Choices and Outcomes in Assignment Mechanisms: The Allocation of Deceased Donor Kidneys*†

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Abstract

While the mechanism design paradigm emphasizes notions of efficiency based on agent preferences, policymakers often focus on alternative objectives. School districts emphasize educational achievement; and transplantation communities focus on patient survival. It is unclear whether choice-based mechanisms perform well when assessed based on these outcomes. This paper evaluates the assignment mechanism for allocating deceased donor kidneys on the basis of patient life-years from transplantion (LYFT). We examine the role of choice in increasing LYFT and compare equilibrium assignments to benchmarks that remove choice. Our model combines choices and outcomes in order to study how selection induced in the mechanism affects LYFT. We show how to identify and estimate the model using quasi-experimental variation resulting from the mechanism. The estimates suggest that the design in use selects patients with better post-transplant survival prospects and matches them well. It results in an average LYFT of 8.78, which is 0.92 years higher than a random assignment. However, there is scope for increasing the aggregate LYFT to 13.84. Realizing the majority of the gains requires transplanting relatively healthy patients, who would have longer life-expectancy even without a transplant. Therefore, a policymaker faces a dilemma between transplanting patients that are sicker and those for whom life will be extended the longest.

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1 Introduction

Assignment mechanisms are commonly used to allocate scarce resources without using monetary transfers. Examples include public schools, public housing and organ allocation. An influential theoretical and a growing empirical literature studies the design of these mechanisms. In this literature, notions of efficiency derived from choices are central to evaluating a design. This desideratum often differs from objectives emphasized by policymakers. School districts emphasize student achievement and organ transplant systems emphasize patient survival.

Because canonical choice-based mechanisms are not designed with these outcomes in mind, it is unclear whether they perform well on this dimension. Choices made by agents who may not be well-informed about the benefits of various options and co-ordination failures may undercut this objective.[1] If so, a planner who can dictate assignments based on benefits estimated using extensive administrative data on outcomes may be able to do better. On the other hand, agents may also have private information about the outcomes that result and using a choice-based mechanism may serve the policymaker's objective.

This paper evaluates the assignment mechanism used to assign kidneys from deceased donors on the basis of the survival outcomes. We compare the performance and distributional consequences of the mechanism to two benchmarks – the survival maximizing assignment and the random assignment. And, we assess the role of choice by examining its relationship to survival and by considering alternatives that dictate assignments using observables alone.

We make several methodological and empirical contributions. First, we build on the literature on Roy selection to analyze a joint model of choices and outcomes in an assignment mechanism. We show how to identify and estimate the effects of counterfactual assignments by using variation generated by the mechanism and instruments that only affect choices but are excluded from outcomes. Second, we estimate the Life-

[1] Moreoever, in the kidney allocation context that we study below, surgeons that advise patients may suffer from agency problems that can misalign decisions relative to maximizing survival outcomes.

Years from Transplantation (LYFT), defined as the difference between median survival with and without a transplant, as a function of patient-donor specific observed and unobserved characteristics. Third, using these estimates we compare the mechanism used in practice to alternative assignments to assess its performance and to identify the scope for further improvements.

Organs from deceased donors are a scarce and valuable resource. Approximately 100,000 patients suffering from kidney failure are currently waiting for a life-saving transplant. In 2018, only 14,725 patients were transplanted through this waitlist, while thousands died and more than 35,000 new patients were added to the list.[2] The best estimates suggest that the average transplant extends a patient's life by several years while also saving the healthcare system $270,000 or more due to reduced expenditures on dialysis (Irwin et al., 2012; Held et al., 2016).

When a kidney becomes available, patients on the waitlist are offered the organ in a priority order. They are informed about the organ's attributes and may choose to reject an offer in order to wait for a more preferable one. This decision may therefore depend on the perceived benefits of a transplant from the offered organ. We jointly consider the decision to accept or refuse an offer along with the potential survival outcomes, and incorporate the potential for selection.

Our model has three components. The first component models the choices made by patients as a function of the patients' and the organs' attributes; the second governs the survival of the patient without a transplant; and the third governs the post-transplant surivival with the offered organ. Our method allows for unobserved attributes that are correlated across the equations.

The model can generate selection into transplantation along three important margins from the perspective of evaluating assignments. Transplanted patients could be selected on untransplanted survival, post-transplant survival from an average kidney, or patient-kidney match specific survival. Selection on these margins can be induced due to two reasons. First, the priority types and waiting times built into the mechanism in-

[2]Source: https://optn.transplant.hrsa.gov/data/view-data-reports/national-data/

duces selection. For example, the mechanism gives priority to patients who have waited longer, thereby selecting patients with high untransplanted survival into transplantation. Second, selection may be induced by patient choice. Organs that are particularly well-suited to a patient may be more likely to be accepted by that patient.

These sources of selection create an identification challenge because they may be driven by unobservables. We prove that our model is non-parametrically identified if two sources of variation are available. The first source of variation is due to randomness in the offers made to a given patient, conditional on the patient's priority-type in the mechanism. This source of variation allows us to compare the outcomes of patients whose final assignments differed due to variation in which organs were offered to the patient. Therefore, it identifies a local-average treatment effect – a difference between the survival outcomes for the select group of patients whose assignment is affected an offer.

An important limitation of using only this first source of variation is that it does not readily allow us to predict survival from counterfactual assignments. Doing so is necessary in order to consider changes in the set of patients that are transplanted or changes in the kidneys to which a patient is matched. To fill this gap, we show that an instrument that shifts choices while holding the (distribution of) outcomes fixed can be used to identify the model. A similar approach has been used to correct for selection Geweke et al. (e.g. 2003); Heckman and Navarro (e.g. 2007); Walters (e.g. 2018); Hull (e.g. 2018); van Dijk (e.g. 2019), and to estimate marginal treatment effects Heckman and Vytlacil (2005). For our application, we use variation in scarcity across geography and time after showing that our measures are balanced on patient-specific observables. We estimate the model using a Gibbs' sampler similar to Geweke et al. (2003).

Our estimates suggest that choices and assignments are positively correlated with survival outcomes, both due to observed and unobserved factors. Patients are more likely to accept kidneys that result in longer survival and those with match-specific benefits. These patterns are also reflected in the final transplants – transplanted patients have a higher LYFT from the average organ as compared to untransplanted patients. Taken

together, these results suggest that prior approaches that do not account for selection on unobservable factors (e.g. Wolfe et al., 2008, 2009) yield biased estimates. While our estimates suggest that the mechanism used during our sample period resulted in an average LYFT of 8.64 years, an approach that does not use a quasi-experimental research design places this estimate at 7.94 years.

Next, we benchmark this assignment from the perspective of a planner interested in maximizing survival effects as measured by LYFT. We focus on survival as an objective because it is a focal outcome in our empirical context.[3] We compare the observed assignment to alternatives ranging from a random assignment to one that maximizes LYFT by reallocating patients and donors. The latter represents the maximum LYFT achievable by an assignment of patients to organs. Because distributional constraints may limit the ability to select which patients get a transplant, we also consider alternatives that assigns organs to different patients while fixing the set of transplanted patients. Finally, we measure the increase in LYFT that can be achieved by a planner who can dictate assignments based on observed patient and donor characteristics.

Our results suggest that the mechanism does better than a random allocation, but that there is significant scope for improvement. A random assignment yields an average LYFT of 7.87, much lower than an average of 8.78 in the mechanism used during our sample period. Compared to a random assignment, the equilibrium assignment transplants patients that have a higher than average LYFT from the average transplant. It also matches these patients to donors that are more suitable for them. Most of this gain in LYFT comes from allowing patient choice. Assignment to patients based on existing priority rules without allowing for choice only achieves an average LYFT of 8.01. However, there is scope for further increasing LYFT to 13.84 by changing the assignment. A significant portion of these gains – specifically, an increase to 10.48 years – can be achieved if a planner can dictate assignments using observables in our dataset. The drop from the optimal assignment suggests that choice may not be dispensible if

[3]Observe that there is no natural numeraire good that is transferable in the organ allocation context. This fact poses challenges to utilitarian objectives that are often justified based on a Kaldor-Hicks criteria.

the unobserved types are private information.

These improvements in LYFT have important distributional consequences that may present real-world challenges. Specifically, we find that realizing the increase in LYFT requires transplanting patients that are relatively healthy and will live longer without a transplant. Such re-distribution is necessary because we find that survival with and without a transplant is strongly correlated, and most of the heterogeneity in LYFT is across patients. Therefore, the planner faces a dilemma between maximizing survival benefits and transplanting urgently sick patients.

Related Literature

This paper contributes to several literatures. We contribute an alternative perspective for evaluating assignments relative to the literature studying assignment mechanisms (Abdulkadiroglu and Sönmez, 2003; Pathak, 2017). This literature typically takes the preferences of students as the welfare relevant object. For example, the empirical literature, which has focused on school choice problems, uses a willingness to travel measure for welfare comparisons (see Agarwal and Somaini, 2020, for a survey). The most closely related paper is on the assignment of deceased donor organs (Agarwal et al., 2019), which uses a decision-theoretic notion of welfare by comparing a change in the mechanism to an equivalent increase in donor supply.

Our evaluation of counterfactual allocations on treatment outcomes is related to the concept of empirical welfare maximzing assignment rules introduced by **?**, who discuss the statistical properties of assignments that maximize treatment outcomes conditional on observable covariates in a setting without selection on unobservables.

Our paper is also related to recent approaches that leverage quasi-experimental variation in school choice mechanisms to estimate school quality (e.g. Abdulkadiroglu et al. 2011; Abdulkadiroglu et al., 2017). The focus of this literature has been to estimate a local average treatment effect. In our context, this estimand would preclude analyzing outcomes from alternative assignments because the set of compliers would change. Our model explicitly incoporates choices in the mechanism as a means to estimate the

distribution of effects.

The techniques we use build on a large literature studying selection models (Roy, 1951; Heckman and Honore, 1990). Our methods are most closely related to papers that combine outcomes with choice models to correct for selection when estimating treatment effects Geweke et al. (e.g. 2003); Heckman and Navarro (e.g. 2007); Walters (e.g. 2018); Hull (e.g. 2018); van Dijk (e.g. 2019). In particular, Geweke et al. (2003) use a Gibbs' sampling in a model that allows for selection on gains, and Heckman and Navarro (2007) study a setting with dynamic treatments. Our use of a Bayesian approach is, as far as we know, new in the literature on estimating survival models with quasi-experimental variation (e.g. Abbring and Van den Berg, 2003). The main difference relative to the aforementioned papers is that we use our methods to estimate heterogenous treatment effects in order to evaluate alternative assignments. This requires us to simultaneously estimate selection on three margins: baseline outcomes, average outcomes under an assignment, and match-specific effects. Our results avoid relying on identification at infinity arguments by combining variation in the offers received by an agent with a choice shifter.

This paper contributes to a medical literature that constructs measures of LYFT (Wolfe et al., 2008). These measures are commonly used to guide organ policy design[4] and to calculate cost savings from transplantation. To the best of our knowledge, this prior literature does not incorporate quasi-experimental variation in the analysis. We find a significant selection bias that could ultimately influence these analyses.

Overview

Section 2 describes the institutions, the data, and presents descriptive evidence. Section 3 presents the model. Section 4 describes the instruments. Section 5 presents our identification results and specifies the empirical model that we take to the data. Section 6 describes our estimates. Section 7 presents our results on LYFT generated by the

[4]The U.S. considered a priority system based on LYFT in the past, and the U.K. uses a "transplant benefit score" for allocating kidneys (Watson et al., 2020).

mechanism, and section 8 compares it to alernatives. Section 9 concludes.

2 Background, Data and Descriptive Evidence

This section begins with the basics of kidney transplation before describing the allocation system. We then detail our data and present key descriptive facts to motivate our study.

2.1 Institutional Features

2.1.1 Basics of Kidney Transplantation

Approximately 750,000 patients are afflicted with End-Stage Renal Disease (ESRD) in the United States (USRDS, 2018). Medicare provides near universal coverage to these patients for costs related to ESRD, irrespective of age. This program cost the federal government $35.4 billion in 2016, accounting for 7.2 percent of overall Medicare paid claims (USRDS, 2018) or approximately 1 percent of the federal budget.

Transplantation is considered to be the best treatment for ESRD – it is estimated to increase the length of an average patient's life by approximately seven years for a patient that is more than 50 years of age and eleven years for a young adult (Wolfe et al., 2008). In addition, a transplant also saves on expensive dialysis treatment. Current estimates suggest that each transplant is expected to save between $195,000 – $400,000 over the life of a transplanted patient depending on insurance status (Irwin et al., 2012; Held et al., 2016; USRDS, 2018). These estimates are based on survival models that control for patient and donor characteristics and a comparison of healthcare costs for patients with and without a transplant. Our methods improve the estimates of the former set of components by relying on quasi-experimental variation.

There is significant potential for heterogeneity in survival effects along several important dimensions, even amongst compatible patient-donor pairs.[5] First, survival both with

[5]To receive a kidney transplant, the patient must be considered biologically compatible. Compatibility requires that a patient does not have a pre-existing immune response to the organ's cells. After

and without a transplant can differ based on the patient's health conditions. Some patients may tolerate dialysis better than others. Similarly, the underlying cause of kidney disease and other co-morbidities can affect a patients' post-transplant survival prospects. Second, donor quality can significantly influence transplants. For example, the circumstances of the donor's death, kidney function, and the donor's heath prior to death are some factors that are considered important determinants of organ quality. Finally, there are match-specific factors that affect post-transplant survival. Examples include size and weight match, and similarity of tissue-protein between the patient and the donor. Our methods will aim to estimate the effects of these factors on life-year benefits.

2.1.2 The Allocation of Deceased Donor Kidneys

The allocation of organs from deceased donors is organized using a prioritized waiting list in which patients receive offers when an organ becomes available and may choose to accept or reject it. This allocation system is co-ordinated using a system called UNet. It collects detailed information about the donor's medical history and organ characteristics, and transmits it to biologically compatible patients who are being offered the kidney. Each donor's kidneys are allocated to the highest priority patients on the waitlist that are willing to accept the organs.

Prior to 2014, patient priority in the kidney assignment system was based primarily on waiting time and tissue-type similarity between the patient and the donor. Specifically, each kidney is first offered to patients with a perfect tissue-type match, then to patients from the local area in which the organs were recovered, then regionally, and finally nationally.[6] Within each priority group, the points system is based on tissue type

transplantation, medications can limit new immune response. We hold medical practices related to the determination of compatibility and post-transplant management as constant when we measure survival benefits. Danovitch (2009) provides further details about kidney biology and medical practices.

[6]The local regions are defined along state boundaries in most cases with exceptions to make sure that a metropolitan area is not split into two regions. This was done, in part, because some regions did not want to disadvantage their patients if others had a high demand for organs. But, local allocation also helps reduce the amount of time an organ needs to be preserved on specialized equipment outside the donor's body.

similarity, whether or not the patient is pediatric, patient sensitization, and waiting time (see OPTN, 2014, for details).

A new kidney allocation system aimed at improving survival benefits was implemented on December 4, 2014. The most important change gives greater priority to the healthiest patients for the highest quality organs because these patients are believed to have the largest survival benefit from these organs. In addition, the system also increases priority for extremely hard to match patients and reduces emphasis on wait time. We refer the reader to OPTN (2017) for a detailed description of the priorities and points used. Using survival models that control for patient and donor covariates, Israni et al. (2014) predict that this change should increase post-transplant survival and improve access for highly sensitized candidates.

There are two features of the kidney allocation system that are worth highlighting. First, unlike the assignment systems for some other organs (for example, livers), the kidney assignment system does not use patient urgency to determine priority. Second, patients who reject an offer remain on the list and may choose to accept the next offer with no penalty in priority for refusing an offer.

2.2 Data and Descriptive Analysis

2.2.1 Data Sources

This study uses data from the Organ Procurement and Transplantation Network (OPTN). The OPTN data system includes data on all donors, wait-listed candidates, and transplant recipients in the US, submitted by the members of the OPTN. The Health Resources and Services Administration (HRSA), U.S. Department of Health and Human Services provides oversight to the activities of the OPTN contractor.

The data includes detailed information on patient and donor characteristics, survival and graft failure outcomes from the Standard Transplantation Analysis and Research dataset. They also include all offers made by the system and accept/reject decisions from the Potential Transplant Recipient dataset. These data are populated using in-

formation gathered in UNet and forms submitted by transplant centers from patient follow-ups after a transplant is performed.

We restrict attention to patients that first joined the kidney waiting list between January 1st, 2000 and December 31st, 2010.[7] From this set, we exclude patients that needed multiple organ transplants and those that received a living donor kidney. Correspondingly, we only use data on donor offers and acceptance decisions for these patients.

The data allow us to measure survival outcomes using information on patient death merged from social security records and transplant center reports. These records are consistently populated until December 31st, 2015.[8] For patients without death records, we use information from the waitlist for untransplanted patients and from annual post-transplant follow-ups for transplanted patients to construct a censored measure of patient survival.

2.2.2 Descriptive Analysis

Patients and Donors

Patients on the waiting list face extreme scarcity, with a significant portion of patients dying while waiting for a transplant. Table 1 describes the sample of patients, and their transplant and survival outcomes. An average of 15956 patients from our sample registered each year on the kidney waiting list. Panel A shows that 27.4% of patients that join the list die within five years of registering, while only 47.2% receive a transplant during this time-period. The chances of receiving a transplant decline after the first five years as only 54% of the full sample of patients ultimately receive a deceased donor kidney. The remaining patients either still await a kidney or leave the list.

Panel B shows that patients receiving a transplant from a deceased donor are younger and appear to have been in better health at the time of registration. Transplanted patients are less likely to be on dialysis at the time of registration, less likely to be

[7] For patients with multiple listings, we keep the earliest registration if the patients never received a transplant; we keep the earliest registration with transplant record otherwise.

[8] Our data use agreement allows for periodic updates, which we plan to include in future iterations of the paper.

Table 1: Patient Characteristics

	All Patients		Received Deceased Donor Transplant	
	Mean	S.D.	Mean	S.D.
New Patients per Year	15956		8393	
Panel A: Outcomes				
Died by Year Five (%)	27.4	44.6	9.3	29.1
Survived Five Years (%)	64.2	47.9	86.2	34.4
Censored by Year Five (%)	8.4	27.7	4.4	20.6
Transplanted by Year Five (%)	47.2	49.9	89.7	30.4
Panel B: Characteristics				
Age at Registration	51.4	14.2	48.9	15.2
On Dialysis at Registration (%)	77.3	41.9	75.1	43.2
Diabetic Patient (%)	42.9	49.5	33.4	47.2
BMI at Registration	28.2	5.9	27.6	5.7

diabetic and have a lower body mass index. These observations are consistent with high waiting times and the hypothesis that differences in these characteristics correlate with longer survival without a transplant.

Despite this scarcity, undesirable organs have to be offered to many patients in an attempt to allocate them. Table 2 shows that across donors, the mean number of biologically compatible offers that met the pre-set screening criteria is 543.5, but the median is much lower, at 51. This skewed distribution arises because undesirable kidneys are rejected by many patients, while desirable kidneys are accepted quickly. Indeed, 18.9% of donors have at least one of their viable kidneys discarded. Organs from these donors were refused by an average of 1890.5 patients.

Our observable donor covariates, which should predict organ quality, are correlated with number of offers and discards in the expected ways. Table 2 summarizes selected donor characteristics by the allocation outcome for a donor's kidneys. Donors whose kidney(s) were discarded are older, less likely to die of head trauma, more likely to be diabetic or hypertensive, have a higher creatinine level (an indicator of lower kidney function),

Table 2: Donor Characteristics

	All Donors		Any Kidney Discarded			
			Yes		No	
	Mean	S.D.	Mean	S.D.	Mean	S.D.
Number of Donors per Year	6181		1169		5012	
Median Number of Offers per Donor	51		482		40	
Average Number of Offers per Donor	543.5	1927.9	1890.5	3684.3	229.3	946.7
Donor Age	39.2	18.4	52.0	16.6	36.2	17.5
Cause of Death -- Head Trauma (%)	39.7	48.9	19.5	39.6	44.5	49.7
Hypertensive Donor (%)	28.6	45.2	55.4	49.7	22.4	41.7
Donor Creatinine	1.2	1.0	1.4	1.1	1.1	0.9
Non-Heart Beating Donor (%)	7.9	26.9	10.4	30.6	7.3	26.0
KDPI	0.5	0.3	0.8	0.2	0.4	0.3

and more likely to have donated after cardiac death. The transplantation community aggregates these and other indicators of quality into the Kidney Donor Profile Index (KDPI), which is the percentile of the estimated quality of a donor's organ. [9]

Survival

Our study will focus on survival as the primary outcome of interest for several reasons. First, this outcome is arguably the most important one from the perspective of the patient and also the policy-makers. Predicted LYFT from observational models was explicitly used by the OPTN Kidney Transplantation Committee to evaluate proposed designs. As we will show below, ESRD patients that do not receive a transplant have a life-expectancy of about half of those that do. Second, moving an ESRD patient from dialysis to transplantation saves on expensive dialysis treatment. While we do not directly evaluate this component, future research can use our estimates to revisit cost-benefit analyses. Third, this outcome can be measured relatively easily. The other most commonly discussed effect is on quality of life, which is hard to quantify.

Figure 1 shows the survival curves for patients that receive a transplant and those that do not using the (non-parametric) Kaplan-Meier estimator. We separate the survival

[9] See https://optn.transplant.hrsa.gov/resources/guidance/kidney-donor-profile-index-kdpi-guide-for-clinicians/.

curves for young and old patients (above/below the median age of 54), and for donors that had at least one of their kidneys discarded, which indicates that the transplanted organ was likely undesirable. The vertical dashed lines depict the average waiting time for organs from the two types of donors. Donors with at least one of their kidneys discarded are much more likely to have undesirable organs as compared to those that did not. Indeed, the average waiting time for a patient that receives a kidney from a donor without a discard is higher than that for a donor with a discard.

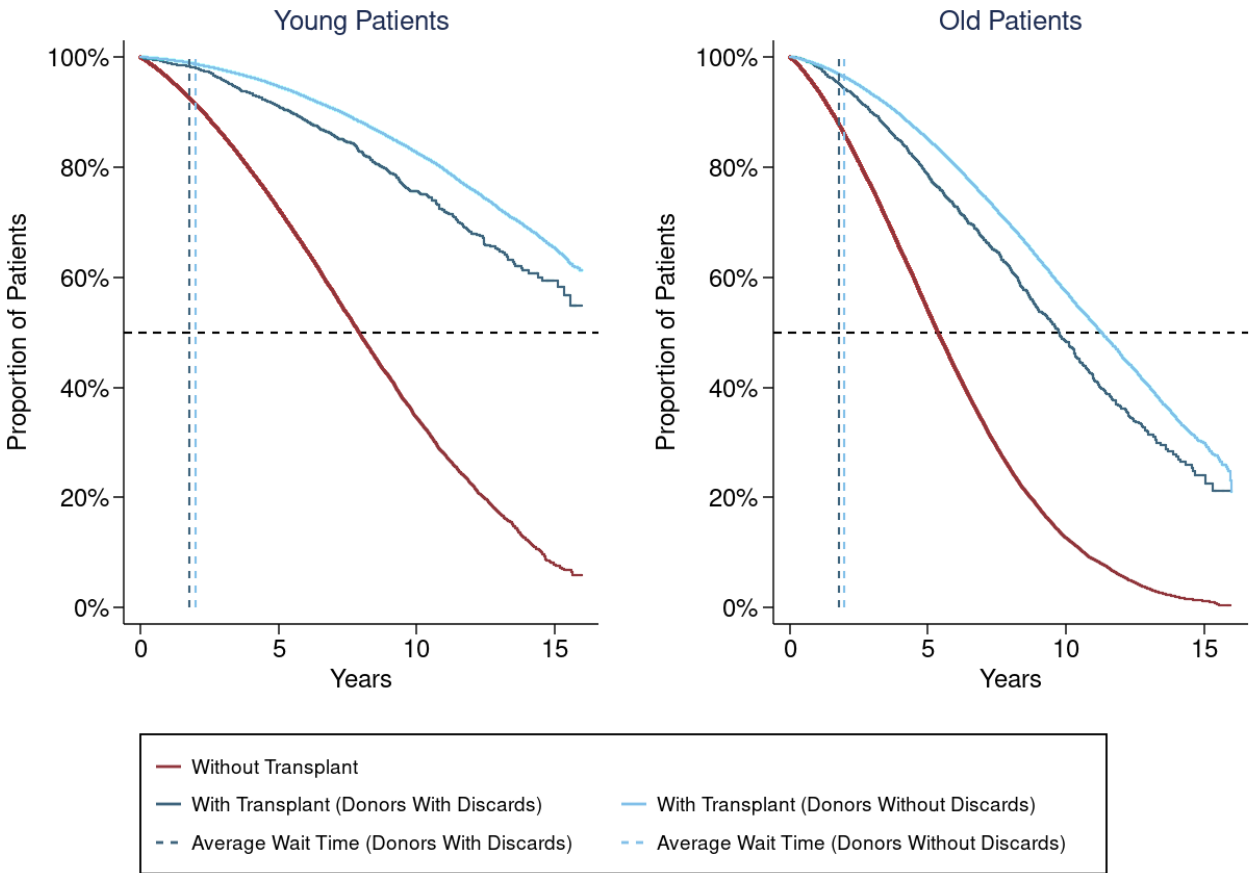


Figure 1: Patient Survival

Notes: The figure shows Kaplan-Meier survival curve for young and old patients (above/below the median age of 54) who registered on the waitlist between 2000 and 2010. Survival with transplant is measured as time since registration.

These survival curves show that transplanted patients live significantly longer than patients that do not receive a transplant. Moreover, these survival curves are substantially different for young and old patients, and also for patients transplanted with a desirable

versus undesirable organ. Only about half of the young patients who do not received a transplant survive more than 7.9 years. But, more than half of the young patients that receive a transplant from a donor with desirable organs live past 16 years. These statistics are 5.4 and 11.3 years respectively for older patients, indicating that older patients have shorter half-lifes both with and without a transplant. In fact, some young patients survive more than eighteen years, which is rare for an older patient.[10] For both groups of patients, a transplant using an undesirable organ is associated with half-lifes that are shorter by about a year or more.

Taken together, these observations point to the potential for choices and assignments to be correlated with survival outcomes. Choices are important because discards occur only when many patients have refused the organ. Next, we turn to a model that incorporates these sources.

3 A Model of Decisions and Outcomes

Our model considers assignment mechanisms in which object, indexed by j, are assigned to agents, indexed by i. When an object arrives, offers are made to agents on a waiting list who must decide to accept or reject it. These decisions translate into an assignment, and an outcome is realized. We now describe the mechanism, observed outcomes and the primitives of our model in further detail.

