaired* kidney exchange—to tackle the problem of double coincidence of wants without creating a repugnant market. The fundamental idea is that "memory" can serve as a medium of exchange (Kocherlakota, 1998). In essence, we propose creating a barter market, where agent i can receive the (compatible) object of agent j, even if agent i's object is not compatible to agent j. When such a trade happens, the system will "remember" that agent j has the right to receive an object in future and that agent i's object can be given to some other agent in future.

[1] The U.S. Medicare's dialysis cost in 2018 was more than 1.2% of the *entire federal budget*.

[2] Indeed, the regulated market for kidneys in Iran has increased the supply (Akbarpour et al., 2019).

Memory and money both break the double coincidence of wants problem. On the other hand, while money is likely to increase the supply of kidneys, the Unpaired algorithm by design avoids encouraging kidney donation for pecuniary benefits. This is why the Unpaired algorithm escapes the repugnance concerns. Donors give kidneys because they love someone who needs one, not because of money. Poor people cannot get a check by selling a kidney. Creditors cannot demand a kidney in return for discharging a debt. Technically, the key difference between money and memory is fungibility. The fungibility of money allows for potentially repugnant uses. The fact that memory is not fungible means that society can control how it is used to avoid concerns about repugnance.

In this paper, we investigate the Unpaired algorithm theoretically and empirically, and discuss two of its incentive-related practical challenges. In Section 2, we study a dynamic kidney exchange model with two types of patients. In this model, patient-donor pairs arrive with some rate n. A fraction λ of patients are *hard-to-match* and a fraction $1-\lambda$ of patients are *easy-to-match*. Hard-to-match patients and easy-to-match patients are compatible to a random donor with probabilities p_H and p_E, respectively, where $p_H < p_E$.[3] Agents stay in the system until they are matched. The planner, everything else constant, wishes to match patients as early as possible. Since under any matching algorithm that we study, easy-to-match patients have negligible waiting times, the main objective of interest is the average waiting time of hard-to-match patients.

The Unpaired algorithm works as follows: whenever a new patient-donor pair enters the market, match the patient to a compatible donor (if any), and match the donor to a compatible patient (if any), breaking ties in favor of patients whose donors have already donated. To evaluate the (relative) performance of the Unpaired algorithm, we study three alternative matching algorithms. The first algorithm—the *Pairwise* algorithm—matches two patient-donor pairs whenever they are pairwise compatible. The second algorithm—the *Chain* algorithm—starts with a finite number of altruistic donors and matches agents whenever there exists a chain. The third one—the *Optimal* algorithm—is the optimal algorithm in the class of all matching algorithms that converge to a stationary distribution, with the (natural) feature that hard-to-match patients wait no shorter (on average) than easy-to-match patients.[4]

We prove the following theoretical results: First, for small values of p_H, the Unpaired algorithm substantially outperforms the Pairwise algorithm. In particular, if more than half of patients are hard to match, this ratio of these waiting times is $O(1/p_H)$. Even if there are more easy-to-match pairs, the Unpaired algorithm outperforms Pairwise. For instance, when only 30% of pairs are hard-to-match, the waiting time of hard-to-match patients in Pairwise

[3]For tractability, we assume $p_E = 1$. The results will go through for any constant p_E, but the analysis is more tedious for other constants.

[4]Since our objective is to minimize waiting time of hard-to-match patients, an algorithm can avoid matching easy-to-match patients and save all of them for hard-to-match patients. To avoid such scenarios, we impose the condition that hard-to-match patients wait at least as much as easy-to-match patients

is at least twice more than the Unpaired.

Second, we prove that for any value of p_H and λ, the Unpaired algorithm outperforms the Chain algorithm. In addition, for small values of p_H, when the fraction of hard-to-match patients is large, the Chain algorithm's relative performance gets *substantially* worse. For instance, if 60% of patients are hard-to-match, the Unpaired algorithm matches hard-to-match patients nearly 2 times faster than the Chain algorithm.

Our final theoretical result compares the Unpaired algorithm with the Optimal algorithm. We prove that, for any value of p_H and λ, the Optimal algorithm's waiting time is at least 50% of the waiting time of the Unpaired algorithm. In addition, if the Optimal algorithm is restricted to provide easy-to-match patients with an average waiting time as small as their waiting time in the Unpaired algorithm, then it can never provide hard-to-match patients with an average waiting time lower than 1.38 of the Unpaired algorithm. Note that the Unpaired algorithm is matching agents greedily, while the Optimal matching is forward-looking and can in principle wait to thicken the market. This result, nevertheless, shows that the additional gains from such considerations are relatively small.

After stating our theoretical results, we go on to empirically investigate the performance and challenges of the Unpaired algorithm. We rely on a dataset provided by the Biomedicine Agency (*Agence de la Biomédecine*), a government agency that oversees all organ transplants in France. It covers the period of December 2013 to February 2018, including all transplants with deceased and living donors kidneys, as well as discarded kidneys from deceased donors.

Our main simulation focuses on the 78 pairs who participated in France's kidney exchange program in our sample period. We run counterfactual simulations to compare four algorithms: Pairwise, Chains, Unpaired, and Optimal. We evaluate an algorithm's performance by the transplant rate (the fraction of the 78 patients receiving a transplant in the simulation period), as well as the average waiting time for transplant. Since computing the Optimal algorithm is complex and requires additional assumptions on the data generating process, we instead simulate the *Omniscient* algorithm by assuming that the planner has perfect foresight about future arrivals. This algorithm performs *better* than the Optimal. Thus, the Omniscient algorithm's transplant rate is an upper bound and its waiting time is a lower bound for what the Optimal algorithm can achieve.

Simulations show that Unpaired dominates the Pairwise and Chain algorithms and is very close to the Omniscient algorithm. In particular, both Pairwise and Chain have a transplant rate around 31%, while Unpaired obtains 57%, similar to Omniscient's transplant rate, 57.9%. The same pattern holds for waiting time – 695 days for Pairwise, 676 days for Chain, 424 days for Unpaired, and more than 410 days for Omniscient.

Next, we focus on how the Unpaired algorithm deals with hard-to-match patients. We define a patient to be hard-to-match if she is *hypersensitized*. There are 21 such patients (out of 78) in our data. If one replaces Pairwise or Chain by Unpaired, the transplant rate among

hard-to-match patients is nearly doubled, while their waiting time is reduced by about 140 days. Again, the Omniscient algorithm does not significantly improve upon Unpaired.

The Unpaired algorithm comes with two practical challenges, and simulations show that these challenges can be significant. First, there may be patients who have to wait for a long time *after* their donors have already donated, and such waits may be hard to accept ex ante. In our simulations, 28 unpaired patients have to wait on average 601 days (the 90th percentile, 1365 days) after their donors have already donated. In addition, there may be donors who have to wait for a long time after their patients have already received a kidney, which increases the chance that they renege. In our simulations, 28 unpaired donors have to wait on average 610 days (the 90th percentile, 1355 days) after their patients have already received a transplant. While important, we emphasize that these issues are not special to the Unpaired algorithm. For instance, the concern that donors may renege is more serious in the Chain algorithm, where *all* donors donate after their patient receives a transplant. In addition, unpaired patients who have to wait for a long time are precisely those patient who may never receive a kidney under other algorithms. In essence, some patients confront a trade-off between an increased likelihood of receiving a kidney and donating a kidney before being sure that they will receive one.

Nonetheless, we propose a modified version of the Unpaired algorithm, Practical Unpaired, that can potentially address the two above-mentioned issues. We take advantage of the frequent arrival of deceased donor kidneys and select the good-quality ones to be used for unpaired patients waiting after their donors have donated. For every deceased donor kidney used in Practical Unpaired, an unpaired donor, who is waiting to donate after her patient has transplanted, immediately donates to the deceased donor list. This practical version reduces the average waiting time among unpaired patients to 34 days (the 90th percentile, 129 days) and the average waiting time among unpaired donors to 31 days (the 90th percentile, 92 days). These reductions are not at the expenses of the algorithm's overall performance: relative to the Unpaired algorithm, the transplant rate in fact increases to 87.1%, while the waiting time among all patients reduces to 141 days.

To investigate the sensitivity of our results to different assumptions, we conduct an extensive set of robustness checks. For example, we allow pairs to exit without transplant, introduce multiple chains, and construct a large market. We demonstrate that the performance of the Unpaired algorithm relative to others remain qualitatively the same.

1.1 Related work

The economics literature on kidney exchange starts with Roth et al. (2004). In a subsequent paper, Roth et al. (2007) demonstrate the efficiency gains of creating a large kidney exchange marketplace, as well as those from allowing 3-way or larger cycles.

The double coincidence of wants problem has been a known challenge since the beginning of kidney exchange. We now review the two approaches that have been used to tackle it in practice.

The first approach is to create a sufficiently thick market:

> *And we will show that, even without a medium of exchange, if the market is thick enough, the problem of the coincidence of wants can be substantially ameliorated by the organization of an appropriate clearinghouse. (Roth et al., 2007)*

Given the likelihood of biological compatibility, this approach requires an extremely thick market to be effective. This is not the case in, for instance, France, where the arrival rate of patient-donor pairs to the kidney exchange market has been less than 20. Even in the U.S. market with hundreds of pairs per year, thickening the market alone has not been enough to overcome the coincidence of wants, largely due to the abundance of hypersensitized patients who are extremely hard to match.

A second approach to tackle this challenge is to use non-simultaneous altruistic donor chains (Roth et al., 2006). In a chain, an altruistic donor initiates a chain by donating a kidney to a patient, whose corresponding donor then donates to another patient, and so on. Transplants may happen simultaneously, or sequentially. Such chains are responsible for a large part of today's kidney exchange platform transplants. Such chains need not form a closed loop, and thus, can alleviate the problem of double coincidence of wants:

> *Developing the capability to arrange trades in longer cycles and chains helps overcome this [double coincidences of wants] barrier... In the case of kidney exchange, long non-simultaneous chains of the sort proposed in Roth et al. (2006) are proving increasingly important. (Ashlagi et al., 2012)*

While clever, chains confront three practical challenges. First, their efficiently is limited by the number of available altruistic donors. Second, in places where altruistic donation is illegal (e.g., France and Germany), such chains are infeasible. Last but not the least, even with a reasonable number of altruistic donors, they go only half-way in solving the double coincidence problem, because they do not want the donor to give a kidney before the corresponding patient receives one.

There is a third approach that has been proposed to overcome coincidence of wants, although it has not yet been employed in practice. Ausubel and Morrill (2014) introduce the idea of "sequential kidney exchange," where a donor donates before her patient receives a kidney. They study this proposal in an overlapping generations (OLG) model. This is exactly the reverse of what chains do. In this sense, our model combines chains and sequential kidney exchange by allowing donations before or after receiving a transplant. Their main efficiency

result requires an identical population that enter every period, since their proposal matches each patient precisely one period after their donor donates.

Our theoretical model is related to those of dynamic kidney exchange. Ünver (2010) studies a model of dynamic exchange with blood-type considerations. Akbarpour et al. (Forthcoming) studies a dynamic kidney exchange model with stochastic departures and shows that optimal timing can be highly valuable; their focus, however, is only on pairwise exchanges. The two-type model studied here builds on the model of Ashlagi et al. (Forthcoming), where they compare Chains and Pairwise exchange.

Introducing memory as a medium of exchange relates our paper to the literature on the role of money in an economy (Kocherlakota, 1998). In this sense, our paper demonstrates an application of the classic monetary models.

2 Model

We now introduce the pieces of a continuous-time, infinite-horizon model of a dynamic kidney exchange market.

Arrivals and types. Patients arrive at the market joint with an incompatible donor and wish to find a donor they find compatible. We assume patients are indifferent between all compatible donors and prefer to get matched as early as possible.

There are two types of patients in our model: *hard-to-match* and *easy-to-match*. We refer to these types as H and E, respectively. Agents arrive to the market at rate n. A fraction $\lambda > 0$ of agents are hard-to-match and a fraction $(1 - \lambda)$ are easy-to-match. A type H patient is compatible with any donor with probability p_H and a type E patient is compatible with any donor with probability p_E. For tractability, we focus on a setting where $p_E = 1$, so that easy-to-match patients are compatible to everyone. These two assumptions bring us analytical tractability without a huge sacrifice in the economics of the problem—we discuss this in subsection 2.1.

For any $t \geq 0$, let V_t^p and V_t^d be the set of patients and donors in the market at time t, respectively, and let $S_t = |V_t^p|$ and $Z_t = |V_t^d|$. Let $\mathcal{E}_t \subseteq V_t^p \times V_t^d$ be the set of compatible patient-donor pairs. Let $\mathcal{G}_t = (V_t^p, V_t^d, \mathcal{E}_t)$ be the (bipartite) *compatibility graph* at time t. We refer to $\mathcal{E}_t$ as the set of *edges*. When a new incompatible patient-donor $v_i = (p_i, d_i)$ arrives at time t, edges are formed between p_i and all compatible existing donors in V_t^d, as well as between d_i and all compatible patients in V_t^p.

Objective. Agents (patients or donors) stay in the market until they are matched. For a patient p_i who enters the market at time t_0 and gets matched at time t_1, let $w(p_i) = t_1 - t_0$ be its waiting time. The planner's objective is to minimize the average waiting time in steady

state. By Little's law, this is equivalent to minimizing the average number of agents in the system[5]. Since easy-to-match patients are compatible to everyone, their waiting time will be negligible in all algorithms we analyze. Thus, our focus is on the average waiting time of hard-to-match patients—which is indeed the main challenge in real-world kidney markets. Let $\mathbf{W}(ALG)$ denote the average waiting time of hard-to-match patients for a given matching algorithm ALG in steady state.

Matching algorithms. A set of edges (possibly empty) is a *matching* if no two edges share the same endpoints. A *matching algorithm*, at any time t, selects a matching M_t in the graph $\mathcal{G}_t$. The endpoints of the edges in M_t leave the graph immediately. This definition of a matching algorithm does not require a donor d_i and her patient p_i to be in the same matching. Thus, it includes algorithms that are currently logistically infeasible. For instance, the usual pairwise kidney exchange—which is the only legal form of exchange in France—substantially limits the set of feasible matchings: A *pairwise compatibility* happens when two incompatible patient-donor pairs v_i and v_j are cross-compatible; that is, there is an edge between (p_i, d_j) and (p_j, d_i). In pairwise kidney exchange, only pairwise compatible pairs can be matched.

We study three myopic matching algorithms. The first two have been extensively studied before (Akbarpour et al., Forthcoming; Ashlagi et al., Forthcoming). The last one, *Unpaired exchange*, is the core of the theoretical contribution of this paper.

Definition 2.1 (Pairwise)**.** *If any new patient-donor pair v_i enters the market at time t, then match her with any cross-compatible patient-donor pair (if any), breaking ties arbitrarily.*

The next matching algorithm, the *Chain exchange*, is feasible only in settings where altruistic donors exist. The definition is taken from Ashlagi et al. (Forthcoming).

Definition 2.2 (Chain)**.** *There is a bridge or altruistic donor in the market at any given time. Consider a new arriving agent $v_1 = (p_1, d_1)$. If p_1 does not have an edge to the bridge donor then no matches happen. Otherwise, a chain-segment begins with matching p_1 and the bridge donor and advances as follows. First we search for an unmatched H patient that has an edge to d_1; if there is one or more such H agents, we select one uniformly at random; otherwise, if no such an H exists, we search for an unmatched E patient that has an edge to v_1 (again breaking ties uniformly at random). This process repeats itself immediately from the selected agent (selected agents cannot be reselected) until we reach an agent that cannot match any other agent, forming a disjoint path. All agents in the disjoint path leave the market except the last agent who then becomes a bridge agent.*

[5]Note that, unlike in Akbarpour et al. (Forthcoming), our agents do not depart. This makes our analysis less tedious, without creating any difference in the objective function. Our goal here is to minimize the total waiting time, whereas in a model with departures the goal is a mix of waiting time and deaths. With linear waiting cost and Poisson departures, Little's law implies that both of these objectives are minimized by minimizing the pool size.

