A Random Graph Model of Kidney Exchanges: Efficiency, Individual-Rationality and Incentives

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ABSTRACT

In kidney exchanges, hospitals share patient lists and receive transplantations. A kidney-paired donation (KPD) mechanism needs to promote full sharing of information about donor-patient pairs, and identify a Pareto efficient outcome that also satisfies participation constraints of hospitals. We introduce a random graph model of the KPD exchange and then fully characterize the structure of the efficient outcome and the expected number of transplantations that can be performed. Random graph theory allows early experimental results to be explained analytically, and enables the study of participation incentives in a methodological way. We derive a square-root law between the welfare gains from sharing patient-donor pairs in a central pool and the individual sizes of hospitals, illustrating the urgent need for the nationwide expansion of such programs. Finally, we establish through theoretical and computational analysis that enforcing simple individual rationality constraints on the outcome can mitigate the negative impact of strategic behavior by hospitals.

Categories and Subject Descriptors

J.4 [**Computer Applications**]: Social and Behavioral Sciences—*Economics*; G.2 [**Discrete Mathematics**]: Graph Theory—*Matchings in random graphs*

General Terms

Algorithms, Theory, Economics, Experimentation

Keywords

kidney exchange, random graph theory, maximum matching, individual rationality, mechanism design

1. INTRODUCTION

The scarcity of cadaver kidneys and significant medical benefits from live kidney donation has promoted the expansion of kidney-paired donation (KPD) in recent years. The idea is that kidney patients with one or more incompatible donors, might be able to receive compatible transplants through barter exchanges. It is typical for this to be performed as a two-way exchange, which involves four (typically simultaneous) operations.[1] Currently, there is a handful of such kidney-exchange programs in the USA and several others around the world [14]. Their expansion in large-scale has been hitherto hindered by the ethical, logistical and even incentive issues they entail.

Nevertheless, there are numerous reports favoring the benefit of kidney exchanges. From the medical literature, survival rates up to 100% are reported in a sample including 10 two-way, paired donations [8]. Further benefits in terms of total saved lives can be found where larger than two-way exchanges are considered [14]. Recent history has seen an increase in (KPD) through multi-regional KPD programs [11].

Naturally enough, if we would like to represent the patient-donor set as a graph, with each pair as a vertex, and focusing on two-way exchanges, then we could think of the compatibility relationships as being the edges. An edge indicates a two-way compatibility between the donor and patient of pair one and pair two, and vice-versa. If one considers utility to be achieved by a compatible transplant to a patient, then the Pareto-efficient solution with only two-way exchanges is a *maximum matching* [12]. In this paper, we make a clean start by defining a comprehensive *random graph* model of (two-way) KPD exchanges. The use of a random-graph model is appropriate here, because there are well defined probabilistic models of the blood and tissue type compatibility of donor-patient pairs entering KPD exchanges.

In addition to efficiency, an important consideration is in regard to the incentives of hospitals to participate, where a typical concern is that an individual hospital will hold back some pairs (to match locally, before or after the exchange clears) in order to increase the number of hospital-specific matches. This kind of strategic hiding of pairs can lead away from Pareto-efficient solutions. In Ashlagi et al. [3], this loss is shown to be 50% in the worst case for strategyproof

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[1] Longer than 2-way exchanges are also possible. In 2007, a chain of 10 kidney transplantations was performed that lasted over 8 months [10] and that was triggered by a single altruistic donor with no designated recipient. Here, we will focus on 2-way exchanges that are easier to perform in practice and thus more prevalent

mechanisms, in short because one has to find the maximum matching individually for every hospital before looking at the global maximum. By adopting a random-graph model, we are able to complement the worst-case analysis in the literature with a meaningful average-case analysis. The main technical content of this paper involves developing a structural analysis of maximum matchings on domain-appropriate random graph models, and the main message is positive: our analytical and simulation results suggest that an appropriate exchange design can be very effective in mitigating incentives to hospitals for hiding patient-donor pairs.

We completely characterize the maximum matching properties of our model (i.e. Pareto-optimal outcomes). In stating our results, we work under two assumptions: the first is a *perfect matching (PM) assumption*, which is that any bipartite random graph, with the probability of an edge between two vertices defined in a way that is appropriate to the kidney domain, will assume a perfect matching. This is easily justified even for small-size patient lists of less than 10 pairs, and the resulting analytical model is very accurate, explaining early experimental results [1, 13, 15]. The second is a *regularity assumption* on the existence of optimal exchanges that possess a particular graph structure. We derive a square-root relationship between the welfare gains of sharing patient-donor pairs in a central pool and the individual sizes of hospitals. This serves as a formal proof for the necessity of collaborative, nationwide kidney exchange programs.