3.1 Assignment Mechanism and Observed Outcomes

Objects arrive sequentially and the mechanism assigns each one as follows. It orders agents on the waiting list according to a priority score that may be object specific and depend on the time that an agent has waited. Offers are made in priority order

[10] In our sample, 61.2% young patients and 21.0% old patients that received a desirable organ survived more than 16 years. We cannot track survival outcomes for any longer than sixteen years because the earliest cohort in our study registered in the year 2000, and our survival data are up to date as of December 31, 2015. This fact also motivates our focus on median survival half-lifes instead of expected life-years – the former does not depend on the right-tail of survival outcomes. This focus is also consistent with prior work measuring the life-year benefits from transplantation (see Wolfe et al., 1999, 2008, for example).

and each agent may decide to accept or reject the object. We denote acceptance with $D_{ij} = 1$. Objects are assigned to the highest priority agents that accepts the offer. The mechanism may elicit multiple decisions at once, but agents may not be skipped. Finally, agents that have been assigned an object are removed from the list. Other agents may also leave the list.

Now consider the set of objects that are feasible for a given agent. Holding fixed the decisions of the other agents, define J_i to be the sequence of objects offered to agent i if the agent refuses all the offers made to her and the agent participated in the mechanism indefinitely. Because we allow agents to depart from the list prior to assignment due to death or for other reasons, an agent may only receive a subset of offers. Let $\tilde{J}_i$ be this subset. That is, $\tilde{J}_i$ is an ordered set of objects that the agent would have been offered prior to departure from the list if she refused all objects.

The object that an agent is assigned depends both on the feasible set of objects and her decisions. Specifically, let $T_{ij} = 1$ denote agent i being assigned object j. Indexing objects in sequence of arrival, we have that

$$T_{ij} = \prod_{j' < j,\, j' \in \tilde{J}_i} \left(1 - D_{ij'}\right) D_{ij},$$

where $D_{ij} = 1$ if agent i accepts object j. Therefore, each agent i is assigned to the first object that they accept from the set $\tilde{J}_i$.

The outcomes we observe are determined by whether or not, and which object an agent is assigned. Let the observed outcome be given by

$$Y_i = \sum_{j \in \tilde{J}_i} T_{ij} Y_{ij} + \left(1 - \sum_{j \in \tilde{J}_i} T_{ij}\right) Y_{i0},$$

where Y_{ij} is the outcome of agent i from being assigned object j, and Y_{i0} is the outcome for agent i if the agent is not assigned any object.

This formulation, for the moment, abstracts away from potential truncation of the observed survival outcome. That is, if agent i is assigned to object j then we observe

Y_{ij}. Otherwise, we observe Y_{i0}. In our empirical context, we observe a censored survival outcome for some set of patients. For these patients, we will be able to deduce that $Y_i > \bar{Y}_i$, where $\bar{Y}_i$ is the censoring time. Throughout, we will make the standard assumption that the duration for censoring is independent of the true duration (see equation 20.22 in Wooldridge, 2010).

3.2 Latent Outcomes and Decisions

There are three key sets of primitives in our model:

Unassigned Outcome: The outcome for agent i if the agent is not assigned any object is given by

$$Y_{i0} = g_0\left(x_i, \nu_{i,0}\right), \tag{3.1}$$

where, with some abuse of notation, $x_i \in \mathbb{R}^{d_x}$ are agent-specific observables; $\nu_{i,0} \in \mathbb{R}$ denotes a vector of agent-specific unobservables; and $Y_{i0} \in \mathbb{R}$.

Assignment Outcome: The outcome of agent i from being assigned object j is given by

$$Y_{ij} = g_1\left(q_j, x_i, \nu_{i,1}, \varepsilon_{ij,1}\right), \tag{3.2}$$

where $x_i \in \mathbb{R}^{d_x}$ is a vector of agent-specific observed characteristics; $q_j \in \mathbb{R}^{d_q}$ denotes the type for each object j; $\nu_{i,1} \in \mathbb{R}$ denotes a vector of agent-specific unobservables; $\varepsilon_{ij,1} \in \mathbb{R}$ denotes unobservables that are agent- and object-specific; and $Y_{ij} \in \mathbb{R}$.

Since Y_{ij} and Y_{i0} denote survival outcomes in our application, they can be written as arising from survival models with time-varying hazard rates given by $\lambda_{ij,1}(t) = \lambda_1(t; x_i, q_j, \nu_{i,1})$ and $\lambda_{i,0}(t) = \lambda_1(t; x_i, \nu_{i,0})$ respectively. In this formulation, $\nu_{i,1}$ and $\nu_{i,0}$ yield the distribution of the resulting survival times. The main restriction for the purposes of our application is that the survival curve for a given patient does not evolve over time. That is, the agent-level unobserved heterogeneity terms ν_{i1} and ν_{i0} do not vary with time. It is difficult to relax this restriction because we only observe a single

survival outcome for each patient (see Unkel et al., 2014; Heckman and Navarro, 2007). The model does allow for survival to depend on time waited prior to transplant since x_i and q_j can include the dates on which patient i and organ j arrive.

Decision Equation: We model the acceptance decision as

$$D_{ij} = g_D\left(q_j, x_i, z_i, \nu_{i,D}, \varepsilon_{ij,D}\right) \in \{0, 1\} \tag{3.3}$$

where $D_{ij} = 1$ denotes accept; $\nu_{i,D} \in \mathbb{R}$ denotes unobserved selectivity of agent i; $\varepsilon_{ij,D} \in \mathbb{R}$ is a shock that is specific to the agent and the object; and $z_i \in \mathbb{R}^{d_z}$ are observables that influence the decision on an agent. Without loss of generality, we assume that g_D is non-increasing in $v_{i,D}$ and non-decreasing in $\varepsilon_{ij,D}$.

The primary restriction in the choice model is that an agent's decision does not depend directly on the specific decisions of other agents or on the feasible set $\tilde{J}_i$. Nonetheless, it accomodates agents refusing an offer in expectation of the future offers that the agent may receive in equilibrium. Although we do not need to commit to a specific equilibrium model of choice, Agarwal et al. (2019) describe an optimal stopping problem for which the present formulation is a reduced form. Specifically, an offer is accepted if the (perceived net present) value from accepting the organ exceeds the option value of waiting. In this formulation, z_i could include variables that influence this decision, say through the distribution of future offers, but is unrelated to the benefits of accepting the given organ.

The main difference between X_i and Z_i is that the latter is excluded from the outcome equations described above. We have used uppercase letters to denote the random variables that describe the process of sampling from the patient population and reserve lowercase letters to denote their realized values. This exclusion restriction, combined with Assumption 1(i) below introduces instruments in the model that we will use in the empirical strategy and identification results developed in Section 4. This section also introduces the specific instruments Z_i used in our application.

Throughout the paper, we will make the following assumptions:

Assumption 1. *(i)* $\{\varepsilon_{ij}\}_j$, ν_i *and* Z_i *are mutually independent conditional on* x_i *and* $(q_j)_j$.

(ii) The random vector $\nu_i = (\nu_{i,0}, \nu_{i,1}, \nu_{i,D})$ *is distributed iid across* i.

(iii) The random vector $\varepsilon_{ij} = (\varepsilon_{ij,1}, \varepsilon_{ij,D})$ *is distributed iid across* i *and* j.

Assumption 1(ii) and 1(iii) above are currently without loss of generality, but will imply restrictions when we restrict the functions $g_0(\cdot)$, $g_1(\cdot)$, and $g_D(\cdot)$. In our specifications, dependence between the components of ν_i and the components of ε_{ij} will allow Y_{ij} and Y_{i0} to be correlated with each other and with D_{ij}.

3.3 Sources of Selection

The model allows for selection on three dimensions: untransplanted survival Y_{i0}; survival from the average transplant $\bar{Y}_i = \frac{1}{J}\sum_j Y_{ij}$, and selection on match-specific survival $Y_{ij} - \bar{Y}_i$. There may be selection on these dimensions either due to choice or due to the mechanism.

Selection due to choice occurs if agents' choices D_{ij} are correlated with survival outcomes Y_{i0} or Y_{ij}. For example, such selection occurs if patients with higher expected survival without a transplant due to unobserved health conditions are more selective. This type of selection can occur due to either observables or unobservables. For example if $E(Y_{i0}|\nu_{i,D}, x_i)$ varies with x_i or $\nu_{i,D}$ there is selection on untransplanted outcomes. Similarly, patients may be more likely to accept an organ with an idiosyncratic survival benefit. These sources of selection are generalized versions of Roy (1951) selection.

Selection due to the mechanism occurs for two reasons, even after conditioning on decisions D_{ij}. First, an organ that arrives after the patient's survival outcome without a transplant is not feasible. Therefore, $\tilde{J}_i$ can only include organs that arrive prior to the untransplanted survival duration, Y_{i0}. This fact results in selection on untransplanted survival via both x_i and ν_{i0} because these attributes may be correlated with transplanted survival. Second, $\tilde{J}_i$ depends on the priorities and the set of patients on the waiting list, which also affects which transplants occur. For example, priority is given to patients

who have a perfect tissue-type match with the kidney who may have idiosyncratically large survival benefits.[11] Similarly, priority for waiting time implies that transplanted patients may have larger than average values of survival without a transplant, Y_{i0}, which may be correlated with transplanted survival, Y_{ij}.

Because some of these sources of selection can be driven by unobservables, comparing survival with and without a transplant can yield biased estimates of the causal effect of a transplant. Both sources result in T_{ij} being correlated with unobserved factors that determine outcomes. The aim of the instruments discussed in Section 4 is to address the resulting endogeneity concerns.

4 Instruments

Our solution to the selection problems discussed above will require two sources of variation. We describe each of these in turn. Section 5 will formally prove identification under these two sources of variation.

4.1 Conditionally Independent Potential Offers

The first source of variation we will exploit arises from randomness in the objects offered to an agent. Recall that J_i is the sequence of offers to agent i if the agent refuses all the offers made to her and participated in the mechanism indefinitely. We will impose the following assumption on J_i:

Assumption 2. *The sequence of offers J_i is conditionally independent of (ν_i, ε_i) given x_i.*

This assumption is satisfied if x_i controls for a sufficiently rich set of agent types such that the remaining variation in the offers that the agent could have received is independent of unobserved determinants of outcomes and decisions. The assumption parallels the exclusion restriction required for the validity of an instrument.

[11] Organs with a perfect tissue-type match are significantly less likely to cause a adverse immune response, resulting in greater survival benefits.

We now argue that this assumption is plausible in our setting on theoretical and empirical grounds. Our theoretical justification is based on the mechanism used to allocate deceased donor kidneys and the assumptions on the model made above. The set J_i depends only on the kidneys that arrive after a patient registers on the waiting list, the decisions of other patients on the waiting list and determinants of the agent's priority and points on the list. It does not depend on the realized decisions made by agent i. Our knowledge of the mechanism allows us to construct rich controls x_i for each patient's priority. Conditional on these controls, the remaining variation in J_i is only due to the stochastic arrival of organs and the decisions of agents other than i. It is plausible to assume that the former is independent of (ν_i, ε_i) because organ availability depends primarily on deaths in the local area. And, as we argued in Section 3 above, the latter is independent of (ν_i, ε_i) in a natural equilibrium model of the the waiting list.

While we will use the full set of offers to estimate the model, we now use a specific function of J_i to investigate this source of variation. To do this, we construct a set of desirable donors that are achievable for patient i in the two years following the patient's registration. Specifically, we calculate whether a patient, denoted i, would be placed above the patient on the 10th position on the list for a given donor. A patient is highly likely to receive an offer for an organ from such a donor because only 22.7% of deceased donors are offered to fewer than ten patients. We then calculate the number of donors in a given category that satisfy this criteria for each patient in the two years following the registration date of the patient.[12]

The variation in this variable comes from two sources: variation in the organs that arrived in the two years following patient i's registration and variation in the patients on the waiting list when the organ arrived. Moreover, the results below control for differences in a patient's priority, geographical area and time trends using fixed effects. We therefore need to argue that Assumption 2 is satisfied for this variable conditional

[12]We include a donor in the calculation irrespective of whether the patient accepted a prior offer or departed from the list during the period. Throughout, we restrict attention to blood type compatible donors that arrived in the same donor area and assume a fixed waiting time of two years.

on these controls. We claim that the first source of variation is independent of patient i's decisions because specific patients are not considered in organ donation decisions. The second source of variation is also plausibly exogenous because a given patient's decision is unlikely to affect the priority of the patient ranked in the tenth position.[13] Consistent with these claims, Table D.5 in the appendix shows that our measures are not significantly correlated with the vast majority of various patient characteristics (age, diabetes, female, height and weight).

Given this exclusion restriction, we now turn to showing how this measure of a patient's potential offers is related to transplant and survival. These correspond to the first-stage and reduced-form relationships in an instrumental variables model. Columns (1) to (4) in Table 3 present estimates from linear probability models to examine the relationship between the number of potential top 10 offers from donors that are either above or below median quality (as measured by KDPI) and transplant outcomes. Columns (5) and (6) show the survival effects of these potential offers using estimates from a Cox proportional hazards model. All models include fixed effects for the patient's donor service area (DSA), year of registration, blood type and determinants of priority (pediatric status and calculated panel reactive antibody (CPRA) categories).

The first conclusion from Table 3 is that potential offers strongly influence whether or not a patient receives a transplant as well as the type of organ transplanted. Columns (1) and (2) show that the number of offers in both donor categories are positively related with the probability of a transplant, whether or not we control for a rich set of patient characteristics. Columns (3) and (4) show that the type of organ transplanted depends on the number of potential offers from the corresponding type of donor. Specifically, a patient with a greater number of potential offers from above median quality organs is more likely to receive a transplant from such an organ. Conversely, the probability of a transplant from a below median organ decreases with more offers from above median quality organs. An analogous relationship holds for offers from below median quality

[13] The only potential effect is if patient i, in our sample, accepts a kidney that would otherwise have been accepted by another patient who would been pivotal in determining whether i would be in the top ten positions for a different donor.

donors. The F-statistic is large and much higher than the conventional cutoff of 10 used to assess whether an instrument is strong (Stock and Watson, 2012). Therefore, the evidence points to a strong first-stage relationship.

Table 3: Top 10 offers: First Stage

	Transplant				Hazard Rate	
	Any Kidney	Any Kidney	KDPI <= 50%	KDPI > 50% or Missing		
	(1)	(2)	(3)	(4)	(5)	(6)
log(1 + # Top 10 Offers in 2 Years)						
KDPI <= 50%	0.0322***	0.0334***	0.0439***	-0.0105***	-0.0163*	-0.0321***
	(0.00441)	(0.00441)	(0.00306)	(0.00287)	(0.00730)	(0.00736)
KDPI > 50% or Missing	0.0303***	0.0297***	-0.0128***	0.0425***	0.0000307	-0.00321
	(0.00475)	(0.00478)	(0.00314)	(0.00294)	(0.00711)	(0.00715)
DSA FE, year FE, and blood type FE	x	x	x	x	x	x
Control for Pediatric at Listing	x	x	x	x	x	x
CPRA Category Controls	x	x	x	x	x	x
Patient Characteristics		x	x	x		x
F-statistic	93.20	92.23	108.0	130.6		
Number of Observations	132715	131105	131105	131105	132715	131105
R-Squared	0.210	0.219	0.171	0.065		

Notes: * p<0.05, ** p<0.01, *** p<0.001. The sample restricts to patients who registered between 2000 and 2008 because the instrument is calculated using offers in the two years post registration. Columns (5) and (6) use the Cox proportional hazards model. Survival duration is measured since the date of registration. All regressions control for donor service area (DSA) fixed effect, registration year fixed effect, blood type fixed effect, an indicator for pediatric at registration, and indictors for CPRA = 0, 20 <= CPRA < 80, CPRA >= 80, and CPRA missing at registration. Patient characteristics include an indicator for female, indicators for age 18-35, 35-50, and 50-65, indicators and linear controls for dialysis time 1-3, 3-5, 5-10, and >10 years, and an indicator for diabetes. Standard errors, clustered by DSA, registration year, and blood type in Columns (1) through (4), are in parentheses. F-test tests against the null hypothesis that the coefficients on the instruments are zero.

The second conclusion from Table 3 is that having a high potential number of offers from organs that are above median quality, as measured by KDPI, improves survival. Column (5) shows results that do not control for patient characteristics. Offers from a higher quality organ reduces the hazard rate of departure, thereby increasing survival. Column (6) shows that this relationship is robust to controlling for patient characteristics. However, both columns suggest that potential offers from a lower than median quality organ do not affect survival. Under Assumption 2, this relationship can only

occur through the transplant a patient ultimately receives. Therefore, together with the results in columns (1) to (4), the results suggest that patients that receive an above median quality kidney have improved survival outcomes.

While we demonstrated this instrument using a particular measure of potential offers, our empirical approach will not directly use a specific measure. Instead, we will make use of all variation in offers conditional on the patient's geographical area, registration year, blood type and priority type.

4.2 A Choice Shifter: Scarcity

The second source of variation that we leverage is based on instruments that alter an agent's acceptance decision, but are independent of latent outcomes. In the model, the variables z_i affect the decisions, D_{ij}, but are excluded from the functions $g^1(\cdot)$ and $g^0(\cdot)$. Moreover, Assumption 1(i) required that, conditional on x_i, (ν_i, ε_i) is distributed independently of z_i. Therefore, these instruments are useful in identifying the model as they can be used to vary the selectivity of patients while holding survival outcomes fixed.

The instruments that we construct for our setting are motivated by the observation that patients face an optimal stopping problem. Therefore, two otherwise identical patients that have different beliefs about their option value of waiting will make different acceptance decisions even when offered the same type of organ. In particular, patients who expect greater transplant opportunities in the future (lower scarcity) should be less willing to accept a given kidney than otherwise identical patients with fewer opportunities (higher scarcity). The scarcity instruments we need to construct must be correlated with decisions, but independent of latent outcomes.

We construct two measures of scarcity as choice shifters. The first is a proxy for the offers a patient can expect in the future. Fix an offer o made to patient i in the calendar quarter t. Consider the set of offers made in the four quarters after t to other patients in a comparison group. This comparison group consists of other patients with the same blood type as i that registered in the same DSA as i. We count the subset of offers

made to this group of patients when they had the same number of waiting time priority points as the offer o. The second is a proxy for donor supply, which is constructed analogously to the first but counts the number of donors instead.

Our analysis will include fixed effects for the DSA, blood-type and the calendar year of the assignment. Therefore, both instruments exploit variation in the relative scarcity of organs in a patient's location while controlling for secular trends across locations. In order to evaluate the assumption that (ν_i, ε_i) are distributed independently of z_i, conditional on x_i, we investigated whether variations in our measures of scarcity are significantly correlated with the characteristics of patients that register in a given year. Reassuringly, table D.6 in the appendix shows that our scarcity instruments are not significantly correlated with our patient characteristics (age, diabetes, female, height and weight). The threat to the instrument therefore needs to be a DSA-specific trend in scarcity are correlated with outcomes for some reason that is not reflected in patient characteristics.

These instruments are relevant to decisions if these ex-post measures are correlated with beliefs, even if they are not precisely known to the agents at the time the decision is being made. Columns (1) to (6) of Table 4 show the results from a linear probability model that regresses a dummy on whether an offer is accepted on two measures of scarcity and a variety of controls. The sample is restricted to the first one hundred offers made for a donor. Both measures of scarcity are negatively correlated with acceptance. Columns (3) and (4) show that the number of donors or number of offers to patients in the comparison group in the four quarters is negatively correlated with acceptance rates, controlling for patient characteristics, and fixed effects for DSA, allocation year and years waited. This relationship is strong and is robust to adding an extensive set of controls for donor and match-specific characteristics. Figure D.1 in the appendix shows a residualized binscatter plot suggesting that this relationship is monotonic.

These results suggest that our measure of scarcity has the expected relationship with patient acceptance decisions while satisfying the required exclusion restrictions.

5 Identification and Estimation

The previous section introduced two sources of variation that are orthogonal to an agent's latent outcomes Y_{i0} and Y_{ij} – the potential offers that an agent could receive and the scarcity faced by an agent, z_i. This section shows that these two sources of variation can be used to identify the decision model and measure the sources of selection discussed in section 3. Our results condition on the agent type x_i and omits it for simplicity of notation. We assume that the analyst observes the offer sequence J_i, the object types q_j, the choices D_{ij} and the survival outcomes.

The argument proceeds in four parts. First, we show that variation in the offers received by an agent can be used to learn the expected outcomes conditional the value of scarcity, assignment status, and the sequence of offer types. Second, we show that the choice model described in equation (3.3) is identified conditional on scarcity. Third, we use the variation in scarcity to identify selection on unobservables. The second and third parts consider the case when all objects arrive at the same time as the agent. The fourth part relaxes this restriction. All proofs are in Appendix C.

5.1 Identification of Conditional Expected Outcomes

The first result shows what can be learned about expected outcomes using variation in offers. Let $j_{i,n}$ denote the n-th offer, and let $q_{j_i} = \left(q_{j_{i,1}}, \ldots, q_{j_{i,|j_i|}}\right)$ be the associated sequence of offer types. We have the following result:

Lemma 1. *Suppose that Assumption 2 is satisfied, and* $\left(q_{j_{i,1}}, \ldots, q_{j_{i,n}}\right)$ *and* $\left(q_{j_{i,1}}, \ldots, q_{j_{i,n-1}}\right)$ *belong to the support of the distribution of offer-types induced by the distribution of* J_i*. If* $P\left[T_{ij_{i,n}} = 1 | q_{j_i}, z\right] > 0$*, then the quantities* $E\left[Y_{ij_{i,n}} | T_{ij_{i,n}} = 1, q_{j_i}, z\right]$ *and* $E\left[Y_{i0} | T_{ij_{i,n}} = 1, q_{j_i}, z\right]$ *are identified.*

This result shows that we can identify the expected outcomes with and without assignment for agents with an offer-type sequence q_{j_i} who were assigned to the $n-$th offer. Note that the assignments of agents with the offer sequence q_{j_i} allows us to observe

$P\left[T_{ij_{i,n}}=1|q_{j_i},z\right]$. Additionally, since we observe the outcome $Y_{ij_{i,n}}$ for agents with $T_{ij_{i,n}}=1$, we also observe $E\left[Y_{ij_{i,n}}|T_{ij_{i,n}}=1,q_{j_i},z\right]$. The challenge is to recover the expected value of Y_{i0} for the group of agents that would have been assigned the $n-$th offer had they received the offer sequence q_{j_i}. We construct this quantity using the expected outcomes of unassigned agents with an offer-type sequences $\left(q_{j_{i,1}},\ldots,q_{j_{i,n}}\right)$ and $\left(q_{j_{i,1}},\ldots,q_{j_{i,n-1}}\right)$. The former group only includes agents with $T_{ij_{i,n}}=0$ while the latter group includes agents with both values of $T_{ij_{i,n}}$ with known probability $P\left[T_{ij_{i,n}}=1|q_{j_i},z\right]$.

This result shows identification of outcomes for a selected set of agents. In particular, the assignment status, the types of offers an agent receives, and the scarcity introduce selection on the distribution of $\nu_{i,D}$. For example, two agents with the same sequence of offers that are assigned to the $n-$th and the $(n+1)-$st offers likely differ in their selectivity. This result is similar in spirit to those in the treatment effects literature (e.g. Imbens and Angrist 1994; Heckman et al., 2010). A similar estimand has been the target in Abdulkadiroglu et al. (2017) where offers in a school choice mechanism are used as instruments to estimate treatment effects.

Although our formal result is stated for the conditional expectations of the outcome variables, we can identify the whole distribution of Y. This follows from Lemma 1 because we can identify the conditional expectation of $\psi(Y)$ for any function ψ as long as the appropriate expectations exists.

Identification of $E\left[Y_{ij_{i,n}}|T_{ij_{i,n}}=1,q_{j_i},z\right]$and $E\left[Y_{i0}|T_{ij_{i,n}}=1,q_{j_i},z\right]$ is not sufficient for evaluation the expected values of $Y_{ij_{i,n}}$ and Y_{i0} under a counterfactual assignment of kidneys to patients. This is because patients with $T_{ij_{i,n}}=1$ are selected into treatment on unobservable selectivity, $\nu_{i,D}$. To obtain counterfactual predictions, we need to recover the distribution of outcomes conditional on unobservables. To do this we first identify the distribution of ν_D conditional on observed choices and selectivity, z, and then use variation in z to "trace out" the expected values of Y_{i0} and Y_{ij} conditional on ν_D and ε_D

5.2 Identification of the Choice Model

Our next result shows that we can use the variation in offers also to identify the function $g_D(\cdot)$. [14] To fix ideas, we focus on donor types whose arrival time coincides with the patient arrival time. That is, if t_j denotes the time difference between donor arrival and patient arrival, we focus on the case when $t_j = 0$ so that the distribution of ν_i is not selected due to survival while waiting on the list. This assumption is relaxed in section 5.4 below. We normalize the marginal distributions of $\nu_{i,D}$ and $\varepsilon_{ij,D}$ to be uniform and assume that z is supported in the unit interval. These assumptions are without loss of generality because we have not yet placed restrictions on the functional form of $g_D(\cdot)$.

We need to introduce some notation in order to develop this result. For each value of z and donor type q_j, consider two sets of pairs (ν_D, ε_D) such that one of these sets yield $g_D(q_j, z, \nu_D, \varepsilon_D) = 0$ and the other yields $g_D(q_j, z, \nu_D, \varepsilon_D) = 1$. Figure 2 illustrates the regions for two representative values of $z \in \{z_{low}, z_{high}\}$. The function $v(\varepsilon_D; q_j, z)$ separate these two sets.[15] Therefore, identifying the function $v(\varepsilon_D; q_j, z)$ is equivalent to identifying $g_D(\cdot)$.

Our results make the following assumptions on $v(\cdot; q_j, z)$:

Assumption 3. *For each q_j and z, the function $v(\cdot; q_j, z)$ is differentiable and its image is the unit interval.*

This

assumption implies that extreme values of ε_D move any agent's decision from accept to reject or vice-versa given a fixed value of z_i and $\nu_D \in (0, 1)$. Because g_D is non-increasing in ν_D and non-decreasing in ε_D, $v(\cdot; q_j, z)$ is weakly monotone function. Thus, we can interpret$v(\varepsilon_D; q_j, z)$ as the fraction of agents that reject an offer of type q_j with probability at least ε_D when faced with scarcity z. Therefore, the assumption requires that agent selectivity cannot overwhelm the effects of idiosyncratic preferences.

[14] The function $g_D(\cdot)$ can be derived from micro-funded binary choice models with mean utilities that depend on $(q_j, x_i, z_i, \nu_{i,D})$ and additive errors (Cosslett, 1983; Matzkin, 1991).