Essentially, upon the arrival of a new patient-donor pair, the chain exchange algorithm identifies a chain in a greedy fashion. This policy does not necessarily pick the maximum size chain (since it is searching in a greedy fashion), but it does find a maximal size chain and gives priority to H patients meanwhile.

We are now ready to introduce the *Unpaired* algorithm.

Definition 2.3 (Unpaired)**.** *If any new patient-donor pair $v_i = (p_i, d_i)$ enters the market at time t, match p_i to a compatible donor (if any), breaking ties arbitrarily, and match d_i to a compatible patient (if any), breaking ties arbitrarily.*

In essence, the Unpaired exchange algorithm records all transactions in market's memory. If a pair enter the market and the donor donates a kidney, but the patient is not able to receive a kidney from anyone, then the market will remember this and gives the patient the right to receive a kidney in future. Similarly, if the patient receives a kidney but the donor cannot donate to anyone, the market will remember this and will expect the donor to donate a kidney in future.

The Unpaired algorithm comes with two practical challenges. First, some donors may renege once their patients received a kidney. In Section 5, we will discuss that the relatively low empirical renege rate for the Chain algorithm suggests that this may not be an issue for our algorithm as well. The second challenge faced by the Unpaired algorithm is that patients may be reluctant to have their donors donate before they receive, specially if they have to wait for a long time.[6] We discuss this point in Section 4. A practical way to reduce the waiting time of such patients is to give priority to patients whose donors have donated a kidney. This, in equilibrium, incentivizes advanced donation, since it reduces the waiting time of those patients substantially. Our empirical analysis is based on this tie-breaking rule. In addition, in Sections 4 and 5, we will explain how a practical version of the Unpaired algorithm that employs deceased kidneys can alleviate or even eliminate both challenges.

In the rest of the paper, we simply refer to these three algorithms as Pairwise, Chain, and Unpaired.

Optimal solution. In many parts of this paper we compare the performance of a matching algorithm to the performance of an Optimal algorithm. This algorithm is simply defined as the smallest waiting time that can be achieved by matching algorithms. Unlike the other matching algorithm we study, the Optimal algorithm need not be greedy, i.e., for instance, it may wait before matching an agent if this agent is more likely to help pairs who will be in the system in the future. More formally, letting $\mathbf{W}_E(ALG)$ be the waiting time of easy-to-match patients

[6] As discussed in Section 4.1.2, for a patient, her incompatible donor *is* an outside option since he can always get transplanted going through a desensitization procedure.

(recall that $\mathbf{W}(ALG)$ is the waiting time of hard-to-match patients), we define $\mathbf{W}(OPT)$ as

$$\begin{aligned} \inf \quad & \mathbf{W}(ALG) \\ \text{s.t.} \quad & \mathbf{W}_E(ALG) \leq \mathbf{W}(ALG) \end{aligned}$$

where the infimum is taken over all matching algorithms inducing a stochastic process which has an invariant distribution. The constraint that the waiting time of easy-to-match is smaller than waiting time of hard-to-match patients (i.e., $\mathbf{W}_E(ALG) \leq \mathbf{W}(ALG)$) is a natural constraint. We focus on hard-to-match exactly because they have longer waiting time than easy-to-match patients.

While this algorithm may be practically infeasible, it is useful as a theoretical benchmark. Let $\mathbf{W}(OPT)$ denote the waiting time of the Optimal algorithm.

2.1 Discussion of assumptions

Our stylized model does not capture all details of the kidney exchange problem. For instance, there are clearly more than two types of patients since, for a patient, her biological compatibility with a donor depends on blood type and tissue type compatibilities. There are finitely many blood types with a known fixed compatibility relation but the tissue compatibility involves a more subtle comparison of the many types of antibodies of a patient with the antigens in the tissue of the donor. This information is usually summarized using the continuous *Panel Reactive Antibodies* (PRA) variable which gives the probability that a patient is tissue type incompatible with a randomly chosen blood type compatible donor. The higher the PRA, the more difficult it is to find a compatible donor. Even though the PRA variable is continuous, its distribution is mostly bimodal with high concentrations of agents at very low and very high PRA values. This has been confirmed for instance in the U.S. (Anderson et al., 2017). Figure 1 shows a similar bimodal pattern for the patients of the French Kidney Exchange Program (KEP), which we use to perform our simulations in Section 4. Adding the blood type compatibility still induces a bimodal distribution for the probability of overall biological compatibility in our data (see for instance Figure 3 in Section C of the Appendix).

Second, our main theoretical results rely on the probability of compatibility of hard-to-match patients being sufficiently low. In our data, we do observe a relatively low probability of compatibility of patients with high PRA values.[7] In France, patients participating in the KEP with a high PRA are compatible on average with only 1.5% of the donors in the program while other patients are compatible on average with 24.5% of the donors.

Third, our theoretical analysis assumes that the probability of compatibility of an easy-to-match patient is equal to 1. We believe our results on the Unpaired algorithm do not rely

[7] We follow the Biomedecine Agency in France and define hypersensitized / high PRA patients as patients whose PRA is above 85%.

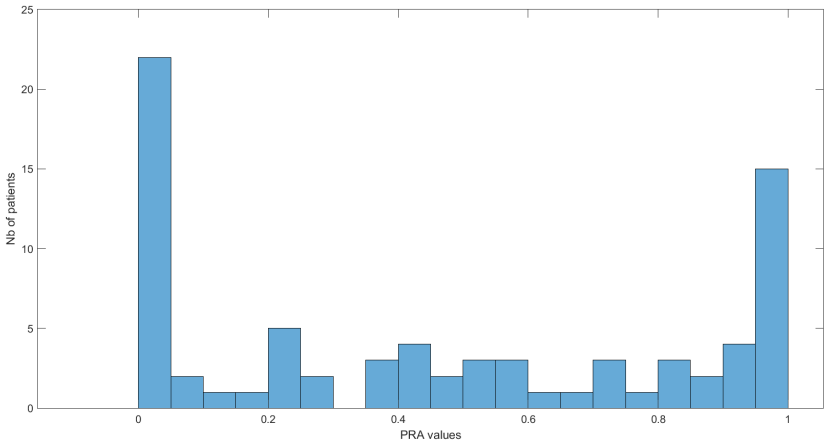


Figure 1: Histogram of PRA values for the French KEP

on this assumption. An heuristic argument is as follows. Since we assume that p_H vanishes, the number of hard-to-match patients remaining in the system explodes and so the number of remaining donors explodes as well. If the probability of compatibility of an easy-to-match patient is $p_E < 1$, the probability of finding a match right away for an arriving easy-to-match agent goes to 1 as p_H vanishes which is an essential component of our analysis.

Finally, we assume that there is no death in our model. This is certainly an unrealistic assumption when one thinks about the overall population of patients waiting for kidney transplant.[8] However, when focusing on the patients participating in the KEP, they are usually patients with better health conditions. On the time span (of more than four years) covered by our data set for France, none of the patients who participated in the French KEP has died while waiting for a kidney. However, some of them do leave the program after waiting. They correspond to patients accepting a kidney from a deceased donor, going through a desensitization process with their incompatible donor (see Section 4.1.2) or finding another living compatible donor. Of course, adding exit choices to the model would add a layer of complexity. However, we do not believe that our main results would be affected. Indeed, at an intuitive level, the longer the waiting time of an algorithm, the most likely it is that patients will exit. As will become clear, our Unpaired algorithm has the smallest expected waiting time among the mechanisms we study (beyond the optimal mechanism). This suggests that our comparison results between the Unpaired algorithm and others will be reinforce in a model with exit. Indeed, our simulations in Section 5 shows how our results are robust to the addition of exit.

[8] In the U.S., in 2014, 4,761 patients died while waiting for a kidney transplant. Another, 3,668 people became too sick to receive a kidney transplant. Source: National Kidney Donation www.kidney.org

3 Theoretical results

We now analyze the expected waiting time for hard-to-match patients under the policies defined in the previous section. Our main goal here is to compare Unpaired algorithm with both standard policies (such as pairwise exchange or chains) and with the optimal solution. In order to achieve this, the following proposition characterizes the expected waiting time of Unpaired algorithm when p_H vanishes.

Proposition 3.1. *Under Unpaired algorithm, the average waiting time of a hard-to-match patient satisfies*

$$\lim_{p_H \to 0} p_H \mathbf{W}(\textit{Unpaired}) = \frac{\ln(1+\lambda)}{n \cdot \lambda}.$$

Proof. See Appendix A.1. □

A very rough intuition for this result is as follows. Under the Unpaired exchange algorithm, agents' average waiting time is inversely proportional to the probability of being compatible with an existing donor. Under this algorithm, for an arriving hard-to-match agent, the probability of being compatible with a donor waiting is p_H. Thus, the scaling factor of the average waiting time for a hard to match patient is $1/p_H$.

The result gives us some basic comparative statics. First, increasing the total arrivals is always good since this thickens the market. Second, waiting time of hard-to-match patients is decreasing in λ. Increasing λ increases the rate of arrival of hard-to-match patients and decreases that of easy-to-match patients. Under the Unpaired algorithm, easy-to-match patients exert a negative externality on hard-to-match patients. Indeed, upon arriving an easy-to-match patient is always sure to be compatible with an existing donor. The removal of this donor makes the pool size smaller. A smaller pool size creates less opportunities for hard-to-match patients arriving in the future and so increases their waiting time. Overall, increasing the fraction of hard-to-match patients arriving reduces this negative externality and reduces waiting time of hard-to-match agents. As we will see, this is in contrast with the Pairwise exchange algorithm under which easy-to-match patients can potentially help hard-to-match patients by increasing their likelihood of being *cross*-compatible.

With this result in hand, we can proceed in comparing Unpaired algorithm with other policies.

3.1 Unpaired versus Pairwise Exchange: Overcoming Double Coincidence of Wants

We start by comparing the expected waiting time under Pairwise and Unpaired exchanges. In full generality, one can construct realizations of the stochastic process under which average waiting time across all agents is larger under Unpaired rather than under Pairwise exchanges.

Indeed, there is a well-known tradeoff between serving agents quickly and thickening the market. With Unpaired algorithm, some agents may be matched quickly but this may impose a cost on future arriving agents who may have benefited from the presence of these agents. On the other hand, the pairwise exchange algorithm, by matching agents less quickly accumulates a number of agents which thicken the market which may be useful for future arriving agents. However, the following result shows that, in expectation, the cost imposed by matching slowly through pairwise exchanges outweighs the benefits of matching agents quickly through Unpaired algorithm.

Theorem 3.2. *For any $p_H > 0$ small enough, the expected waiting times satisfy*

$$\mathbf{W}(\textit{Unpaired}) < \mathbf{W}(\textit{Pairwise}).$$

Proof. See Appendix A.2. □

We can further compare the two algorithms. In particular, we show that when a majority of arrivals are hard-to-match agents, Unpaired algorithm, by overcoming the double coincidence of wants imposed by Pairwise exchanges, reduces waiting time by an order of magnitude.

Theorem 3.3. *We have*

$$\lim_{p_H \to 0} \frac{\mathbf{W}(\textit{Pairwise})}{\mathbf{W}(\textit{Unpaired})} = \begin{cases} O(1/p_H) & \textit{if } \lambda \geq \frac{1}{2} \\ c & \textit{if } \lambda < \frac{1}{2} \end{cases}$$

where $c = \ln\left(\frac{1-\lambda}{1-2\lambda}\right)/\ln(1+\lambda)$ is always greater than 1.

Proof. See Appendix A.2. □

To gain intuition into the result, let us recall that, for pairwise exchanges, Ashlagi et al. (Forthcoming) identify two different possible scaling laws on $\mathbf{W}$(Pairwise) depending on whether a majority of arrivals are hard-to-match agents. Indeed, under the pairwise exchange algorithm, for an arriving hard-to-match agent, the probability of being cross-compatible with an easy-to-match agent in the pool is p_H (recall that $p_E = 1$); while it is p_H^2 with an existing hard-to-match agent. When a majority of arrivals are easy-to-match agents, almost all hard-to-match agents are matched with easy-to-match agents for pairwise exchanges. Thus, in that case, the expected waiting time for the pairwise exchange policy scales with $1/p_H$. The scaling is similar to the one achieved by the expected waiting time of Unpaired algorithm as shown in Proposition 3.1. Nevertheless, the performance gap between Unpaired and the Pairwise algorithm increases with the arrival rate of hard-to-match agents and tends towards infinity as λ approaches to $1/2$. As previously discussed, this is due to the fact that easy-to-match patients exert a negative externality on hard-to-match under Unpaired algorithm while they help to perform more exchanges under the Pairwise algorithm.

In the other regime where hard-to-match arrive more frequently than easy-to-match agents, there are not enough easy-to-match agents. So a significant fraction of hard-to-match agents match with each other and thus, as shown in Ashlagi et al. (Forthcoming), the scaling of the expected waiting time increases to $1/p_H^2$. Thus, in this latter context, by Proposition 3.1, Unpaired algorithm reduces waiting time by an order of magnitude by overcoming the double coincidence of wants imposed by the pairwise exchange algorithm.

3.2 Ordering Policies

We now go beyond the comparison with pairwise exchanges and further compare expected waiting times under Unpaired algorithm with that under chain exchange and under the optimal solution. Many kidney exchange programs are now successfully using chains initiated by altruistic donors to facilitate patients' access to transplants. In our dynamic environment, the comparison between Unpaired and Chain exchanges is a priori not obvious for the same reason that the comparison between Unpaired and Pairwise algorithm was a priori not straightforward: Unpaired exchange can potentially match agents too quickly which may make the market too thin and hurt future arriving agents. Furthermore, Chain exchange, unlike Pairwise exchange, does not rely on the double coincidence of compatibilities. Still, while it is possible to construct realization of the stochastic process where Chain beats Unpaired algorithm, here again, we show that, in expectation, the waiting time is smaller under Unpaired rather than under chain exchanges. In particular, we prove the following ordering in terms of waiting times:

Theorem 3.4. *For any $p_H > 0$ small enough, the expected waiting times satisfy*

$$\mathbf{W}(\textit{Unpaired}) < \mathbf{W}(\textit{Chains}) < \mathbf{W}(\textit{Pairwise}).$$

Proof. See Appendix A.3. □

On theoretical grounds, Ashlagi et al. (Forthcoming) have shown that under the chain exchange algorithm, expected waiting time has a scaling factor of $1/p_H$ exactly as the optimal solution. However, the following result gives a sense in which there may be an important gap in practice between chain exchanges and the optimal solution. Importantly, the proposition shows that this gap can be largely filled by Unpaired algorithm. This is true even though Unpaired algorithm is purely greedy while the optimal solution may be forward looking, for instance, by waiting before matching agents who are likely to help future arriving agents.

Theorem 3.5. *The following facts are true about the waiting times:*

1. $\lim_{p_H \to 0} \frac{\mathbf{W}(\textit{Chains})}{\mathbf{W}(\textit{Unpaired})}$ *is increasing in* λ.

2. *As* $\lambda \to 1$, $\lim_{p_H \to 0} \frac{\mathbf{W}(Chains)}{\mathbf{W}(Unpaired)} \to \infty$.[9]

3. $\lim_{p_H \to 0} \sup \frac{\mathbf{W}(Unpaired)}{\mathbf{W}(OPT)} \leq 2$.

Proof. See Appendix A.4. □

Remark 3.6. *One may simply want to see how much the waiting time of hard-to-match patients under Unpaired can be decreased without increasing the waiting time of easy-to-match agents. The above upper bound can be improved under this additional constraint on waiting time of easy-to-match patients. Indeed, we show in the appendix that for any matching algorithm ALG satisfying* $\mathbf{W}_E(ALG) \leq \mathbf{W}_E(Unpaired)$, $\lim_{p_H \to 0} \sup \frac{\mathbf{W}(Unpaired)}{\mathbf{W}(ALG)} \leq 2\ln(2) \simeq 1.38$.