Based on our analysis of the structure of the matching problem, the strategic problem facing hospitals is reduced to a game of adding nodes on a bipartite graph, which enables us to show empirically that non-truthful sharing in a non-IR mechanism is hurtful in expectation to truthful hospitals. We also quantify this expected loss in a 2-hospital scenario. In the sequel, we consider two variants on individually-rational centralized mechanisms, both of which are efficient under the PM assumption when hospitals fully reveal their patient-donor pairs. Our preferred mechanism (`xCM`), computes a matching of a particular structure individually for each hospital, and completes with a random maximum matching of the remainder donor-patient pairs. We establish under an additional regularity assumption on the realized structure of maximum matchings in KPD graphs, that `xCM` is individually-rational, efficient and supports full sharing of donor/patient pairs in a Bayesian-Nash equilibrium.

In detailed simulations, we validate the incentive compatibility of the `xCM` mechanism. In comparison, a randomized, non-IR mechanism allows a strategic hospital to achieve $\sim 20\%$ more transplantations than the truthful ones. `xCM` eliminates this benefit and also keeps efficiency. Our model remains robust after the introduction of extra nuisance parameters (for example PRA sensitivity of patients) in which `xCM` is also able to restore fairness and retain almost 96% of efficiency.

Some proofs are omitted from this version of the paper in the interest of space and will be available in an extended version.

1.1 Related Work

Roth et al. [13] study priority mechanisms in which patients decide how to reveal the sets of their incompatible donors and the transplants they are willing to accept. Hospital incentives are analyzed in Ashlagi et al. [3], although in worst-case rather than random-graph framework.

Ashlagi and Roth [2], independently of our work, adopt a random-graph model with which to study individually-rational, multiple hospital mechanisms (including 3-way exchanges). While the themes and qualitative observations are quite similar, our results differ. First, we provide a detailed, quantified analysis of the welfare gains from a centralized pool (Theorem 2, Corollary 2 and 3.) Through this, we are also able to provide an almost perfect analytical explanation for existing numerical results in the literature. Second, our main equilibrium, IR and efficiency results are presented for the `xCM` *mechanism* and made under the PM and regularity assumptions. In comparison, Ashlagi and Roth [2] introduce a different mechanism, termed the *Bonus mechanism* and provide an equilibrium analysis under a different regularity assumption. In particular, we both focus on the set Ω of efficient outcomes, but Ashlagi and Roth [2] assume an expected property over the entire set, namely the *regular size assumption*, while we make a claim on the existence of an outcome $\alpha \in \Omega$ of a specific structure. Interestingly, we show (under our assumptions) that for 2-way exchanges, IR and efficiency can be achieved in a Bayes-Nash equilibrium of the xCM mechanism, while Ashlagi & Roth [2] establish (under their assumptions), and while allowing for 3-way exchanges, that IR can be achieved with a small efficiency loss that is about 1% of the individual hospital sizes in an epsilon Bayes-Nash equilibrium of the Bonus mechanism. In this sense, our works can be considered complementary. In addition, our positive results on xCM hold in both a truthful equilibrium and an equilibrium in which each hospital follows a canonical deviation and only hides pairs that form part of a maximum matching with a particular structure on its own, local graph.

2. MISE-EN-SCÈNE

Human blood has four different types, namely O, A, B and AB, depending on the presence or absence of the proteins A and B. Two people are blood-type compatible if the donor does not introduce new proteins to the recipient. For example, a donor with blood type A can donate to patients with type A or AB and a donor with type O can donate to any blood type since O denotes the absence of both proteins.

Blood-type compatibility is the first requirement for a kidney transplantation. In addition, the donor and the recipient should share as many common HLA antigens as possible to prevent a *positive crossmatch*, i.e. the transplant being rejected. The probability of a crossmatch between a donor and a patient selected at random has been calculated around 11% [17]. However, this number varies greatly among patients and we will adopt the analysis in [14] which identifies three distinct categories of tissue-type sensitivities, namely low, medium and high PRA, as shown in Table 1:

Sensitivity type	Distribution	p_c probability
Low-PRA	70.19%	0.05
Medium-PRA	20%	0.45
High-PRA	9.81%	0.9

Table 1: Positive crossmatch [14]

In this paper we will denote the positive crossmatch proba-

bility with p_c and we will fix its value to $p_c \approx 0.2$ to produce numerical results, i.e. the weighted average of the aforementioned distribution. In this case the probability that two pairs that are already blood-type compatible, are also tissue-type compatible is $(1-p_c)^2 = 0.64$, since every donor has to be compatible with the patient of the other pair. We therefore make the strong, simplifying assumption that tissue-type compatibilities are independent random events, ignoring blood and PRA sensitivity types for the moment. However, in Section 5.2 we show that our results remain robust even under these nuisance parameters.