[15] Formally, define $v(\varepsilon_D; q_j, z) = \sup\{\nu_D \in [0,1] : g_D(q_j, z, \nu_D, \varepsilon_D) = 1\}$, where we adopt the convention that the supremum of the empty set is 0.

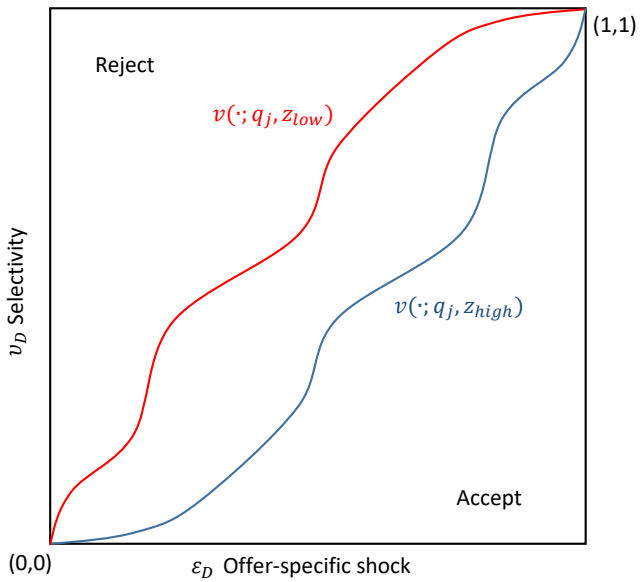


Figure 2: Acceptance and Rejection Regions

If it did, then there would be (interior) values of ν_D that would yield a degenerate acceptance probability for a given value of z. In addition, the assumption places a weak smoothness restriction on $v(\cdot; q_j, z)$.

With these assumptions, we show that variation in offers can be used to identify the function $g_D(\cdot)$:

Lemma 2. *Let q_j^n be a sequence composed by n offers of type q_j with $t_j = 0$, and let $v_{n-1}(\cdot; q_j, z)$ be the $(n-1)$-st order Fourier-Legendre approximation of $v(\cdot; q_j, z)$. If Assumptions 2 and 3 are satisfied, and q_j^n is in the support of the distribution of offer-types induced by J_i, then $v_{n-1}(\cdot; q_j, z)$ is identified for each $z \in (0,1)$ and q_j. In particular, if the hypotheses hold for all n, then $v(\cdot; q_j, z)$ and therefore $\mathbb{P}(D_{ij} = 1 | \nu_{i,D} = \nu_D)$ are identified.*

The main challenge for identification is that there are two latent reasons that drive an agent's decisions, namely $\nu_{i,D}$ and $\varepsilon_{ij,D}$. We must also identify how each of these map to acceptance decisions. For any n, we observe the probability $P\left(D_{ij_{i,1}} = D_{ij_{i,2}} = \ldots = D_{ij_{i,k}} = 0 | q_j^n, z\right)$

for all $k \leq n$. Because $v(\varepsilon_D; q_j, z)$ is equal to the fraction of agents that reject an offer of type q_j with probability at most ε_D when faced with scarcity z, we can write

$$P\left(D_{ij_{i,1}} = D_{ij_{i,2}} = \ldots = D_{ij_{i,k}} = 0 | q_j^n, z\right) = \int_0^1 \varepsilon_D^k \mathrm{d}v(\varepsilon_D; q_j, z).$$

Therefore, the quantity $P\left(D_{ij_{i,1}} = D_{ij_{i,2}} = \ldots = D_{ij_{i,k}} = 0 | q_j^n, z\right)$ is the k-th moment of a random variable with cumulative distribution function $v(\cdot; q_j, z)$. The problem of recovering this function is therefore equivalent to solving the Hausdorff moment problem (Casella and Berger, 2002). That is, we need to learn the CDF $v(\cdot; q_j, z)$ with information on its moments. This can be done if infinitely many moments are known.

In fact, our result is stronger – it shows that observing decisions of finite n is informative even without variation in the number of offers. Formally, it implies that $v(\cdot)$ can be well-approximated by observing decisions from a *given* sequence of offer-types q_j^n. We accomplish this by showing that the moments described above determine the n-th order Fourier-Legendre approximation of $v(\cdot)$. As shown in Talenti (1986), as n become large, this approximation converges to the true function $v(\cdot; q_j, z)$ uniformly over $\varepsilon_D \in (0, 1)$.

5.3 Identification of Selection on Unobservables

Next, we turn our attention to identifying the components that determine selection on unobservables. This result requires an additional regularity assumption:

Assumption 4. *(i) For each $z \in (0,1)$ and q_j, the derivative $v'(\cdot; q_j, z) = \frac{\partial}{\partial \varepsilon_D} v(\cdot; q_j, z)$ is a continuous, bounded and strictly positive function of $\varepsilon_D \in (0,1)$.*

(ii) For each z and q_j, the functions $E(Y_{i0}|\nu_D)$ and $E(Y_{ij}|\nu_D, \varepsilon_{ij,D} \geq \varepsilon_D, q_j)$ are continuous, and the first and second moments of Y_{i0} and Y_{ij} exist.

The first part strengthens the monotonicity and differentiability of $v(\varepsilon_D; q_j, z)$ imposed in Assumption 3(i) slightly by requiring a strictly positive and bounded derivative. Given our interpretation of $v(\cdot)$, observe that $v'(\cdot; q_j, z)$ is the density function of the distribution of the probability with which an agent rejects an offer of type q_j. Therefore,

the assumption requires that this density function bounded and is non-zero for all interior values of ε_D and z. The second part imposes weak regularity assumptions on conditional expectations and the moments of Y_{i0} and Y_{ij}.

With this assumption, we can identify the components resulting in selection:

Theorem 1. *Suppose that Assumption 4 and the hypotheses for Lemma 2 hold for all n. Then, the quantities $\mathbb{E}[Y_{i0}|\nu_{i,D} = \nu_D]$ and $\mathbb{E}[Y_{ij}|\nu_{i,D} = \nu_D, \varepsilon_{ij,D} \geq \varepsilon_D]$ are identified for all $\varepsilon_D \in (0,1)$ and $\nu_D \in (0,1)$ such that there exists z in the support of its distribution with $\nu_D = v(\varepsilon_D; q_j, z)$.*

This result shows non-parametric identification of the expected value of outcomes conditional on values of selectivity and idiosyncratic preferences. The proof begins by using results in Lemma 1 to identify the conditional expectations given scarcity z, offer-types and assignment. It then rewrites these quantities in terms of the primitives and uses arguments similar to those in Lemma 2 to recover quantities that depend on both the model of outcomes and the model of choices. Next, we use the identification results for $v(\cdot)$ in Lemma 2 to recover the objects of interest. For example, Lemma 1 implies that $E\left(Y_{i0} \times 1\{T_i = 0\}|q_j^k, z_i\right)$ is identified from variation in offers. This quantity can be re-written as

$$E\left(Y_{i0} \times 1\{T_i = 0\}|q_j^k, z_i\right) = \int_0^1 E(Y_{i0}|\nu_D = v(\varepsilon_D; z_i, q_j))\,\varepsilon_D^k \mathrm{d}v(\varepsilon_D; z_i, q_j).$$

If we observe this quantity for all $k \leq n$, then we can recover the n-th order Fourier-Legendre approximation of $E(Y_{i0}|\nu_D = v(\varepsilon_D; q_j, z))\,v'(\varepsilon_D; q_j, z)$ when viewed as a function of ε_D. Under the maintained assumptions, results in Talenti (1986) and Freud (1971) imply that the Cesàro mean of thisseries converges uniformly to the true function. Finally, since $v'(\varepsilon_D; q_j, z) > 0$ and bounded and the function $v(\varepsilon_D; q_j, z)$ is identified (Lemma 2), we can identify $E(Y_{i0}|\nu_D)$ for all $\nu_D \in (0,1)$ if we can find values of z and ε_D such that $v(\varepsilon_D; q_j, z) = \nu_D$. The intuition for identifying $E(Y_{ij}|\nu_D, \varepsilon_{ij,D} \geq \varepsilon_D)$ is similar in spirit, although a little more notationally involved.[16]

[16]Again, Lemma 1 implies that $E\left(Y_{ij} \times 1\left\{T_{ij_{i,k}} = 1\right\}|q_j^k, z_i\right)$ is identified. It can be re-written

In this way, the scarcity instrument is used to "trace-out" the expected values of Y_{i0} and Y_{ij} conditional on ν_D and ε_D (see Heckman and Vytlacil, 2005; Lewbel, 2007; Heckman and Navarro, 2007). Notice that our results do not rely on values of z that push choice probabilities to degenerate values that obviate the selection problem. Therefore, we do not rely on an "identification at infinity" argument. But, as is common, we can only identify the expected outcomes conditional on the latent variable ν_D for values of ν_D that are spanned by variation in the observable z. Moreover, it is easy to see if the image of $v(\varepsilon_D; \cdot, q_j)$ across values in the support of z is the unit interval, then we can identify the unconditional values of the latent outcomes, namely $E[Y_{i0}]$ and $E[Y_{ij}]$.

5.4 Dynamic Selection

The results in Lemma 2 and Theorem 1 above apply to objects q_j that arrive at the same time as the agent ($t_j = 0$). We now extend our results to the case when $t_j > 0$. Considering negative values of t_j is not necessary because patients cannot be assigned donors that arrived before them. The main challenge in considering the case when $t_j > 0$ is that the distribution of $\nu_{i,D}$ conditional on waiting until t_j is no longer unselected. In our empirical example, selectivity may be correlated with survival without a transplant. Therefore, we cannot normalize the marginal distribution to be uniform, except at $t_j = 0$.

We now extend the identification results to account for this type of dynamic selection. While the results in the previous subsection allows Y_{ij} and Y_{i0} to denote arbitrary outcomes of interest, the results in this subsection explicitly assumes that Y_{i0} denotes survival. Therefore, we will assume that agent i may be assigned object j only if $Y_{i0} > t_j$. This allows for selection in transplanted survival outcomes due to the use of waiting time in the mechanism.

Our main result requires a mild restriction on the conditional distribution of Y_{i0}:

as $\int_0^1 E(Y_{ij}|\nu_D = v(\varepsilon_D; z_i, q_j), \varepsilon_{ij,D} \geq \varepsilon_D)(1-\varepsilon_D)\varepsilon_D^{k-1}\mathrm{d}v(\varepsilon_D; z_i, q_j)$. As done above, we use this expression to identify $E(Y_{ij}|\nu_D = v(\varepsilon_D; z_i, q_j), \varepsilon_{ij,D} \geq \varepsilon_D)(1-\varepsilon_D)v'(\varepsilon_D; q_j, z)$ and finally recover $E(Y_{ij}|\nu_D, \varepsilon_{ij,D} \geq \varepsilon_D)$ by finding a value of z such that $\nu_D = v(\varepsilon_D; q_j, z)$. One qualitative difference is that identification of $E(Y_{i0}|\nu_D)$ allows us to use variation in either z or ε_D to trace-out ν_D, whereas the result for $E(Y_{ij}|\nu_D, \varepsilon_{ij,D} \geq \varepsilon_D)$ must condition on ε_D.

Assumption 5. *For any interval $I \subset \mathbb{R}_+$, $\mathbb{P}(Y_{i0} \in I | \nu_D)$ is a continuous function of ν_D.*

With this assumption, we show the identification in the presence of dynamic selection:

Theorem 2. *Suppose that Assumption 5 and the hypothesis of Theorem 1 hold, allowing for $t_j > 0$. Then, the probability $\mathbb{P}(D_{ij} = 1 | \nu_{i,D} = \nu_D, Y_{i0} \geq t_j)$ and $\mathbb{E}(Y_{ij} | \nu_{i,D} = \nu_D, \varepsilon_{ij,D} \geq \varepsilon_D, Y_{i0} \geq t_j$ are identified for all $\varepsilon_D \in (0,1)$ and $\nu_D \in (0,1)$ such that there exist z in the support of its distribution with $\nu_D = v(\varepsilon_D; q_j, z)$ and $\mathbb{P}(Y_{i0} \geq t_j | \nu_D, x_i) > 0$.*

The argument is developed in two steps. In the first step, we identify the conditional distribution of ν_D for agents that survive until time t. Lemma 6 in Appendix C.5 shows that this function is identified. The proof applies Theorem 1 to show identification of $\mathbb{P}(Y_{i0} \geq t | \nu_D) = \mathbb{E}[1\{Y_{i0} \geq t\} | \nu_D]$, which implies the identification of the conditional distribution of ν_D for agents that survive until time t.

The second step takes this conditional distribution and combines it with the arguments in Lemma 2 and Theorem 1. Specifically, we first identify the function $v(\varepsilon_D; q_j, z_i)$, which delimits the acceptance region in the (ε_D, ν_D)-space, by using the cdf of the probability that a patient which survives until $t_j > 0$ rejects a kidney of type q_j.[17] This result is analogous to Lemma 2 for the case when $t_j > 0$. Then, we use arguments similar to those in Theorem 1.

Taken together with Theorem 1, the result implies the identification of the quantities $\mathbb{E}(Y_{ij} | \nu_{i,D} = \nu_D, \varepsilon_{ij,D} \geq \varepsilon_D, Y_{i0} \geq t_j)$ and $\mathbb{E}(Y_{i0} | \nu_{i,D} = \nu_D, Y_{i0} \geq t_j)$ where the conditioning on x_i and q_j has been subsumed for simplicity. These quantities are sufficient for evaluating the expected survival with and without a transplant for any agent under a counterfactual in which the agent is assigned object j by fiat. Moreover, we since we have also identified $\mathbb{P}(D_{ij} = 1 | \nu_{i,D} = \nu_D, Y_{i0} \geq t_j)$, we can use Bayes' rule to identify the conditional distribution of v_D for agents that have or have not received an assignment under the current mechanism by conditioning on their decisions

[17] These two quantities were identical when $\nu_{i,D}$ was uniformly distributed on the unit interval as in the previous subsections. This was the relevant case when $t_j = 0$.

and observed survival time. Combined with $\mathbb{E}\left(Y_{ij}|\,\nu_{i,D}=\nu_D,\varepsilon_{ij,D}\geq\varepsilon_D,Y_{i0}\geq t_j\right)$ and $\mathbb{E}\left(Y_{i0}|\,\nu_{i,D}=\nu_D,Y_{i0}\geq t_j\right)$, we can obtain the expected survival with and without a transplant conditional on observed decisions and survival duration. This latter quantity allows us to measure the selection induced in the current mechanism.

5.5 Estimation

Non-parametric estimation is cumbersome because we would like to use a rich set of observables when estimating the model. We therefore estimate a parametrized version of equations (3.1) – (3.3).

$$y_{i0}=B\left(Y_{i0};\rho_0\right)=x_i\beta_x+\nu_{i.0} \tag{5.1}$$

$$y_{ij}=B\left(Y_{ij};\rho_1\right)=\chi\left(x_i,q_j\right)\alpha_{x,q}+\alpha_\eta\eta_j+\nu_{i,1}+\varepsilon_{ij,1} \tag{5.2}$$

$$D_{ij}=1\left\{\chi\left(x_i,q_j\right)\gamma_{x,q}+z_i\gamma_z+\eta_j+\nu_{i,D}+\varepsilon_{ij,D}>0\right\}, \tag{5.3}$$

where Y_{i0} is survival since registration without a transplant; Y_{ij} is survival since transplantation if patient i is transplanted organ j; $B\left(\cdot;\rho\right)$ denotes a Box-Cox transformation of the argument with parameter ρ (Box and Cox, 1964);[18] $\chi\left(x_i,q_j\right)$ is a flexible function of agent observables x_i and object types q_j; η_j is distributed $\mathcal{N}\left(0,\sigma_\eta^2\right)$ with the parameter σ_η^2 to be estimated; $\varepsilon_{ij}=\left(\varepsilon_{ij,D},\varepsilon_{ij,1}\right)'$ is distributed $\mathcal{N}\left(0,\Sigma_\varepsilon\right)$ where $\Sigma_{\varepsilon,11}$ is normalized to 1 without loss of generality; and ν_i is a mean-zero multi-variate normal with a distribution via the following factor structure:

$$\nu_{i,1}=\delta_{1,D}\nu_{i,D}+\nu_{i,f} \tag{5.4}$$

$$\nu_{i,0}=\delta_{0,D}\nu_{i,D}+\delta_{0,f}\nu_{i,f}+\tilde{\nu}_{i,0}, \tag{5.5}$$

where $\nu_{i,D}$, $\nu_{i,f}$ and $\tilde{\nu}_{i,0}$ are independently distributed mean-zero normal random variables with variances to be estimated. This factor stucture is without loss given the

[18]The Box-Cox transformation of y with parameter ρ is given by $B\left(Y;\rho\right)=\frac{Y^\rho-1}{\rho}$. A special case when $\rho=0$ is $B\left(Y,\rho\right)=\log Y$. Our initial guess of ρ is based on comparing an estimated survival curve using the non-parametric Kaplan-Meier estimator to those implied by assuming that $B\left(Y,\rho\right)$ is normally distributed.

normality of ν_i.

This empirical model maps the patient and kidney types into characteristic space, which allows us to keep the dimension of the parameter space manageable.[19] It also allows us to include η_j, which represents unobserved heterogeneity in organ quality. This term can be seen as capturing the cumulative effect of organ characteristics observed to patients and surgeons, but not included in the empirical specifications.[20]

This choice of functional form is motivated by several considerations. First, we wish to allow for and interpret the correlations between $\nu_{i,0}$, $\nu_{i,1}$ and $\nu_{i,D}$, and between $\varepsilon_{ij,1}$ and $\varepsilon_{ij,D}$. For example, the factor $\nu_{i,f}$ captures the component of a patient's unobserved frailty that is not correlated with decisions. If $\delta_{0,f}$ is small or negative, then, all else equal, transplanting a patients with lower frailty (higher $\nu_{i,f}$) results in higher survival benefits.

Second, the decision model is similar to the probit binary choice used in Agarwal et al. (2019) for the kidney waitlist. These two considerations point us to using multivariate normals to model the distributions of ν_i and ε_{ij}.

Third, we are interested in analyzing (censored) survival data, and appropriately fitting the shape of the survival curve is important for obtaining meaningful estimates. Box-Cox transformations yield a tractable likelihood function while generalizing the functional form (see Spitzer 1982, for example). We hold the Box-Cox transformations ρ_0 and ρ_1 fixed and conduct robustness analysis to alternative choices.

Estimating this model via maximum likelihood is difficult because the likelihood for each patient's data depends on the decisions over many donors as well as (potentially censored) survival outcomes. Computing it requires integrating a nonlinear function over a high dimensional space. Instead, we estimate the parameters of the model using a Gibbs' sampler (McCulloch and Rossi, 1994; Geweke et al., 2003; Gelman et al.,

[19] Our framework can also accomodate coarsely defined patient and donor types. In this case, x_i and q_j would be a vector indicating to which a patient or donor belongs. As is common, introducing a very large number of types would result in imprecise results.

[20] Agarwal et al. (2019) argue, using an analogy to measurment error models (see Kotlarski's Theorem in Rao, 1992; Hu and Schennach, 2008), that the distribution of this variable can be identified based on the correlation between acceptances between a given donor's first and second kidney. For consistency with the formal results presented in this paper, we will also estimate models that exclude this term.

2014). This method generates a sequence of draws of the parameters of the model, collected in θ, and the latent variables ν_i, ε_{ij} and η_j given the parameters from their respective posterior distributions. Our chosen parametrization is ammenable to this approach because the latent variables can be partitioned so that each group has a posterior distributions given the draws of the other groups that can be solved in closed-form.[21] The distribution this method generates is asymptotically equivalent to that of the maximum likelihood estimator (see van der Vaart, 2000, Theorem 10.1 (Bernstein-von-Mises)). Details on the method are provided in Appendix B.1.

An advantage of our approach is that it allows for a rich set of patient-level covariates x_i and organ types q_j, to be included in the model. This richness is important for understanding the extent to which observables can capture the selection on outcomes induced by choices. The cost of this approach is the somewhat heavier reliance on parametric assumptions and computational burden. For example, Hull (2018) studies a semi-parametric model and proposes a indirect inference method that targets a subset of quasi-experimental moments that can be identified directly in a first-step. The main drawback of this alternative for our purposes is that the number of moments that need to be estimated in the first step increase with the dimension of the parameter space, making it hard to include the covariates x_i and types q_j.

6 Survival and Choice Estimates

We present estimates from four different specifications. The first specification only relies on the randomness of offers, and does not employ the scarcity instruments. The second specification, which is our preferred one, includes both the number of future offers and the number of future donors as scarcity instruments. The third and fourth specifications employ one of the two scarcity instruments each in order to assess robustness. All specifications include a rich set of patient and donor covariates to capture medical history and match quality. They include all of the characteristics used in the leading

[21] These considerations also motivate Geweke et al. (2003) to also use a similar parametrization and estimation approach when studying hospital quality in a selection model.

models for predicting pre- and post-transplant survival for patients with kidney failure (see Wolfe et al., 2008, for example) as well as characteristics used to determine patient priority on the transplant list.

6.1 Choice

Table 5 presents the marginal effects of select characteristics on the probability of acceptance, equation (3.3). The table reports the effects for a one standard deviation increase in a continuous characteristic or a unit change in an indicator.

Our results suggest that proxies for donor quality and for match-specific benefits are positively correlated with acceptance. Patients are significantly more likely to accept kidney offers from younger donors and donors who died of head trauma, and less likely to accept offers from donors with a history of hypertension. Patients are also significantly more likely to accept kidneys with which they have a perfect tissue type match. Note that patients are also significantly more likely to accept offers of kidneys which have higher unobservable quality, η_j, suggesting that decisions respond to information that is not perfectly captured by the observable organ characteristics included in the model. This information can include results from a battery of medical tests and the report from a physical examination of the kidney.

The last two rows record the effects of the scarcity instruments on the probability of acceptance. Consistent with the results in Table 4, each of the two instruments has a significant negative effect on the probability of acceptance. Because these instruments are correlated, the marginal effect of scarcity as measured by future donors is positive but marginally significant when both instruments are included. Other parameter estimates are similar across the three instrumented specifications. The robustness of these co-efficients across the last three columns suggests that the choice between these two instruments is unlikely to be an important driver of our final results.

6.2 Survival

Panels A and B of Table 6 respectively present estimates for survival without and with a transplant, equations (3.1) and (3.2). They show the marginal half-life effects associated with select characteristics.[22]

Observable proxies for baseline patient health predicts survival both with and without a transplant. A patient who is older, diabetic, or on dialysis at registration has a significantly shorter half-life without a transplant. These patient characteristics also have lower survival with a transplant, with effects that are slightly larger in magnitude. For example, a diabetic patient's half-life without transplant is lower than a non-diabetic patient by 1.36 years, and a half-life with a transplant that is lower by 2.98 years.

We also find that the proxies for donor quality, waiting time and tissue-type similarity are predictive of post-transplant survival, but donor characteristics have lower estimated effects as compared to tissue-type matching and patient characteristics. For example, a donor with a history of hypertension results in a lower half-life by 0.34 years, which is much smaller than the patient effects described above. Receiving a kidney with a perfect tissue-type match has a large effect of half-life, which is consistent with the fact that they are less likely to result in an adverse immune reaction post-transplantation. These estimates are quite stable across our instrumented specifications.

A comparison of estimates in Tables 5 and 6 indicates that many of the measures of organ quality have positive effects on both choice and survival. Tissue type match and donor death by head trauma are both strongly associated with both choice and survival. That said, the association is not perfect: organs from younger donors are more likely to be accepted even though the survival effects are not significant. Likewise, the kidney unobservable characteristic, η_j, has a significant effect on choice, but a small, insignificant effect on survival.

[22] We avoid marginal expected life-years in order to limit extrapolation into extremely long survival durations. Our current dataset allows us to observe a patient for at most sixteen years. This approach is consistent with the medical literature (e.g. Wolfe et al., 2008).

6.3 Selection on Unobservables

An advantage of our framework is that it can be used to measure the correlation between survival and choice induced by unobservable characteristics. The correlation on observable characteristics discussed above suggests that this channel may also be important.

Table 7 presents these effects for the three specifications that use the scarcity instruments. The top panel shows the effects of an increase in selectivity on acceptance and on survival. We measure these effects by increasing $\nu_{i,D}$ in equation (3.3) by one standard deviation. The effects on survival are measured by computing the changes on unobserved frailties $\nu_{i,0}$ and $\nu_{i,1}$ induced by their estimated correlation with $\nu_{i,D}$. The bottom panel shows the correlation between unobserved match-specific determinants of choice and survival. We present these effects by reporting the impact of a one standard deviation increase in $\varepsilon_{ij,D}$ on choices and post-transplant half-lifes.

We find that selective patients typically survive longer without a transplant and benefit less from the typical transplant. A one standard deviation increase in $\nu_{i,D}$ selectivity decreases the probability of acceptance by 3.9 percentage points. This magnitude is of a similar order as the effect of a kidney from a donor that had a history of hypertension. The net effect on survival due to a typical transplant is therefore negative. This patient would need a sufficiently high quality or well-matched donor in order to benefit from a transplant. Therefore, there is positive selection into treatment on the patient-specific component of survival benefits. A comparison of the specifications shows that our conclusion is not sensitive to the choice of instrument.

In contrast to selectivity, patient-donor specific factors do not induce significant selection via choices. While we estimate the covariance between $\varepsilon_{ij,D}$ and $\varepsilon_{ij,1}$ to be positive, the effect is not statistically significant. This suggests that there is limited positive selection into specific treatments based on unobservable match-level benefits.

7 LYFT in the Current Mechansism

7.1 Calculating Life Years from Transplant

Our model allows us to measure survival benefits for every potential transplant. For each patient-donor pair, we compute the difference between the median survival time with a transplant and median survival time without a transplant, measured from the date of transplant. This measure is widely used in the literature on organ transplantation (Wolfe et al., 2008), and is arguably the focal outcome for patients with kidney failure.

Specifically, for each pair (i, j), we define LYFT conditional on a set of covariates $I_{ij} = \{x_i, q_j, D_{ij}, \eta_j, \nu_{i,D}, \nu_{i,f}\}$ in our model as follows:

$$LYFT\left(I_{ij}\right) = M(Y_{ij}|I_{ij}) - M(Y_{i0} - t_{ij}(x_i, q_j)|I_{ij}, Y_{i0} > t_{ij}), \tag{7.1}$$

where $M(Y|X)$ is the median of random variable Y conditional on X and $t_{ij}(x_i, q_j)$ is the time between patient i's registration and the arrival of kidney j. We then compute the expectation of $LYFT\left(I_{ij}\right)$ by drawing η_j, $\nu_{i,D}$ and $\nu_{i,f}$ from their conditional distributions given observables, decisions and observed survival outcomes using a Gibbs' sampler.[23] Therefore, this measure accounts for selection on unobservables induced by the mechanism.