The first two parts of the Theorem 3.5 state that Unpaired algorithm performs better and better (relative to the chains algorithm) as the fraction of hard-to-match agents in the market increases. Perhaps more importantly, the ratio of the waiting time between Chain and Unpaired exchanges *explodes* as nearly all patients become hard-to-match. The basic intuition behind this result can be given as follows. Easy-to-match agents are critical for chain exchanges. Indeed, intuitively, the larger the probability of starting a new chain-segment, the best the performance of chains will be. When a hard-to-match agent arrives, the probability that she finds the bridge agent acceptable is p_H which vanishes. When an easy-to-match agent arrives she will always be matched by one of the bridge agents and proceed to advance the chain-segment. Thus, when only a small minority of arrivals are easy-to-match agents, the probability of starting a new chain-segment is small and chains perform poorly. On the contrary, Unpaired algorithm does not depend so much on easy-to-match. Loosely speaking, this latter algorithm does not need to wait for easy-to-match agents to arrive in order to implement a chain-segment.

To conclude, the theoretical analysis provides some guidance for how different policies may perform in practice. In particular, under the assumption that a majority of arrivals are hard-to-match agents, we expect the difference (in terms of waiting times) between unpaired exchanges and paired exchanges to be large and much larger than the difference between unpaired exchanges and the optimal solution. Further, the waiting time of chain exchanges should be bounded away from that of the optimal solution and, here again, we expect waiting time of Unpaired algorithm to be much closer to the waiting time achieved by the optimal solution. The empirical analysis below will confirm these results.

4 Evaluating the Matching Algorithms with French Data

With an administrative dataset on kidney transplants in France, we now evaluate the algorithms studied in the model. Section 4.1 describes the institutional background and data. We

[9] The ratio is equal to $-\ln(1-\lambda)/\ln(1+\lambda)$.

start with a baseline setting for simulation similar to the theoretical model, as detailed in Section 4.2. By assumption, a patient/donor never exits without a kidney transplant/donation, and a donor never reneges after her patient has received a transplant. The performance of the four algorithms (i.e., Pairwise, Chain, Optimal, and Unpaired) are presented in Section 4.3, and we highlight that the empirical results are consistent with the theoretical predictions. We also point out that the two potential incentive issues (discussed in Section 2) are present in Unpaired. To address them, we introduce a practical version of the Unpaired algorithm in Section 4.4. Our results show that it preserves the performance of the Unpaired algorithm while essentially removing the two incentive issues. In Section 5, we relax some of the assumptions in the simulation and present robustness checks.

4.1 Institutional Background and Data

Our analysis relies on administrative data from France provided by the Biomedicine Agency (*Agence de la Biomédecine*, ABM), a government agency that oversees all organ transplants in France. Our data covers the period of December 2013 to February 2018, including all transplants with deceased and living donors kidneys, as well as discarded kidneys from deceased donors.

We focus on three types of kidney transplants: kidney exchange, living donor with desensitization, and deceased donor kidneys. In France, when a patient is diagnosed as requiring a kidney transplant, her doctor registers her at the national deceased donor list (DDL) to wait for a kidney. If a patient finds an incompatible living donor, she may either join the kidney exchange or go through a desensitization procedure whereby she can receive an incompatible kidney from her donor. Below, we provide institutional details and describe the data by transplant type.

4.1.1 Kidney Exchange Program in France

France's kidney exchange program (KEP) started in 2013, following the revision of the bioethics law (*loi de bioéthique*) that regulates the medical practices in France and is revised and revoted every four years. Unlike the U.S., France only has a single KEP at the national level and is administered by the ABM. By law, any exchange of living donors must be done through the KEP. In particular, a hospital is not allowed to implement an exchange of donors between its pairs and has to register these pairs at the national KEP.

In general, the KEP executes a match run every three months, leading to 15 in our sample period.[10] Only Pairwise exchange is allowed in the KEP, while non-directed kidney donations

[10] In the sample period, December 2013 to February 2018, the first match run happened in December 2013. There were only three match runs each in 2014, 2015, and 2017 due to low participation. Additionally, our data covers one match run in February 2018.

and chains are prohibited. The KEP's objective is to maximize the total number of transplants in each match run. If a match run contains multiple solutions reaching the maximal number of transplants, a point system is used to choose among the solutions. For a possible transplant, its number of points is determined by blood type compatibility (accounting for 20% of the total points), human leukocyte antigen (HLA) compatibility (20%), age difference between the donor and the patient (20%), and the patient's chance of obtaining a graft on average (40%).

In total, there are 78 pairs participating in at least one of the 15 match runs. On average, a pair stays for 3.4 match runs, and a match run has 17.5 participating pairs. 12 pairs were engaged in an exchange in our sample period.

Table 1: Kidney Patients and Donors: Summary Statistics

	KEP Pairs		Desensitization Pairs		DDL Kidneys[d]
	Patient	Donor	Patient	Donor	
	(1)	(2)	(3)	(4)	(5)
N	78	78	571	571	15,417
Patient grafted/Donor donated	69%[a]	23%[a]	100%	100%	100%
Age	49.86	50.67[b]	45.58	50.64	54.69
	(12.90)	(10.95)	(14.46)	(11.72)	(18.47)
Female	47%[c]	51%[b]	37%	62%	43%
Blood type					
A	31%	51%	24%	47%	44%
B	10%	18%	17%	16%	10%
O	56%	23%	57%	31%	43%
AB	3%	8%	2%	6%	4%
Sensitization type					
Hypersensitized (= hard-to-match)	27%		24%		
Sensitized	23%		27%		
Non-sensitized	50%		49%		
Blood type compatible b/t the pair	42%		47%		
HLA Compatible b/t the pair	32%		45%		

Notes: This table presents characteristics of kidney patients and donors in France from December 2013 to February 2018. Columns (1) and (2) are on paired patients and donors who ever participated in the KEP. There are 78 pairs participated in at least one of the 15 match runs; on average, a pair stays for 3.4 match runs, and a match run has 17.5 participating pairs. Columns (3) and (4) are on paired patients and donors who did desensitization. Column (5) are all the DDL kidneys that were grafted to a patient.

[a] Patients in the KEP can receive a graft outside the KEP, and a donor can donate outside the KEP too. There are 12 pairs (15.4%) engaged in an exchange in the KEP during the sample period.

[b] These percentages are calculated among the 45 donors with non-missing values for the respective variable. These two variables have missing values for the 8 Swiss donors and 25 French donors.

[c] This percentage is calculated among the 70 patients with non-missing gender information. The other 8 patients are Swiss.

[d] A DDL donor may provide two kidneys, and the statistics in column (5) are calculated at individual kidney level.

Columns (1) and (2) of Table 1 present more summary statistics on the 78 KEP pairs. Some patients receive a graft from the DDL or a living donor kidney outside the KEP, leading to 69% of them receiving a transplant. For the same reason, only 23% of the donors donate,

with some of them donating outside the KEP. Many of the patients are of blood type O (56%) and hypersensitized (27%), consistent with the hypothesis that it is hard to find a match for them. The most common blood type among the donors is A (51%), while only 23% of them are of blood type O. Among the pairs, 42% are blood type compatible, and 32% are HLA compatible.

4.1.2 Desensitization Pairs in France

Recent developments in immunosuppressive protocols have introduced a new option of transplants from incompatible donors. Desensitization is an immunosuppressive treatment that enables transplants from incompatible donors and the medication used in this procedure is called immunosuppressants. For most compatible transplants, immunosuppressants have been commonly used to relax minor immunological constraints. Since 1980s, however, they have been developed to eliminate blood-type compatibility constraints, enabling transplants from blood-type incompatible donors. More recently, they are developed further to eliminate all immunological compatibility constraints. When a patient uses immunosuppressant and goes through the desensitization procedure, she becomes essentially compatible with any donor, so is able to receive a transplant from an incompatible donor. For a brief review of desensitization, please see Andersson and Kratz (2017) and Heo et al. (2018) as well as the references therein.

In France, desensitization is a popular choice for incompatible pairs. In our data, there are 571 incompatible pairs that never participate in the KEP and take this option. These transplants, as well as the associated patients and donors, are recorded by the ABM. In some of our simulations (Section 5), we assume that some of these pairs participate in the exchange.

Columns (3) and (4) of Table 1 present more summary statistics on desensitization pairs. Compared to the donors in the pairs, the patients are younger (45.48 versus 50.64 years old), have fewer females (37% versus 62%), and are more likely to be of blood type O (57% versus 31%). 24% of the patients in the desensitization pairs are hypersensitized. Relative to the KEP pairs, the desensitization pairs are slightly more likely to be blood type compatible (47% versus 42%) or HLA compatible (45% versus 32%).

4.1.3 Deceased Donor List in France

Once a patient is medically diagnosed as needing a kidney transplant, her doctor is required to register her at the national DDL and thus becomes associated with one of the 184 organ retrieval centers across the country. The patient's associated center puts her into a local waiting list as well as a regional waiting list. Each center has its unique local list, while several centers share a regional list. However, no center can be associated with multiple regional list. On any given day in our sample period, there are about $9,000$ patients waiting on the DDL.

The allocation of a DDL kidney are based on geographical locations of the kidney and the priorities of patients on the DDL. Typically, when a donor deceases, a team from the closest organ retrieval center will harvest the two kidneys. The team then allocates one kidney to the patient who has the highest priority score among all patients its local list. The other kidney, "the national kidney," goes to the national list and then the center's regional list.[11]

National and regional priorities are given to patients who are in critical conditions, hypersensitized, younger than 18 years old, or waiting for transplants of multiple organs. To calculate a patient's priority score in the local, regional, or national allocation of a given kidney, it takes into account the patient's total waiting time and time on dialysis, her HLA match with the kidney, her potential of finding a good match, the age difference between the patient and the donor, and the time needed to ship the kidney to the patient.

During our sample period, there are 14,944 kidneys from deceased donors being transplanted in patients on the DDL. Moreover, there are 473 deceased donors whose kidneys are offered to the DDL patients but discarded in the end due to either refusals or last minute cancellations.[12] These two together give us 15,417 DDL kidneys. Column (5) of Table 1 present more summary statistics. On average, the kidneys are 54.69 years old, and 43% are from a female donor. The top two blood types are A (44%) and O (43%). In some of our simulations (Sections 4.4 and 5), we assume that some of the "high-quality" DDL kidneys can be used in the exchange, where high quality is to be defined.

4.2 Definitions and Assumptions in the Simulations

The following definitions, assumptions, and data preparations are needed in our simulations.

Hard to match. We define that a patient is hard to match if she is hypersensitized. There are 21 such patients from the KEP pairs and another 135 from the desensitization pairs (Table 1). As mentioned in Section 2.1, even when we abstract from blood type incompatibility, the probability of compatibility of those patients is very low (the mean PRA among those patients is 1.5%).

Arrival and exit dates. Among the KEP pairs, arrival dates are recorded in the form of participation in the KEP programs. We observe the pairs participated in each match run

[11] The allocation rules were changed in February 2015 to address the regional inequality concerns in kidney transplants. The retrieving team still allocates one kidney to a patient on its local list in a similar way, but the national kidney is now allocated differently. Specifically, after exhausting patients with national and then regional priorities, the pre-reform rules allocate the national kidney to the patients in the region, and, by contrast, the kidney is allocated to a patient on the national list by the post-reform rules.

[12] For some of these donors, we do not know how many kidneys are available for the DDL. We assume each of them has only one kidney available.

and the date of the match run. Among the desensitization pairs, we observe the date of each transplant.

Our main simulations consider the 78 KEP pairs. If a KEP pair arrives between the k-th and $(k+1)$-th match runs, we draw an arrival day uniformly between these two dates. For each pair participating in the first match run, we independently draw a date uniformly among the 110 days before the match run.

Most departures of pairs from the KEP are due to accepting a kidney from a deceased donor or desensitization. As discussed in Section 2.1, there is no death of the patient in a pair, because patients who are allowed to participate in the KEP are in relatively good health.

In some of our simulations, we allow a KEP pair to exit without receiving a transplant. Exit dates are simulated as follows: for the pairs that accepted a KEP kidney or participated in the last match run in the data, they are assumed to stay until the end of the time horizon for our simulation (to be defined below); for all other pairs, we draw a date uniformly between the k-th and $(k+1)$-th match run, with the k-th being the last match run in which they participated.

In some other simulations, we also use the desensitization pairs. For each pair independently, we uniformly draw a date from the 110 days before its transplant date as its arrival date. A pair's exit date is set at its desensitization transplant date in the data.

In all simulations, we draw 100 sets of arrival and exit dates and use the same draws to calculate outcomes of all policies. We then report the averages over the 100 simulations for any given policy.

In our baseline simulations (Section 4.3), we assume there is no exit. Equivalently, every one who has not received a transplant or has not donated stays until the end of our simulation.

Time horizon in simulations. Time in our simulations are measured by days. For a given set of simulated arrival and exit dates, the time horizon starts with the arrival of the first pair and ends on the date when the last pair arrives.

"Waiting rooms" for unpaired patients and donors (P and D). As we already mentioned in Section 2, the potential incentive issues of the Unpaired algorithm involve unpaired patients and donors. Namely, a patient may not be willing to let her donor donate before she receives a kidney; a donor may renege if her patient has already received a transplant from someone else. Some definitions will be useful in our simulation analysis. We let P be the "waiting room" for patients who are still waiting for a kidney but whose paired living donors have already donated; D is the "waiting room" for donors who wait to donate but whose paired patients have already received transplant.

4.3 Evaluating the Algorithms: Baseline Simulations

We now simulate the matching algorithms studied in Section 2 (Pairwise, Unpaired, Chain, and Optimal), starting with the baseline in which there is neither pair exit nor donor reneging.

We describe our simulation for a given set of simulated arrival and exit dates, and the same simulation procedure is applied to all 100 sets of simulated arrival and exit dates. Pairs are ordered by arrival date: $i = 1, \ldots, n$. Let $a(i)$ and $e(i)$ be respectively the dates of arrival and exit of pair i. For two dates t and t', we write $t < t'$ if the date t is before date t'. We also define $t - t'$ as the number of days between t and t', which can be negative if t is after t'. Let $T := a(n)$ be the arrival date of the last pair. We assume there is no exit, or equivalently $e(i) = T$ for all i. That is, before the last day (T), once a pair arrives, the patient leaves only if she receives a kidney and the donor leaves only if she donates a kidney. This no-exit assumption is motivated in Section 2.1 and is relaxed in Section 5.

We simulate the first three policies (i.e., Pairwise, Chain, Unpaired) by following their definitions in Section 2 (Definitions 2.1, 2.2, and 2.3). To initiate the Chain exchange algorithm, we select a DDL kidney to arrive on the first day of the simulation, $a(1)$, as an altruistic donor.[13] In other words, there is at most one single chain. Note that, for sake of realism, pairwise exchanges are still allowed in Chain while this was not the case in our theoretical analysis. For Optimal we take the following detour. We study the Omniscient solution which assumes that the designer has full information about the future, i.e., he knows who will be in the system in the future and the edges between them. Equipped with this information, it matches agents in such a way to minimize the overall sum of the waiting times of all patients, regardless of transplant status. While this algorithm is clearly practically infeasible, it is useful to learn about the performance of the Optimal solution. Indeed, our empirical results show that Unpaired and Omniscient are extremely close in terms of expected waiting time. Hence, since the Optimal solution must be "squeezed" inbetween the Unpaired and the Omniscient in terms of waiting time, this result implies that the waiting times under Optimal and Unpaired must also be extremely close to each other. This detour is convenient since it avoids to make any assumption on the data generating process which, in principle, is needed to study the Optimal algorithm. Further, we can formulate the Omniscient solution as an Integer Linear Programming (ILP) problem as detailed in Appendix B.