Formally, a donor-patient pair is defined on $S \times S$, where $S = \{O, A, B, AB\}$ is the blood-type set. Following the terminology in Ünver [15], we break up the entire set into 4 distinct subsets as follows:

Definition 1. A donor-recipient pair is *under-demanded* (denoted U), if the donor is not ABO compatible with the patient. If in addition the pair contains only the types A and B, then it is called *reciprocal* (denoted by R).

Definition 2. A pair is *over-demanded* (denoted by O) if the donor and the patient are ABO compatible. If they also have the same type then the pair is called *self-demanded* (denoted by S).

The following table summarizes.

patient	O	A	B	AB
donor				
O	S	O	O	O
A	U	S	R	O
B	U	R	S	O
AB	U	U	U	S

Table 2: ABO subsets

The compatibilities of Lemma 1 are depicted graphically in Figure 1. It is now easy to establish the following:

LEMMA 1. *An under-demanded pair can only be matched to an over-demanded one. A reciprocal pair can be paired with an over-demanded or another reciprocal pair. A self-demanded pair can me matched to an over-demanded or another self-demanded pair.*

2.1 The random graph model

We model the donor-patient pairs of a hospital as a graph where a node represents one such pair and an edge represents the fact that two pairs can perform a paired donation. Obviously, an efficient two-way kidney exchange is a maximum matching on this graph. Our goal is then to study the expected properties of such a matching under two probabilistic assumptions: that blood types are drawn from some discrete blood-type distribution and that tissue-type compatibilities are independent Bernoulli trials with probability $1-p_c$ (robustness against these assumptions will be checked in subsequent sections). Random graph theory is therefore a natural way to study the expected properties of efficient outcomes and the Bayes-Nash equilibria of multi-hospital participation in KPD markets.

More formally, a *random donor-patient graph* that has n pairs is denoted by $\widetilde{G_n}$ and its vertex set is constructed by

the following random process:

```
REPEAT until G_n has n pairs
      Draw 2 people ∼Blood Type Frequencies
          IF not Blood Type Compatible
                Add to G_n
          ELSE
                Add to G_n with probability p_c
REPEAT ∀u,v ∈ V(G_n),
      IF u,v ABO compatible AND x ∼ U(0,1), x > p_c
          ADD (u,v) to E(G_n)
```

In general, the O group is the most common, and A, B, AB follow in that order. For our analysis, we will consider a fixed distribution over the blood types. To produce arithmetical results we will consider a distribution of $O(50\%)$, $A(30\%)$, $B(15\%)$ and $AB(5\%)$ which is close to the world average (see [16]) but we will also check for robustness in the experimentation section of the paper.[2]

Unfortunately, the aforementioned process does not adhere to any well-known random graph model. Nevertheless, we will soon show how to combine known combinatorial results with the specific properties of $\widetilde{G_n}$, aiming to identify the structural properties that *most* of the model-generated graphs share with each other.

We start by identifying the vertex sets and the induced subgraphs in $\widetilde{G_n}$ that correspond to the pair types introduced in Definitions 1 and 2. In particular denote with O, U, S, R the vertex sets containing the over-demanded, under-demanded, self-demanded and reciprocal pairs respectively. The expected sizes of these sets are given by the following lemma.

LEMMA 2. *Denote with p_x the probability that a random pair in $\widetilde{G_n}$ belongs to the x vertex set, $x \in \{O, U, S, R\}$ and f_y the frequency of blood type y. Then it holds:*

$$p_O = \frac{w \cdot p_c}{V}, p_S = \frac{s \cdot p_c}{V}, p_U = \frac{w}{V}, p_R = \frac{r}{V} \quad (1)$$

Also (see Table 2),

$$V = w + w \cdot p_c + s \cdot p_c + r$$
$$w = f_O \cdot (f_A + f_B) + f_{AB} \cdot (f_O + f_A + f_B)$$
$$s = f_O^2 + f_A^2 + f_B^2 + f_{AB}^2$$
$$r = 2 \cdot f_A \cdot f_B$$

Furthermore, the expected sizes of the subgraphs of $\widetilde{G_n}$ are:

$$|O| = p_O \cdot n = \frac{w \cdot p_c}{V} \cdot n$$
$$|U| = p_U \cdot n = \frac{w}{V} \cdot n \quad (2)$$
$$|S| = p_S \cdot n = \frac{s \cdot p_c}{V} \cdot n$$
$$|R| = p_R \cdot n = \frac{r}{V} \cdot n$$