In order to assess the role of selection on choices and on unobservables, we also be interested the expectation of $LYFT\left(I_{ij}\right)$ given only the observables x_i and q_j. In this case, we integrate $LYFT\left(I_{ij}\right)$ over the unconditional distributions of $\eta_j, \nu_{i,D}$, $\nu_{i,f}$ and D_{ij}.

[23]The sampler provides us with simulated draws of $LYFT\left(I_{ij}\right)$ from its distribution. To do this, we generate a chain that fixes the parameters at the estimate $\hat{\theta}$. We generate 200,000 draws, burn-in the first half and take one every 1,000 draws.

7.2 Life Years from Transplant in the Mechanism

Table 8 presents the average estimated LYFT over all realized transplants. The first row presents the average LYFT accounting for patient- and kidney-specific unobservables and the decision to accept. The second row presents the results conditioning only on the observables. The columns correspond to the specifications in Tables 5 and 6. The average LYFT from our preferred specification is 8.64 years (column 2). Ignoring selection on unobservables yields an an average LYFT of 7.94 years. This difference suggests that there is positive selection on LYFT of patients into transplantation based on unobservables. Column (1) reports analogous estimates from a specification that does not use quasi-experimental variation from our scarcity instruments. The estimated LYFT is biased and about one year smaller than our preferred estimate. This suggests that observational methods such as those in Wolfe et al. (1999) may underestimate gains from transplantation.

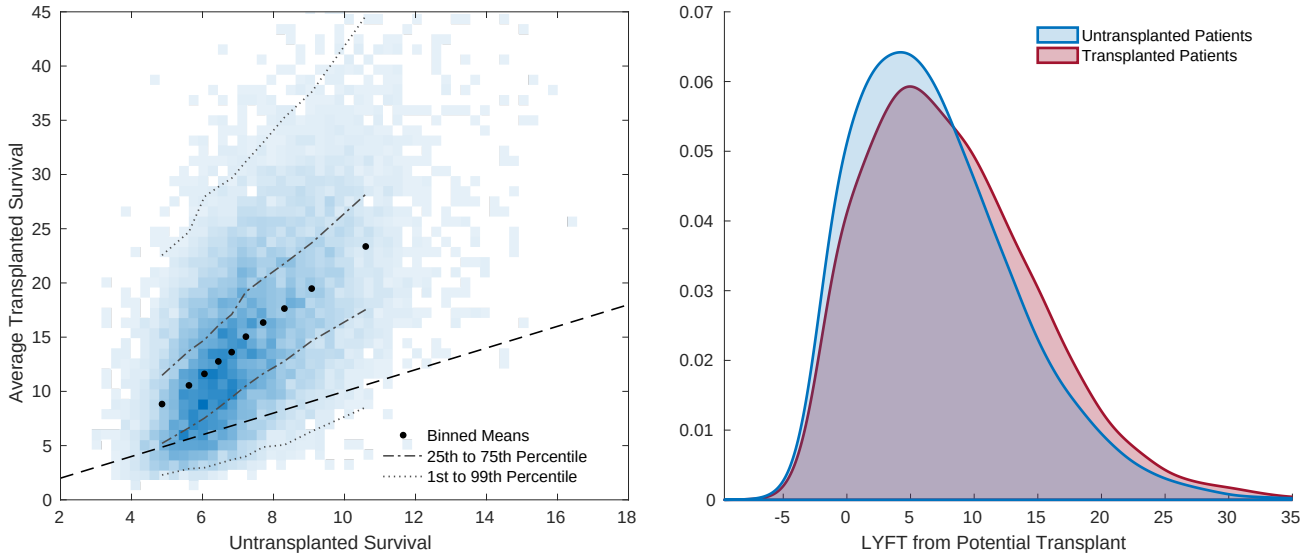
The second pair of rows of Table 8 report average survival without a transplant, separately for the all patients and the subset of patients who received a transplant. Across specifications, the untransplanted survival for patients that are transplanted is higher than the patients thar are not. This postive selection on untransplanted survival aggregates both selection due to choice and due to the mechanism.

7.3 Selection and LYFT

The positive selection on LYFT and on untransplanted survival reported in Table 8 above can take place along two margins: the patients that are transplanted and the kidneys to which they are matched. This subsection further investigates these sources.

7.3.1 Patient Selection

To understand the importance of patient selection, we present the relationship between (median) untransplanted survival and the average (median) transplanted survival from all potential donors for each patient. Figure 3(a) presents the joint density between



(a) Transplanted and Untransplanted Survival

(b) LYFT by Transplant Status

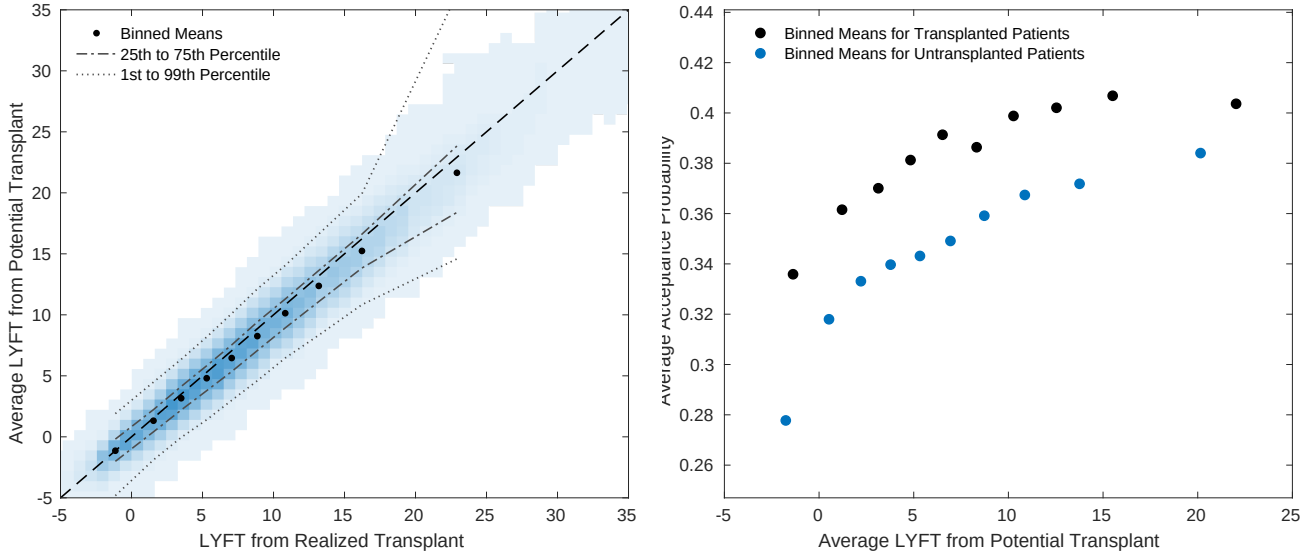
Figure 3: Patient Selection

these two quantities overlayed with a binscatter plot. Transplant and untransplanted survival are strongly correlated with a slope of the conditional mean that is larger than one. Therefore, patients that are expected to live long without a transplant also have the highest life-year gains from a transplant. This result implies strong complementarities between baseline health and transplantation.

When combined with the observation in Table 8 that transplanted patients have a higher baseline survival, this complementarily suggests that patients that are transplanted are likely to have higher LYFT due to selection on baseline health. However, there are additional components of patient selection, from choice and from the priorities in the mechanism.

The overall selection on LYFT by observed transplant status is presented in Figure 3(b). This figure plots the distribution of predicted LYFT across all of these potential transplants. This distribution is shifted to the right for transplanted patients. The mean LYFT for this group is 1.2 years higher than the untransplanted group.

Taken together, we find that the mechanism selects patients with higher average LYFT



(a) Transplanted Survival from Potential and Realized Donors

(b) LYFT and Choice

Figure 4: Patient-Kidney Matching

and that some of this selection comes from transplanting patients that are relatively healthy at baseline. One way in which the mechanism achieves this is by making patients wait.

7.3.2 Patient-Kidney Matching

The realized allocation also matches patients to kidneys from which they have greater survival benefits as compared to the average kidney. Figure 4(a) plots the joint distribution of LYFT from the realized donor for a transplanted patient against the LYFT from all potential donors. The binscatter is below the 45-degree line, indicating that the realized transplants generate greater than the average LYFT for a patient. This finding that *matches* are selected advantageously complements the finding described by Figure 3 which showed that the mechanism selects *patients* with higher than average gains from transplantation.

The estimates of the choice and survival equations reported in Section 6 suggest that

part of this advantageous matching comes from the correlation of patients' acceptance decisions with LYFT. Figure 4(b) summarizes this relationship in binscatter plots of kidney-patient acceptance probability against LYFT for all potential transplants. It shows two features. First, transplanted patients have a higher predicted probability of acceptance than untransplanted patients. This pattern is expected given that acceptance is necessary for a transplant to occur.

Second, the predicted probability of accepting an offer is increasing in LYFT. As our estimates suggest, patients are more likely to accept kidneys with greater life-year benefits (based on both observable and unobservable characteristics). A regression of acceptance probability on average LYFT, controlling for patient and donor fixed effects, underlines this point.[24] A one standard deviation increase in the match-specific component of LYFT increases the probability of acceptance by 0.59 percentage point.

Taken together, we find that the allocation matches kidneys to patients based on LYFT, and that at least some of this selection is induced by choices in the mechanism.

7.3.3 Patient Selection vs Rematching

Figure 4(b) also provides insight into which of these two margins of assignment dominates. The heterogeneity in survival across patients swamps the heterogeneity across donors within a patient. In fact, a decomposition of the total variance in LYFT into a patient-specific, donor-specific and a match-specific component (the remainder) shows that the patient-specific component constributes to 6.58 years of the standard deviation in LYFT. The donor-specific and the match-specific components account for 1.04 years and 0.48 years respectively.[25]

These results suggest that the potential for increasing life-years by improving the match between patients and donors without changing which patients are transplanted (rematching) is limited. Therefore, distributional constraints may limit the potential

[24] Specifically, we regressed the expected value of $LYFT_{ij}$ conditional on $\{x_i, q_j, \eta_j, \nu_{i,D}, \nu_{i,f}\}$ on the probablility of acceptance given these same covariates, controlling for patient- and donor-specific fixed effects.

[25] The standard deviation in LYFT is 6.68 years, which is the pythagorean sum of the three components.

gains from improved matching. In particular, maximizing life-year gains may mean reallocating transplants away from the most urgent cases towards patients with longer expected survival without a transplant, suggesting a potential trade-off between equity and efficiency.

8 Potential for Further Increasing LYFT

We now turn to evaluating the performance of the mechanism on LYFT and quantifying the importance of patient selection versus rematching. We do this by comparing the average LYFT achieved by the realized assignment to alternatives, ranging from a random assignment to one that maximizes LYFT. Throughout this exercise, we restrict the sample to the set of patients that registered in 2000 to ease computation.

As we argued in Section 2, extending patients' lives is a prima facie objective of the medical profession. However, it may differ from the objective of a planner if the planner's objective depends on other factors or if the weights the planner places on life year gains depend on how urgently sick a patient is. A byproduct of our exercise will be a comparison of the types of patients that are transplanted under the alternative assignments. These results provide insight into the trade off between maximizing LYFT and distributional or ethical motivations for evaluating an assignment.

8.1 Comparison with Benchmark Assignments

We start with two extremal benchmarks – random assignment, and optimal assignment:

- The **random assignment** is simulated by sorting patients in a random order, and successively assigning patients to kidneys at random from the set of feasible kidneys. For a kidney to be feasible for a patient, it must be biologically compatible and should arrive between the patient's registration date and a simulated death date without a transplant. The latter is drawn from that patient's predicted survival distribution.

- The **optimal assignment** is computed by maximizing the total LYFT from all transplants. This benchmark considers an omniscient planner who knows x_i, q_j, $\nu_{i,D}$, $\nu_{i,f}$, η_j, each patient's arrival and death dates, and each kidney's arrival date. The planner computes LYFT conditional on these characteristics and can dictate assignments. Only feasible transplants are allowed and each patient can receive at most one transplant.[26]

Comparison to the random assignment allows us to measure the increase in LYFT achieved by the mechanism. Both selection of patients and advantageous matching of kidneys to patients drive the difference. To decompose these sources, we evaluate an alternative that allocated kidneys randomy among patients that were actually transplanted:

- The **random amongst transplanted** assignment is simulated by sorting *transplanted* patients in a random order, and successively assigning only these patients to a kidney at random from the set of feasible kidneys.

The increase in LYFT due to the mechanism is a result of both the mechanism's priority rules for kidney offers, and the choices made by patients on the waiting list. To separate the gain in LYFT over the random allocation achieved by the mechanism's targeting of patients from the gain in LYFT that comes from choice, we evaluate a counterfactual assignment with no patient choice.

- The **no choice assignment** is computed by assigning each kidney to the patient with the highest priority among untransplanted patients. Offers cannot be rejected by patients. Kidneys are assigned in a random order, and priority is computed as in the existing mechanism.

[26]Specifically, we simulate the unobservables $\nu_{i,D}$, $\nu_{i,f}$, η_j from the distribution of these random variables conditional on the estimated parameters and the decisions observed in the data.We also draw a death date from the estimated untransplanted survival distribution. Call a simulated draw for each patient/donor pair $LYFT^s_{ij}$. Let $a_{ij} = 1$ if i is assigned j and $a_{ij} = 0$ otherwise. Let $c_{ij} = 1$ if i is feasible for j and $c_{ij} = 0$ otherwise. We solve the problem $\max_a \sum_{i,j} a_{ij} LYFT_{ij}$ subject to $a_{ij}(1 - c_{ij}) = 0$, $\sum_i a_{ij} \leq k_j$, where k_j is the number of kidneys available from donor j, and $\sum_j a_{ij} \leq 1$.

Comparison of the realized assignment to the optimal assignment is a measure of the maximum theoretical gain in LYFT that could be achieved over the existing mechanism. As with the comparison of the realized and random assignments, this gain is driven both by selection of patients and matchinof patients to kidneys. To decompose these sources, we evaluate an alternative that only reassigns kidneys among transplanted patients:

- The **optimal rematching** assignment is computed by maximizing the total LYFT from all transplants under the same information set as in the optimal assignment. In addition to the feasibility constraint, a patient in this assignment can be transplanted only if she was transplanted in the data.[27]

The theoretical bounds based on optimal assignments use information on factors that induce selection, $\nu_{i,D}$, $\nu_{i,f}$ and η_j. However, the factors $\nu_{i,D}$ and $\nu_{i,f}$ may not be observed by the planner and may be hard to ellicit in a mechanism. Similarly, η_j may be hard to condition on. These observations motivate a benchmark that uses only the information in the current set of observables:

- The **optimal assignment based on observables** is computed by maximizing the total expected LYFT conditional on x_i and q_j by assigning patients to a feasible kidney. For tractibility, we assume that the planner has foresight on when patients arive and depart, and when kidneys arrive.[28][29]The solution describes the highest possible LYFT that can be achieved by a planner who can dictate assignments based on this information.

Figure 5 presents the results. The average LYFT for the realized assignment amongst patients who registered in 2000 is 8.78 years. This is analogous to the results in Table 8 above.

[27]As in calculations of average $LYFT\,(I_{ij})$, we simulate the unobservables from their conditional distributions given the data of these random variables to generate draws $LYFT^s_{ij}$. We then solve the problem in footnote 26 above with the additional constraint $a_{ij} = 0$ if i was not transplanted in the data.

[28]Relaxing foresight would require solving a dynamic assignment problem with uncertainty about the future.

[29]We modify the problem in footnote 26 by replacing $LYFT^s_{ij}$ with its expectation given x_i and q_j. The factors $\nu_{i,D}$, $\nu_{i,f}$ and η_j are drawn from their unconditional distributions.

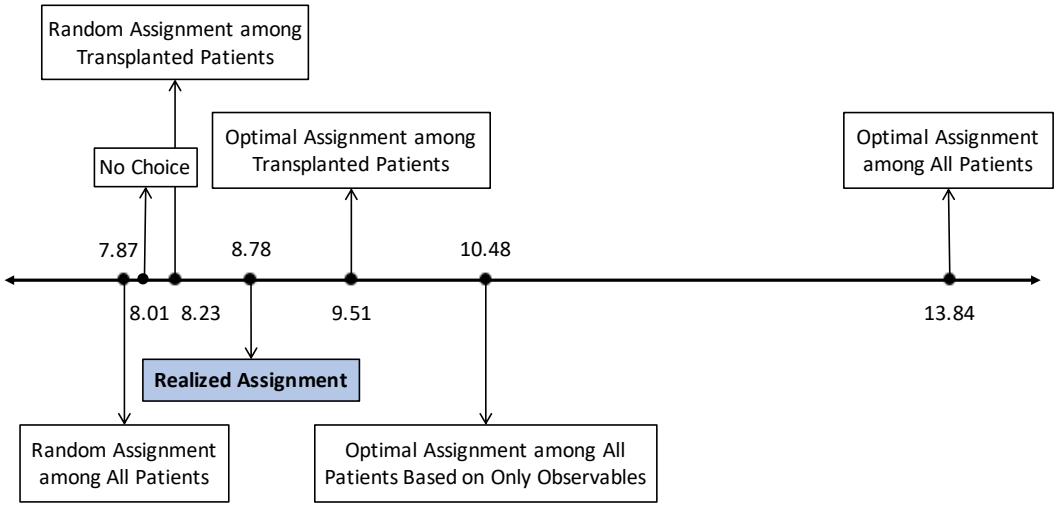


Figure 5: LYFT Under Counterfactual Allocations

The realized assignment achieves about a 0.92 year or 11.6% improvement in average LYFT over random assignment. Both selection of patients and the matching of patients to kidneys are important. If the transplanted patients were assigned a random kidney, then the increase would only be 4.4 months. This quantity represents the increase relative to random assignments that is accounted for by patient selection. The remainder is due to patient-kidney matching.

To achieve these gains over random assignment, the mechanism leverages patient choice. The no choice assignment achieves a 0.14 year increase in LYFT over the random assignment. Thus, assignment to patients based on the existing priority rules without allowing patients to decline kidneys would achieve only 15.8% of the increase in LYFT achieved by the realized assignment. Given the priority rules of the mechanism, it is clear that allowing for patient choice is necessary to attain most of the gains in LYFT.

Although the mechanism does better than a random assignment, there is significant scope for further increasing LYFT. Under the optimal assignment, average LYFT is 13.84 years, about 5.1 years higher than the LYFT achieved in the realized assignment. A significant fraction, 14.4%, of these potential gains require only rematching patients and kidneys while keeping the set of transplanted patients fixed. However, consistent with Figure 4(a), most of the potential gains from the optimal allocation come from

changing the set of patients that are transplanted.

Finally, we find that a planner that can dictate assignments using the observable characteristics could achieve a significant fraction, but not all of the potential increase. The observables in our model have either been used to determine priority, or have been considered explicitly in proposed reforms.[30] The average LYFT under the optimal assignment based on observables is 10.48 years. Although this is 3.4 years less than the theoretical maximum, it is about 1.7 year higher than the average LYFT achieved by the mechanism. Therefore, in principle, average LYFT could be substantially increased by targeting transplants using observed characteristics rather than choices.

8.2 The Planner's Dilemma

An important conclusion from Figure 5 is that LYFT could be increased by up to 57.6%. But, this requires changing the set of patients that are transplanted. We now show that this change creates shifts in the demographics and health conditions of transplanted patients, creating a potential barrier due to distributional considerations and the need to weigh patient urgency.

Table 9 presents the distribution of patient age, share diabetic, and share on dialysis at registration for patients transplanted under the random assignment, the no choice assignment, the actual assignment and the optimal assignment. Patients who are transplanted under the realized assignment are younger, less likely to be diabetic, and less likely to be on dialysis than patients selected at random. Similarly, transplanted patients are younger and healthier under the optimal assignment than under the realized assignment.

The comparison between the realized assignment and the no choice assignment illustrates the role of choice in increasing LYFT. Allowing for choice improves the patient-kidney match, improving average LYFT for each of the patient categories listed. Choice also changes the selection of who is transplanted, shifting the age distribution towards

[30]This claim is based on an examination of the minutes of the OPTN Kidney Transplantation Committee. A determination of whether other health conditions can be used to the assignment system is beyond the scope of this paper.

younger patients. The existing priority rules target patients with no HLA mismatches. Under the no choice assignment, 15.5% of assignments are to zero mismatch patients. Only 12.5% of assignments are to such patients under the realized assignment and 8.1% under the optimal assignment. While patients benefit from kidneys with a perfect tissue type match, all else equal, these results indicate that the selection on other patient and match characteristics induced by choice in the mechanism increases LYFT by reassigning kidneys to patients without perfect tissue type matches.

The final row shows the average predicted survival without a transplant among the patients who are transplanted. The average untransplanted survival for patients transplanted in the optimal assignment is 0.5 years longer than under the random assignment and 0.5 years longer than under the realized assignment.

These shifts highlight the distributional effects of optimizing LYFT. The realized outcome increases LYFT over random assignment in part by selecting younger, healthier patients to transplant. The optimal assignment exacerbates these distributional changes. These results are driven by the strong correlation between survival with and without a transplant illustrated in Figure 3(b). Therefore, in order to maximize LYFT given the scarcity of kidneys available, the planner must transplant healthier patients and let sicker patients go untransplanted.

This stark trade-off represents a moral dilemma for several reasons. First, society may have a moral imperative to transplant sick patients who may soon die, even if doing so implies reducing total life years gained from transplantation. Second, concerns about discriminating based on patient characteristics stand in the way. In particular, our results suggest that an optimal assignment should target transplants at younger patients. Proposed priorities based on age have came into conflict with concerns about age discrimination when previous reforms were being considered.

9 Conclusion

An hitherto overlooked goal in the design of assignment mechanisms is to produce matches that improve associated outcomes such as patient survival or student achievement. We take a first step towards an empirical analysis that incorporates these outcomes by studying the LYFT generated using the pool of deceased donor organs. To do this, we show how to use variation generated in an assignment mechanism to estimate and identify a model that jointly considers choices and outcomes.

We find that the waitlist mechanism used to allocate deceased donor kidneys does better than a random allocation, but leaves much scope for improvement. As compared to the average patient, the mechanism transplants patients for whom life would be extended longer and matches them to more suitable than average kidneys. However, there is scope for increasing the average LYFT by a total of 5.1 years per kidney. The potential economic value of realizing these gains is enormous. Approximately 14.4% of these benefits could be realized if dictating assignments based on observed patient and donor characteristics were possible. Aldy and Viscusi (2007) place the value of a statistical life year at $300,000. At even half this value and ignoring costs savings on dialysis, the potential benefits from an increase of 1 year of life from the approximately 13,000 deceased donor kidneys transplanted each year accrues to almost $2 billion per year.

Realizing most of these gains will require confronting important distributional considerations. Specifically, we find that survival with and without a transplant is strongly correlated, and that most of the heterogeneity in the benefits from a transplant is across patients rather than match-specific. Therefore, the planner faces a dilemma between transplanting the sick and transplanting those for whom life will be extended the longest.

We open several important avenues for further research. First, our current approach evaluates benchmark assignments, rather than the equilibria of alternative mechanisms that allow agents to express choice. It would be useful to combine recent approaches for analyzing equilibria of alternative mechanisms with a model of outcomes. Such a

model would allow us to consider the selection induced via choices in a counterfactual environment. Second, we focus on an aggregate measure of LYFT that abstracts away from distributional considerations. Formalizing these constraints and incorporating them into the design problem is valuable. Solving these two challenges would allow a design approach that better speaks to the considerations central to policymaking. The trade-off between equity and efficiency, which is central to the exercise of designing mechanisms particularly when outcomes are the target, deserves further research in other contexts as well.

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Table 4: Scarcity Instruments: First Stage

	Acceptance						Hazard Rate			
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
Log(1 + No. Donors)	-0.0632***		-0.0480***		-0.0361***		-0.0107		-0.0328	
	(0.00373)		(0.00338)		(0.00323)		(0.0207)		(0.0208)	
Log(1 + No. Offers)		-0.0640***		-0.0528***		-0.0409***		-0.0156		-0.0371**
		(0.00203)		(0.00183)		(0.00182)		(0.0113)		(0.0115)
Offer Year FE	x	x	x	x	x	x				
Registration Year FE							x	x	x	x
DSA FE and blood type FE	x	x	x	x	x	x	x	x	x	x
Years Waited at Offer FE	x	x	x	x	x	x	x	x	x	x
Patient Characteristics			x	x	x	x	x	x	x	x
Donor Characteristics					x	x			x	x
Match Characteristics					x	x			x	x
F-statistic	287.8	991.0	201.2	829.8	125.0	506.3				
Number of Observations	912761	912761	912761	912761	900669	900669	64703	64703	63959	63959
R-Squared	0.101	0.109	0.169	0.174	0.265	0.268				

Notes: * p<0.05, ** p<0.01, *** p<0.001. For Columns (1) through (6), we use the first 100 offers from each donor between 2000 and 2009, and the dependent variable is accpetance of an offer. For Columns (7) through (10), we use patients who received a transplant through deceased donor offers between 2000 and 2009. All regressions control for DSA fixed effect, blood type fixed effect, and a fixed effect for the number of years waited at the offer. Patient characteristics include Calculated Panel Reactive Antibody (CPRA) via indicators for CPRA=0, 0.8>CPRA>=0.2, CPRA>=0.8, and CPRA missing, an indicator for female, indicators for age <=18, 18-35, 35-50, and 50-65, indicators and linear controls for dialysis time 1-3, 3-5, 5-10, >10 years, and an indicator for diabetes. Donor characterstics include linear age, indicators and linear controls for donor creatinine > 0.6 and >1.8, and indicators for diabetes, donation after cardiac death, and expanded criteria donor. Match characteristics include the number of Human Leukocyte Antigen (HLA) mismatches via indicators for 0 HLA mismatch, 0 and 1 DR antigen mismatch, identical blood type, local offers, and linear controls for (+) and (-) age difference, interactions between CPRA indicators and # HLA mismatches, donor age over 40 and pediatric patient, donor age over 55 and patient age 18-35, donor age over 60 and patient age 35-50, and donor age below 60 and patient age 50-65. Columns (1) through (6) report standard errors clustered by DSA, offer year, number of years waited at offer, and blood types in parentheses.