Our simulation results in Table 2 are in line with the theory. Waiting time under Unpaired

[13] To ensure that a DDL kidney is of "high quality" for a given patient, we require that the DDL kidney be compatible with the patient and have a Kidney Donor Profile Index (KDPI), a risk index of post-transplant graft failure, below the Living Kidney Donor Profile Index (LKDPI) of the patient's paired incompatible donor. The LKDPI is an index for living donor kidneys corresponding to the KDPI, and they are of the same scale. See Appendix D for more details on KDPI and Appendix E for more details on LKDPI. Among the DDL kidneys meeting this selection criterion for at least one KEP patient, we randomly pick one, regardless of its arrival date. We assume that this DDL kidney arrives at the beginning of the time horizon, $a(1)$, and waits until at least one compatible patient arrives or until the end of the simulation. We redraw a new DDL kidney for each set of simulated dates of the KEP pairs.

is lower than Pairwise and Chain (Theorems 3.2 and 3.4). While Omniscient achieves the lowest waiting time, it does not outperform Unpaired much (Theorem 3.5).

Table 2: Performance of Matching Algorithms

	Pairwise Exchange	Chain (+ Pairwise)	Omniscient	Unpaired Exchange	
				Original	Practical
	(1)	(2)	(3)	(4)	(5)
Transplants					
Total number of transplants	24.1	24.2	45.2	44.4	67.9
to hard-to-match patients	*3.3*	*3.3*	*8.0*	*6.4*	*15.2*
from deceased donors	*0*	*1*	*0*	*0*	*28.2*
% patients receiving transplant	30.9	31.1	57.9	57.0	87.1
% hard-to-match patients receiving transplant	15.5	15.5	38.1	30.7	72.1
Waiting time (days)					
All patients	695	676	410	424	141
Hard-to-match patients	724	720	539	580	249
Patients going through P					
Total number			28.0	24.2	29.7
# days in P: mean			601	406	34
# days in P: median			456	218	2
# days in P: 90th percentile			1365	1127	129
Hard-to-match patients going through P					
Total number			11.8	10.7	14.0
# days in P: mean			577	623	70
# days in P: median			473	509	20
# days in P: 90th percentile			1096	1167	213
Donors going through D					
Total number			27.6	22.9	32.0
# days in D: mean			610	433	31
# days in D: median			451	289	7
# days in D: 90th percentile			1355	1019	92

Notes: There are in total 78 incompatible pairs, among which 21 have a hard-to-match patient. The statistics reported are from the 100 sets of simulations, each of which contains a draw of arrival dates of the 78 pairs. Note that the waiting time for a patient or a donor may be censored from above if she has not received or donated a kidney by the last date of the simulation, T. The same censoring applies to the number of days in P or D. Pairwise exchange (column 1) is defined in Definition 2.1, Chain exchange is defined in Definition 2.2 and is combined with Pairwise exchange (column 2), and Omniscient solution (column 3) uses full information about the future to match patients and donors to minimize the total waiting time (also see Equation (9)). In columns (4), the "original" Unpaired Exchange, as defined in Definition 2.3, only uses living donors in the 78 pairs. In the Practical Unpaired Exchange (column 5), which is defined in Definition 5.1, qualified DDL kidneys are used in the algorithm and for each DDL kidney that is used, a living donor gives a kidney to the DDL. A qualified DDL kidney for a given patient must have a KDPI below that of her own paired donor.

Specifically, columns (1)-(4) show the performance of each algorithm. In terms of the percentage of patients transplanted, Unpaired is very close to Omniscient (57.0% versus 57.9%) and far above the other two (30.9% under Pairwise Exchange and 31.1% Chain Exchange). A similar pattern holds true among hard-to-match patients.

Regarding waiting time, we again observe the performance of Unpaired being close to Omniscient and dominating Pairwise and Chain. This is true overall and for hard-to-match patients.

On the other hand, Table 2 also shows two potential issues with Unpaired. A patient

enters in P whenever her donor donates before she receives a kidney. Column (4) shows that patients going through P can wait a long time, although they wait less than Omniscient solution (column 3). The mean waiting time is 406 days, the median is 218, and the 90th percentile is 1127. If a patient has to wait a long time in P, pairs can be discouraged from joining the Unpaired exchange.

The second potential issue is that donors going through D also have to wait for a long time. The mean waiting time is 433 days, the median is 289, and the 90th percentile is 1019. A long wait in D increases the chance that a donor reneges or becomes unfit for donation. That is, after the patient in a pair receives a kidney, the donor refuses or becomes unable to donate. Potentially, this can be an issue, as no donor can be contractually forced to donate in current legal systems.

We now propose a practical version of Unpaired to solve these two potential incentive issues.

4.4 Practical Unpaired Exchange

The key idea of the practical proposal is to use kidneys from deceased donors, i.e., DDL kidneys (cf. Table 1).

Definition 4.1 (Practical Unpaired)**.** *In addition to the Unpaired procedure as in Definition 2.3, whenever a qualified DDL kidney arrives, match the kidney to a compatible patient in P (if any), while prioritizing patients by waiting time. Whenever a DDL kidney is taken by a patient, the donor in D who has the longest waiting time gives a kidney to some patient in the DDL.*

Note that in Practical Unpaired, P and D always have the same size. Therefore, if a patient in P takes a DDL kidney, there must be some donor in D who can donate to the DDL. This to some extent balances the interaction between the DDL and the exchange.

The algorithm only takes *qualified* DDL kidneys to ensure that they are of high quality. As described in footnote 13, we use KDRI to screen DDL kidneys. The details are presented in Appendix D. Each qualified DDL kidney is available in the algorithm for a day, i.e., the date of its arrival. Importantly, for every DDL kidney that the algorithm takes, it gives back a living donor kidney. Column (5) of Table 2 presents the outcome of a version of the Practical Unpaired exchange. Specifically, a DDL kidney is qualified for a patient in P if it has a KDRI below her incompatible donor's LKDPI; we assume that a patient in P always accepts such a kidney.

With the Practical Unpaired algorithm, the two potential incentive issues essentially disappear. The waiting times in P and D are substantially reduced. On average, patients in P only wait for 34 days (median: 2 days; 90th percentile: 129 days), while donors in D wait for 31 days (median: 7 days; 90th percentile: 92 days). With such short waiting time, one would

not be too concerned with the lack of incentives of pairs to accept donating before the patient receives. Further, the issue with reneging of donors is likely to be small. We further discuss this in Section 5 and explain how Practical Unpaired can be further modified to entirely solve the reneging issue without sacrificing on its performance.

Finally, the practical version dominates the original one on every dimension that is reported in the table. The average waiting time among all patients or among hard-to-match patients is more than halved. Noticeably, hard-to-match patients now have a 72.1% transplant rate, a substantial increase from 30.7%. The DDL kidneys help significantly, as 28.2 transplants use a DDL kidney. This also implies that 28.2 living donor kidneys are donated to the DDL.

5 Discussion and Robustness Checks

To investigate the sensitivity of our results to different assumptions, we now present an extensive set of robustness checks. In particular, we relax the assumption of no reneging, try an alternative selection of DDL kidneys for the Practical Unpaired exchange, allow pairs to exit before getting a transplant from the KEP, introduce multiple chains, and show some large market results, one by one. That is, in each of the following robustness checks, we only make one change relative to the benchmark case of the Practical Unpaired exchange (column 5, Table 2).

Reneging of Donors in D. Column (2) in Table 3 considers donor reneging when they are in D. We allow a donor in D to renege with probability 0.17% each day when she is in D. Equivalently, a donor reneges with a probability of 5% in a month, which is the same as the rate assumed by Gentry et al. (2009). On average there are 32 donors going through D, among them 1.38, or 4.3%, renege, which is higher than what is documented by Cowan et al. (2017), 1.5%, in a dataset from the National Kidney Registry of the U.S.

Relative to the benchmark case of Practical Unpaired exchange (column 1), we hardly see any effects of reneging on transplant rates. However, waiting time and the number of days in P and D increase. In particular, hard-to-match patients now have to wait for 425 days, instead of 249 days.

Column (3) considers another policy wherein a donor immediately donates a kidney to the DDL whenever her paired patient receives a kidney. Therefore, no donors waits in D and there is no reneging.

Definition 5.1 (Practical Unpaired without Donor in D)**.** *In addition to the Unpaired procedure as in Definition 2.3, whenever a qualified DDL kidney arrives, match the kidney to a compatible patient in P (if any), while prioritizing patients by waiting time. Moreover, whenever the patient in a pair receives a living donor kidney and the paired donor cannot donate to any patient, the donor immediately donates to the DDL.*

Table 3: Practical Unpaired Exchange with Reneging and Alternative Selection of DDL Kidneys

	Benchmark	Reneging		Selection of DDL Kidneys
		Reneging at 0.17% daily	No donor in D	Median KDPI of Living Donors
	(1)	(2)	(3)	(4)
Transplants				
Total number of transplants	67.9	67.2	68.4	61.5
to hard-to-match patients	*15.2*	*14.4*	*15.5*	*10.4*
from deceased donors	*28.2*	*27.7*	*29.2*	*20.8*
% patients receiving transplant	87.1	86.2	87.6	78.9
% hard-to-match patients receiving transplant	72.1	68.7	73.6	49.4
Waiting time (days)				
All patients	141	152	142	209
Hard-to-match patients	249	425	249	429
Patients going through P				
Total number	29.7	30.1	30.8	25.8
# days in P: mean	34	57	34	157
# days in P: median	2	2	2	12
# days in P: 90th percentile	129	230	128	692
Hard-to-match patients going through P				
Total number	14.0	14.0	14.3	11.8
# days in P: mean	70	120	71	334
# days in P: median	20	24	19	159
# days in P: 90th percentile	213	393	217	831
Donors going through D				
Total number	32.0	32.0	0	32.4
# days in D: mean	31	66	0	127
# days in D: median	7	27	0	47
# days in D: 90th percentile	92	177	0	383

Notes: There are in total 78 incompatible pairs, among which 21 have a hard-to-match patient. The statistics reported are from the 100 sets of simulations. Note that the waiting time for a patient or a donor may be censored from above if she has not received or donated a kidney by the last date of the simulation, T. The same censoring applies to the number of days in P or D. Column (1) contains the benchmark case of the Practical Unpaired exchange, which is copied from column (5) of Table 2. In this case, there is no reneging and a qualified DDL kidney for a given patient must have a KDRI below that of her own paired donor. In columns (2) and (3), the selection of DDL kidneys is the same as the benchmark. However, column (2) allows each donor in D to renege with probability 0.17% every day; column (3) avoids the possibility of reneging by letting a donor immediately donates a kidney to the DDL whenever her paired patient receives a kidney. The only difference between the benchmark and column (4) is that in the latter, a qualified DDL kidney for any patient must have a KDPI below the median KDPI among all 78 living donors.

The results are almost identical to those in the benchmark case (column 1).

Alternative selection of DDL kidneys. The results from the Practical Unpaired exchange is not too sensitive to alternative selection of DDL kidneys. Recall that only qualified DDL kidneys can be used in the algorithm. To qualify for the algorithm, we now require a DDL kidney to be below the median KDRI among compatible donors in Europe as reported in Rehse et al. (2018).

Column (4) of Table 3 shows that the performance of the algorithm is reduced by the new selection of DDL kidneys. In particular, hard-to-match patients now have a lower rate of

transplant and have to wait longer. The number of days patients in P is increased overall, so is the number of days of donors in D. However, the practical version still outperforms the original Unpaired exchange (column 4 of Table 2) in terms of waiting time as well as the numbers of days in P and D.

Exits of pairs. We now relax the no-exit assumption. Recall that the exit date of (p_i, d_i) is denoted by $e(i)$ and that Section 4.2 describes how it is simulated. Furthermore, we make the following assumption: if (p_i, d_i) are still waiting at $e(i)$, both of them exit at $e(i)$; if d_i donates before $e(i)$ and if p_i has not received a kidney by $e(i)$, p_i leaves at $e(i)$; if p_i receives a kidney from someone else before $e(i)$, d_i stays until the end of our simulation, T. Recall that for pairs who do not exit, we set $e(i) = T$.

With these assumptions on exits, we can simulate the first three policies (i.e., Pairwise, Chain, Unpaired) following their definitions (Definitions 2.1, 2.2, and 2.3), while taking into account some pairs and patients may exit. We again use the ILP problem in Appendix B to find the Omniscient solution , except that the exit constraints, E_i, can now be binding.

The five columns of results in Table 4 show the same pattern across algorithms as in Table 2, which implies that pair exits do not affect the performance ranking of the algorithms. Compared to column (5) of Table 2, the performance of the Practical Unpaired exchange is only slightly less effective when pairs may exit (column 5 of Table 4).

Multiple Chains. In practice, multiple altruistic donors may arrive, making multiple chains possible. Column (3) of Table 5 presents an example. We draw 30 qualified DDL kidneys as altruistic donors and assume that they arrive on the date they become a DDL kidney. Similar to the previous Chain exchange that allows at most one chain, we assume that after arrival, every DDL kidney remains available until either the end of our simulation or when it is transplanted. This may lead up to 30 chains.

We set 30 as the number of altruistic donors, more than the 28.2 DDL kidneys that Practical Unpaired uses (column 1, Table 5). Note that for every DDL kidney that Practical Unpaired assigns to a KEP patient, a KEP living donor donates a kidney to the DDL. By contrast, Chain does not require any KEP donor to donate to the DDL. These specifications of the two algorithms favor Chain and thus may overestimate its performance relative to Practical Unpaired.

The results show that allowing for multiple chains improves the Chain exchange upon the single-chain exchange, but it is still outperformed by the Practical Unpaired exchange.

Large market results. We now investigate the performance of the algorithms in a large market. In addition to the 78 pairs, we on average add 285 desensitization pairs, 50% of the

Table 4: Performance of the Matching Algorithms when Pairs May Exit

	Pairwise Exchange	Chain (+ Pairwise)	Omniscient	Unpaired Exchange	
				Original	Practical
	(1)	(2)	(3)	(4)	(5)
Transplants					
Total number of transplants	17.3	18.8	44.0	43.5	56.6
to hard-to-match patients	*2.3*	*2.2*	*5.0*	*5.4*	*10.6*
from deceased donors	*0*	*1*	*0*	*0*	*16.0*
% patients receiving transplant	22.2	24.1	56.5	55.7	72.6
% hard-to-match patients receiving transplant	10.9	10.4	23.8	25.5	50.4
Waiting time (days)					
All patients	374	364	185	244	162
Hard-to-match patients	429	430	387	393	277
Patients going through P					
Total number			25.9	23.6	25.3
# days in P: mean			343	312	167
# days in P: median			225	155	10
# days in P: 90th percentile			753	678	359
Hard-to-match patients going through P					
Total number			11.9	10.0	11.4
# days in P: mean			398	438	180
# days in P: median			311	404	22
# days in P: 90th percentile			848	870	557
Donors going through D					
Total number			35.1	24.0	29.4
# days in D: mean			565	433	147
# days in D: median			412	316	72
# days in D: 90th percentile			1333	976	429

Notes: There are in total 78 incompatible pairs, among which 21 have a hard-to-match patient. A pair or a patient may exit before receiving a kidney. The statistics reported are from the 100 sets of simulations, each of which contains a draw of arrival dates of the 78 pairs. Note that the waiting time for a patient or a donor may be censored from above if she has not received or donated a kidney by her exit day or by the last date of the simulation, T. The same censoring applies to the number of days in P or D. Pairwise exchange (column 1) is defined in Definition 2.1, Chain exchange is defined in Definition 2.2 and is combined with Pairwise exchange (column 2), and Omniscient solution (column 3) uses full information about the future to match patients and donors to minimize the total waiting time (also see Equation (9)). In columns (4), the "original" Unpaired Exchange, as defined in Definition 2.3, only uses living donors in the 78 pairs. In the Practical Unpaired Exchange (column 5), which is defined in Definition 5.1, qualified DDL kidneys are used in the algorithm and for each DDL kidney that is used, a living donor gives a kidney to the DDL. A qualified DDL kidney for a given patient must have a KDPI below that of her own paired donor.