PROOF. By considering a fixed distribution of ABO blood-types, equations (1) and (2), follow immediately by the elementary properties of the uniform distribution. For the

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[2]Blood-type distribution among human population varies a lot [16]. For example, Koreans are evenly distributed in types O, A and B while the Bororo people in Brazil are 100% of type O.

aforementioned distribution, the coefficients are $w = 0.2725$, $s = 0.365$, $r = 0.09$. $\square$

By Lemma 2, the size of every vertex set is proportional to the total size n of a graph in $\widetilde{G_n}$. However, by inspection, the set O is much smaller than the set U since $\frac{|O|}{|U|} = p_c < 1$. A similar argument holds for the set S as well. In summary, Lemma 1 gives information about compatibilities among different pair types and Lemma 2 offers insight on their respective sizes. Figure 1 is a graphical depiction of the structure of a $\widetilde{G_n}$ graph. The edges in the figure correspond to compatibility relationships but the intra-type compatibilities (i.e. self-loops) have been omitted.
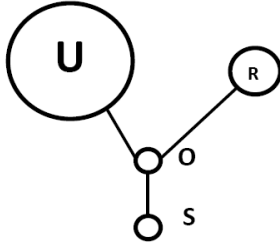

Figure 1: Vertex sets in $\widetilde{G_n}$

The sizes were calculated by considering the positive cross-match probability equal to $p_c = 0.2$. Obviously, the over-demanded pairs are more centrally placed within the graph and thus more likely to participate in a maximum matching. In addition, a large portion of the under-demanded pairs are left unmatched by any matching, due to the blood-type incompatibilities with each other, as shown in Lemma 1. These and similar remarks are summarized in the following lemma:

LEMMA 3. *The O subgraph (induced by the O vertex set) is connected to all other subgraphs. The U subgraph is isolated, i.e. it has no edges. The subgraph R is bipartite. The S subgraph is comprised by four disconnected components comprising the pairs $(O,O), (A,A), (B,B)$ and (AB,AB)*

PROOF. No under-demanded pair can be matched to an under-demanded pair by Lemma 1, thus the U subgraph is isolated. Pairs within the R subgraph are symmetric in Table 2 and hence R is bipartite with the vertex classes (A, B) and (B, A). Pairs in the S subgraph are on the main diagonal of Table 2 and hence S has 4 disconnected components, one for each blood type. $\square$

As first shown in Roth et al. [13], the Pareto-optimal solution is essentially a maximum matching on the graph. It is therefore important to characterize the maximum matchings of $\widetilde{G_n}$, which in fact is a random graph as well. In the following section we will achieve approximate results which will form the basis for our subsequent analysis.

3. MAXIMUM MATCHING IN $\widetilde{G_N}$

In graph theory [4], the maximum matching of a graph is a subset of its edges with no common vertices and with the maximum cardinality possible. It has numerous applications as a combinatorial problem [9], and luckily it can be solved deterministically in polynomial time by Edmond's algorithm [6]. Random graph theory [5] on the other hand, studies distributions over graphs normally referred to as *random graph models*. For example, $G_{n,p}$ is often defined as a process producing graphs with n nodes such that each of the $\binom{n}{2}$ possible edges exists independently with a probability p. Combinatorial arguments are then used to explore graph invariants such as size, connectivity or chromatic number.

Despite the extensive research literature and to the best of our knowledge, no random graph model could be applied directly for the problem defined in this paper. However, it will suffice to prove a specific result regarding matchings in bipartite graphs and then make a few reasonable assumptions on how to proceed. In particular, let us denote with $G_{n \times n,p}$ the bipartite graph with n nodes in each class such that any node is connected to any node of the other class with probability p. It then holds:

THEOREM 1. *Graphs in model $G_{n \times n,p}$ with $p > \phi - 1$ (ϕ being the golden ratio) assume a perfect matching for sufficiently large n.*

Theorem 1 is sufficient in unveiling that a bipartite random graph always assumes a near-perfect matching. In order to facilitate our mathematical analysis for the rest of our technical results, we make the following assumption:

ASSUMPTION 1. **Perfect matching (PM)** *Every graph drawn from $G_{n \times n,p}$ assumes a perfect matching*

For example, under our kidney exchange model where $p = 1 - p_c = 0.8$ the probabilities of a perfect matching for $n = 4$ and $n = 6$ are 0.985 and 0.999 respectively. In addition, any graph in $G_{2n,p}$ can be reduced to a graph in $G_{n \times n,p}$ and thus inherit its matching properties. As a consequence of the PM assumption, we conclude that:

COROLLARY 1. *Under the PM assumption, every graph drawn from $G_{n,p}$ with n even, assumes a perfect matching*

We now proceed to characterize the maximum matching on $\widetilde{G_n}$. We make the PM assumption throughout the rest of the paper.