Table 5: Choice Estimates

	(1)	(2)	(3)	(4)
Patient Characteristics				
Diabetic	-0.003	-0.005	-0.005	-0.006
	(0.000)	(0.001)	(0.001)	(0.001)
CPRA	-0.008	-0.008	-0.008	-0.013
	(0.000)	(0.000)	(0.000)	(0.001)
On Dialysis at Registration	0.001	0.003	0.003	0.003
	(0.001)	(0.001)	(0.001)	(0.001)
Age at Registration	0.002	0.004	0.004	0.003
	(0.000)	(0.001)	(0.001)	(0.001)
Donor Characteristics				
Age < 18	0.140	0.153	0.154	0.152
	(0.008)	(0.008)	(0.008)	(0.009)
Age 18-35	0.079	0.098	0.098	0.134
	(0.008)	(0.008)	(0.008)	(0.010)
Age 50+	-0.060	-0.071	-0.069	-0.072
	(0.002)	(0.003)	(0.003)	(0.003)
Cause of Death - Head Trauma	0.057	0.065	0.064	0.068
	(0.006)	(0.007)	(0.007)	(0.007)
History of Hypertension	-0.025	-0.029	-0.028	-0.029
	(0.001)	(0.001)	(0.001)	(0.002)
Unobservable (η_j)		0.224	0.219	0.219
		(0.002)	(0.002)	(0.002)
Offer Characteristics				
Perfect Tissue Type Match	0.146	0.143	0.145	0.114
	(0.008)	(0.009)	(0.009)	(0.008)
Log Waiting Time (Years)	0.010	0.026	0.016	0.024
	(0.000)	(0.001)	(0.001)	(0.001)
Scarcity				
Log(1+#Future Donors)		-0.010		
		(0.001)		
Log(1+#Future Offers)			-0.020	
			(0.001)	
Log(1+#Past Donors)				-0.009
				(0.001)
Instruments	No Instruments	# Past Donors	# Past Offers	# Future Donors

Notes: Selected estimates of the marginal effect on the probability of acceptance of a one standard deviation increase in each continuous covariate and a unit increase in each binary covariate Marginal effects are computed at the median value of observable covariates, integrating over the distribution of all unobservables. We generate 850000 draws and burn-in the first 50000 draws. We thin the chain by taking every 10 draws. All columns control for DSA fixed effects, blood type fixed effects, and registration year fixed effects. Other patient characteristics include dialysis time at registration, BMI at departure, patient serum albumin, indicators for female, diabetic, CPRA=0 and prior transplant. Donor characteristics include indicators for other causes of death, expanded criteria donor, donation after cardiac death and male, and bins of creatinine levels. Other offer characteristics include indicators for 2 A, 2 B, 2 DR mismatches, not the same blood type but compatible, regional offer, and local offer, indicator and interactions between several patient and donor characteristics. See Appendix Table D.11 through D.13 for detailed estimates.

Table 6: Survival Estimates

	(1)	(2)	(3)	(4)
	Panel A: Survival without Transplant			
Patient Characteristics				
Diabetic	-1.380	-1.361	-1.361	-1.378
	(0.030)	(0.030)	(0.030)	(0.030)
CPRA	0.089	0.089	0.089	0.082
	(0.031)	(0.031)	(0.031)	(0.030)
On Dialysis at Registration	-1.019	-1.013	-1.013	-0.902
	(0.042)	(0.041)	(0.041)	(0.039)
Age at Registration	-1.070	-1.060	-1.060	-1.052
	(0.025)	(0.025)	(0.025)	(0.024)
	Panel B: Survival with Transplant			
Patient Characteristics				
Diabetic	-2.959	-2.980	-2.977	-3.212
	(0.099)	(0.113)	(0.111)	(0.110)
CPRA	-0.027	-0.026	-0.031	-0.064
	(0.098)	(0.098)	(0.097)	(0.096)
On Dialysis at Registration	-2.384	-2.395	-2.389	-2.075
	(0.118)	(0.125)	(0.123)	(0.115)
Age at Registration	-3.183	-3.192	-3.181	-3.416
	(0.118)	(0.126)	(0.124)	(0.121)
Donor Characteristics				
Age < 18	1.595	1.604	1.647	0.784
	(0.906)	(0.916)	(0.916)	(0.830)
Age 18-35	-0.267	-0.282	-0.249	-0.547
	(0.973)	(0.981)	(0.980)	(0.930)
Age 50+	3.383	3.381	3.296	0.635
	(2.243)	(2.252)	(2.241)	(1.864)
Cause of Death - Head Trauma	0.662	0.665	0.691	0.673
	(0.313)	(0.316)	(0.314)	(0.317)
History of Hypertension	-0.340	-0.342	-0.357	-0.410
	(0.122)	(0.124)	(0.123)	(0.125)
Unobservable (η_j)		0.107	0.181	0.194
		(0.183)	(0.177)	(0.176)
Offer Characteristics				
Perfect Tissue Type Match	2.272	2.269	2.322	1.946
	(0.944)	(0.959)	(0.954)	(0.896)
Log Waiting Time (Years)	-0.487	-0.543	-0.539	-0.646
	(0.062)	(0.168)	(0.161)	(0.155)
Instruments	No Instruments	# Past Donors	# Past Offers	# Future Donors

Notes: Select estimates of the marginal effect on half-life of a one standard deviation increase in each continuous covariate and a unit increase in each binary variable. Marginal effects are computed at the median value of observable covariates, integrating over the distribution of all unobservables. The specifications have the same patient, donor and offer covariates as in Table 5 other than the scarcity instruments. Standard errors are in parentheses. See Appendix Table D.7 through D.10 for detailed estimates.

Table 7: Correlation Table

	(1)	(2)	(3)
Selectivity ($v_{i,D}$)			
Probability of Acceptance	-0.039	-0.039	-0.044
	(0.001)	(0.001)	(0.001)
Post-Transplant Survival	0.008	-0.025	-0.121
	(0.138)	(0.134)	(0.136)
Survival without a Transplant	0.330	0.323	0.229
	(0.060)	(0.059)	(0.059)
Match value ($\varepsilon_{ij,D}$)			
Probability of Acceptance	0.068	0.066	0.068
	(0.001)	(0.001)	(0.001)
Post-Transplant Survival	0.022	0.122	0.091
	(0.258)	(0.251)	(0.253)
Instruments	# Past Donors	# Past Offers	# Future Donors

Notes: Estimates of the effects of one standard deviation increases in choice unobservables on probability of acceptance and survival. Survival durations are calculated using half-lifes. Survival effects from changes in $\varepsilon_{ij,D}$ are computed using the expected change in $\varepsilon_{ij,1}$ from a one standard deviation increase in $\varepsilon_{ij,D}$ from zero, given the estimated covariance between $\varepsilon_{ij,D}$ and $\varepsilon_{ij,1}$. Likewise, survival effects from changes in $\nu_{i,D}$ are computed using the expected changes in $\nu_{i,1}$ and $\nu_{i,0}$ from a one standard deviation increase in $\nu_{i,D}$ from zero, given the estimated covariances between $\nu_{i,D}$, $\nu_{i,1}$, and $\nu_{i,0}$. All effects are computed at the median value of observable covariates. Columns (1) through (3) use specifications corresponding to columns (2) through (4) in Tables 6 and 5.

Table 8: Life-Years from Transplantation

	(1)	(2)	(3)	(4)
Life Years from Transplant				
Accounting for Unobservables	7.98	8.64	8.63	8.63
Observables Only	7.95	7.94	7.83	7.71
Untransplanted Survival				
All Patients	6.89	6.95	6.95	6.86
Transplanted Patients	7.24	7.21	7.21	7.17
Post-Transplant Survival	15.22	15.84	15.84	15.80
Instruments	No Instruments	# Past Donors	# Past Offers	# Future Donors

Notes: Life years from transplant and survival durations presented in the table are calculated using half-lifes. Future donors (offers) is defined as the number of donors (offers) in the next 4 quarters (see Table 4 for detailed definition). All columns control for patient, donor and offer characteristics, which are defined analogously as in Table 6 Panel B and Table 5.

Table 9: Characteristics of Transplanted Patients

		Random Assignment		No Choice		Realized Assignment		Optimal Assignment	
	All Patients	Transplanted Patients	LYFT	Transplanted Patients	LYFT	Transplanted Patients	LYFT	Transplanted Patients	LYFT
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
Age < 18	3.1%	3.2%	13.29	5.9%	13.70	5.4%	14.89	5.4%	15.87
Age 18 - 35	11.6%	12.3%	10.63	11.9%	11.61	13.0%	12.45	16.8%	12.02
Age 36 - 59	54.8%	55.8%	7.50	53.0%	8.17	54.7%	8.86	57.5%	9.09
Age >= 60	30.5%	28.8%	4.64	29.2%	5.11	26.9%	5.61	20.3%	5.51
Diabetic	41.4%	40.2%	5.34	37.7%	5.80	33.3%	6.51	31.6%	6.45
On Dialysis at Registration	83.0%	82.3%	6.99	82.0%	7.74	80.2%	8.50	80.7%	8.90
0 HLA Mismatches	-	0.0%	10.18	15.5%	8.18	12.5%	8.59	8.1%	11.16
0 DR Mismatches	-	4.2%	7.35	35.6%	8.11	21.9%	8.86	13.1%	10.26
HLA Mismatches	-	4.75	-	3.62	-	3.92	-	3.80	-
Untransplanted Survival	6.68	6.75	-	6.72	-	6.81	-	7.27	-

Appendix for "Choices and Outcomes in Assignment Mechanisms"

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A Data Appendix

A.1 Obtainting Original Data Files

The data reported here have been supplied by UNOS as the contractor for the Organ Procurement and Transplantation Network (OPTN). The interpretation and reporting of these data are the responsibility of the author(s) and in no way should be seen as an official policy of or interpretation by the OPTN or the U.S. Government.

We will retain copies of the data until permitted by our Data Use Agreement with the Organ Procurement and Transplantation Network (OPTN). Further, we plan to send OPTN a copy of our replication archive if and when we are required to destroy our dataset. Researchers interested in using our dataset should directly contact OPTN to obtain permission: https://optn.transplant.hrsa.gov/data/request-data/ We are happy to provide copies of our data to researchers with permission and a data use agreement with the OPTN.

A.2 Data Description

Our data on patients, donors, transplants, and offers are based on information submitted to the Organ Procurement and Transplant Network (OPTN) by its members. The main datasets are the Potential Transplant Recipient (PTR) dataset and the Standard Transplantation Analysis and Research (STAR) dataset.

The PTR dataset contains offers made to patients on the deceased donor kidney waitlist that were not automatically rejected based on pre-specified criteria. Information includes identifiers for the donor, patient, and patient history record that generated the offer; the order in which the offers were made; each patient's acceptance decision;

and if the offer was not accepted, a reason of rejection. Each offer record also contains certain characteristics of the match, including the number of tissue type mismatches.

The STAR dataset contains separate files on deceased donor characteristics, patient histories, patient characteristics and transplant outcomes, and follow-up data, which are collected at six months and then annually, for kidney transplants. The patient and donor characteristics from these datasets are used to estimate our models of acceptance behavior and patient survival. The patient characteristics and transplant outcomes dataset contains patient death information. For patients who received a transplant through the deceased kidney donor waitlist, the follow-up dataset records whether the patient is still alive at the follow-up point. This information allows us to compute a survival duration for each patient. UNOS also provided supplemental information, including the ordering of distinct match runs conducted for the same deceased donor; the transplant centers of donors and patients in our dataset; and dates of birth for pediatric candidates, who joined the waitlist before turning 18 years of age.

The data contain identifiers that allow us to link the offer and acceptance data to patient and donor characteristics. Each deceased donor has a unique identifier. Similarly, each patient registration generates a unique patient waitlist identifier. Because patients may move to different transplant centers or be registered in multiple centers simultaneously, some individual patients have multiple waitlist identifiers. For this study, we focus on the earliest registration of each patient. The follow-up data contain a unique identifier for each transplant, allowing us to connect the follow-up information to each transplanted patient. The patient history file contains a unique patient record identifier corresponding to a particular state of the patient on the waitlist, including the patient's CPRA, activity status, and pre-set screening criteria. Each offer in the PTR dataset contains the identifiers for the donor, the patient registration, and the patient history record that were used in the match run. When appropriate, we de-duplicate offers so that each patient can receive at most one offer from each donor.

A.3 Sample Selection

We consider the first waiting period for patients who were actively waiting for a deceased donor kidney between January 1, 2000 and December 31, 2010. This restriction is to avoid selection arising from patients that remain on the list at the begining of the sample period. We omit patients who received a living donor transplant as their first transplant or were cross-registered for other organs simultaneously. Most patients that can receive a living donor receive one within the first year of registration and would prefer such a transplant to a deceased donor transplant. The latter restriction is made to focus on a more homogeneous group of patients.

In addition, we made a number of other more minor adjustments to work with a more cohesive sample of patients. The number of patients that survive each step of the sample selection process is described in Table A.1.

A small minority of patients are simultaneously registered in multiple donor service areas – our analysis keeps only one waitlist record from each patient. If the patient received a kidney transplant through the deceased donor waitlist before December 31, 2015, we keep the waitlist record with the earliest transplant date; if the patient remained untransplanted as of December 31, 2015, we keep the waitlist record with the earliest registration date.[31] Next, we exclude a small number of patients who received a prior kidney transplant to focus on survival effects from the first transplant. We also exclude patients removed for administrative reasons. These are patients who were listed on the waitlist by error, who departed because transplant took place but no transplant was recorded in the STAR dataset, and who could no longer be contacted while waiting on the waitlist. These departure reasons are recorded in the STAR patient and the transplant outcome dataset.

Then, we keep the waitlist records with registration dates between Janurary 1, 2000 and December 31, 2010 because we do not have data on offers prior to 2000. For example, an untransplanted patient active between 2000 and 2010 may not be included in the

[31] We use transplant data through December 31, 2015 to be consistent with the sample period during which we observe patient survival.

final sample because said patient's first waitlist registration is before 2000. This step amounts to be one of the largest cuts.

Finally, we exclude patients who received a transplant through non-standard allocations rules. This can occur, for example, if the donor is an armed service member; if the donor specified a particular recipient (directed donation); if there is a medical emergency or expedited placement attempt; if the kidney is not offered due to operational issue. We identify these cases by analyzing the PTR data as a large number of offers will be bypassed with a code indicating one of these reasons. In some cases, there is also text specifying specific circumstances justifying a rejection, which we parse to identify invalid offers in cases where the refusal code does not provide a specific reason.

Table A.1: Sample Selection: Patients

	Number of Patients	Number of Wait List Records
Patient's first waiting period that intersects the period 2000-2010	308,370	372,681
Exclude patients who received living donor transplants in their first waiting period	241,209	295,075
Exclude patients were waiting for other organs in their first waiting period	213,685	244,580
Keep one kidney waitlist record for each patient	213,685	213,685
Patients with multiple waitlist records	32,191	32,191
Patients with single waitlist record	181,494	181,494
Exclude patients who had a previous kidney transplant	212,258	-
Exclude patients with administrative waitlist removal reason	207,316	-
Restrict to patients whose remaining waitlist registration is between 2000 and 2010	178,944	-
Exclude patients who received non-standard kidney allocations	175,518	-

Our sample of deceased kidney donors comes from the intersection of the STAR deceased donor dataset and the PTR dataset. These are deceased donors whose kidneys were allocated between January 1, 2000 and December 31, 2010 to patients on the waitlist. We further exclude donors allocated using non-standard rules and restrict to donors who were offered to patients in the sample.

Table A.2 details the number of donors that survive each filter. The largest cuts come from the last step. This is because the priority for waiting time implies that many offers are only given to patiens that registered prior to 2000.

We consider a sample of offers made betwee January 1, 2000 and December 31, 2010 that could have resulted in transplants between our patient and donor samples. The

Table A.2: Sample Selection: Donors

	Number of Donors
Deceased donors offered to any kidney waitlist patients between 2000 and 2010	71,738
Exclude deceased donors offered through non-standard kidney allocations	67,993
Restrict to deceased donors offered to patients in the sample	61,453

PTR dataset includes records of all initial patient contacts and patients skipped due to administrative reasons irrespective of whether an offer was made. This happens mainly for three reasons. First, some patients that were contacted have lower priority than the patients that accepted and were transplanted the kidneys from a donor. In this case, we determine the cutoff point for each donor, and exclude all offers made after the cutoff. Second, some match runs were abandoned due to logistical reasons, and were re-run. We only keep the offers from the last match run for a donor. Third, in some cases, the PTR dataset records administrative or logistical reasons for skipping patients in the offer sequence. This can occur, for example, if the kidney has antigens that would result in an immune response; a patient was bypassed due to logistical reasons; or if the kidney does not meet the patient's minimum criteria. We also exclude non-responsive offers, for example, because either the surgeon or the patient is unavailable or because the patient is temporarily inactive/unsuitable for transplantation. Finally, we restrict to offers made to the patients in the sample. This step cuts the offer sample by 41% because many offers are made to patients that were not in our sample, for example, to patients that registered prior to 2000. Table A.3 describes how we arrive at the final sample of offers.

Table A.3: Sample Selection: Offers

	Number of Offers
Offers made between 2000 and 2010 from donors in the sample	14,888,539
Exclude non-responsive offers	14,239,214
Restrict to offers made to patients in the sample	8,444,106

A.4 Patient Survival

The patient characteristics and transplant outcomes dataset collects patient death dates from the waitlist record and periodically from the social security master file. In a small minority of cases, death dates are inconsistent across multiple waitlist records for a patient, in which case we assume that earlier death dates take precedence over later ones. Transplant dates and death dates are truncated on December 31, 2015, because death records after this date are inconsistently populated. For patients who received a transplant or died after December 31, 2015, we treat them as untransplanted or alive, respectively, as of December 31, 2015.

Among 175518 patients in the sample, we observe death dates before December 31, 2015 for 80168 of them. Of these, 55476 are untransplanted patients and 24692 are transplanted. Patients from whom we do not observe death are censored with an observed survival duration needs to be computed. The rules differ for transplanted and untransplanted patients. For transplanted patients, we censor on the date of the second transplant if a second transplant took place before December 31, 2015; on the day after transplant if there is no follow-up information for the patient corresponding to the transplant; on the date when the patient is lost to follow-up if the patient is lost to follow-up prior to December 31, 2015; and on Decmeber 31, 2015 if the patient is known to be alive as of December 31, 2015. For untransplanted patients, we censor on December 31, 2015 if the patient is known to be alive as of December 31, 2015; and on the date when the patient exits the waitlist if no death date is available and the exit day is prior to December 31, 2015.

Table A.4 presents a break down of censor reasons and their corresponding censor dates for the patient sample. Nearly one half of the patient sample is uncensored, and among censored patients, the vast majority (73%) are censored on December 31, 2015. Since December 31, 2015 is an exogenously determined date, patients censored on the date should be similar to uncensored patients in terms of potential outcomes. We expect that this censoring date does not induce selection bias that might confound our survival analysis.

Table A.4: Censor Reason

Censor Reason	Censor Date	# Patients
Transplanted Patients		
Retransplant before Dec 31, 2015	Retransplant date	3,581
No follow-up information	One day after transplant	979
Lost to follow-up before Dec 31, 2015	Date lost to follow up	5,856
Known to be alive as of Dec 31, 2015	December 31, 2015	57,215
Untransplanted Patients		
Known to be alive as of Dec 31, 2015	December 31, 2015	12,370
No death date and depart the waitlist before Dec 31, 2015	Date departing waitlist	15,349

B Estimation Appendix

B.1 Gibbs' Sampler

Recall that our model is given by

$$\begin{aligned}
y_{i0} &= B\left(Y_{i0};\rho_0\right) = x_i\beta_x + \nu_{i,0} \\
y_{ij} &= B\left(Y_{ij};\rho_1\right) = \chi\left(x_i,q_j\right)\alpha_{x,q} + \alpha_\eta\eta_j + \nu_{i,1} + \varepsilon_{ij,1} \\
D_{ij} &= 1\left\{y_{ij,D} = \chi\left(x_i,q_j\right)\gamma_{x,q} + z_i\gamma_z + \eta_j + \nu_{i,D} + \varepsilon_{ij,D} > 0\right\},
\end{aligned}$$

where we allow for $\nu_i = (\nu_{i,D}, \nu_{i,1}, \nu_{i,2}) \sim \mathcal{N}(0, \Sigma_\nu)$ and $\varepsilon_{ij} = (\varepsilon_{ij,1}, \varepsilon_{ij,D}) \sim \mathcal{N}(0, \Sigma_\varepsilon)$.

There are several challenges in estimating this model. First, we often observed censored values of y_{i0} and y_{ij}. We perform a data augmentation step given the parameters and the censoring point to solve this issue. For y_{ij}, the data augmentation step is necessary only in cases for which $T_{ij} = 1$.

Second, D_{ij} is a binary variable. As is standard in discrete choice models, we perform a data augmentation step to draw $y_{ij,D}$ given the observed decisions. This step is necessary for the observed values of D_{ij}.

Third, the model incorporates rich correlations between the different observations via η_j, ν_i and ε_{ij}. In particular, due to these terms, the covariance matrix between $\{y_{i0}\}_i \{y_{ij}\}_{ij}$

and $\{y_{ij,D}\}_{ij}$ conditional on the obserables and the parameters does not have a simple block-diagonal structure that would allow us to compute simple posterior distributions. To solve this problem, we re-write these variables using a factor structure such that the posterior distribution of the parameters of each equation is conditionally independent of the others given the factors. Specifically, we rewrite ν_i as

$$\begin{aligned}\nu_{i,D} &= f_{i,1} \\ \nu_{i,f} &= f_{i,2} \\ \nu_{i,0} &= \beta_{\nu 1} f_{i,1} + \beta_{\nu 2} f_{i,2} + \tilde{\varepsilon}_{i0}\end{aligned}$$

where $f_{i,1}$, $f_{i,2}$ and ε_{i0} are each independently distributed mean-zero normal random variables with variances σ_1^2, σ_2^2 and $\sigma_{\tilde{\varepsilon},0}^2$. This structure places no restrictions on the covariance matrix Σ_ν. Similarly, we write ε_{ij} as

$$\begin{aligned}\varepsilon_{ij,1} &= \alpha_\varepsilon f_{ij,3} + \tilde{\varepsilon}_{ij,1} \\ \varepsilon_{ij,D} &= f_{ij,3} + \tilde{\varepsilon}_{ij,D}\end{aligned}$$

where $f_{ij,3}$, $\tilde{\varepsilon}_{ij,1}$ and $\tilde{\varepsilon}_{ij,D}$ are independently distributed mean-zero normal random variables with variances σ_3^2, $\sigma_{\tilde{\varepsilon},1}^2$ and $\sigma_{\tilde{\varepsilon},D}^2$. We normalize the variances σ_3^2, and $\sigma_{\tilde{\varepsilon},D}^2$ to 1. Finally, we set

$$\eta_j = f_{j,4}$$

with variance σ_4^2. The main difference between $f_\cdot$and $\tilde{\epsilon}_\cdot$ is that it is sufficient to condition on the former in order to render the models above as conditionally independent.

Therefore, the parameters we are interested estimating in are the co-efficients in each equation, $\beta = (\beta_x, \beta_{\nu 1}, \beta_{\nu 2})$, $\alpha = (\alpha_{x,q}, \alpha_\eta, \alpha_{\nu 1}, \alpha_\varepsilon)$, $\gamma = (\gamma_{x,q}, \gamma_z)$, and the variances $\sigma_{\tilde{\varepsilon},0}^2 = V(\tilde{\varepsilon}_{i0})$, $\sigma_{\tilde{\varepsilon},1}^2 = V(\tilde{\varepsilon}_{ij,1})$ and $\sigma_l^2 = V(f_l)$ where $l \in \{1, 2, 4\}$ is the l-th factor.

For simplicity of notation, we will collect the coefficients in the vector θ and the standard deviations in the vector σ, with $\sigma_{\tilde{\varepsilon}}$ and σ_f denoting the sub-vectors for $\tilde{\varepsilon}$ and f respectively. And, with some abuse of notation, we collect y_{i0}, y_{ij} and $y_{ij,D}$ for all i and

j in y.

Following standard practice, we assume diffuse conjugate and independent priors for each of these parameters. Specifically, we model the priors α, β and γ using a mean-zero independent normal distribution with variances equal to 1000 and the prior for the variances $\sigma^2_{\tilde{\varepsilon},0}$, $\sigma^2_{\tilde{\varepsilon},1}$ and σ^2_l using independent inverse-Wishart distributions with parameters $(3, 3)$. These priors are diffuse; thus, they have a negligible impact on our estimates.

The Gibbs' sampler starts with an initial draw y^0, θ^0, σ^0 and f^0 and generates a chain of length K by iterating through the following steps for each $k \in \{0, \ldots, K-1\}$:

1. **Data Augmentation:** Sample y^{k+1}_{i0}, y^{k+1}_{ij} for censored observations and $y^{k+1}_{ij,D}$ for observed decisions given θ^k, σ^k and f^k from truncated normal distributions.

2. **Sample Coefficients:** Sample θ^{k+1} given y^{k+1}, f^k, the standard deviations σ^k and the prior distribution from a multi-variate normal distribution.

3. **Sample Variances:** Sample $\sigma^{2,k+1}_{\tilde{\varepsilon},0}$ and $\sigma^{2,k+1}_{\tilde{\varepsilon},1}$ given y^{k+1}, f^k, the parameters θ^{k+1} and the prior distribution from a inverse-Wishart distribution.

4. **Sample Factors:** For each $l \in \{1, 2, 3, 4\}$, sample $f^{k+1}_{\cdot,l}$ given y^{k+1}, the parameters θ^{k+1}, $\sigma^{k+1}_{\tilde{\varepsilon}}$, σ^k_f, and the remaining factors $f^{k+1}_{\cdot,1}, \ldots, f^{k+1}_{l-1}$ and $f^k_{\cdot,l+1}, \ldots, f^k_4$.

5. **Sample Factor Variances:** Sample $\sigma^{2,k+1}_l$ for $l \in \{1, 2, 4\}$ given f^{k+1} and the prior distribution from an inverse-Wishart distribution.

We draw a chain of length K =200,000 and burn 50,000 draws to allow the chain to convergence. We only keep one every 10 draws to save some computation time and reduce the autocorrelation in the resulting chain. We visually inspect the chains and ensure that the potential scale reduction factor is below 1.1 for each of the parameters. The distributions in each step can be solved for in closed-form as detailed below:

1. Conditional distributions for y_{i0}, y_{ij} and $y_{ij,D}$ given θ, f and σ:

(a) For each i, j pair such that D_{ij} is observed, the distribution of $y_{ij,D}$ conditional on γ, f and D_{ij} is a one-sided truncated with mean $\mathbb{E}\left[g_{ij,D}|\gamma, f_{ij}\right]$ and unit standard deviation. The distribution is truncated below at 0 if $D_{ij} = 1$ and above at 0 otherwise.

(b) For each i such that y_{i0} is censored, the distribution of y_{i0} conditional on β and f is a one-sided truncated normal with mean $\mathbb{E}\left[y_{i0}|\beta, f_{i1}, f_{i2}\right]$ and standard deviation $\sigma_{\tilde{\varepsilon},0}$. The distribution of y_{i0} is truncated below at the censoring duration.