Table 5: Alternative Chain Exchanges

	Unpaired Exchange	Chain Exchange	
		Long Chain (+ Pairwise)	Multiple Long Chain
	(1)	(2)	(3)
Transplants			
Total number of transplants	67.9	24.2	48.1
to hard-to-match patients	*15.2*	*3.3*	*4.4*
from deceased donors	*28.2*	*1*	*19.5*
% patients receiving transplant	87.1	31.1	61.6
% hard-to-match patients receiving transplant	72.1	15.5	21.1
Waiting time (days)			
All patients	141	676	469
Hard-to-match patients	249	720	699

Notes: There are in total 78 incompatible pairs, among which 21 have a hard-to-match patient. The statistics reported are from the 100 sets of simulations. Column (1) contains the benchmark case of the Practical Unpaired exchange, which is copied from column (5) of Table 2. Column (2) is copied from Column (2) of Table 2. Column (3) uses 30 qualified DDL kidneys to be used as bridge donors and thus contains up to 30 chains.

desensitized pairs (cf. Table 1). This market size is similar to what we observe in Spain, the second largest kidney exchange program in Europe (see (Biró et al., 2019)).

Recall that we simulate the policies in 100 sets of simulated arrival and exit dates of the KEP pairs. Given a set of the simulated dates, in any trimester, each desensitization pair that has a transplant in that trimester has a 50% chance being drawn. We redraw desensitization pairs across the sets of simulated dates. Arrival dates of desensitization pairs are simulated according to Section 4.2.

This procedure leads to a market that has on average 352 incompatible pairs, among which 89 have a hard-to-match patient. Table 6 presents the results, and we observe the same patterns across algorithms as in Table 2, a smaller market.

Table 6: Performance of the Matching Algorithms in a Large Market

	Pairwise Exchange	Chain (+ Pairwise)	Omniscient	Unpaired Exchange	
				Original	Practical
	(1)	(2)	(3)	(4)	(5)
Transplants					
Total number of transplants	150.2	154.1	241.6	235.1	329.1
to hard-to-match patients	*21.3*	*21.6*	*49.5*	*50.0*	*79.4*
from deceased donors	*0*	*1*	*0*	*0*	*114.3*
% patients receiving transplant	42.7	43.8	68.6	66.8	93.5
% hard-to-match patients receiving transplant	23.9	24.3	55.6	56.2	89.2
Waiting time (days)					
All patients	503	488	265	286	87
Hard-to-match patients	712	706	491	488	169
Patients going through P					
Total number			138.7	116.6	122.6
# days in P: mean			437	298	45
# days in P: median			296	152	2
# days in P: 90th percentile			1354	1308	137
Hard-to-match patients going through P					
Total number			52.1	47.2	56.6
# days in P: mean			646	560	95
# days in P: median			534	418	24
# days in P: 90th percentile			1354	1308	321
Donors going through D					
Total number			137.9	113.3	172.7
# days in D: mean			440	306	32
# days in D: median			318	219	21
# days in D: 90th percentile			1057	671	78

Notes: There are on average 352 incompatible pairs, among which 89 have a hard-to-match patient. The statistics reported are from the 100 sets of simulations. Other than the market size, everything is the same as in Table 2. For more details, please see the table notes of Table 2.

References

Akbarpour, Mohammad, Farshad Fatemi, and Negar Matoorian, "Market for kidneys," *Working paper*, 2019.

_ , Shengwu Li, and Shayan Oveis Gharan, "Thickness and information in dynamic matching markets," *Journal of Political Economy*, Forthcoming.

Anderson, Ross, Itai Ashlagi, David Gamarnik, and Yash Kanoria, "Efficient dynamic barter exchange," *Operations Research*, 2017, *65* (6), 1446–1459.

Andersson, Tommy and Jörgen Kratz, "Kidney Exchange over the Blood Group Barrier," Working Papers 2016:11, Lund University, Department of Economics June 2017.

Ashlagi, Itai, David Gamarnik, Michael A Rees, and Alvin E Roth, "The need for (long) chains in kidney exchange," Technical Report, National Bureau of Economic Research 2012.

_ , Maximilien Burq, Patrick Jaillet, and Vahideh Manshadi, "On matching and thickness in heterogeneous dynamic markets," *Operations Research*, Forthcoming.

Ausubel, Lawrence M and Thayer Morrill, "Sequential kidney exchange," *American Economic Journal: Microeconomics*, 2014, *6* (3), 265–85.

Becker, Gary S. and Julio Jorge Elias, "Introducing incentives in the market for live and cadaveric organ donations," *Journal of Economic Perspectives*, 2007, *21* (3), 3–24.

Bentall, A, LD Cornell, JM Gloor, WD Park, MJ Gandhi, JL Winters, MF Chedid, PG Dean, and Mark D Stegall, "Five-year outcomes in living donor kidney transplants with a positive crossmatch," *American Journal of Transplantation*, 2013, *13* (1), 76–85.

Biró, Péter, Bernadette Haase-Kromwijk, Tommy Andersson, Eyjólfur Ingi Ásgeirsson, Tatiana Baltesová, Ioannis Boletis, Catarina Bolotinha, Gregor Bond, Georg Böhmig, Lisa Burnapp, Katarína Cechlárová, Paola Di Ciaccio, Jiri Fronek, Karine Hadaya, Aline Hemke, Christian Jacquelinet, Rachel Johnson, Rafal Kieszek, Dirk R. Kuypers, Ruthanne Leishman, Marie-Alice Macher, David Manlove, Georgia Menoudakou, Mikko Salonen, Bart Smeulders, Vito Sparacino, Frits C.R. Spieksma, María Oliva Valentín, Nic Wilson, and Joris van der Klundert, "Building Kidney Exchange Programmes in Europe—An Overview of Exchange Practice and Activities," *Transplantation*, 2019, *103* (7), 1514–1522.

Calvillo-Arbizu, Jorge, Miguel A. Pérez-Valdivia, Miguel A. Gentil-Govantes, Pablo Castro de-la Nuez, Auxiliadora Mazuecos-Blanca, Alberto Rodríguez-Benot, María C. Gracia-Guindo, Francisco Borrego-Utiel, Mercedes Cabello-Díaz, Rafael Bedoya-Pérez, Manuel Alonso-Gil, Mercedes Salgueira-Lazo, and Laura M. Roa-Romero, "Does the Kidney Donor Profile Index (KDPI) predict graft and patient survival in a Spanish population?," *Nefrología (English Edition)*, 2018, *38* (6), 587–595.

Cowan, N, HA Gritsch, Nima Nassiri, Joseph Sinacore, and J Veale, "Broken chains and reneging: A Review of 1748 kidney paired donation transplants," *American Journal of Transplantation*, 2017, *17* (9), 2451–2457.

Gentry, Sommer E, Robert A Montgomery, Bruce J Swihart, and Dorry L Segev, "The roles of dominos and nonsimultaneous chains in kidney paired donation," *American Journal of Transplantation*, 2009, *9* (6), 1330–1336.

Heo, Eun Jeong, Sunghoon Hong, and Youngsub Chun, "Kidney exchange with Immunosuppressants," Technical Report, Vanderbilt University Department of Economics 2018.

Jevons, William Stanley, *Money and the Mechanism of Exchange*, Vol. 17, Kegan Paul, Trench, 1885.

Kocherlakota, Narayana R, "Money is memory," *Journal of Economic Theory*, 1998, *81* (2), 232–251.

Lehner, Lukas Johannes, Anna Kleinsteuber, Fabian Halleck, Dmytro Khadzhynov, Eva Schrezenmeier, Michael Duerr, Kai-Uwe Eckardt, Klemens Budde, and Oliver Staeck, "Assessment of the kidney donor profile index in a European cohort," *Nephrology Dialysis Transplantation*, 2018, *33* (8), 1465–1472.

Massie, Allan B, Joseph Leanza, Lara M Fahmy, Eric KH Chow, Niraj M Desai, Xun Luo, Elizabeth A King, Mary G Bowring, and Dorry L Segev, "A risk index for living donor kidney transplantation," *American Journal of Transplantation*, 2016, *16* (7), 2077–2084.

Organ Procurement and Transplant Network, "A Guide to Calculating and Interpreting the Kidney Donor Profile Index (KDPI)," May 2019. Accessed: July 11, 2019.

Rao, Panduranga S, Douglas E Schaubel, Mary K Guidinger, Kenneth A Andreoni, Robert A Wolfe, Robert M Merion, Friedrich K Port, and Randall S Sung, "A comprehensive risk quantification score for deceased donor kidneys: the kidney donor risk index," *Transplantation*, 2009, *88* (2), 231–236.

Rehse, Gregor, Fabian Halleck, Dmytro Khadzhynov, Lukas J Lehner, Anna Kleinsteuber, Anja Staeck, Michael Duerr, Klemens Budde, and Oliver Staeck, "Validation of the Living Kidney Donor Profile Index in a European cohort and comparison of long-term outcomes with US results," *Nephrology Dialysis Transplantation*, 2018, *34* (6), 1063–1070.

Roth, Alvin E, "Repugnance as a Constraint on Markets," *Journal of Economic perspectives*, 2007, *21* (3), 37–58.

_ , Tayfun Sönmez, and M Utku Ünver, "Kidney exchange," *The Quarterly Journal of Economics*, 2004, *119* (2), 457–488.

_ , _ , and _ , "Efficient kidney exchange: Coincidence of wants in markets with compatibility-based preferences," *American Economic Review*, 2007, *97* (3), 828–851.

_ , _ , _ , Francis L Delmonico, and Susan L Saidman, "Utilizing list exchange and nondirected donation through 'chain' paired kidney donations," *American Journal of transplantation*, 2006, *6* (11), 2694–2705.

Ünver, M Utku, "Dynamic kidney exchange," *The Review of Economic Studies*, 2010, *77* (1), 372–414.

A Proofs from the Theoretical Model

A.1 Proof of Proposition 3.1

For ease of notation in proofs, we define $\lambda_H = n\lambda$ and $\lambda_E = n(1-\lambda)$ as the arrival rate of hard-to-match and easy-to-match pairs.

We make several preliminary remarks. First, under the unpaired exchange algorithm, one can easily check that the number of patients remaining in the system equals the number of donors remaining ($S_t = Z_t$ for all t). This is useful since we can simply focus on the evolution of the number of patients of each type remaining in the system.

Second, since $p_E = 1$, the Markov chain induced by the unpaired exchange policy is "almost one-dimensional". Indeed, any easy-to-match pair arriving in the system will be matched right away provided that there is at least one donor remaining. Hence, there will always be at most one easy-to-match remaining in the system. Formally, the state space for our Markov chain is $(k_E, k_H) \in \{(1,0) \cup (\{0\} \times \mathbb{N})\}$ where k_E (resp. k_H) is the number of easy-to-match (hard-to-match, resp.) patients remaining in the system. Note that the state space is homeomorphic to $\{-1\} \cup \mathbb{N}$ which we will consider as being the state space hereafter (-1 stands for the state $(1,0)$ while state $k \geq 0$ stands for the state $(0,k)$).

We denote by Q the transition rate matrix over states $\{-1\} \cup \mathbb{N}$. This is described as follows. For $k \geq 1$:

$$Q(k,k') = \begin{cases} \lambda_H (1-p_H)^{2k} \text{ if } k' = k+1 \\ \lambda_H 2(1-p_H)^k \left[1-(1-p_H)^k\right] + \lambda_E (1-p_H)^k \text{ if } k' = k \\ \lambda_H \left[1-(1-p_H)^k\right]^2 + \lambda_E \left[1-(1-p_H)^k\right] \text{ if } k' = k-1 \\ 0 \text{ otherwise} \end{cases}$$

and

$$Q(0,k') = \begin{cases} \lambda_H \text{ if } k' = 1 \\ \lambda_E \text{ if } k' = -1 \\ 0 \text{ otherwise} \end{cases}$$

and

$$Q(-1,k') = \begin{cases} \lambda_E + \lambda_H p_H \text{ if } k' = 0 \\ \lambda_H (1-p_H) \text{ if } k' = 1 \\ 0 \text{ otherwise} \end{cases} .$$

Let us first recall that the Global Balance Equations (GBE) are a set of equations that characterize the invariant distribution of a Markov chain, when such a distribution exists. The above stochastic process is a Markov chain which has an invariant distribution. In the sequel, we let π be this invariant distribution. The GBE can be stated as follows: for any subset

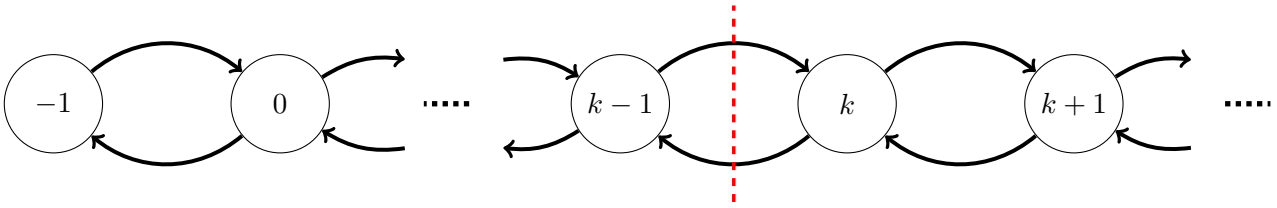


Figure 2: An illustration of the transition paths of the Markov Chain under the Unpaired algorithm

$S \subset \{-1, 0, 1, 2, \ldots\}$, we must have

$$\sum_{j \in S} \pi(j) \sum_{i \notin S} Q(j,i) = \sum_{i \notin S} \pi(i) \sum_{j \in S} Q(i,j).$$

In our context, the GBE implies a simple condition on the invariant distribution. Indeed, fix any $k \geq 1$, and let $S := \{-1, 0, 1, ..., k\}$. We have

$$\sum_{j \in S} \pi(j) \sum_{i \notin S} Q(j,i) = \pi(k) Q(k, k+1)$$

and

$$\sum_{i \notin S} \pi(i) \sum_{j \in S} Q(i,j) = \pi(k+1) Q(k+1, k).$$

By the GBE, we must have

$$\pi(k) Q(k, k+1) = \pi(k+1) Q(k+1, k). \tag{1}$$

for any $k \geq 1$. Note that this may not hold for $k = -1, 0$.

We also define k^* as the real number ensuring

$$\lambda_H (1 - p_H)^{2k^*} = \lambda_H \left[1 - (1 - p_H)^{k^*}\right]^2 + \lambda_E \left[1 - (1 - p_H)^{k^*}\right]$$

i.e., if $k^* \geq 1$, this real number ensures $Q(k^*, k^* + 1) = Q(k^*, k^* - 1)$. Simple algebra shows that

$$\frac{2\lambda_H + \lambda_E}{\lambda_H + \lambda_E} (1 - p_H)^{k^*} = 1 \tag{2}$$

and so

$$k^* = \ln\left(\frac{2\lambda_H + \lambda_E}{\lambda_H + \lambda_E}\right) \Big/ - \ln(1 - p_H).$$

The remaining part of the proof shows that π is highly concentrated around k^*. We start by showing that at the invariant distribution there is exponential decay of the tail distribution when moving away from k^* provided that p_H is sufficiently small.

Lemma A.1. *Assume p_H is small enough. For any integer $k \geq k^*$*

$$\frac{\pi(k+1)}{\pi(k)} \leq \exp\left(-(k-k^*)p_H\right)$$

and for any $k \leq k^*$

$$\frac{\pi(k-1)}{\pi(k)} \leq \exp\left(-(k^*-k+1)p_H\right)$$

Before moving to the proof of the above lemma, we state a first useful result.