LEMMA 4. *The probability that the O subgraph cannot be completely matched to the U subgraph in random graph $\widetilde{G_n}$ decreases exponentially in n.*

PROOF. An O pair (x, y) is compatible with its symmetric (y, x) U pair. By Lemma 2, pairs (y, x) are expected to be $\frac{1}{p_c}$ times more than the pairs (x, y). Therefore, with n O pairs, $\frac{1-p_c}{p_c} \cdot n$ pairs in U will remain unmatched on average. This means that there will be $\alpha \cdot n$ pairs in U that will be unmatched, for some constant α. The probability that an over-demanded pair remains unmatched if subgraph O is matched only against the U subgraph is therefore equal to $p_c^{\alpha \cdot n}$. This tends to 0 for large n. $\square$

The S subgraph is even more densely connected as shown in the following lemma:

LEMMA 5. *Consider the subgraph S with k pairs contained in some $\widetilde{G_n}$. Also denote with $s(k)$ the expected number of pairs that are matched in a maximum matching of S, and with β some value $O(1)$. Then:*

$$s(k) = k - \beta$$

For sufficiently large k it holds that $\beta = 2$.

We now turn our attention to the R subgraph. This is a bipartite graph (see Lemma 3) but it is unbalanced and therefore we cannot apply Assumption 1 directly.

LEMMA 6. *Consider the R subgraph with k pairs contained in some $\widetilde{G_n}$. Also denote with $r(k)$ the expected number of pairs that are matched in a maximum matching of R. It holds:*

$$r(k) = k - \Theta(\sqrt{k})$$

In particular,

$$k - r(k) \sim \sqrt{\frac{2}{\pi} \cdot k}$$

The unmatched pairs in the R subgraph actually follow the *folded binomial* distribution. Formally, if $X \sim Binom(n, p), p = 0.5$ then the variable defined by $Y = |2 \cdot X - n|$ follows a folded binomial. By Lemma 6 we have that $E[Y]$ approximates the value $\sqrt{\frac{2}{\pi} \cdot n}$. Now it is easy to prove the following:

LEMMA 7. *Consider m independent random variables X_i, such that $X_i \sim Binom(n, 0.5)$. Also define:*

$$Y_m = |(2X_1 - n) + \cdots + (2X_m - n)| = |2\sum_i X_i - m \cdot n|$$

Then it holds,

$$E[Y_m] \sim \sqrt{\frac{2}{\pi} \cdot n \cdot m} \qquad (3)$$

PROOF. The sum of m random variables X_i defined as above follows $Binom(m \cdot n, 0.5)$. Applying Lemma 6 and a substitution of variables will get us the desired result. □

We can now put the pieces together and characterize maximum matchings globally on $\widetilde{G_n}$ by calculating the expected cardinality of a maximum matching.

THEOREM 2. *If $\mu(n)$ is the expected cardinality of a maximum matching in $\widetilde{G_n}$, then given the PM assumption, there exist positive constants $\gamma < 1$ and β such that:*

$$\mu(n) = \gamma \cdot n - \Theta(\sqrt{n}) - \beta$$

PROOF. Consider a matching in $\widetilde{G_n}$ where all O pairs are matched with pairs in U and subgraphs S and R assume maximum matchings internally. It is not possible to construct an alternating path for this matching since by Lemma 1 the U subgraph is isolated. Therefore, the matching is maximum (see also [9]). In expectation and in a population of n donor patient pairs and given equations (2), the unmatched pairs are equal to $|U| - |O| + \Theta(\sqrt{n}) + \beta = \lambda \cdot n + \Theta(\sqrt{n}) + \beta$. Therefore the expected number of matches is given by equation:

$$\mu(n) = n - (\lambda \cdot n + \Theta(\sqrt{n}) + \beta) \qquad (4)$$

Setting $\gamma = 1 - \lambda$, we conclude that

$$\mu(n) = \gamma \cdot n - \Theta(\sqrt{n}) - \beta$$

□

In particular by equations (2) and $p_c = 0.2$ we have that $\lambda = (1 - p_c) \cdot \frac{w}{V} \approx 0.44$ and hence $\gamma = 1 - \lambda = 0.56$. We now make the following definition, which will be helpful when considering incentives.