(c) For each observed transplant such that y_{ij} is censored, the distribution of y_{ij} conditional on α^k, f^k is a one-sided truncated normal with mean $\mathbb{E}\left[y_{ij}|\alpha, f\right]$ and standard deviation $\sigma_{\tilde{\varepsilon},1}$. The distribution of y_{ij} is truncated below at the censoring duration.

2. Posterior distributions of the co-efficients α, β and γ given y, f, σ and the priors. Since y_{i0}, y_{ij} and $y_{ij,D}$ are mutually independent conditional on f, the parameters α, β and γ are each co-efficients in a linear regression model with normally distributed errors. Therefore, the posterior distributions of each of these terms is given by a multivariate normal distribution with closed-form means and variances (see Gelman et al., 2014, Chapter 14.2).

3. Posterior distributions of $\sigma^2_{\tilde{\varepsilon},0}$ and $\sigma^2_{\tilde{\varepsilon},1}$ given y, f, σ and the priors. As argued above, y_{i0}, y_{ij} are mutually independent conditional on f. Therefore, the distributions of $\sigma^2_{\tilde{\varepsilon},0}$ and $\sigma^2_{\tilde{\varepsilon},1}$ are inverse-Wishart with parameters given in Chapter 14.2 of Gelman et al. (see 2014).

4. Posterior distributions of f given y, θ and σ:

(a) The distribution of $f_{i,1}$ conditions on the residual $f_{i,1}+\frac{1}{\beta_{\nu 1}}\tilde{\varepsilon}_{i0} = \frac{1}{\beta_{\nu 1}}\left(y_{i0} - \left(x_i\beta_x + \beta_{\nu 2}f_{i,2}\right)\right)$ and σ_1 throughout; on the residual $f_{i,1}+\tilde{\varepsilon}_{ij,D} = y_{ij,D}-\left[\chi\left(x_i, q_j\right)\gamma_{x,q} + z_i\gamma_z + \eta_j + f_{ij,3}\right]$ for all j such that D_{ij} is observed; and on the residual $f_{i,1} + \frac{1}{\alpha_{\nu 1}}\tilde{\varepsilon}_{ij,1} = \frac{1}{\alpha_{\nu 1}}\left[y_{ij} - \left(\chi\left(x_i, q_j\right)\alpha_{x,q} + \alpha_\eta\eta_j + + f_{i,2} + \alpha_\varepsilon f_{ij,3}\right)\right]$ if $T_{ij} = 1$. These residuals

have prior mean zero and variances $\sigma_1^2+\frac{\sigma_{\tilde{\varepsilon},0}^2}{\beta_{\nu 1}^2}$, $\sigma_1^2+\sigma_{\tilde{\varepsilon},1}^2$ and $\sigma_1^2+\frac{\sigma_{\tilde{\varepsilon},1}^2}{\alpha_{\nu 1}^2}$ repectively. The mean is the precision-weighted average of the residuals conditioned on, and the variance is the inverse of the sum of σ_1^{-2} and the precisions of each residual.

(b) The distribution of $f_{i,2}$ is analogous, where we condition on the residual $\frac{1}{\beta_{\nu 2}}\left(y_{i0}-\left(x_i\beta_x+\beta_{\nu 1}f_{i,1}\right)\right)$ and σ_2 throughout; and on the residual $y_{ij}-\left[\chi\left(x_i,q_j\right)\alpha_{x,q}+\alpha_\eta\eta_j+\alpha_{\nu 1}f_{i,1}\right]$ if $T_{ij}=1$.

(c) The distribution of $f_{ij,3}$ is analogous, where we conditions on α_ε throughout; on $y_{ij,D}-\left[\chi\left(x_i,q_j\right)\gamma_{x,q}+z_i\gamma_z+\eta_j+f_{i,1}\right]$ for all j such that D_{ij} is observed; and on $\frac{1}{\alpha_\varepsilon}\left(y_{ij}-\left[\chi\left(x_i,q_j\right)\alpha_{x,q}+\alpha_\eta\eta_j+f_{i,2}\right]\right)$ if $T_{ij}=1$. Observe that σ_3 is normalized to 1.

(d) The distribution of $f_{j,4}$ is analogous, where we condition on σ_4 throughout; on $y_{ij,D}-\left[\chi\left(x_i,q_j\right)\gamma_{x,q}+z_i\gamma_z+f_{i,1}+f_{ij,3}\right]$ for all i such that D_{ij} is observed; and on $\frac{1}{\alpha_\eta}\left(y_{ij}-\left[\chi\left(x_i,q_j\right)\alpha_{x,q}+f_{i,2}+\alpha_\varepsilon f_{ij,3}\right]\right)$ if $T_{ij}=1$.

5. The variances σ_l^2 for $l\in\{1,2,4\}$ follow an inverse-Wishart distributions given the prior and respectively, $\{f_{i,1}\}$, $\{f_{i,2}\}$ and $\{f_{j,4}\}$.

C Theoretical Appendix

C.1 Proof of Lemma 1

For simplicity of notation, denote $q_n=\left(q_{j_{i,1}},\ldots,q_{j_n}\right)$, $q_{n-1}=\left(q_{j_{i,1}},\ldots,q_{j_{i,n-1}}\right)$, and the vector $\tilde{D}_{i,n}=\left(D_{ij_{i,1}},\ldots,D_{ij_n}\right)$. Assumption 2 implies that $P\left[T_{ij_{i,n}}=1|q_{j_i},z\right]=P\left[\tilde{D}_{i,n-1}=0,D_{ij_{i,n}}=1|q_{j_i},z\right]$ is equal to the observed quantity $P\left[T_{ij_{i,n}}=1|q_n,z\right]$, and is therefore identified. Similarly, if $P\left[T_{ij_{i,n}}=1|q_{j_i},z\right]>0$, then Assumption 2 implies that

$$E\left[Y_{ij_{i,n}}|T_{ij_{i,n}}=1,q_{j_i},z\right]=E\left[Y_{ij_{i,n}}|\tilde{D}_{in-1}=0,D_{ij_{i,n}}=1,q_{j_i},z\right]$$

is identified because it is equal to $E\left[Y_{ij_{i,n}}|T_{ij_{i,n}}=1,q_n,z\right]$. Therefore, it remains to show that $E\left[Y_{i0}|T_{ij_{i,n}}=1,q_{j_i},z\right]$ is identified. First, re-write

$$\begin{aligned}
&E\left[Y_{i0}|T_{ij_{i,n}}=1,q_{j_i},z\right]\Pr\left[T_{ij_{i,n}}=1|q_{j_i},z\right]\\
=&E\left[Y_{i0}|T_{ij_{i,n}}=1,q_n,z\right]\Pr\left[T_{ij_{i,n}}=1|q_n,z\right]\\
=&E\left[Y_{i0}|\tilde{D}_{i,n-1}=0,D_{ij_n}=1,q_n,z\right]\Pr\left[\tilde{D}_{in-1}=0,D_{ij_n}=1|q_n,z\right]\\
=&E\left[Y_{i0}|\tilde{D}_{i,n-1}=0,q_n,z\right]\Pr\left[\tilde{D}_{i,n-1}=0|q_n,z\right]-E\left[Y_{i0}|\tilde{D}_{i,n}=0,q_n,z\right]\Pr\left[\tilde{D}_{i,n}=0|q_n,z\right]\\
=&E\left[Y_{i0}|\tilde{D}_{i,n-1}=0,q_{n-1},z\right]\Pr\left[\tilde{D}_{i,n-1}=0|q_{n-1},z\right]-E\left[Y_{i0}|\tilde{D}_{i,n}=0,q_n,z\right]\Pr\left[\tilde{D}_{i,n}=0|q_n,z\right]
\end{aligned}$$

where the last expression is observed. The first equality above follows from Assumption 2, the second equality is definitional, the third equality follows from set inclusion and the last from Assumption 2. Thefore, since $\Pr\left[T_{ij_{i,n}}=1|q_{j_i},z\right]$ is identified and strictly positive, $E\left[Y_{i0}|T_{ij_{i,n}}=1,q_{j_i},z\right]$ is identified.

C.2 Proof of Lemma 2

For any $k\leq n$, Assumptions 1 and 2 imply that the observed probability that $D_{i,j_{i,1}}=D_{i,j_{i,2}}=\ldots=D_{i,j_{i,k}}=0$ can be re-written as follows:

$$P\left(D_{i,j_{i,1}}=D_{i,j_{i,2}}=\ldots=D_{i,j_{i,k}}=0|q_j^n,z_i\right)=\int_0^1\varepsilon_D^k\mathrm{d}v\left(\varepsilon_D;q_j,z_i\right).$$

Observe that $a_k=\int_0^1\varepsilon_D^k\mathrm{d}v\left(\varepsilon_D;q_j,z_i\right)$ is identified for $k\in\{1,\ldots,n\}$. Moreover, 3(i) and (ii) together imply that

$$a_0=\int_0^1 1\mathrm{d}v\left(\varepsilon_D;q_j,z_i\right)=1.$$

Therefore, to complete the proof, we need to show that $v_{n-1}\left(\cdot;q_j,z_i\right)$ is determined by the values of $a_k=\int_0^1\varepsilon_D^k\mathrm{d}v\left(\varepsilon_D;q_j,z_i\right)$ for $k\leq n$ where $v_{n-1}\left(\cdot;q_j,z_i\right)$ is the $(n-1)$-st order Fourier-Legendre approximation of $v\left(\cdot;q_j,z\right)$. In what follows, we will drop conditioning on z_i and q_j^n for simplicity of notiation.

To complete the proof, we write the co-efficients of $(n-1)$ −st Fourier-Legendre series of $v(\cdot)$ in terms of a_k. Let $\Gamma_m(x)$ be the m-th shifted Legendre Polynomial. Observe that each $\Gamma_m(\cdot)$ is given by

$$\Gamma_m(x) = \sum_{l=0}^{m} \gamma_{m,l} x^l,$$

with known co-efficients $\gamma_{m,l}$.[32]The $m-$th co-efficient in the (shifted) Fourier-Legendre series of $v(x)$ is given by

$$\begin{aligned} c_m &= (2m+1)\int_0^1 \Gamma_m(x)\, v(x)\, \mathrm{d}x \\ &= (2m+1)\left[\int_0^1 \Gamma_m(x)\, \mathrm{d}x - \int_0^1 \int_0^x \Gamma_m(y)\, \mathrm{d}y \mathrm{d}v(x)\right], \end{aligned}$$

where the second equality follows from integration by parts. Observe that $\int_0^1 \Gamma_m(x)\, \mathrm{d}x = \int_0^1 \Gamma_m(x)\Gamma_0(x)\, \mathrm{d}x = 0$ for $m > 0$. Therefore, for $m > 0$,

$$\begin{aligned} c_m &= -(2m+1)\int_0^1 \int_0^x \Gamma_m(y)\, \mathrm{d}y \mathrm{d}v(x) \\ &= -(2m+1)\int_0^1 \int_0^x \sum_{l=0}^{m} \gamma_{m,l} y^l \mathrm{d}y \mathrm{d}v(x) \\ &= -(2m+1)\int_0^1 \sum_{l=0}^{m} \gamma_{m,l} \frac{1}{l+1} x^{l+1} \mathrm{d}v(x) \\ &= -(2m+1)\sum_{l=0}^{m} \gamma_{m,l} \frac{1}{l+1} \int_0^1 x^{l+1} \mathrm{d}v(x) \\ &= -(2m+1)\sum_{l=0}^{m} \gamma_{m,l} \frac{1}{l+1} a_{l+1}. \end{aligned} \tag{C.1}$$

And, finally, we have

$$\begin{aligned} c_0 &= \int_0^1 \Gamma_0(x)\, v(x)\, \mathrm{d}x \\ &= \int_0^1 v(x)\, \mathrm{d}x \\ &= v(1) - \int_0^1 x \mathrm{d}v(x), \end{aligned} \tag{C.2}$$

[32]The shifted Legendre-Polynomials on $[0,1]$ satisfy the orthogonality relationship $\int_0^1 \Gamma_m(x)\Gamma_n(x)\, \mathrm{d}x = \frac{1}{2n+1}\delta_{m,n}$where $\delta_{m,n}$ is the Kronecker delta. The first few polynomials are $\Gamma_0(x) = 1$, $\Gamma_1(x) = 2x-1$, $\Gamma_2(x) = 6x^2 - 6x + 1$.

where the last equality follows from integration by parts. The term $v(1) = 1$ since $v(\cdot)$ is non-decreasing with image $[0,1]$. Equations (C.1) and (C.2) imply that all c_m for $m < n$ can be written in terms of the observed quantities $a_0, \ldots, a_n$. Therefore, $v_{n-1}(\cdot)$ is identified.

Let $\tilde{\Gamma}_m(y)$ be the m-th unshifted Legendre Polynomial defined over $[-1,1]$ satisfying$\tilde{\Gamma}_m(y) = \Gamma_m\left(\frac{y+1}{2}\right)$.[33] The $(n-1)$-st order Fourier-Legendre approximation of $\tilde{v}(y) = v\left(\frac{y+1}{2}\right)$ is $\tilde{v}_{n-1}(y) = \sum_{k=0}^{n-1} \tilde{c}_m \tilde{\Gamma}_m(y)$ where,

$$\tilde{c}_m = \frac{(2m+1)}{2} \int_{-1}^{1} \tilde{\Gamma}_m(y)\, \tilde{v}(y)\, dy = c_m,$$

where the last equality follows after a change of variables $x = \frac{y+1}{2}$. Since the function $\tilde{v}(\cdot)$ has a compact domain and image, we have that $\int_{-1}^{1} \tilde{v}(y)^2 \, dy$ is bounded. Theorem 8.1 in Pollard (1947) shows that the Legendre polynomials form a basis in $L^2(-1,1)$, or equivalently, that $\tilde{v}_n(y)$ converges in the L^2-norm to $\tilde{v}(y)$ as $n \to \infty$. Therefore, $\|v_{n-1}(\cdot) - v(\cdot)\|_2 \to 0$ as $n \to \infty$. Therefore, $v(\cdot)$ is identified if the hypotheses of the Lemma are satisfied for all n. Since $v(\cdot; q_j, z_i)$ is increasing in its argument, $\mathbb{P}(D_{ij} = 1 | \nu_{i,D} = v(\varepsilon_D; q_j, z_i); q_j, z_i)$ is identified.

C.3 Preliminaries for Theorem 1

Lemma 3. *Let f_n and g_n be sequences of functions such that $f_n \to f$ and $g_n \to g$ pointwise. Assume that f is continuous.*

(i) If f_n converges to f uniformly in $[a,b]$ and $g_n(x) \in (a,b)$ for all x, then $f_n(g_n(x))$ converges to $f(g(x))$ for each x in the domain of g.

(ii) If f_n and g_n respectively converge to f and g uniformly in $[a,b]$ and $\inf_{x\in[a,b]} |g(x)| = k > 0$, then $\frac{f_n(x)}{g_n(x)}$ converges to $\frac{f(x)}{g(x)}$ uniformly in $[a,b]$.

(iii) If f_n converges to f uniformly in $[a,b]$ and f is strictly increasing on $[a,b]$, and the function $f_n^{-1}(y)$ is defined as $\inf\{x : f_n(x) > y\}$, then for all $x \in (a,b)$, $f_n^{-1}(f(x)) \to$

[33] The unshifted Legendre-Polynomials on $[-1,1]$ satisfy the orthogonality relationship $\int_0^1 \tilde{\Gamma}_m(y)\tilde{\Gamma}_n(y)\, dy = \frac{2}{2n+1}\delta_{m,n}$where $\delta_{m,n}$ is the Kronecker delta. The first few polynomials are $\tilde{\Gamma}_0(y) = 1$, $\tilde{\Gamma}_1(y) = y$, $\tilde{\Gamma}_2(x) = \frac{1}{2}(3x^2 - 1)$.

x.

Proof. Part (i). By the triangle inequality, we have that

$$\begin{aligned}|f_n(g_n(x)) - f(g(x))| &\leq |f_n(g_n(x)) - f(g_n(x))| + |f(g_n(x)) - f(g(x))| \\ &\leq \sup_{x\in[a,b]} |f_n(y) - f(y)| + |f(g_n(x)) - f(g(x))|.\end{aligned}$$

The first term converges to zero since f_n converges to f uniformly in $[a,b]$. The argument of f in the second term, $g_n(x)$, converges to $g(x)$. Since f is continuous, the sequential definition of continuity implies that the second term also converges to zero. Therefore, $|f_n(g_n(x)) - f(g(x))| \to 0$ as $n \to \infty$.

Part (ii). By the triangle inequality, we have that

$$\begin{aligned}\sup_{x\in[a,b]} \left|\frac{f_n(x)}{g_n(x)} - \frac{f(x)}{g(x)}\right| \leq{}& \sup_{x\in[a,b]} |f_n(x) - f(x)| \sup_{x\in[a,b]} \left|\frac{1}{g_n(x)} - \frac{1}{g(x)}\right| \\ &+ \sup_{x\in[a,b]} |f(x)| \sup_{x\in[a,b]} \left|\frac{1}{g_n(x)} - \frac{1}{g(x)}\right| \\ &+ \sup_{x\in[a,b]} \left|\frac{1}{g(x)}\right| \sup_{x\in[a,b]} |f_n(x) - f(x)|.\end{aligned}$$

By assumption, $\sup_{x\in[a,b]} |f_n(x) - f(x)|$ converges to zero and $\sup_{x\in[a,b]} \left|\frac{1}{g(x)}\right| = k^{-1}$ is finite. Further, $\sup_{x\in[a,b]} |f(x)|$ if finite because f is continuous and $[a,b]$ is a compact set. Therefore, the left-hand side converges to zero as required if $\sup_{x\in[a,b]} \left|\frac{1}{g_n(x)} - \frac{1}{g(x)}\right|$ converges to zero.

To show this, observe that

$$\sup_{x\in[a,b]} \left|\frac{1}{g_n(x)} - \frac{1}{g(x)}\right| \leq \sup_{x\in[a,b]} \left|\frac{1}{g_n(x)}\right| \sup_{x\in[a,b]} \left|\frac{1}{g(x)}\right| \sup_{x\in[a,b]} |g_n(x) - g(x)|$$

converges to zero. Since $\lim_{n\to\infty} \sup_{x\in[a,b]} |g_n(x) - g(x)| = 0$ and $\sup_{x\in[a,b]} \left|\frac{1}{g(x)}\right| = k^{-1}$ exists by assumption, it is sufficient to show that $\sup_{x\in[a,b]} \left|\frac{1}{g_n(x)}\right|$ exists. Let N be such that for all $n > N$, we have that $\sup_{x\in[a,b]} |g(x) - g_n(x)| \leq \frac{k}{2}$. Such a value of N exists because g_n converges to g uniformly in $[a,b]$ and $\inf_{x\in[a,b]} |g(x)| = k > 0$. Hence, for all

$n > N$, $\sup_{x\in[a,b]} \left|\frac{1}{g_n(x)}\right| < \left(\frac{k}{2}\right)^{-1}$, which is finite.

Part (iii). Define $f_n^{-1}(y) = \inf\{x : f_n(x) > y\}$. Fix $x \in (a,b)$. For any $\varepsilon > 0$, define $\tilde{\varepsilon} = \min\left\{\frac{\varepsilon}{2}, x-a, b-x\right\}$ and $\delta_{\tilde{\varepsilon}} = \min\{f(x+\tilde{\varepsilon}) - f(x), f(x) - f(x-\tilde{\varepsilon})\}$. Observe that $\tilde{\varepsilon} > 0$ and $\delta_{\tilde{\varepsilon}} > 0$ because and f is strictly increasing. Pick N such that for all $n > N$ $\sup_{x'\in[a,b]} |f_n(x') - f(x')| < \delta_{\tilde{\varepsilon}}$. Such an N exists because f_n converges to f uniformly in $[a,b]$. To complete the proof, we will show that for all $n > N$, $f_n^{-1}(f(x)) > x - \varepsilon$ and $f_n^{-1}(f(x)) < x + \varepsilon$.

Since f is strictly increasing, for all $x' < x - \tilde{\varepsilon}$, $f(x') + \delta_{\tilde{\varepsilon}} < f(x)$. Therefore, for all $n > N$ and $x' < x - \tilde{\varepsilon}$, $f_n(x') < f(x)$. Hence, $f_n^{-1}(f(x)) \geq x - \tilde{\varepsilon} > x - \varepsilon$ for all $n > N$.

Similarly, for all $x' > x + \tilde{\varepsilon}$, $f(x') > f(x)$. Therefore, for all $n > N$ and $x' > x + \tilde{\varepsilon}$, $f_n(x') - \delta_{\tilde{\varepsilon}} > f(x)$. Hence, $f_n^{-1}(f(x)) \leq x + \tilde{\varepsilon} < x + \varepsilon$ for all $n > N$. □

Lemma 4. *Let $g \in L^2(0,1)$ be continuous and $s_n(g;x)$ be its Fourier-Legendre approximation of degree n evaluated at x. For any $[a,b] \in (0,1)$, the partial average $S_n(g;x) = \frac{1}{n}\sum_{k=0}^{n-1} s_k(g;x)$ converges to $g(x)$ uniformly in $[a,b]$.*

Proof. The result is a corollary of Theorem IV.3.2 in Freud (1971). To apply this result, we will use the cumulative distribution function of the uniform distribution on $[0,1]$ as the function $\alpha(x)$.

Let $p_n(d\alpha;x)$ for $n = 0,1,2...$ be the sequence of orthogonal polynomials defined in Theorem I.1.2 of Freud (1971). It is straightforward to check that, for our chosen $\alpha(x)$,

$$p_n(d\alpha;x) = \sqrt{2m+1}\Gamma_m(x),$$

where $\Gamma_m(x)$ be the m-th shifted Legendre Polynomial on $[0,1]$,[34]

satisfied the conditions in Theorem I.1.2 because (i) each $\Gamma_m(x)$ is a polynomial, (ii) the leading co-efficient of $\Gamma_m(x)$ is positive and (iii) $\int \Gamma_n(x)\Gamma_m(x)\,dx = \delta_{mn}$ where δ_{mn}

[34]The shifted Legendre-Polynomials on $[0,1]$ satisfy the orthogonality relationship $\int_0^1 \Gamma_m(x)\Gamma_n(x)\,dx = \frac{1}{2n+1}\delta_{m,n}$where $\delta_{m,n}$ is the Kronecker delta. The first few values are $\Gamma_0(x) = 1$, $\Gamma_1(x) = 2x-1$, $\Gamma_2(x) = 6x^2 - 6x + 1$.

is the Kronecker delta. Moreover, $p_n(d\alpha; x)$ is unique as noted in the remark below Theorem I.1.2 in Freud (1971).

Therefore, it remains to show that $p_n(d\alpha; x)$ satisfies requirement (3.2) in Chapter IV of Freud (1971). As noted following this requirement, it is sufficient to show that for every pair x_2 and x_1 in a neighborhood of $x_0 \in [a, b] \subset (0, 1)$,

$$\frac{\alpha(x_2) - \alpha(x_1)}{x_2 - x_1} \geq m > 0,$$

for some constant m. This the case because for our chosen $\alpha(x)$, because the left hand side is identically equal to 1 for every $x_1, x_2 \in (0, 1)$.

Finally, $s_k(g; x)$, as defined in equations IV(1.1) and IV(1.2) of Freud (1971) is the $k-$th order shifted Fourier-Legendre approximation of g. Therefore, by a direct corollary of Theorem IV.3.2 in Freud (1971), $S_n(g; x)$ converges to $g(x)$ uniformly in $[a, b] \subset (0, 1)$. □

Lemma 5. *Let $v'_n(\cdot; q_j, z)$ be the n-th order Fourier-Legendre approximation of $v'(\cdot; q_j, z)$. If the hypotheses of Lemma 2 are satisfied, then $v'_n(\cdot; q_j, z)$ is identified for each $z \in (0, 1)$ and q_j.*

Proof. We drop the parameters z, q_j for simplicity of notation as they are held fixed. As argued in the proof of Lemma 2, Assumptions 1 and 2 imply that the quantities

$$a_k = \int_0^1 \varepsilon_D^k \mathrm{d}v(\varepsilon_D; q_j, z_i)$$

are identified for all $k \leq n$. Let b_m be the (shifted) $m-$th Fourier-Legendre co-efficient of $v'(\cdot)$ defined on $[0, 1]$

$$b_m = (2m + 1) \int_0^1 \Gamma_m(x) v'(x) \mathrm{d}x$$

where $\Gamma_m(\cdot)$ is the $m-$th shifted Legendre polynomial on $[0, 1]$. Observe that each

$\Gamma_m(\cdot)$ is given by

$$\Gamma_m(x) = \sum_{l=0}^{m} \gamma_{m,l} x^l,$$

with known co-efficients $\gamma_{m,l}$. Therefore, the co-efficients

$$\begin{aligned} b_m &= (2m+1) \sum_{l=0}^{m} \gamma_{m,l} \int_0^1 x^l v'(x)\, \mathrm{d}x \\ &= (2m+1) \sum_{l=0}^{m} \gamma_{m,l} a_l, \end{aligned}$$

are identified. The second equality follows from the definition of a_l. □

C.4 Proof of Theorem 1

Identification of $E(Y_{i0}|\nu)$. Define $y_0(\nu) = E(Y_{i0}|\nu)$. For a given ν, fix z such that there exists $\varepsilon_D \in (0,1)$ with $v(\varepsilon_D; q_j, z) = \nu$ and drop the conditioning on z in what follows, for simplicity of notation. As in the main text, we are also conditioning and dropping x_i from the notation.

Let s and $\tilde{s}$ be a pair of models satisfying the hypotheses of Theorem 1, and let $\{y_0(\cdot), v(\cdot)\}$ and $\{\tilde{y}_0(\cdot), \tilde{v}(\cdot)\}$ be features that are associated with s and $\tilde{s}$ respectively. We will show that if $\{y_0(\cdot), v(\cdot)\} \neq \{\tilde{y}_0(\cdot), \tilde{v}(\cdot)\}$, then there exists n, such that if q_j^k is in the support of the distribution of offer types for all $k \leq n$, then the joint distribution of $Y_{i0}, \left\{T_{ij_{i,1}}, \ldots, T_{ij_{i,k}}\right\}$ conditional on q_j^k differs for some $k \leq n$ under models s and $\tilde{s}$.