Lemma A.2. *The following must hold*

$$\frac{\lambda_H\left[1-(1-p_H)^{k+1}\right]^2+\lambda_E\left[1-(1-p_H)^{k+1}\right]}{\lambda_H(1-p_H)^{2k}} \geq \frac{\lambda_H\left[1-(1-p_H)^{k+1}\right]+\lambda_E\left[1-(1-p_H)^{k+1}\right]}{\lambda_H(1-p_H)^{k}}$$

if $k \geq k^*$. The inequality holds in the other direction if $k \leq k^*-1$.

Proof. Using simple algebra one can show that the inequality stated in Lemma A.2 is equivalent to

$$\lambda_H+\lambda_E \geq \lambda_H(1-p_H)^{k+1}+(1-p_H)^k\lambda_H+(1-p_H)^k\lambda_E.$$

If $k \geq k^*$, using (2), we have that $(2\lambda_H+\lambda_E)(1-p_H)^k \leq \lambda_H+\lambda_E$. Since

$$(2\lambda_H+\lambda_E)(1-p_H)^k \geq \lambda_H(1-p_H)^{k+1}+(1-p_H)^k\lambda_H+(1-p_H)^k\lambda_E,$$

we are getting the above inequality for $k \geq k^*$, as claimed. If $k \leq k^*-1$, using (2) again, $(2\lambda_H+\lambda_E)(1-p_H)^{k+1} \geq \lambda_H+\lambda_E$. Since

$$(2\lambda_H+\lambda_E)(1-p_H)^{k+1} \leq \lambda_H(1-p_H)^{k+1}+(1-p_H)^k\lambda_H+(1-p_H)^k\lambda_E,$$

we are getting the reverse inequality for $k \leq k^*-1$, as claimed. □

We are ready to complete the proof of Lemma 3.1.

Proof of Lemma 3.1. We will be using the following inequalities. First, for all $z \geq 0$:

$$\frac{\alpha}{(1-p_H)^{z-k^*}}-(1-p_H)-\frac{\alpha-1}{(1-p_H)^{z-k^*}}\begin{cases}\geq 0 & \text{if} \quad z+1 \geq k^* \\ \leq 0 & \text{if} \quad z+1 \leq k^*\end{cases} \tag{3}$$

Second, for all x,

$$1-x \leq e^{-x} \tag{4}$$

Let us now prove the first part of the Lemma ($k \geq k^*$). We must have

$$\begin{aligned}
\frac{\pi(k)}{\pi(k+1)} &= \frac{\lambda_H \left[1-(1-p_H)^{k+1}\right]^2 + \lambda_E \left[1-(1-p_H)^{k+1}\right]}{\lambda_H (1-p_H)^{2k}} \\
&\geq \left(\frac{\lambda_H+\lambda_E}{\lambda_H}\right) \frac{\left[1-(1-p_H)^{k+1}\right]}{(1-p_H)^k} \\
&= \left(\frac{\lambda_H+\lambda_E}{\lambda_H}\right) \frac{\left[\frac{2\lambda_H+\lambda_E}{\lambda_H+\lambda_E}(1-p_H)^{k^*} - (1-p_H)^{k+1}\right]}{(1-p_H)^k} \\
&\geq \left(\frac{\lambda_H+\lambda_E}{\lambda_H}\right) \left(\frac{\frac{\lambda_H}{\lambda_H+\lambda_E}}{(1-p_H)^{k-k^*}}\right) = \frac{1}{(1-p_H)^{k-k^*}} \\
&\geq \exp\left((k-k^*)p_H\right)
\end{aligned}$$

where the first equality comes from the fact that, for p_H is sufficiently small, $k^* \geq 1$ and so we can use (1) and the expressions of the transition rates since $k \geq k^*$. The first inequality comes from Lemma A.2 and $k \geq k^*$. The second equality uses expression (2), the penultimate inequality uses expression (3) with $z+1 = k+1 > k^*$ and $\alpha = \frac{2\lambda_H+\lambda_E}{\lambda_H+\lambda_E}$ and the last inequality uses (4).

Let us turn now to the proof of the second part of the lemma ($k \leq k^*$). Let us first consider that $k \geq 2$. We must have

$$\begin{aligned}
\frac{\pi(k-1)}{\pi(k)} &= \frac{\lambda_H \left[1-(1-p_H)^{k}\right]^2 + \lambda_E \left[1-(1-p_H)^{k}\right]}{\lambda_H (1-p_H)^{2(k-1)}} \\
&\leq \left(\frac{\lambda_H+\lambda_E}{\lambda_H}\right) \frac{\left[1-(1-p_H)^{k}\right]}{(1-p_H)^{k-1}} \\
&= \left(\frac{\lambda_H+\lambda_E}{\lambda_H}\right) \frac{\left[\frac{2\lambda_H+\lambda_E}{\lambda_H+\lambda_E}(1-p_H)^{k^*} - (1-p_H)^{k}\right]}{(1-p_H)^{k-1}} \\
&\leq \left(\frac{\lambda_H+\lambda_E}{\lambda_H}\right) \left(\frac{\frac{\lambda_H}{\lambda_H+\lambda_E}}{(1-p_H)^{k-1-k^*}}\right) = \frac{1}{(1-p_H)^{k-1-k^*}} \\
&\leq \exp\left(-(k^*-k+1)p_H\right)
\end{aligned}$$

where the first equality comes from (1) and the expression of the transition rates. The first inequality comes from Lemma A.2 and $k \leq k^*$. The second equality uses expression (2), the penultimate inequality uses expression (3) with $z+1 = k \leq k^*$ and $\alpha = \frac{2\lambda_H+\lambda_E}{\lambda_H+\lambda_E}$ and the last equality uses (4).

Now, we have to handle the cases where $k = 0, 1$. We first deal with $k = 0$. From the expression of k^*, $\exp\left(-(k^*-k+1)p_H\right) = \exp\left(-(k^*+1)p_H\right)$ converges to $\frac{\lambda_H+\lambda_E}{2\lambda_H+\lambda_E}$ as p_H

becomes small. Using the GBE for $S = \{-1\}$ gives us

$$\frac{\pi(-1)}{\pi(0)} = \frac{Q(0,-1)}{Q(-1,0)+Q(-1,1)} = \frac{\lambda_E}{\lambda_E+\lambda_H} \leq \frac{\lambda_H+\lambda_E}{2\lambda_H+\lambda_E}.$$

Hence, $\frac{\pi(k-1)}{\pi(k)} \leq \exp\left(-(k^*-k+1)p_H\right)$ holds for $k=0$ provided that p_H is small enough. Now, we deal with $k=1$. Here again, $\exp\left(-(k^*-k+1)p_H\right) = \exp\left(-k^*p_H\right)$ converges to $\frac{\lambda_H+\lambda_E}{2\lambda_H+\lambda_E}$ as p_H becomes small. Using the GBE for $S=\{0\}$ gives us

$$\frac{\pi(0)}{\pi(1)} = \frac{Q(1,0)}{Q(0,-1)+Q(0,1)-\frac{\pi(-1)}{\pi(0)}Q(-1,0)} = \frac{p_H(\lambda_E+\lambda_H p_H)}{\lambda_E+\lambda_H-\frac{\lambda_E}{\lambda_H+\lambda_E}(\lambda_E+\lambda_H p_H)}$$

Clearly, this expression vanishes as p_H goes to 0. Hence, here again, $\frac{\pi(k-1)}{\pi(k)} \leq \exp\left(-(k^*-k+1)p_H\right)$ holds for $k=1$ provided that p_H is small enough. □

Lemma A.3. *For p_H small enough, for any $\sigma > 0$:*

$$\pi\left\{k : k \geq k^* + 1 - \sigma\sqrt{2/p_H}\right\} \leq \frac{\exp(-\sigma^2)}{\min\{1/2, \sigma\sqrt{2/p_H}\}}$$

Proof. Let us consider $k \geq k^*$ and let us define $\lceil k^* \rceil$ as the smallest integer larger than k^*. Then we have:

$$\pi(k) \leq \frac{\pi(k)}{\pi(\lceil k^* \rceil)} = \frac{\pi(\lceil k^* \rceil+1)}{\pi(\lceil k^* \rceil)} \times \frac{\pi(\lceil k^* \rceil+2)}{\pi(\lceil k^* \rceil+1)} \times \ldots \times \frac{\pi(k)}{\pi(k-1)} \leq \exp\left[-p_H \sum_{i=\lceil k^* \rceil}^{k-1} (i-k^*)\right]$$

where the last inequality directly comes from Lemma A.1. Moreover, since $k^*+1 \geq \lceil k^* \rceil \geq k^*$ we have:

$$\sum_{i=\lceil k^* \rceil}^{k-1} (i-k^*) = \frac{(k-\lceil k^* \rceil)(\lceil k^* \rceil - k^* + k - 1 - k^*)}{2} \geq \frac{(k-k^*-1)^2}{2}$$

Hence it must be the case that

$$\pi(k) \leq \exp\left[-(k-k^*-1)^2 p_H/2\right].$$

Then, for any $\sigma > 0$:

$$\begin{aligned}\sum_{k=k^*+1+\sigma\sqrt{2/p_H}}^{+\infty} \pi(k) &\leq \sum_{k=k^*+1+\sigma\sqrt{2/p_H}}^{+\infty} \exp\left[-(k-k^*-1)^2 p_H/2\right] \\ &= \sum_{k=0}^{+\infty} \exp\left[-(k+\sigma\sqrt{2/p_H})^2 p_H/2\right] \\ &\leq \frac{\exp(-\sigma^2)}{\min\{1/2, \sigma\sqrt{2/p_H}\}}\end{aligned}$$

where the last inequality comes from Akbarpour et al. (Forthcoming), Appendix I. □

Lemma A.4. *For p_H small enough, for any $\sigma > 0$:*

$$\pi\left\{k : k \leq k^* - 1 - \sigma\sqrt{2/p_H}\right\} \leq \frac{\exp(-\sigma^2)}{\min\{1/2, \sigma\sqrt{2/p_H}\}}$$

Proof. Let us consider $k \leq k^*$ and let us define $\lfloor k^* \rfloor$ as the largest integer smaller than k^*. Then we have:

$$\pi(k) \leq \frac{\pi(k)}{\pi(\lfloor k^* \rfloor)} = \frac{\pi(\lfloor k^* \rfloor - 1)}{\pi(\lfloor k^* \rfloor)} \times \frac{\pi(\lfloor k^* \rfloor - 2)}{\pi(\lfloor k^* \rfloor - 1)} \times \ldots \times \frac{\pi(k)}{\pi(k+1)} \leq \exp\left[-p_H \sum_{i=k}^{\lfloor k^* \rfloor - 1} (k^* - i)\right]$$

where the last inequality is directly deduced from Lemma A.1. Moreover, since $k^* \geq \lfloor k^* \rfloor \geq k^* - 1$ we have:

$$\sum_{i=k}^{\lfloor k^* \rfloor - 1} (k^* - i) = \frac{(\lfloor k^* \rfloor - k)(k^* - k + k^* - \lfloor k^* \rfloor + 1)}{2} \geq \frac{(k^* - k - 1)(k^* - k + 1)}{2} \geq \frac{(k^* - k - 1)^2}{2}$$

Hence it must be the case that

$$\pi(k) \leq \exp\left[-(k^* - k - 1)^2 p_H/2\right]$$

Then, for any $\sigma > 0$:

$$\begin{aligned}
\sum_{k=-1}^{k^*-1-\sigma\sqrt{2/p_H}} \pi(k) &\leq \sum_{k=-1}^{k^*-1-\sigma\sqrt{2/p_H}} \exp\left[-(k^*-k-1)^2 p_H/2\right] \\
&= \sum_{n=\sigma\sqrt{2/p_H}-k^*+1}^{1} \exp\left[-(k^*+n-1)^2 p_H/2\right] \\
&\leq \sum_{n=\sigma\sqrt{2/p_H}-k^*+1}^{+\infty} \exp\left[-(k^*+n-1)^2 p_H/2\right] \\
&= \sum_{n=0}^{+\infty} \exp\left[-(n+\sigma\sqrt{2/p_H})^2 p_H/2\right] \\
&\leq \frac{\exp(-\sigma^2)}{\min\{1/2, \sigma\sqrt{2/p_H}\}}
\end{aligned}$$

where the last inequality comes from Akbarpour et al. (Forthcoming), Appendix I. □

The following result is immediately obtained by combining Lemma A.3 and A.4,

Corollary A.5. *For p_H small enough, for any $\sigma > 0$:*

$$\pi\left\{k : k^* - \sigma\sqrt{2/p_H} \leq k \leq k^* + \sigma\sqrt{2/p_H}\right\} \geq 1 - \frac{2\exp(-\sigma^2)}{\min\{1/2, \sigma\sqrt{2/p_H}\}}$$

This result implies that π is highly concentrated around k^*.

Corollary A.6. *Let K be the random variable associated to π, we have*

$$\frac{K}{1/p_H} \xrightarrow{p} \ln\left(\frac{2\lambda_H + \lambda_E}{\lambda_H + \lambda_E}\right)$$

as $p_H \to 0$.

Proof. Given that p_H tends to $-\ln(1-p_H)$ as p_H vanishes, it is enough to show

$$\frac{K}{1/(-\ln(1-p_H))} \xrightarrow{p} \ln\left(\frac{2\lambda_H + \lambda_E}{\lambda_H + \lambda_E}\right).$$

Fix any $\delta > 0$. We need to show:

$$\pi\left\{k : \ln\left(\frac{2\lambda_H + \lambda_E}{\lambda_H + \lambda_E}\right) - \delta \leq \frac{k}{1/(-\ln(1-p_H))} \leq \ln\left(\frac{2\lambda_H + \lambda_E}{\lambda_H + \lambda_E}\right) + \delta\right\} \to 1$$

as p_H vanishes. This is equivalent to showing

$$\pi\left\{k : k^* - \delta/(-\ln(1-p_H)) \le k \le k^* + \delta/(-\ln(1-p_H))\right\} \to 1$$

as p_H vanishes. Using the above corollary for $\sigma = \frac{\delta}{-\ln(1-p_H)}\frac{1}{\sqrt{2/p_H}}$, we have

$$\pi\left\{k : k^* - \delta/(-\ln(1-p_H)) \le k \le k^* + \delta/(-\ln(1-p_H))\right\} \ge 1 - \frac{2\exp(-\sigma^2)}{\min\{1/2, \sigma\sqrt{2/p_H}\}}.$$

Now, we observe that $\frac{2\exp(-\sigma^2)}{\min\{1/2,\sigma\sqrt{2/p_H}\}}$ vanishes as p_H vanishes, which completes the proof. □

We obtain the following straightforward corollary.

Corollary A.7. *Let K be the random variable associated to π, we have*

$$\lim_{p_H\to 0} \mathbb{E}\left[\frac{K}{1/p_H}\right] = \ln\left(\frac{2\lambda_H + \lambda_E}{\lambda_H + \lambda_E}\right).$$

Since by Little's law, $\mathbf{W}(\text{Unpaired}) = \frac{\mathbb{E}[K]}{\lambda_H}$, we obtain Proposition 3.1.

A.2 Proofs of Theorem 3.2 and Proof of Theorem 3.3

We know from the Theorem 1 in Ashlagi et al. (Forthcoming) that

$$\lim_{p_H\to 0} p_H \mathbf{W}(\text{Pairwise}) = \begin{cases} \frac{\ln\left(\frac{2\lambda_H}{\lambda_H+\lambda_E}\right)}{\lambda_H p_H} & \text{if} \quad \lambda_H \ge \lambda_E \\ \frac{\ln\left(\frac{\lambda_E}{\lambda_E-\lambda_H}\right)}{\lambda_H} & \text{if} \quad \lambda_H < \lambda_E \end{cases} \tag{5}$$

Moreover, we know from Proposition 3.1 that

$$\lim_{p_H\to 0} p_H \mathbf{W}(\text{Unpaired}) = \frac{\ln\left(\frac{2\lambda_H+\lambda_E}{\lambda_H+\lambda_E}\right)}{\lambda_H} \tag{6}$$

The result stated in the Theorem 3.2 directly follows from the comparison between (5) and (6).