Definition 3. Maximum matchings of $\widetilde{G_n}$ in which O is matched completely to U and the S and R subgraphs assume a maximum matching internally, are themselves random graphs denoted by $\widetilde{M_n}$. The remainder graph, $\widetilde{D_n} = \widetilde{G_n} - \widetilde{M_n}$ is also random and on expectation it contains:

- Pairs in the U subgraph, proportional to size n
- Pairs in R all of the *same* class (either A-B or B-A) proportional to $\sqrt{n}$
- A total of 2 pairs of the S type

Notice also that graphs from $\widetilde{D_n}$ are isolated, i.e. they contain no edges. The proof of Theorem 2 establishes that matchings of the form $\widetilde{M_n}$ exist with high probability for a given $\widetilde{G_n}$.

3.1 Interpretation of results

Using Theorem 2 and Lemma 6, and adopting $|R|$ as the size of the reciprocal subgraph, we can use the following approximation for the expected number of matched pairs in $\widetilde{G_n}$:

$$\mu(n) \approx 0.556 \cdot n - \sqrt{\frac{2}{\pi} \cdot |R|} - 2 \qquad (5)$$

Using equation (2) we know that $|R| = \frac{r}{V} \cdot n = 0.18n$. Substituting in (5) we get:

$$\mu(n) \approx \gamma \cdot n - \delta \cdot \sqrt{n} - 2 \qquad (6)$$
$$\gamma = 0.556, \ \delta = 0.342$$

We can now explain much of the assumptions and empirical observations of previous related work. The abundance of unmatched undemanded pairs is established in Lemma 2. The deviation from the *maximal-size* matching in Roth et al. [13] (See Propositions 1 & 2 and Table 2), are explained by virtue of Theorem 2. In particular, for the simulation with $n = 100$ the deviation from the expected ~ 56 exchanges is explained by equation (6) which yields $55.6 - 0.34 \cdot 10 - 2 = 50.2$. This result is very close to the value 49.7 that is reported in Roth et al. [13].

Similarly, simulation results in Table 1 of Abraham et al. [1], although they were based on few samples (100 trials), is also explained in light of Theorem 2. In particular, equation (6) almost always provides estimations between the reported mean and max values. Finally, Lemmas 4,5,6 prove analytically the assumptions behind kidney exchange models that focus on the reciprocal R subgraph, as in Ünver [15] which uses the number of (A, B) pairs as the representative state of a Markov chain model.

4. INCENTIVES IN KPD MARKETS

We now turn our attention to the case of multiple hospitals contributing their donor-patient graphs to a KPD market. We make this model more succinct through the following definitions:

Definition 4. The addition of two donor-patient graphs G_1, G_2 is defined by $G_1 \bigoplus G_2 = G_1 \bigcup G_2 \bigcup C$, where $C = \{(u, v)\}, u \in V(G_1), v \in V(G_2)$, and pair u is blood-type compatible and tissue-type compatible with pair v, the latter independently with probability p_c. Let $V(G), E(G)$ and $M(G)$ denote the vertex set, the edges set and some maximum matching of graph G respectively.

Definition 5. A *hospital* h of size n has a donor-patient graph G_h as a type, which is a realization of random graph $\widetilde{G_n}$. A *strategy* s_h of a hospital h is a function such that $s_h(G_h) \subseteq G_h$. If $s_h(G_h) = G_h$ the strategy is *truthful*. If $s_h(G_h) \subset G_h$ it is *non-truthful*. A *selfish* strategy is defined by $s_h(G_h) = \oslash$

Definition 6. A *centralized mechanism CM* defined on m hospitals each of size n, and with graph type profile $G = (G_1, \cdots, G_m)$ and a strategy profile $s = (s_1, \cdots, s_m)$, computes a matching $CM(s, G)$ on graph $\hat{G} = \bigoplus_h s_h(G_h)$. The set of nodes on $CM(s, G)$ that belong to hospital h will be denoted by $CM_h(s, G)$.

The *utility* of a hospital from some outcome is given by $U_h(s, G) = |CM_h(s, G)| + |M(G_h - CM_h(s, G))|$. The implicit assumption is that hospitals will try to maximize the matches on the patients that were not matched by the mechanism. For a specific type G_h of h and a strategy profile s, the *expected utility* is $\overline{U_h}(s) = \mathbb{E}_{G_{-h}}[U_h(s, G_h \bigcup G_{-h})]$, where $G_{-h} = (G_1, \cdots, G_{h-1}, G_{h+1}, \cdots, G_m)$

The welfare $W(s, G)$ produced by the mechanism is thus equal to $W(s, G) = \sum_h U_h(s, G)$. For a strategy profile s, $\forall G$, an *efficient CM* allocates welfare $W(s, G) = |M(\bigoplus_h G_h)|$

An outcome $CM(s, G)$ is *individually rational* (IR) if $\forall h$ $CM_h(s, G) \geq |M(s_h(G_h))|$. Finally, a strategy profile $s = (s_h, s_{-h})$ is a Bayes-Nash equilibrium (BNE) if $\forall h$, $\forall s'_h$ it holds that $\overline{U_h}(s_h, s_{-h}) \geq \overline{U_h}(s'_h, s_{-h})$

4.1 Mechanisms

Definition 7. rCM is a *CM* which, given $\hat{G}$, outputs a uniformly sampled, maximum matching $M(\hat{G})$. A uniform sample from the maximum matchings of some graph G can be implemented through a relabeling of $V(G)$ and a generic maximum matching algorithm.