Consider a value of $\bar{\nu} \in (0,1)$ such that $y_0(\bar{\nu}) \neq \tilde{y}_0(\bar{\nu})$ and $\bar{\nu} = v(\bar{x}; q_j)$ for some $\bar{x} \in (0,1)$. Lemmas 2 and 5 imply that if either $v(\bar{x}; q_j) \neq \tilde{v}(\bar{x}; q_j)$ or $v'(\bar{x}; q_j) \neq \tilde{v}'(\bar{x}; q_j)$ for some $\bar{x} \in (0,1)$, then there exists N such that for all $n > N$ the joint distribution of $\left\{T_{ij_{i,1}}, \ldots, T_{ij_{i,n}}\right\}$ conditional on q_j^k for some $k \leq n$ differs for models s and $\tilde{s}$. Therefore, it is sufficient to focus on the case when $v(\bar{x}; q_j) = \tilde{v}(\bar{x}; q_j)$ and $v'(\bar{x}; q_j) = \tilde{v}'(\bar{x}; q_j)$. Moreover, since $\bar{x} \in (0,1)$, we have that $v'(\bar{x}; q_j) > 0$ (Assumption 4(i)) implying that it is sufficient to show that that if $y_0(v(\bar{x}; q_j))\, v'(\bar{x}; q_j) \neq \tilde{y}_0(v(\bar{x}; q_j))\, v'(\bar{x}; q_j)$, then the joint distribution of $Y_{i0}, \left\{T_{ij_{i,1}}, \ldots, T_{ij_{i,k}}\right\}$ conditional on q_j^k differs for some $k \leq n$

under models s and $\tilde{s}$.

We prove this by showing that if $y_0\left(v\left(\bar{x};q_j\right)\right)v'\left(\bar{x};q_j\right) \neq \tilde{y}_0\left(v\left(\bar{x};q_j\right)\right)v'\left(\bar{x};q_j\right)$, then there exists n such that if q_j^k is in the support of the distribution of offer types for all $k \leq n$, then$Y_{i0}, \left\{T_{ij_{i,1}}, \ldots, T_{ij_{i,k}}\right\}$ conditional on q_j^k differs for some $k \leq n$ under models s and $\tilde{s}$.

To do this, we first show that the Fourier-Lebesgue approximation of the function $u\left(x\right) = y_0\left(v\left(x;q_j\right)\right)v'\left(x;q_j\right)$ can be determined from observables. Assumptions 1 and 2 imply that for each $k \leq n$, we can re-write

$$\begin{aligned} E\left(Y_{i0} \times 1\left\{T_i = 0\right\}|q_j^k\right) &= \int_0^1 E\left(Y_{i0}|\nu_D = v\left(x;q_j\right)\right)x^k \mathrm{d}v\left(x;q_j\right) \\ &= \int_0^1 x^k y_0\left(v\left(x;q_j\right)\right)v'\left(x;q_j\right)\mathrm{d}x. \end{aligned}$$

The argument in the proof of Lemma 5 implies that the $n-$th order Fourier-Legendre approximation of $u\left(x;q_j\right) = y_0\left(v\left(x;q_j\right)\right)v'\left(x;q_j\right)$, denoted as $u_n\left(x;q_j\right)$, is a function of the observables $\left\{E\left(Y_{i0} \times 1\left\{T_i = 0\right\}|q_j^k\right)\right\}_{k=1}^n$. Similarly, let $\tilde{u}_n\left(x;q_j\right)$ be the (shifted) Fourier-Legendre series associated with model $\tilde{s}$ with associated feature $\left\{\tilde{y}_0\left(\cdot\right), \tilde{v}\left(\cdot\right)\right\}$ such that $\tilde{v} = v$.

Lemma 4 implies that for any subinterval $[a,b] \subset (0,1)$, $\frac{1}{n}\sum_{k=0}^{n-1} u_k\left(x;q_j\right)$ converges uniformly to $u\left(x;q_j\right)$ if $u\left(x;q_j\right)$ is square-integrable and continuous. Assumption 4(i) and (ii) imply continuity of $u\left(x,q_j\right)$ since the product of continuous functions is continuous. To show square-integrability of $y_0\left(v\left(x;q_j\right)\right)v'\left(x;q_j\right)$ observe that

$$\begin{aligned} \int_0^1 y_0\left(v\left(x;q_j\right)\right)^2 v'\left(x;q_j\right)^2 \mathrm{d}x &= \int_0^1 E\left(Y_{i0}|v\left(x;q_j\right)\right)^2 v'\left(x;q_j\right)^2 \mathrm{d}x \\ &\leq \sup_x |v'\left(x;q_j\right)| \int_0^1 E\left(Y_{i0}|v\left(x;q_j\right)\right)^2 v'\left(x;q_j\right)\mathrm{d}x \\ &= \sup_x |v'\left(x;q_j\right)| \int_0^1 E\left(Y_{i0}|\nu\right)^2 \mathrm{d}\nu, \end{aligned}$$

where the second equality follows from a change of variables. Observe that Assumption

4(i) holds that $\sup_x |v'(x;q_j)|$ is finite. The term $\int_0^1 E(Y_{i0}|\nu)^2 \,\mathrm{d}\nu$ is finite since

$$\begin{aligned}\int_0^1 E(Y_{i0}|\nu)^2 \,\mathrm{d}\nu &= V(E[Y_{i0}|\nu]) + E(E(Y_{i0}|v))^2 \\ &= V(E[Y_{i0}|\nu]) + E(Y_{i0})^2 \\ &\leq V(Y_{i0}) + E(Y_{i0})^2,\end{aligned}$$

where the inequality follows from the law of total variance. 4(ii) implies that the right hand side is bounded. Therefore, $\bar{u}_n(x,q_j)$ converges uniformly to $u(x;q_j)$. An identical argument implies that $\frac{1}{n}\sum_{k=0}^{n-1}\tilde{u}_n(x;q_j)$ converges uniformly to $\tilde{u}(x;q_j)$ over $x \in [a,b]$. Since $\bar{x} \in (0,1)$, we can pick $[a,b]$ such that $\bar{x} \in [a,b]$.

Now, let $\delta = |y_0(v(\bar{x};q_j))\, v'(\bar{x};q_j) - \tilde{y}_0(v(\bar{x};q_j))\, v'(\bar{x};q_j)| > 0$. Pick n such that

$$\left| y_0(v(\bar{x};q_j))\, v'(\bar{x};q_j) - \frac{1}{n}\sum_{k=0}^{n-1} u_k(\bar{x};q_j) \right| < \frac{\delta}{2}$$

and

$$\left| \tilde{y}_0(v(\bar{x};q_j))\, v'(\bar{x};q_j) - \frac{1}{n}\sum_{k=0}^{n-1} \tilde{u}_k(\bar{x};q_j) \right| < \frac{\delta}{2}.$$

Such an n exists because Lemma 4 implies that $\frac{1}{n}\sum_{k=0}^{n-1} u_k(\bar{x};q_j)$ and $\frac{1}{n}\sum_{k=0}^{n-1}\tilde{u}_k(\bar{x};q_j)$ converge to $y_0(v(\bar{x};q_j))\, v'(\bar{x};q_j)$ and $\tilde{y}_0(v(\bar{x};q_j))\, v'(\bar{x};q_j)$ respectively. Therefore, if q_j^k is in the support of the distribution of offer types for all $k \leq n$, then

$$\left| \frac{1}{n}\sum_{k=0}^{n-1} u_k(\bar{x};q_j) - \frac{1}{n}\sum_{k=0}^{n-1} \tilde{u}_k(\bar{x};q_j) \right| > 0.$$

Because each $u_n(\bar{x};q_j)$ and $\tilde{u}_n(\bar{x};q_j)$ is determined by the conditional expectations $\left\{E\left(Y_{i0} \times 1\{T_i = 0\} \,|q_j^k\right)\right\}_{k=1}^n$, we have shows that the joint distribution of $Y_{i0}, \left\{T_{ij_{i,1}}, \ldots, T_{ij_{i,k}}\right\}$ conditional on q_j^k differs for some $k \leq n$ under models s and $\tilde{s}$.

Identification of $E(Y_{ij}|\nu_D, \varepsilon_{ij,D} \geq \varepsilon_D, q_j)$. Define $y_1(\nu_D, \varepsilon_D; q_j) = E(Y_{ij}|\nu_D, \varepsilon_{ij,D} \geq \varepsilon_D, q_j)$. Consider a pair of models s and $\tilde{s}$. As argued above, we can restrict to pairs such that $v(x;q_j,z) = \tilde{v}(x;q_j,z)$ for all $x \in (0,1)$ and all z. For a given $\nu \in (0,1)$ and $\bar{x} \in (0,1)$, and let $\bar{z}$ be such that $\nu = v(\bar{x};q_j,\bar{z})$. We will show that if $y_1(v(\bar{x};q_j,\bar{z}),\bar{x};q_j)\, v'(\bar{x};q_j,\bar{z}) \neq$

$\tilde{y}_1\left(v\left(\bar{x};q_j,\bar{z}\right),\bar{x};q_j\right)v'\left(\bar{x};q_j,\bar{z}\right)$, then there exists n such that if q_j^k is in the support of the distribution of offer types for all $k\leq n$, then the joint distribution of Y_{ij}, $\left\{T_{ij_{i,1}},\ldots,T_{ij_{i,k}}\right\}$ conditional on q_j^k and $\bar{z}$ differs for some $k\leq n$ under models s and $\tilde{s}$.

Assumptions 1 and 2 imply that for each $k\leq n$, we can re-write the observed quantity

$$\begin{aligned}E\left(Y_{ij_k}\times 1\left\{T_{ij_k}=1\right\}|q_j^k,\bar{z}\right) &= \int_0^1 E\left(Y_{ij_n}|\nu_D=v\left(x;q_j,\bar{z}\right),\varepsilon_{ij,D}\geq x,q_j\right)x^{k-1}\left(1-x\right)\mathrm{d}v\left(x;q_j,\bar{z}\right)\\ &= \int_0^1 x^{k-1}\left(1-x\right)y_1\left(v\left(x;q_j,\bar{z}\right),x;q_j\right)v'\left(x;q_j,\bar{z}\right)\mathrm{d}x.\end{aligned}$$

Arguments similar to those above imply that for any $[a,b]\subset(0,1)$, we can uniformly approximate the function

$$u\left(x;q_j,\bar{z}\right)=\left(1-x\right)y_1\left(v\left(x;q_j,\bar{z}\right),x;q_j\right)v'\left(v\left(x;q_j,\bar{z}\right);q_j,\bar{z}\right)$$

over $x\in[a,b]\subset(0,1)$ with $\frac{1}{n}\sum_{k=0}^{n-1}u_n\left(x;q_j,\bar{z}\right)$, where $u_n\left(x;q_j,\bar{z}\right)$ is determined as a function of observed conditional distributions given $\bar{z}$ and q_j^k for $k\leq n$. This claim required continuity and square-integrability of $u\left(v\left(x;q_j,\bar{z}\right);q_j,\bar{z}\right)$ in x. Continuity follows because $y_1\left(\nu,x;q_j\right)$, $v\left(x;q_j,\bar{z}\right)$ and $v'\left(x;q_j,\bar{z}\right)$ are assumed to be continuous (Assumption 4) and the composition and product of continuous functions is continuous. Square integrability follows similarly to the argument above because

$$\begin{aligned}&\int_0^1\left(1-x\right)^2y_1\left(v\left(x;q_j,\bar{z}\right),x;q_j\right)^2v'\left(x;q_j,\bar{z}\right)^2\mathrm{d}x\\ &\leq\sup_x\left|v'\left(x;q_j\right)\right|\int_0^1\left(\left(1-x\right)E\left(Y_{ij}|v\left(x;q_j,\bar{z}\right),\varepsilon_{ij,D}\geq x\right)\right)^2v'\left(x;q_j,\bar{z}\right)\mathrm{d}x\\ &=\sup_x\left|v'\left(x;q_j\right)\right|\int_0^1\int_0^1E\left(Y_{ij}|v\left(x;q_j,\bar{z}\right),\varepsilon\right)^2 1\left\{\varepsilon\geq x\right\}v'\left(x;q_j,\bar{z}\right)\mathrm{d}x d\varepsilon\\ &=\sup_x\left|v'\left(x;q_j\right)\right|\int_0^1\int_0^1E\left(Y_{ij}|\nu,\varepsilon\right)^2 1\left\{v\left(\varepsilon;q_j,\bar{z}\right)\geq\nu\right\}\mathrm{d}\nu d\varepsilon\\ &\leq\sup_x\left|v'\left(x;q_j\right)\right|\int_0^1\int_0^1E\left(Y_{ij}|\nu,\varepsilon\right)^2\mathrm{d}\nu d\varepsilon,\end{aligned}$$

where the second equality follows from a change of variables and the fact that $v\left(x;q_j,z\right)$ is strictly monotonic in x. As above, Assumption 4(i) implies that $\sup_x\left|v'\left(x;q_j,z\right)\right|$ is

finite and

$$\begin{aligned}\int_0^1 E\left(Y_{ij}|\nu,\varepsilon\right)^2 \mathrm{d}\nu &= V\left(E\left[Y_{ij}|\nu,\varepsilon\right]\right) + E\left(E\left(Y_{ij}|v,\varepsilon\right)\right)^2 \\ &= V\left(E\left[Y_{ij}|\nu,\varepsilon\right]\right) + E\left(Y_{ij}\right)^2 \\ &\leq V\left(Y_{ij}\right) + E\left(Y_{ij}\right)^2,\end{aligned}$$

Therefore, if $\delta = |(1-\bar{x})\, y_1\left(v\left(\bar{x};q_j,\bar{z}\right),\bar{x};q_j\right) v'\left(\bar{x};q_j,\bar{z}\right) - (1-\bar{x})\, \tilde{y}_1\left(v\left(\bar{x};q_j,\bar{z}\right),\bar{x};q_j\right) v'\left(\bar{x};q_j,\bar{z}\right)|$, then, as argued above, Lemma 4 implies that there exists n such that $\left|\frac{1}{n}\sum_{k=0}^{n-1} u_n\left(\bar{x};q_j,\bar{z}\right) - \frac{1}{n}\sum_{k=0}^{n-1} \tilde{u}_n\left(\bar{x};\right.\right.$ 0. Because each $u_n\left(\bar{x};q_j,\bar{z}\right)$ and $\tilde{u}_n\left(\bar{x};q_j,\bar{z}\right)$ is determined by the conditional expectations $\left\{E\left(Y_{ij_k}\times 1\left\{T_{ij_k}=1\right\}|q_j^k,\bar{z}\right)\right\}_{k=1}^n$, we have shown that thejoint distribution of $Y_{ij}, \left\{T_{ij_{i,1}},\ldots,T_{ij_{i,k}}\right\}$ conditional on q_j^k and $\bar{z}$ differs for some $k\leq n$ under models s and $\tilde{s}$.

C.5 Dynamic Selection

Let $h_t\left(v\right)$ be the cdf of ν_D conditional on surviving until t. It is given by

$$h_t\left(v\right) = \int^v \frac{\Pr\left(Y_{i0}\geq t|\,\nu_D\right)}{\Pr\left(Y_{i0}\geq t\right)} d\nu_D.$$

Observe that the types ν_D of surviving patients will be uniformly distributed only if the event $Y_{i0}\geq t$ is independent of ν_D.

Lemma 6. *Suppose that the hypothesis of Theorem 1 hold.* The function $h_t\left(v\right) = \int^v \frac{\Pr(Y_{i0}\geq t|\nu_D)}{\Pr(Y_{i0}\geq t)} d\nu_D$ is identified for every $t\geq 0$.

Proof. Let q_j be a donor-type that arrives at the same time time as patient i. Because the image of $v(\cdot,q_j,z)$ is the unit interval (Assumption 3), for any $\nu_D\in(0,1)$ and z, there exists $\varepsilon_D\in(0,1)$ such that $\nu_D = v\left(\varepsilon_D;q_j,z\right)$. Theorem 1 implies that for every $t\geq 0$, $\mathbb{P}\left(Y_{i0}\geq t|\nu_D\right) = \mathbb{E}\left[1\left\{Y_{i0}\geq t\right\}|\,\nu_D\right]$ is identified. Thus, $\Pr\left(Y_{i0}\geq t\right)$ and the function $h_t\left(v\right)$ is identified. □

Define the cdf of the probability that a patient which survives until t_j rejects a kidney of

type q_j as $v_j(\varepsilon_D; q_j, z_i) = h_{t_j} \circ v(\varepsilon_D; q_j, z_i)$. Our next result shows that $v_j(\varepsilon_D; q_j, z_i)$ and $v(\varepsilon_D; q_j, z_i)$ are identified under additional smoothness assumptions on the distribution of $Y_{i0}|\nu_D$. Lemma 2 discussed the identification of the function $v(\varepsilon_D; q_j, z_i)$ for donor types q_j with $t_j = 0$. We extend this result to the case when $t_j > 0$.

Lemma 7. *Suppose that Assumption 5 and the hypothesis of Theorem 1 hold. Then, $v_j(\varepsilon_D; q_j, z_i)$ and $v(\varepsilon_D; q_j, z_i)$ are identified for every ε_D such that $\mathbb{P}(Y_{i0} \geq t_j | \nu_D = v(\varepsilon_D; q_j, z_i)) > 0$.*

Proof. Fix ε_D is such that $\mathbb{P}(Y_{i0} \geq t_j | \nu_D = v(\varepsilon_D; q_j, z_i)) > 0$. Note that $h_{t_j}(\cdot)$ is differentiable because $\mathbb{P}(Y_{i0} \geq t_j | \nu_D) > 0$ and Assumption 5 is satisfied. Moreover, it is increasing in v and has image equal to the unit interval. Therefore, we have that $v_j(\varepsilon_D; q_j, z_i)$ satisfies Assumption 3. By arguments identical to those in Lemma 2, $v_j(\varepsilon_D; q_j, z_i)$ is identified. Assumption 5 implies that $\mathbb{P}(Y_{i0} \geq t_j | \nu_D)$ is also positive in a neighborhood around ν_D and that h_{t_j} is strictly increasing at that point. Thus, $v(\varepsilon_D; q_j, z_i) = h_{t_j}^{-1} \circ v_j(\varepsilon_D; q_j, z_i)$ is identified because the terms on the right hand side are identified. □

We are now ready to prove our main identification result for donor types that arrive at any $t_j > 0$:

Proof of Theorem 2:

Proof. Take any $\varepsilon_D \in (0,1)$ and $\nu_D \in (0,1)$ satisfying the stated hypotheses. As argued in the proof of Lemma 7, $v_j(\cdot; q_j, z_i)$ satisfies Assumption 3 and is identified. Since $v_j(\cdot; q_j, z_i)$ is increasing in its argument, $\mathbb{P}(D_{ij} = 1 | \nu_{i,D} = v(\varepsilon_D; q_j, z_i), Y_{i0} \geq t_j)$ is identified.

By the chain rule $\frac{\partial}{\partial \varepsilon} v_j(\varepsilon_D; q_j, z_i) = \frac{\partial}{\partial \nu} h_{t_j}(\nu_D) \frac{\partial}{\partial \varepsilon} v(\varepsilon_D; q_j, z_i)$. Note that $\frac{\partial}{\partial \varepsilon} v(\varepsilon_D; q_j, z_i)$ is continuous, bounded and strictly positive. Also, $\frac{\partial}{\partial \nu} h_{t_j}(\nu_D) = \frac{\Pr(Y_{i0} \geq t_j | \nu_D)}{\Pr(Y_{i0} \geq t_j)}$ is continous, bounded and strictly positive because the denominator is strictly positive by the assumption that there exists ν_D with $\mathbb{P}(Y_{i0} \geq t_j | \nu_D, x_i) > 0$ and Assumption 5. Therefore, $\frac{\partial}{\partial \varepsilon} v_j(\varepsilon_D; q_j, z_i)$ is continuous and bounded and strictly positive. Therefore, the function

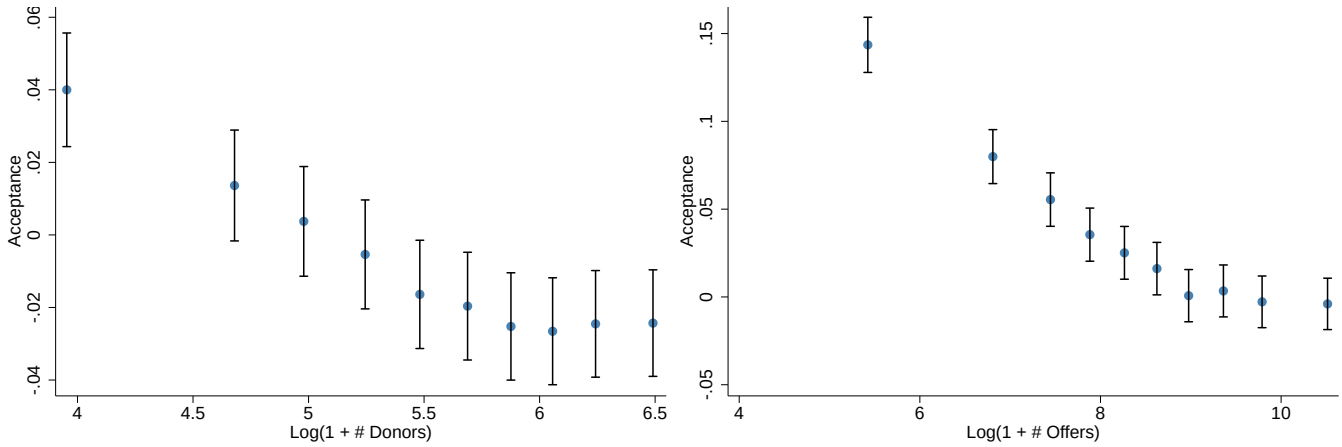
$\frac{\partial}{\partial \varepsilon} v_j(\cdot; q_j, z_i)$ it is strictly positive in a neiborhood of ε_D. Arguments identical to those used for proving Theorem 1 imply that $\mathbb{E}\left(Y_{ij} | h_{t_j}(\nu_{i,D}) = h_{t_j}(\nu_D), \varepsilon_{ij,D} \geq \varepsilon_D, Y_{i0} \geq t_j\right)$ is identified. Because $\mathbb{P}(Y_{i0} \geq t_j | \nu_D, x_i) > 0$, we have that $h_{t_j}(\nu_D)$ is strictly increasing at ν_D, the event $h_{t_j}(\nu_{i,D}) = h_{t_j}(\nu_D)$ is equivalent to $\nu_{i,D} = \nu_D$. □

D Additional Figures and Tables

Table D.5: Top 10 offers: Balance

	Age	Diabetes	Female	Weight	Height
	(1)	(2)	(3)	(4)	(5)
log(1 + # Top 10 Offers in 2 Years)					
KDPI <= 50%	-0.0479	0.00134	-0.00158	-0.269*	0.0253
	(0.0772)	(0.00302)	(0.00277)	(0.108)	(0.0732)
KDPI > 50% or Missing	-0.0233	-0.00427	0.000269	0.104	0.0137
	(0.0683)	(0.00294)	(0.00276)	(0.101)	(0.0819)
DSA FE, Year FE, and Blood Type FE	x	x	x	x	x
Control for Pediatric at Listing	x	x	x	x	x
CPRA Category Controls	x	x	x	x	x
F-test p-Value	0.499	0.267	0.787	0.037	0.828
Number of Observations	128949	127414	128949	127363	126619
R-Squared	0.026	0.022	0.074	0.038	0.034

Notes: * p<0.05, ** p<0.01, *** p<0.001
The sample for all regressions is patients who registered between 2000 and 2008. Dependent variables are as indicated in the column headers. All regressions control for DSA fixed effect, registration year fixed effect, blood type fixed effect, an indicator for pediatric at registration, and indictors for CPRA = 0, 20 <= CPRA < 80, CPRA >= 80, and CPRA missing at registration. Standard errors, clustered by DSA, registration year, and blood type, are in parentheses. F-test tests against the null hypothesis that the coefficients on the instruments are zero.



(a) Donors (b) Offers

Figure D.1: Scarcity Instrument: First Stage

Notes: Figures are plotted using binsreg (Cattaneo et al., 2019) with the same specification as Columns (5) and (6) in Table 4. Dependent variable is acceptance of an offer. Independent variables include DSA fixed effect, offer year fixed effect, number of years waited at offer fixed effect, blood type fixed effect, patient characteristics, donor characteristics, and match characteristics.

Table D.6: Scarcity Instruments: Balance

	Age	Diabetes	Female	Weight	Height
	(1)	(2)	(3)	(4)	(5)
Log(1 + No. Donors)					
Patients Waited 0-1 years	-0.319	0.00271	-0.00105	0.151	-0.254
	(0.331)	(0.0125)	(0.0115)	(0.516)	(0.328)
Patients Waited 1-2 years	0.135	-0.0129	0.00164	0.330	0.0594
	(0.299)	(0.0117)	(0.0109)	(0.457)	(0.307)
Patients Waited 2-3 years	-0.256	0.000252	0.0130	-0.290	-0.0133
	(0.272)	(0.0104)	(0.00902)	(0.397)	(0.269)
Patients Waited 3-4 years	0.286	0.0160	-0.0272***	0.114	0.109
	(0.223)	(0.00910)	(0.00800)	(0.348)	(0.225)
Patients Waited 4-5 years	-0.0248	-0.0117	0.0120*	-0.393	-0.212
	(0.153)	(0.00603)	(0.00533)	(0.220)	(0.152)
Log(1 + No. Offers)					
Patients Waited 0-1 years	0.395*	0.0165*	-0.00352	0.301	0.350
	(0.195)	(0.00817)	(0.00765)	(0.323)	(0.218)
Patients Waited 1-2 years	-0.0375	0.0000856	-0.00111	-0.228	-0.174
	(0.215)	(0.00847)	(0.00764)	(0.328)	(0.228)
Patients Waited 2-3 years	0.0897	0.000332	-0.00488	0.300	0.0110
	(0.213)	(0.00817)	(0.00698)	(0.315)	(0.223)
Patients Waited 3-4 years	-0.123	-0.0124	0.0189**	-0.1000	-0.0956
	(0.196)	(0.00766)	(0.00666)	(0.299)	(0.196)
Patients Waited 4-5 years	0.0748	0.0125*	-0.0130**	0.234	0.114
	(0.133)	(0.00527)	(0.00475)	(0.197)	(0.132)
Year FE, DSA FE, and blood type FE	x	x	x	x	x
Control for Pediatric at Listing	x	x	x	x	x
CPRA Category Controls	x	x	x	x	x
F-test p-Value	0.319	0.166	0.201	0.555	0.692
Number of Observations	87205	87200	87205	86078	85500
R-Squared	0.025	0.021	0.076	0.036	0.038

Notes: * p<0.05, ** p<0.01, *** p<0.001
The sample for all regressions is adult patients who registered on the waitlist between 1999Q4 and 2005Q4. Each regression is on patient level, where the dependant variable is the patient characteristics in the column header at registration. Each regression has five regressors indexed by $k = 0, 1, 2, 3, 4$, where the kth regressor for patient i is computed as the number of unique donors (offers) such that: the offer is made to patients who are in the same DSA as i, have the same blood type as i, and have waited the same number of years as i; the offer is made between $4k + 1$ and $4k + 4$ quarters, inclusive, from the quarter when i registers (e.g. if i registers in 2002Q1, then the offer must be made between 2003Q2 and 2004Q1 for $k = 1$. All regressions control for DSA fixed effect, registration year fixed effect, blood type fixed effect, an indicator for pediatric at registration, and indictors for CPRA = 0, 20 <= CPRA < 80, CPRA >= 80, and CPRA missing at registration. Robust standard errors, clustered by DSA, registration year, and blood type, are in parentheses. F-test tests against the null hypothesis that the coefficients on the five regressors are zero.