Then, combining (5) and (6) and using the fact that $\lambda_H = n \cdot \lambda$ and $\lambda_E = n(1-\lambda)$, we immediately get that

$$\lim_{p_H\to 0} \frac{\mathbf{W}(\text{Pairwise})}{\mathbf{W}(\text{Unpaired})} = \begin{cases} \frac{\ln(2\lambda)}{\ln(1+\lambda)} \cdot \frac{1}{p_H} & \text{if} \quad \lambda \ge \frac{1}{2} \\ \frac{\ln\left(\frac{1-\lambda}{1-2\lambda}\right)}{\ln(1+\lambda)} & \text{if} \quad \lambda < \frac{1}{2} \end{cases}$$

This completes the proof of Theorem 3.3.

A.3 Proof of Theorem 3.4

We know from the Proposition 1 in Ashlagi et al. (Forthcoming) that

$$\lim_{p_H \to 0} p_H \mathbf{W}(\text{Chains}) = \frac{\ln\left(\frac{\lambda_H+\lambda_E}{\lambda_E}\right)}{\lambda_H} \tag{7}$$

Then, the results stated in the Theorem 3.4 directly follow from Theorem 3.2 and the comparison between (6) and (7).

A.4 Proofs of Theorem 3.5 and statements in Remark 3.6

Combining (6) and (7) we get that:

$$\lim_{p_H \to 0} \frac{\mathbf{W}(\text{Chains})}{\mathbf{W}(\text{Unpaired})} = \frac{\ln\left(\frac{\lambda_H+\lambda_E}{\lambda_E}\right)}{\ln\left(\frac{2\lambda_H+\lambda_E}{\lambda_H+\lambda_E}\right)} = \frac{\ln\left(\frac{1}{1-\lambda}\right)}{\ln(1+\lambda)} = -\frac{\ln(1-\lambda)}{\ln(1+\lambda)}$$

The results stated in the points 1. and 2. of the Theorem Theorem 3.5 immediately follows from the expression above.

In the sequel, given an algorithm ALG we let $\mathbf{W}_E(\text{ALG})$ be the expected waiting time (at the invariant distribution) of an easy-to-match patient under matching algorithm ALG. The following result implies the point 3. of the Theorem 3.5 as well as the statements in Remark 3.6.

Proposition A.8. *Fix a matching algorithm ALG inducing a stochastic process with an invariant distribution. (1) Assume that* $\mathbf{W}_E(ALG) \leq \mathbf{W}_E(Unpaired)$. *Then*

$$\lim_{p_H \to 0} \sup \frac{\mathbf{W}_H(Unpaired)}{\mathbf{W}_H(ALG)} \leq 2\ln(2).$$

(2) Fix any matching algorithm ALG inducing a stochastic process with an invariant distribution. Assume that $\lim_{p_H \to 0} \sup \mathbf{W}_H(ALG) \geq \mathbf{W}_E(ALG)$. *Then*

$$\frac{\mathbf{W}_H(Unpaired)}{\mathbf{W}_H(ALG)} \leq 2.$$

Let us assume that the size of the pool is $\tilde{k} = \tilde{k}_H + \tilde{k}_E$ where $\tilde{k}_H$ and $\tilde{k}_E$ are the number of hard-to-match and easy-to-match patients waiting in the pool. In the sequel, $\tilde{\mathbf{W}}_H(\text{ALG})$ is the random variable describing waiting time of an arriving hard-to-match agent. Note that a necessary condition for hard-to-match agent to be matched is that he is compatible with a donor in the pool upon arriving (in which case his waiting time is simply 0) or, in case this does not occur, he is compatible with a donor in the future. In the former case, his waiting time is

simply 0 while in the latter case, by the Poisson thinning property, the expected waiting time is $\frac{1}{(\lambda_H+\lambda_E)p_H}$. Hence, we obtain

$$\begin{aligned}
\mathbb{E}\left[\tilde{\mathbf{W}}_H(ALG)\,\middle|\,\tilde{k}=k\right] &\geq \left[1-(1-p_H)^k\right]\times 0+(1-p_H)^k\frac{1}{(\lambda_H+\lambda_E)p_H}\\
&= (1-p_H)^k\frac{1}{(\lambda_H+\lambda_E)p_H}\\
&\geq (1-kp_H)\frac{1}{(\lambda_H+\lambda_E)p_H}\\
&= \frac{1}{(\lambda_H+\lambda_E)p_H}-\frac{1}{\lambda_H+\lambda_E}k.
\end{aligned}$$

Thus, using the fact that, by Little's law, $\mathbf{W}_H(\mathrm{ALG})=\frac{\mathbb{E}[\tilde{k}_H]}{\lambda_H}$ and $\mathbf{W}_E(\mathrm{ALG})=\frac{\mathbb{E}[\tilde{k}_E]}{\lambda_E}$, we have

$$\begin{aligned}
\mathbf{W}_H(ALG) &= \mathbb{E}\left[\mathbb{E}\left[\tilde{\mathbf{W}}_H(ALG)\,\middle|\,\tilde{k}=k\right]\right]\\
&\geq \frac{1}{(\lambda_H+\lambda_E)p_H}-\frac{1}{\lambda_H+\lambda_E}\mathbb{E}\left[\tilde{k}\right]\\
&= \frac{1}{(\lambda_H+\lambda_E)p_H}-\frac{1}{\lambda_H+\lambda_E}\left[\mathbb{E}\left[\tilde{k}_H\right]+\mathbb{E}\left[\tilde{k}_E\right]\right]\\
&= \frac{1}{(\lambda_H+\lambda_E)p_H}-\frac{1}{\lambda_H+\lambda_E}\left[\lambda_H\mathbf{W}_H(ALG)+\lambda_E\mathbf{W}_E(ALG)\right].
\end{aligned}$$

This gives us

$$\mathbf{W}_H(ALG)\cdot\left[\frac{2\lambda_H+\lambda_E}{\lambda_H+\lambda_E}\right]\geq\frac{1}{(\lambda_H+\lambda_E)p_H}-\frac{\lambda_E}{\lambda_H+\lambda_E}\mathbf{W}_E(ALG)$$

and so

$$\mathbf{W}_H(ALG)\geq\frac{1}{[2\lambda_H+\lambda_E]\,p_H}-\frac{\lambda_E}{2\lambda_H+\lambda_E}\mathbf{W}_E(ALG). \tag{8}$$

Now, we are in a position to prove the first part of the proposition. Indeed, by Proposition 3.1, when p_H vanishes,

$$\begin{aligned}
\frac{\mathbf{W}_H(\mathrm{Unpaired})}{\mathbf{W}_H(ALG)} &\leq \frac{\frac{\ln\left(\frac{2\lambda_H+\lambda_E}{\lambda_H+\lambda_E}\right)}{\lambda_H}\frac{1}{p_H}}{\frac{1}{[2\lambda_H+\lambda_E]}\frac{1}{p_H}-\frac{\lambda_E}{2\lambda_H+\lambda_E}\mathbf{W}_E(ALG)}\\
&= \frac{\frac{\ln\left(\frac{2\lambda_H+\lambda_E}{\lambda_H+\lambda_E}\right)}{\lambda_H}}{\frac{1}{[2\lambda_H+\lambda_E]}-\frac{\lambda_E}{2\lambda_H+\lambda_E}\mathbf{W}_E(ALG)p_H}.
\end{aligned}$$

Since $\mathbf{W}_E(\text{ALG}) \leq \mathbf{W}_E(\text{Unpaired})$, $\mathbf{W}_E(\text{ALG})p_H = 0$ when p_H vanishes and so we have

$$\lim_{p_H \to 0} \sup \frac{\mathbf{W}_H(\text{Unpaired})}{\mathbf{W}_H(ALG)} \leq \frac{2\lambda_H + \lambda_E}{\lambda_H} \ln\left(\frac{2\lambda_H + \lambda_E}{\lambda_H + \lambda_E}\right).$$

For any λ_H, the above expression is decreasing in λ_E.[14] Hence, it is maximized at $\lambda_E = 0$. We obtain

$$\lim_{p_H \to 0} \sup \frac{\mathbf{W}_H(\text{Unpaired})}{\mathbf{W}_H(ALG)} \leq 2 \ln(2)$$

when p_H vanishes.

Let us move to the proof of the second part of the proposition. By Equation (8) and $\mathbf{W}_H(\text{ALG}) \geq \mathbf{W}_E(\text{ALG})$,

$$\begin{aligned} \mathbf{W}_H(ALG) &\geq \frac{1}{[2\lambda_H + \lambda_E]\, p_H} - \frac{\lambda_E}{2\lambda_H + \lambda_E} \mathbf{W}_H(ALG) \\ &\geq \frac{1}{2} \frac{1}{[\lambda_H + \lambda_E]\, p_H} \end{aligned}$$

Hence, using Proposition 3.1 again,

$$\begin{aligned} \lim_{p_H \to 0} \sup \frac{\mathbf{W}_H(\text{Unpaired})}{\mathbf{W}_H(ALG)} &\leq \frac{\frac{\ln\left(\frac{2\lambda_H+\lambda_E}{\lambda_H+\lambda_E}\right)}{\lambda_H} \frac{1}{p_H}}{\frac{1}{2}\frac{1}{(\lambda_H+\lambda_E)p_H}} \\ &= 2\frac{\lambda_H + \lambda_E}{\lambda_H} \ln\left(\frac{2\lambda_H + \lambda_E}{\lambda_H + \lambda_E}\right) \end{aligned}$$

We claim that the above term is smaller than 2. This holds if and only if

$$\frac{2\lambda_H + \lambda_E}{\lambda_H + \lambda_E} \leq \exp\left(\frac{\lambda_H}{\lambda_H + \lambda_E}\right).$$

This inequality is true since $\exp(x) \geq 1 + x$ for any x. This completes the proof.

Remark 3.6 is directly implied by point (1) of the above proposition. We now complete the proof of Theorem 3.5.

Completion of the proof of Theorem 3.5. Using (2) in the above proposition, we obtain that

$$\frac{\mathbf{W}_H(\text{Unpaired})}{\mathbf{W}_H(\text{OPT})} \leq 2.$$

Indeed, if $\frac{\mathbf{W}_H(\text{Unpaired})}{\mathbf{W}_H(\text{OPT})} > 2$, then there exists a sequence of matching algorithms $\{\text{ALG}_n\}_{n\geq 1}$

[14] The derivative with respect to λ_E gives us $(1/\lambda_H)\left[\ln\left(\frac{2\lambda_H+\lambda_E}{\lambda_H+\lambda_E}\right) - \left(\frac{\lambda_H}{\lambda_H+\lambda_E}\right)\right]$. One can easily show that this is negative using the inequality $\exp(x) \geq 1 + x$ for any x.

such that $\mathbf{W}_H(\mathrm{ALG}_n) \to \mathbf{W}_H(\mathrm{OPT})$ satisfying the constraint $\mathbf{W}(\mathrm{ALG}_n) \geq \mathbf{W}_E(\mathrm{ALG}_n)$. Then, this means that for n large enough, $\frac{\mathbf{W}_H(\mathrm{Unpaired})}{\mathbf{W}_H(\mathrm{ALG}_n)} > 2$, a contradiction with point (2) of the above proposition. $\square$

B Integer Linear Programming for the Omniscient Solution

For the Omniscient solution, some details are in order. We formulate it as an Integer Linear Programming (ILP) problem. The goal is to minimize the overall sum of the waiting times of all patients, regardless of transplant status. Let $X_{ij} \in \{0,1\}$ be a dummy variable that is equal to 1 if d_i gives to p_j. We use $\mathcal{D}_\ell$ to denote the set of all living donors and $\mathcal{P}$ to denote the set of all patients. For d_i and p_j, let $T_{ij} = \max\{0, a(i) - a(j)\}$ be the number of days patient j has to wait to receive a kidney from donor i. Note that $T_{ij} = 0$ if pair i arrives before pair j. For pair j, let $T_j^e = e(j) - a(j)$ be the number of days between its arrival and departure dates. Under the assumption of no exit, $T_j^e = T - a(j)$. Let G be the compatibility matrix between donors and patients so that $G_{ij} = 1$ if donor $i \in \mathcal{D}_\ell$ is compatible with patient $j \in \mathcal{P}$. Finally, let $M = |\mathcal{P}| \times |\mathcal{D}_\ell|$. The Omniscient solution solves the following ILP problem:[15]

$$\min_{(X_{ij})_{ij} \in \{0,1\}^M} \quad \sum_{i \in \mathcal{D}_\ell, j \in \mathcal{P}} X_{ij} \times (T_{ij} - T_j^e) \tag{9}$$

$$\text{s.t.}$$

$$\forall i \in \mathcal{D}_\ell, j \in \mathcal{P}: \qquad (C_{ij}) \qquad X_{ij} \leq G_{ij} \times 1_{\{e(j) \geq a(i)\}} \times 1_{\{(i \in D_\ell) \vee (e(i) \geq a(j))\}}$$

$$\forall j \in \mathcal{P}: \qquad (F_j^p) \qquad \sum_{i \in \mathcal{D}_\ell} X_{ij} \leq 1$$

$$\forall i \in \mathcal{D}_\ell: \qquad (F_i^d) \qquad \sum_{j \in \mathcal{P}} X_{ij} \leq 1$$

$$\forall i \in \mathcal{P}: \qquad (E_i) \qquad \sum_{j \in \mathcal{P}: e(i) < e(j)} X_{ij} \leq \sum_{j \in \mathcal{D}_\ell} X_{ji}$$

The objective function is the total waiting time of all patients, and the constraints are explained below:

- C_{ij}: *Compatibility constraints.* d_i can give to p_j if the following conditions are met: i) they are biologically compatible, and ii) d_i arrives before p_j exits (which is never binding under the no-exit assumption).
- F_j^p: *Feasibility constraints for patients.* Each patient can receive at most one kidney.
- F_i^d: *Feasibility constraints for donors.* Each donor can give to at most one patient.
- E_i: *Exit constraints.* A donor leaves with her patient but stays if her patient has received a kidney. Hence, if p_i does not receive a kidney, then d_i leaves with p_i and thus cannot donate to any patient who arrives after their exit date. Because of the no-exit assumption, this constraint is never binding.

[15] The total waiting time of all patients is $\sum_{i \in \mathcal{D}_\ell, j \in \mathcal{P}} X_{ij} T_{ij} + \sum_{j \in \mathcal{P}} (1 - \sum_{i \in \mathcal{D}_\ell} X_{ij}) T_j^e = \sum_{i \in \mathcal{D}_\ell, j \in \mathcal{P}} X_{ij} \times (T_{ij} - T_j^e)$.