Definition 8. irCM is a *CM* which, given $\hat{G}$, repeatedly calls rCM until the outcome is also IR.

Definition 9. xCM is a *CM* which, operates in two stages: First, it clears internally the graphs $s_h(G_h), \forall h$, by enforcing the constraints of $\widetilde{M_n}$ (see Definition 3) and computing the most efficient matching possible, say L_h. Second, it runs rCM on the union of the individual remainder graphs, i.e. rCM(s, G).

It is straightforward to enforce the constraints of $\widetilde{M_n}$ in xCM through weighted matching (see [9]). Our implementation in Section 5 simply assigns larger weights to the edges between O and U pairs and then performs maximum weighted matching on the entire donor-patient graph.

Our first result, which stems directly from Theorem 2, quantifies the benefit of an institution as simple as rCM. Our baseline is the case when the mechanism is not used at all, or equivalently when all hospitals employ selfish strategies.

COROLLARY 2. *For mechanism* rCM *with m hospitals of size n and the parameters r, V defined in Lemma 2, and under the PM assumption, the welfare surplus $W(s, G)$ when hospitals employ truthful strategies compared to selfish ones is equal to:*

$$W(s, G) = (m - \sqrt{m}) \cdot \sqrt{\frac{2r}{\pi V} \cdot n} + (m - 1) \cdot \beta \quad (7)$$

PROOF. Consider equation (6) of the average maximum matching in $\widetilde{G_n}$. When hospitals are selfish, total welfare is $m \cdot \mu(n)$ and when truthful welfare is $\mu(m \cdot n)$ since all hospitals draw independently from the same random graph model. Therefore, all we need to compute is:

$$W(s, G) = \mu(m \cdot n) - m \cdot \mu(n)$$

Substituting with Equation (6) for the value of $\mu(n)$ we get the desired result. $\square$

By symmetry, the additional matches are distributed evenly among hospitals:

COROLLARY 3. *A hospital of size n that participates in* rCM *with m truthful participants, and under the PM assumption, will receive δU more transplantations on average, for which:*

$$\delta U = (1 - 1/\sqrt{m}) \cdot \sqrt{\frac{2r}{\pi V} \cdot n} + (1 - 1/m) \cdot \beta \quad (8)$$

For large CMs where $m \to \infty$, it holds that,

$$\delta U = \sqrt{\frac{2r}{\pi V} \cdot n} + \beta \quad (9)$$

A nationwide kidney exchange program can therefore yield individual benefits to participating hospitals that follow a square-root law to the size n of their patient lists, given that this sharing is truthful by all participants.

Continuing, we make the following key assumption:

ASSUMPTION 2. **(Regularity)** *For every $\widetilde{G_n}$, there exists a maximum matching drawn from some $\widetilde{M_n}$.*

In words, the regularity assumption claims the existence of a particular type of maximum matchings in $\widetilde{G_n}$. In such a matching all O pairs are completely matched to U pairs, and S and R pairs are self-matched. In the connectivity analysis of Section 3, we showed that this is a fair assumption to make, but simulation data is supportive as well. For example, in $\widetilde{G_n}$ with parameters $n = 40, p_c = 0.2$, the probabilities that there exists a matching of the form $\widetilde{M_n}$ that is either 0 or 1 exchange away from a maximum matching is 0.85 and 0.98 respectively. For a crossmatch probability $p_c = 0.11$ as reported in [17] these numbers are even higher, 0.94 and 0.998 respectively. If we include PRA sensitivity in our model (see Table 1) these numbers for $n = 40$ are 0.71 and 0.95. This hints at our model being robust even under this extra variability.

In order to emphasize the use of our two basic assumptions of perfect matching and regularity for studying incentives, we will make the following definition:

Definition 10. An *idealized* mechanism *CM* is a mechanism operating under the PM and Regularity assumptions.

By definition, the idealized xCM always computes matchings of the form $\widetilde{M_n}$ in the first stage of its operation. Lemma 8 establishes that individual rationality constraints do not affect the efficiency of our idealized mechanisms.