Table D.7: Survival Estimates

	(1)	(2)	(3)	(4)
Panel A: Survival without Transplant				
Constant	0.286	0.282	0.282	0.240
	(0.052)	(0.052)	(0.052)	(0.050)
Patient Characteristics				
Diabetic	-0.054	-0.054	-0.054	-0.055
	(0.001)	(0.001)	(0.001)	(0.001)
CPRA	0.018	0.018	0.018	0.016
	(0.006)	(0.006)	(0.006)	(0.006)
CPRA >= 0.8	0.000	-0.001	-0.001	-0.004
	(0.008)	(0.008)	(0.008)	(0.008)
CPRA = 0	0.003	0.003	0.003	0.002
	(0.002)	(0.002)	(0.002)	(0.002)
CPRA - 0.8 if CPRA >= 0.8	-0.073	-0.067	-0.067	-0.035
	(0.053)	(0.053)	(0.053)	(0.051)
Intial CPRA Missing	-0.129	-0.129	-0.129	-0.120
	(0.005)	(0.005)	(0.005)	(0.004)
Prior Transplant	-0.041	-0.041	-0.041	-0.041
	(0.005)	(0.005)	(0.005)	(0.005)
On Dialysis at Registration	-0.039	-0.039	-0.039	-0.035
	0.002	0.002	0.002	0.002
Blood Type A	0.006	0.006	0.006	0.005
	0.003	0.003	0.003	0.004
Blood Type O	0.019	0.020	0.020	0.018
	0.003	0.003	0.003	0.003
Blood Type B	0.027	0.029	0.029	0.027
	0.004	0.004	0.004	0.004
Age at Registration	0.002	0.002	0.002	0.002
	(0.001)	(0.001)	(0.001)	(0.001)
Age - 18 if Age >= 18	-0.003	-0.003	-0.003	-0.004
	(0.001)	(0.001)	(0.001)	(0.001)
Age - 35 if Age >= 35	-0.002	-0.002	-0.002	-0.002
	(0.000)	(0.000)	(0.000)	(0.000)
Age - 50 if Age >= 50	0.000	0.000	0.000	0.000
	(0.000)	(0.000)	(0.000)	(0.000)
Age - 65 if Age >= 65	-0.001	-0.001	-0.001	0.000
	(0.000)	(0.000)	(0.000)	(0.000)
BMI at Departure	0.004	0.004	0.004	0.005
	(0.003)	(0.003)	(0.003)	(0.003)
BMI - 18.5 if BMI >= 18.5	0.001	0.001	0.001	0.000
	(0.003)	(0.003)	(0.003)	(0.003)
BMI - 25 if BMI >= 25	-0.004	-0.004	-0.004	-0.004
	(0.001)	(0.001)	(0.001)	(0.001)
BMI - 30 if BMI >= 30	-0.001	-0.001	-0.001	-0.001
	(0.001)	(0.001)	(0.001)	(0.001)
BMI Missing	0.050	0.050	0.050	0.076
	(0.053)	(0.053)	(0.053)	(0.052)
Serum Albumin	0.043	0.042	0.042	0.042
	(0.002)	(0.002)	(0.002)	(0.002)
Serum Albumin - 3.7 if >= 3.7	0.011	0.011	0.011	0.012
	(0.004)	(0.004)	(0.004)	(0.005)
Serum Albumin - 4.4 if >= 4.4	-0.060	-0.059	-0.059	-0.060
	(0.005)	(0.005)	(0.005)	(0.005)
Serum Albumin Missing	0.148	0.147	0.147	0.148
	(0.008)	(0.008)	(0.008)	(0.008)
Log Dialysis Time at Registration (Years)	-0.015	-0.015	-0.015	-0.015
	(0.000)	(0.000)	(0.000)	(0.001)
Log Dialysis Time at Registration x 1{> 5 years}	0.000	0.000	0.000	0.006
	(0.005)	(0.005)	(0.005)	(0.005)
Unobservable Characteristics				
Selectivity				0.009
				(0.002)
Survival				0.067
				(0.032)

Table D.8: Survival Estimates (Continued)

	Panel B: Survival with Transplant			
Constant	0.646	1.778	1.758	0.628
	(0.089)	(0.237)	(0.237)	(0.092)
Patient Characteristics				
Diabetic	-0.097	-0.233	-0.234	-0.100
	(0.003)	(0.010)	(0.010)	(0.004)
CPRA	-0.010	-0.011	-0.013	-0.011
	(0.017)	(0.041)	(0.041)	(0.017)
CPRA >= 0.8	0.004	-0.011	-0.012	0.004
	(0.021)	(0.051)	(0.051)	(0.022)
CPRA = 0	0.003	0.007	0.007	0.003
	(0.005)	(0.012)	(0.012)	(0.005)
CPRA - 0.8 if CPRA >= 0.8	-0.072	-0.235	-0.242	-0.075
	(0.144)	(0.347)	(0.347)	(0.144)
Intial CPRA Missing	-0.008	-0.033	-0.031	-0.011
	(0.009)	(0.028)	(0.027)	(0.010)
Prior Transplant	-0.013	-0.044	-0.046	-0.016
	(0.015)	(0.040)	(0.040)	(0.016)
On Dialysis at Registration	-0.063	-0.185	-0.185	-0.064
	(0.004)	(0.010)	(0.010)	(0.004)
Blood Type A	-0.007	-0.019	-0.020	-0.008
	(0.007)	(0.017)	(0.017)	(0.007)
Blood Type O	0.001	0.003	0.000	0.000
	(0.007)	(0.018)	(0.018)	(0.007)
Blood Type B	-0.008	-0.005	-0.006	-0.009
	(0.008)	(0.019)	(0.019)	(0.008)
Age at Registration	-0.007	-0.013	-0.013	-0.006
	(0.002)	(0.004)	(0.004)	(0.002)
Age - 18 if Age >= 18	0.006	0.013	0.013	0.005
	(0.002)	(0.005)	(0.005)	(0.002)
Age - 35 if Age >= 35	-0.006	-0.017	-0.017	-0.007
	(0.001)	(0.003)	(0.003)	(0.001)
Age - 50 if Age >= 50	-0.002	-0.004	-0.004	-0.002
	(0.001)	(0.002)	(0.002)	(0.001)
Age - 65 if Age >= 65	-0.001	-0.002	-0.002	-0.001
	(0.001)	(0.002)	(0.002)	(0.001)
BMI at Departure	0.010	0.011	0.010	0.010
	(0.005)	(0.013)	(0.013)	(0.005)
BMI - 18.5 if BMI >= 18.5	-0.007	-0.001	-0.001	-0.007
	(0.005)	(0.014)	(0.014)	(0.005)
BMI - 25 if BMI >= 25	-0.003	-0.012	-0.012	-0.003
	(0.002)	(0.004)	(0.004)	(0.002)
BMI - 30 if BMI >= 30	-0.003	-0.004	-0.004	-0.003
	(0.001)	(0.003)	(0.003)	(0.001)
BMI Missing	0.205	0.271	0.268	0.205
	(0.091)	(0.235)	(0.235)	(0.090)
Serum Albumin	0.026	0.061	0.062	0.028
	(0.006)	(0.015)	(0.015)	(0.006)
Serum Albumin - 3.7 if >= 3.7	0.028	0.079	0.079	0.029
	(0.011)	(0.027)	(0.027)	(0.011)
Serum Albumin - 4.4 if >= 4.4	-0.056	-0.138	-0.138	-0.059
	(0.010)	(0.027)	(0.027)	(0.010)
Serum Albumin Missing	0.105	0.252	0.253	0.112
	(0.020)	(0.053)	(0.053)	(0.021)
Log Dialysis Time at Registration (Years)	-0.016	-0.042	-0.042	-0.016
	(0.001)	(0.004)	(0.004)	(0.001)
Log Dialysis Time at Registration x 1{> 5 years}	-0.070	-0.171	-0.171	-0.069
	(0.012)	(0.029)	(0.029)	(0.012)

Table D.9: Survival Estimates (Continued)

Donor Characteristics				
Age < 18	0.021	0.116	0.119	0.023
	(0.024)	(0.065)	(0.065)	(0.025)
Age 18-35	-0.017	-0.022	-0.020	-0.016
	(0.029)	(0.074)	(0.074)	(0.029)
Age 50+	0.020	0.235	0.230	0.017
	(0.055)	(0.152)	(0.152)	(0.055)
Cause of Death - Anoxia	0.003	-0.001	0.000	0.004
	(0.009)	(0.023)	(0.023)	(0.010)
Cause of Death - Stroke	0.002	0.000	0.001	0.003
	(0.009)	(0.023)	(0.023)	(0.009)
Cause of Death - CNS	0.010	0.041	0.039	0.009
	(0.019)	(0.050)	(0.050)	(0.019)
Cause of Death - Head Trauma	0.018	0.049	0.051	0.020
	(0.009)	(0.023)	(0.023)	(0.009)
Creatinine 0.5-1.0	-0.005	-0.002	0.000	-0.004
	(0.007)	(0.018)	(0.018)	(0.007)
Creatinine 1.0-1.5	-0.013	-0.023	-0.021	-0.012
	(0.007)	(0.018)	(0.018)	(0.007)
Creatinine >= 1.5	-0.012	-0.027	-0.028	-0.013
	(0.008)	(0.020)	(0.020)	(0.008)
Expanded Criteria Donor (ECD)	-0.019	-0.047	-0.049	-0.020
	(0.006)	(0.015)	(0.015)	(0.006)
Donation After Cardiac Death (DCD)	-0.003	-0.007	-0.009	-0.004
	(0.005)	(0.013)	(0.013)	(0.005)
Male	0.001	0.001	0.001	0.001
	(0.003)	(0.007)	(0.007)	(0.003)
History of Hypertension	-0.012	-0.026	-0.027	-0.013
	(0.004)	(0.009)	(0.009)	(0.004)
Offer Characteristics				
Perfect Tissue Type Match	0.053	0.162	0.167	0.054
	(0.025)	(0.067)	(0.067)	(0.026)
2 A Mismatches	-0.002	0.017	0.017	-0.002
	(0.016)	(0.039)	(0.039)	(0.016)
2 B Mismatches	0.001	-0.018	-0.019	0.001
	(0.017)	(0.042)	(0.043)	(0.017)
2 DR Mismatches	0.000	-0.006	-0.006	0.000
	(0.016)	(0.040)	(0.040)	(0.017)
ABO Compatible	-0.008	-0.011	-0.013	-0.009
	(0.012)	(0.030)	(0.030)	(0.012)
Regional Offer	-0.007	-0.014	-0.012	-0.007
	(0.014)	(0.036)	(0.036)	(0.014)
Local Offer	0.035	0.073	0.080	0.038
	(0.021)	(0.057)	(0.057)	(0.022)
Log Waiting Time (Years)	-0.003	-0.008	-0.008	-0.003
	(0.002)	(0.005)	(0.005)	(0.002)
Log Waiting Time x 1{Over 1 Year}	-0.003	-0.026	-0.025	-0.005
	(0.008)	(0.021)	(0.021)	(0.008)
Log Waiting Time x 1{Over 2 Years}	-0.021	-0.055	-0.055	-0.027
	(0.011)	(0.032)	(0.032)	(0.013)
Perfect Tissue Type Match x Prior Transplant	-0.003	0.012	0.012	-0.003
	(0.032)	(0.082)	(0.082)	(0.032)
Perfect Tissue Type Match x Diabetic Patient	-0.008	-0.011	-0.010	-0.007
	(0.008)	(0.019)	(0.019)	(0.008)
Perfect Tissue Type Match x Patient Age	0.000	-0.002	-0.002	0.000
	(0.000)	(0.001)	(0.001)	(0.000)
Perfect Tissue Type Match x CPRA	-0.016	0.011	0.012	-0.015
	(0.027)	(0.068)	(0.068)	(0.027)
Perfect Tissue Type Match x 1{CPRA > 80%}	-0.015	-0.039	-0.039	-0.015

Table D.10: Survival Estimates (Continued)

	(0.031)	(0.078)	(0.078)	(0.031)
Perfect Tissue Type Match x ECD Donor	0.019	0.044	0.042	0.018
	(0.011)	(0.030)	(0.030)	(0.011)
Perfect Tissue Type Match x DCD Donor	-0.014	-0.044	-0.045	-0.014
	(0.020)	(0.050)	(0.050)	(0.020)
Perfect Tissue Type Match x Local Offer	-0.027	-0.055	-0.056	-0.028
	(0.020)	(0.052)	(0.052)	(0.020)
Perfect Tissue Type Match x ABO Compatible	0.023	0.046	0.047	0.024
	(0.015)	(0.038)	(0.038)	(0.015)
Local Offer x 1{2 A Mismatches}	-0.001	-0.022	-0.022	-0.002
	(0.016)	(0.040)	(0.040)	(0.016)
Local Offer x 1{2 B Mismatches}	0.000	0.022	0.022	0.000
	(0.017)	(0.043)	(0.043)	(0.017)
Local Offer x 1{2 DR Mismatches}	-0.010	-0.011	-0.011	-0.010
	(0.017)	(0.040)	(0.040)	(0.017)
Local Offer x 1{Donor Age < 18}	-0.036	-0.097	-0.099	-0.037
	(0.017)	(0.046)	(0.046)	(0.018)
Local Offer x 1{Donor Age 18-35}	-0.017	-0.032	-0.033	-0.018
	(0.013)	(0.035)	(0.035)	(0.013)
Local Offer x 1{Donor Age 50+}	-0.010	-0.022	-0.022	-0.010
	(0.014)	(0.035)	(0.035)	(0.014)
Patient Age x 1{Donor Age < 18}	0.000	0.000	0.000	0.000
	(0.000)	(0.001)	(0.001)	(0.000)
Patient Age x 1{Donor Age 18-35}	0.001	0.003	0.003	0.002
	(0.001)	(0.002)	(0.002)	(0.001)
Patient Age x 1{Donor Age 50+}	-0.001	-0.008	-0.008	-0.001
	(0.002)	(0.004)	(0.004)	(0.002)
Patient Age - 35 if Age >= 35 x 1{Donor Age 18-35}	-0.001	-0.002	-0.002	-0.001
	(0.001)	(0.002)	(0.002)	(0.001)
Patient Age - 35 if Age >= 35 x 1{Donor Age 50+}	0.002	0.008	0.008	0.001
	(0.002)	(0.005)	(0.005)	(0.002)
Unobserved Covariates				
Selectivity		0.001	-0.002	-0.004
		(0.012)	(0.012)	(0.004)
Survival		1.000	1.000	1.000
		(0.000)	(0.000)	(0.000)
Match Value		0.002	0.009	0.002
		(0.019)	(0.019)	(0.008)
Donor Quality	0.002	0.003	0.005	0.002
	(0.001)	(0.005)	(0.005)	(0.002)
Instruments	No Instruments	# Past Donors	# Past Offers	# Future Donors

Notes: Estimates of the survival equations are presented. The sample includes 7938854 offers made between 2000 and 2009 to patients in the sample. The chain length is 850000, which includes a burn-in of 50000 draws. We thin the chain by taking every 10 draws. All columns control for dummies for DSA fixed effect, blood type fixed effect, and registration year fixed effect. Future donors (offers) is defined as the number of donors (offers) in the next 4 quarters (see Table 4 for detailed definition). Standard errors are in parenthese.

Table D.11: Choice Estimates

	(1)	(2)	(3)	(4)
Constant	-4.080	-4.895	-4.071	-5.266
	(0.175)	(0.356)	(0.356)	(0.381)
Patient Characteristics				
Diabetic	-0.043	-0.090	-0.093	-0.111
	(0.006)	(0.011)	(0.011)	(0.013)
CPRA	-0.721	-1.072	-1.089	-1.504
	(0.032)	(0.064)	(0.065)	(0.067)
CPRA >= 0.8	-0.198	-0.181	-0.132	-0.162
	(0.043)	(0.086)	(0.087)	(0.087)
CPRA = 0	0.053	0.110	0.110	0.110
	(0.009)	(0.018)	(0.019)	(0.019)
CPRA - 0.8 if CPRA >= 0.8	-1.322	-3.142	-3.258	-2.839
	(0.287)	(0.563)	(0.576)	(0.569)
Intial CPRA Missing	0.632	1.178	1.177	1.214
	(0.024)	(0.047)	(0.048)	(0.045)
Prior Transplant	-0.319	-0.468	-0.478	-0.578
	(0.028)	(0.052)	(0.053)	(0.057)
On Dialysis at Registration	0.012	0.050	0.054	0.060
	(0.007)	(0.013)	(0.013)	(0.014)
Blood Type A	-0.307	-0.425	0.053	-0.477
	(0.036)	(0.063)	(0.065)	(0.063)
Blood Type O	-0.553	-0.827	-0.183	-0.871
	(0.037)	(0.066)	(0.068)	(0.065)
Blood Type B	-0.149	-0.652	-0.328	-0.713
	(0.040)	(0.067)	(0.067)	(0.070)
Age at Registration	0.057	0.084	0.083	0.082
	(0.003)	(0.005)	(0.005)	(0.005)
Age - 18 if Age >= 18	-0.055	-0.085	-0.083	-0.082
	(0.003)	(0.006)	(0.006)	(0.006)
Age - 35 if Age >= 35	0.002	0.008	0.009	0.008
	(0.002)	(0.004)	(0.004)	(0.004)
Age - 50 if Age >= 50	-0.003	-0.005	-0.005	-0.006
	(0.001)	(0.002)	(0.002)	(0.003)
Age - 65 if Age >= 65	-0.002	-0.002	-0.003	-0.003
	(0.002)	(0.004)	(0.004)	(0.004)
BMI at Departure	-0.011	-0.010	-0.009	0.019
	(0.009)	(0.018)	(0.018)	(0.019)
BMI - 18.5 if BMI >= 18.5	0.007	0.000	-0.002	-0.033
	(0.010)	(0.020)	(0.020)	(0.021)
BMI - 25 if BMI >= 25	-0.007	-0.011	-0.011	-0.008
	(0.003)	(0.007)	(0.007)	(0.007)
BMI - 30 if BMI >= 30	-0.006	-0.008	-0.008	-0.012
	(0.003)	(0.005)	(0.005)	(0.006)
BMI Missing	-0.593	-0.888	-0.860	-0.283
	(0.164)	(0.328)	(0.333)	(0.354)
Serum Albumin	0.001	-0.003	-0.002	0.018
	(0.011)	(0.022)	(0.022)	(0.024)
Serum Albumin - 3.7 if >= 3.7	0.067	0.102	0.102	0.115
	(0.020)	(0.040)	(0.041)	(0.042)
Serum Albumin - 4.4 if >= 4.4	-0.089	-0.149	-0.151	-0.159
	(0.021)	(0.041)	(0.042)	(0.041)
Serum Albumin Missing	0.082	0.138	0.146	0.216
	(0.039)	(0.078)	(0.078)	(0.084)
Log Dialysis Time at Registration (Years)	0.008	0.025	0.027	0.025
	(0.002)	(0.004)	(0.004)	(0.005)
Log Dialysis Time at Registration x 1{> 5 years}	-0.008	0.050	0.039	0.025
	(0.022)	(0.044)	(0.044)	(0.050)
Donor Characteristics				
Age < 18	1.169	1.930	1.957	1.907
	(0.052)	(0.081)	(0.081)	(0.085)
Age 18-35	0.752	1.359	1.380	1.728
	(0.059)	(0.095)	(0.094)	(0.098)
Age 50+	-1.176	-1.987	-1.990	-2.010
	(0.085)	(0.132)	(0.132)	(0.143)

Table D.12: Choice Estimates (Continued)

Cause of Death - Anoxia	0.097	0.156	0.153	0.203
	(0.054)	(0.089)	(0.086)	(0.089)
Cause of Death - Stroke	0.409	0.678	0.677	0.736
	(0.053)	(0.088)	(0.086)	(0.090)
Cause of Death - CNS	-0.589	-0.894	-0.876	-0.988
	(0.100)	(0.158)	(0.154)	(0.175)
Cause of Death - Head Trauma	0.573	0.969	0.967	0.998
	(0.052)	(0.089)	(0.085)	(0.089)
Creatinine 0.5-1.0	0.757	1.281	1.273	1.270
	(0.038)	(0.068)	(0.067)	(0.058)
Creatinine 1.0-1.5	0.523	0.898	0.890	0.912
	(0.040)	(0.072)	(0.071)	(0.060)
Creatinine >= 1.5	-0.577	-0.927	-0.926	-0.839
	(0.041)	(0.076)	(0.074)	(0.064)
Expanded Criteria Donor (ECD)	-0.733	-1.203	-1.174	-1.247
	(0.034)	(0.053)	(0.054)	(0.052)
Donation After Cardiac Death (DCD)	-0.438	-0.734	-0.737	-0.765
	(0.028)	(0.049)	(0.048)	(0.055)
Male	0.108	0.184	0.184	0.175
	(0.016)	(0.027)	(0.027)	(0.027)
History of Hypertension	-0.351	-0.591	-0.588	-0.598
	(0.023)	(0.029)	(0.029)	(0.036)
Offer Characteristics				
Perfect Tissue Type Match	1.208	1.828	1.876	1.520
	(0.053)	(0.091)	(0.092)	(0.091)
2 A Mismatches	-0.027	-0.039	-0.040	-0.110
	(0.013)	(0.021)	(0.020)	(0.025)
2 B Mismatches	0.020	0.031	0.031	-0.022
	(0.013)	(0.023)	(0.023)	(0.026)
2 DR Mismatches	-0.086	-0.143	-0.147	-0.152
	(0.012)	(0.018)	(0.018)	(0.024)
ABO Compatible	-0.492	-0.820	-0.854	-0.866
	(0.039)	(0.066)	(0.067)	(0.066)
Regional Offer	0.477	0.812	0.817	0.134
	(0.017)	(0.025)	(0.025)	(0.030)
Local Offer	1.698	2.783	2.798	2.508
	(0.030)	(0.046)	(0.045)	(0.050)
Log Waiting Time (Years)	-0.022	0.034	0.025	0.053
	(0.004)	(0.007)	(0.007)	(0.007)
Log Waiting Time x 1{Over 1 Year}	0.161	0.441	0.322	0.419
	(0.016)	(0.027)	(0.027)	(0.028)
Log Waiting Time x 1{Over 2 Years}	0.174	0.484	0.235	0.352
	(0.023)	(0.042)	(0.043)	(0.043)
Perfect Tissue Type Match x Prior Transplant	-0.262	-0.639	-0.658	-0.598
	(0.076)	(0.148)	(0.148)	(0.147)
Perfect Tissue Type Match x Diabetic Patient	0.009	-0.037	-0.034	-0.016
	(0.023)	(0.042)	(0.042)	(0.042)
Perfect Tissue Type Match x Patient Age	0.002	0.005	0.005	0.005
	(0.001)	(0.002)	(0.002)	(0.001)
Perfect Tissue Type Match x CPRA	0.059	0.084	0.087	0.365
	(0.073)	(0.137)	(0.137)	(0.143)
Perfect Tissue Type Match x 1{CPRA > 80%}	0.086	0.057	0.031	0.123
	(0.077)	(0.147)	(0.147)	(0.156)
Perfect Tissue Type Match x ECD Donor	-0.765	-1.229	-1.266	-1.033
	(0.043)	(0.069)	(0.069)	(0.071)
Perfect Tissue Type Match x DCD Donor	-0.556	-0.957	-0.963	-1.057
	(0.076)	(0.128)	(0.127)	(0.129)
Perfect Tissue Type Match x Local Offer	0.147	0.379	0.360	0.699
	(0.039)	(0.061)	(0.060)	(0.063)
Perfect Tissue Type Match x ABO Compatible	0.482	0.850	0.875	0.908
	(0.048)	(0.085)	(0.085)	(0.082)
Local Offer x 1{2 A Mismatches}	-0.007	-0.016	-0.015	0.042
	(0.014)	(0.023)	(0.023)	(0.027)

Table D.13: Choice Estimates (Continued)

Local Offer x 1{2 B Mismatches}	-0.114	-0.181	-0.183	-0.177
	(0.015)	(0.025)	(0.026)	(0.028)
Local Offer x 1{2 DR Mismatches}	-0.149	-0.207	-0.211	-0.243
	(0.014)	(0.020)	(0.020)	(0.026)
Local Offer x 1{Donor Age < 18}	-0.868	-1.416	-1.426	-1.284
	(0.033)	(0.054)	(0.055)	(0.058)
Local Offer x 1{Donor Age 18-35}	-0.414	-0.706	-0.703	-0.960
	(0.031)	(0.050)	(0.049)	(0.052)
Local Offer x 1{Donor Age 50+}	0.100	0.134	0.134	0.024
	(0.028)	(0.043)	(0.043)	(0.050)
Patient Age x 1{Donor Age < 18}	-0.013	-0.021	-0.021	-0.023
	(0.001)	(0.001)	(0.001)	(0.001)
Patient Age x 1{Donor Age 18-35}	0.003	0.003	0.003	0.000
	(0.001)	(0.002)	(0.002)	(0.002)
Patient Age x 1{Donor Age 50+}	0.015	0.028	0.028	0.032
	(0.002)	(0.004)	(0.004)	(0.004)
Patient Age - 35 if Age >= 35 x 1{Donor Age 18-35}	-0.011	-0.016	-0.016	-0.014
	(0.002)	(0.003)	(0.003)	(0.003)
Patient Age - 35 if Age >= 35 x 1{Donor Age 50+}	-0.006	-0.014	-0.014	-0.016
	(0.003)	(0.004)	(0.004)	(0.004)
Scarcity				
Log(1+#Past Donors)		-0.289		
		0.018		
Log(1+#Past Offers)			-0.297	
			0.008	
Log(1+#Future Donors)				-0.268
				0.019
Instruments	No Instruments	# Past Donors	# Past Offers	# Future Donors

Notes: Estimates of the choice equation are presented. The sample includes 7938854 offers made between 2000 and 2009 to patients in the sample. The chain length is 850000, which includes a burn-in of 50000 draws. We thin the chain by taking every 10 draws. All columns control for dummies for DSA fixed effect, blood type fixed effect, and registration year fixed effect. Future donors (offers) is defined as the number of donors (offers) in the next 4 quarters (see Table 4 for detailed definition). Standard errors are in parenthese.