C Additional figures

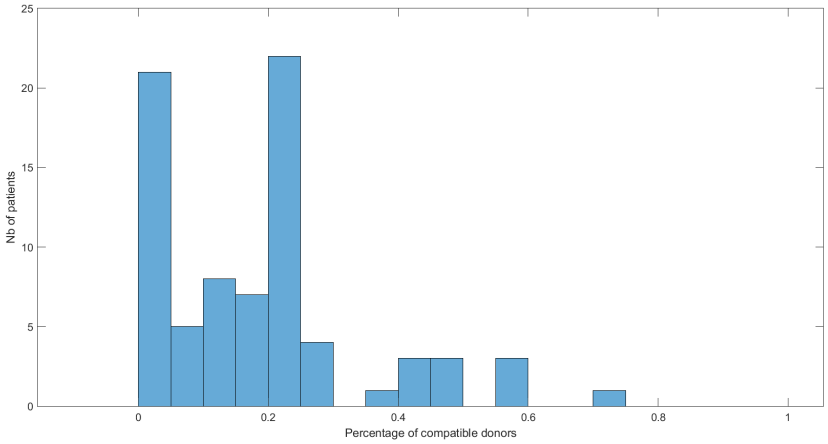


Figure 3: Histogram of PRA values for the French KEP

D Selection of Deceased Donor Kidneys

The donor-only Kidney Donor Risk Index (KDRI, hereafter) is widely used in assessing the quality of kidneys retrieved from deceased donors. The KDRI, developed by Rao et al. (2009) based on US data, combines 10 donor factors to provide an estimated risk of graft failure after a kidney transplant. We apply their estimates to the French data and obtain a value of the KDRI for each DDL kidney offered in France during our simulation period. Lehner et al. (2018) and Calvillo-Arbizu et al. (2018) follow the same methodology, using German and Spanish data, respectively, and they confirm that the estimated KDRI provides an accurate prediction of the graft failure in these two populations.

In the following, Section D.1 reviews the calculation of the KDRI in Rao et al. (2009); Section D.2 describes the data in our study; Section D.3 explains how we deal with the missing values in the donor factors; Section D.5 briefly summarizes the results we obtain; and, finally, we explain how we use the calculated KDRI to select the DDL kidneys to be used in the exchange in Section D.6.

D.1 The Kidney Donor Risk Index (KDRI)

Rao et al. (2009) use the following variables to calculate the KDRI:[16]

- donor's age (in years);
- donor's height (in cm);
- donor's weight (in kg);
- donor's ethnicity (African American *vs.* other);
- donor's history of hypertension (yes or no);
- donor's history of diabetes (yes or no);
- donor's cause of death (Cerebrovascular accident (CVA) *vs.* other);
- donor's serum creatinine (in mg/dL);
- donor's Hepatitis C Virus (HCV) Status (positive *vs.* negative);
- donor's Donation after Circulatory Death (DCD) Status (yes or no).

The association between these variables and graft survival is determined by estimating a multivariate Cox proportional hazards regression model using graft outcomes from nearly

[16] See also Organ Procurement and Transplant Network (2019) for a practical guide to calculate the KDRI.

70,000 adult in the United States from 1995 to 2005. The estimated coefficients derived from this model are shown in the following formula.

$$\begin{aligned} KDRI &= \exp\{0.0128 \times (age - 40) - 0.0194 \times (age - 18) \times 1(age < 18) \\ &+ 0.0107 \times (age - 50) \times 1(age > 50) - 0.0464 \times \left(\frac{height - 170}{10}\right) \\ &- 0.0199 \times \left(\frac{weight - 80}{5}\right) \times 1(weight < 80) + 0.1790 \times 1(African\ American) \\ &+ 0.1260 \times 1(History\ of\ Hypertension) + 0.1300 \times 1(History\ of\ Diabetes) \\ &+ 0.0881 \times 1(Cause\ of\ Death = CVA) + 0.2200 \times (Creatinine - 1) \\ &- 0.2090 \times (Creatinine - 1.5) \times 1(Creatinine > 1.5mg/dL) \\ &+ 0.2400 \times 1(HCV\ positive) + 0.1330 \times 1(DCD)\} \end{aligned}$$

D.2 Data on DDL Kidneys in France

The variables used by Rao et al. (2009) correspond to the following variables in our dataset:

- **donor's age**: *Ageaumomentduprlvementdudonneur* (in year).
- **donor's height**: *Tailleencmdudonneur* (in cm).
- **donor's weight**: *Poidsenkgdudonneur* (in kg).
- **donor's ethnicity**: This information is missing. We assume that all donors are *Caucasian* as in Lehner et al. (2018) and Calvillo-Arbizu et al. (2018). Hence we have $1(African\ American) = 0$ for all donors.
- **donor's history of hypertension**: *HypertensionartrielleSME* / *HypertensionartrielleM12* / *HypertensionartrielleM3* (no *vs.* other[17]).
- **donor's history of diabetes**: *DiabteSME* / *DiabteM12* / *DiabteM3* (no *vs.* other[18]).
- **donor's cause of death**: *EtiologiecausededcsSME* / *EtiologiecausededcsM12* / *EtiologiecausededcsM3* (VAS (vasculaire) *vs.* other[19]).
- **donor's serum creatinine**: *CratininmieSME* / *CratininmieM12* / *CratininmieM3* (in μmol/L). We have to convert the μmol/L in mg/dL in order to express creatinine by the same unity than in Rao et al. (2006): 1μmol/L = 0.011 mg/dL.

[17] Other may take three different values: *yes without medical treatment* / *yes with medical* / *yes and no information about medical treatment.*

[18] Other may take three different values: *yes and insulin dependent* / *yes and non insulin dependent* / *yes and no information about insulin dependence.*

[19] Other may take seven different values: *AVP =Traumatique A.V.P.* / *NAVP =Traumatique Non A.V.P.* / *ANO =Anoxie* / *TUM =Tumeur* / *MEN =Méningite* / *INT =Intoxication* / *AUT =Autre.*

- **donor's Hepatitis C Virus (HCV) Status**: *AnticorpsantiHCVSME* / *AnticorpsantiHCVM12* / *AnticorpsantiHCVM3* (positive *vs.* negative).
- **donor's Donation after Circulatory Death (DCD) Status**: *ArrtcardiaquercuprSME* / *ArrtcardiaquercuprM12* / *ArrtcardiaquercuprM3* (yes *vs.* no).

D.3 Treatment of missing values

In case of missing values, the KDRI is determined by mean substitution of individual missing values according to OTPN methods (see Organ Procurement and Transplant Network, 2019).[20] For instance, if *History of Hypertension* is missing for one donor, we assume that this donor has a probability of having been hypertensive equal to the proportion of deceased donors having a history of hypertension; or, if the *serum creatinine* is missing for one donor, we assume that this donor has a serum creatinine equal to the mean value of serum creatinine in the whole population of deceased donors.

D.4 From KDRI to Kidney Donor Profile Index (KDPI)

It proves to be useful to translate our KDRI measure into a Kidney Donor Profile Index (KDPI). The KDPI is a mapping of the KDRI from a relative risk scale to a cumulative percentage scale.[21] The reference population used for this mapping is all deceased donors in the United States with a kidney recovered for the purpose of transplantation in the prior calendar year. We use the year 2017 as year of reference such that we use the OPTN mapping table 2018 for translating our KDRI into KDPI.[22] For instance, if the KDPI for a particular donor equals 75, it means that only 25% of deceased donor kidneys offered in the US during the year 2017 were of better quality than this particular donor.

One big advantage of the KDPI lies in the fact that it is expressed on the same scale than a risk index for living donor developed by Massie et al. (2016): The Living Kidney Donor Profile Index (LKDPI) (see Section E). For instance, Massie et al. find that the median living donor in US (over the period 2005-2013) had a LKDPI equals to 13 such that only 13% of the deceased donor offers are of better quality than this median living donor (with 2013 as reference year). On European data, Rehse et al. (2018) conclude that the median living donor has a LKDPI equals to 17 (with 2014 as reference year).[23]

[20] The same method is used by Lehner et al. (2018) and Calvillo-Arbizu et al. (2018).
[21] See also Organ Procurement and Transplant Network (2019).
[22] https://optn.transplant.hrsa.gov/media/2150/kdpi_mapping_table.pdf.
[23] Data used by Rehse et al. (2018) come from a single center in Germany over the period 2000-2016.

D.5 Results

The median value for the KDRI in our data is 1.3357 while it is, by construction, equals to 1 in the US. This corresponds to a KDPI equals to 78 meaning that 78% of the deceased donors organs proposed in the US are of better quality than the median deceased donor in France. It is a well known fact that more kidneys, and then kidneys of lesser quality, are proposed in France compared to the US. This is also the case in others European countries but maybe not in the same degree.[24]

D.6 Selection of DDL Kidneys

Our goal is to select the deceased donor offers offered to patients in P in order to keep only the kidneys of sufficiently good quality, i.e., acceptable to patients in P. To do so, one first option consists in keeping only deceased donor kidneys whose quality is comparable to a living donor kidney. This is the rationale for keeping only the deceased donor offers with a KDPI higher than 13 (which corresponds to the median LKDPI in the US as determined by Massie et al. (2016)) or a KDPI higher than 17 (which corresponds to the median LKDPI in Europe as determined by Rehse et al. 2018).

Nevertheless, this filtering strategy can be viewed as too restrictive. Indeed, for patients having registered to the program, the outside option is not a compatible living donor offer but merely an incompatible transplant from their own intended donor. Yet, in many instances, this outside option is really bad. For instance, a substantial proportion of these patients are HLA incompatible with their own donors while HLA incompatible transplants have worse outcomes than many deceased donors transplant Bentall et al. (2013). Having this in mind, an alternative filtering strategy consists in keeping top quality kidneys only for patients who are HLA compatible with their own intended donor while proposing more standard deceased donor kidneys to patients from HLA incompatible pairs. Finally, we might consider the outside option even more seriously by considering as acceptable, for a patient in P, all the offers who have a KDPI higher than the LKDPI of their associated donor. Section E describes in more details how this LDKPI is determined.

[24] Using German data, Lehner et al. (2018) conclude that 66% of the deceased donors organs proposed in the US are of better quality than the median deceased donor organ in their data.

E The Living Kidney Donor Profile Index (LKDPI)

The LKDPI is an index of quality of living donor kidneys expressed on the same scale than the KDPI. It is developed by Massie et al. (2016) who use U.S. data to identify living donor characteristics associated with the risk of post-transplant graft failure. We use the estimation results from their study to our data.[25]

E.1 Estimation Results from Massie et al. (2016)

Massie et al. (2016) use the following variables to calculate the LKDPI:

- donor's age (in year);
- donor's estimated glomerular filtration rate (eGFR in mL/min per 1.73 m^2);
- donor's Body Mass Index (BMI);
- donor's ethnicity (African American *vs.* other);
- donor's history of cigarette use (yes or no);
- donor's systolic blood pressure (SBP in mmHg);
- donation from a male donor to a male recipient (yes or no);
- donor biologically unrelated to the recipient (yes or no);
- number of HLA-B mismatches between the donor and the recipient;
- number of HLA-DR mismatches between the donor and the recipient;
- donor/recipient weight ratio (D/R WR);
- donor ABO incompatible with the recipient (yes or no).

The association between these variables and graft survival was determined by estimating a multivariate Cox proportional hazards regression model using graft outcomes from 36,025 living donor kidney transplantation recipients in the United States from 2005-2013. The estimated coefficients derived from this model are shown in the following formula.

[25] Rehse et al. (2018) apply the same methodology to German data and confirm the validity of the estimation by Massie et al. (2016).

$$
\begin{aligned}
LKDPI &= -11.3 + 1.85 \times (age - 50) \times 1(age > 50) - 0.381 \times eGFR + 1.17 \times BMI \\
&+ 22.34 \times 1(African\ American) + 14.33 \times 1(history\ of\ cigarette\ use) \\
&+ 0.44 \times SBP - 21.68 \times 1(donor\ recipient\ both\ males) \\
&+ 27.30 \times 1(donor\ recipient\ ABO\ incompatible) \\
&- 10.61 \times 1(donor\ recipient\ unrelated) + 8.57 \times (\#HLA - B\ mismatches) \\
&+ 8.26 \times (\#HLA - DR\ mismatches) - 50.87 \times \min(D/R\ WR, 0.9)
\end{aligned}
$$

E.2 Data on Living Donors in France

The variables used by Massie et al. (2016) correspond to the following variables in our dataset:

- **donor's age**: *Ageaumomentduprlvementdudonneur* (in year).
- **donor's eGFR**: this variable is calculated using the CKD-EPI equation (see Levey et al. 2019) under the assumption that none of the donors are African American:

  $$eGFR = 141 \times \min(Creatinine/\kappa, 1)^{\alpha} \times \max(Creatinine/\kappa, 1)^{-1.209} \times 0.993^{age} \times \varphi$$

  with $\kappa = 0.7$ for females and 0.9 for males, $\alpha = -0.329$ for females and -0.411 for males and $\varphi = 1.018$ for females and 1 for males. For the creatinine we use the variable *Créatinine plasmatique DV* (in μmol/L). We have to convert the μmol/L in mg/dL in order to express creatinine by the same unity than in Levey et al. (2019): $1\mu\text{mol/L} = 0.011$ mg/dL.
- **donor's BMI**: this variable is calculated by using the usual formula:

  $$BMI = \frac{weight}{(height)^2}$$

  For the weight and the height of the donor we use respectively the variables *Poids en kg du donneur* and *Taille en cm du donneur*.
- **donor's ethnicity**: This information is missing. We assume that all donors are *Caucasian* as in Rehse et al. (2018). Hence we have $1(African\ American) = 0$ for all donors.
- **donor's SBP**: *PAS DV* (in mmHg).
- **donation from a male donor to a male recipient**: we use information about the sex of the donor and the sex of the patient (*Sexe du donneur* and *Sexe du receveur* respectively).

- **donor biologically unrelated to the recipient**: *Lien donneur-receveur* (yes or no).[26]
- **number of HLA-B mismatches between the donor and the recipient**: we compare the antigens HLA-B of the donor (listed in *HLA B1 du donneur* and *HLA B2 du donneur*) with the antigens HLA-B of the patient (listed in *HLA B1 du receveur* and *HLA B2 du receveur*).
- **number of HLA-DR mismatches between the donor and the recipient**: we compare the antigens HLA-DR of the donor (listed in *HLA DR1 du donneur* and *HLA DR2 du donneur*) with the antigens HLA-DR of the patient (listed in *HLA DR1 du receveur* and *HLA DR2 du receveur*).
- **donor/recipient weight ratio**: ratio of the weight of the donor over the weight of the patient (*Poids en kg du donneur* and *Poids au cours de l'ATT* respectively).
- **donor ABO incompatible with the recipient**: we compare the blood type of the donor with the blood type of the patient (yes or no): variables *Groupe sanguin ABO du donneur* and *Groupe ABO du receveur* respectively.

E.3 Treatment of missing values

As for the KDRI, in case of missing values, the LKDPI is determined by mean substitution (see Section D.3).[27] Note that, even if we are only interested on pairs having registered to the program, the reference population we used in order to determine mean values is the entire population of pairs in our data set: 2737 pairs having participated to the exchange program and/or for which the patient has received a transplant form her/his own intended donor.

When coming to our population of interest (pairs having participated to the program), the *history of cigarette use* is missing for the vast majority of patients. For this particular variable, instead of mean replacement, we apply the assumption made by Rehse et al. (2018) that this variable is negative when cigarette use is not mentioned in the patient medical record. Let us also underline that for 8 pairs (pairs coming from Switzerland) we have a lot of missing values. However, these pairs are HLA incompatible and, thereby, must be considered as particular cases (see the next section). Finally, for three ABO incompatible pairs, most of the information about the donor are missing. These missing values are treated by mean substitution.

[26] Yes may take four different values: *CONJ / CONJPM / LIAFFEST / VIECOM* and No may take five different values: *COLL / ASC / COUSIN / DESC / ONCLE*.

[27] Rehse et al. (2018) use the same method in their study on European Data.

E.4 LKDPI for patients from HLA incompatible pairs

As described in Section E.1, HLA incompatibility is not taken into account in the LKDPI formula estimated by Massie et al. (2016). Nevertheless, we know that HLA incompatibility has a huge negative incidence on graft survival (see, among others, Bentall et al. (2013)). In particular, an HLA incompatible graft is clearly considered as being of poorer quality than an ABO incompatible graft. For this reason, we have attributed to patients of HLA incompatible pairs a LKDPI equals to the highest value of the LKDPI among patients from HLA compatible pairs having participated to the program. This value equals 80.35.