LEMMA 8. *Under truthful strategies, the idealized* **irCM** *and the idealized* **xCM** *are individually rational and efficient.*

However, mechanism `irCM` is not very computationally plausible since it searches blindly for IR and efficient matches, and in a straightforward implementation, takes a long time to finish. Our incentives analysis will thus focus on the `xCM` mechanism.

4.2 Incentives

We start with clarifying the concept of a hospital's deviating strategy.

Definition 11. Define a *proper subgraph* of G, a subgraph $P(G) \subseteq G$, $P(G) \neq \oslash$, such that $\forall u \in V(P(G))$, if $(u, v) \in G$ then $v \in P(G)$.

Definition 12. Given hospital h with graph G_h, a *deviating* strategy d_h is defined by $d_h(G_h) = G_h - P(M_h)$, where $P(M_h)$ is a proper subgraph of some maximum matching M_h of G. If $P(M_h) = M_h$ the strategy is called *fully deviating*. If maximum matching M_h is of the form $\widetilde{M_n}$, then the strategy is called *canonically deviating*.

A strategy is both fully deviating and canonically deviating when a hospital is hiding completely an internal maximum matching of the form $\widetilde{M_n}$. We will soon show that canonical deviations are Bayes-Nash equilibria in kidney exchanges, however our equilibrium analysis will explore the entire space of possible strategies.

Let us first examine cases where hospitals fully deviate. The first natural question is whether this strategy is undesirable. For clarity, we focus on the simplest case of two hospitals, one being truthful and one (fully) deviating, denoted by h_t and h_d respectively. We will also use the following combinatorial definition:

Definition 13. Define $J(a, b, N)$ to be the number of white balls in a chain of N balls created by picking balls randomly from a jar with a white balls and b black balls without replacement.

It is easy to establish that the expected value $\overline{J}(a, b, N)$ is given by $\overline{J}(a, b, N) = \frac{a}{a+b} \cdot N$

We now seek to compute δU_t, the expected gain in utility of h_t being truthful compared to being selfish (i.e. reporting nothing). Also denote with δU_d the gains for hospital h_d. First, we will study `rCM`, as a typical non-IR mechanism and then `xCM`, which is IR by construction.

4.2.1 In mechanism `rCM`

We consider only pairs in the R subgraph since our analysis in Section 3 showed that all other pair types will not affect δU_t as much. In particular, say h_t reports s and w pairs in the two classes, such that $s \geq w$, and that h_d reports y pairs of the some specific kind. Then there are exactly three cases, as shown in Figure 2.

Mechanism `rCM` will allocate the following utilities:

$$\delta U_t = \begin{cases} J(s, y, w) - w & \text{case } (\alpha) \\ y & \text{case } (\beta) \\ s - 2w + J(w, y, s) & \text{case } (\gamma) \end{cases}$$
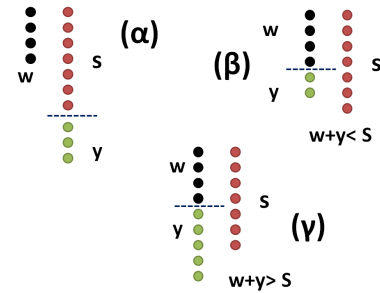

Figure 2: Deviating agent has y pairs of one kind (green). Truthful agent has s, w of both reciprocal pair types

For the fully deviating agent:

$$\delta U_d = \begin{cases} J(y, s, w) & \text{case } (\alpha) \\ y & \text{case } (\beta) \\ J(y, w, s) & \text{case } (\gamma) \end{cases}$$

It is hard to derive analytically the sign of δU_t, since $\delta U_t > 0$ for (α) and some (γ) and $\delta U_t < 0$ for (β) and some (γ). However, we can adopt simulations. Figure 3 depicts the average values of δU_t and δU_d in 1,000 test runs in `rCM`. Also notice from the equations, that $\delta U_d = \Theta(y)$ and since $y \propto \sqrt{|R|}$ by virtue of Lemma 6, it holds that $\delta U_d = \Theta(\sqrt{|R|})$. This is reflected in the shape of the red utility line for the strategic agent. A similar argument holds for the truthful agent as well.
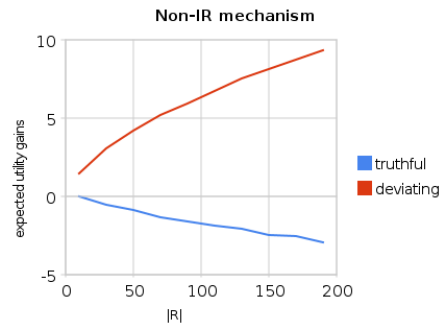
Figure 3: Truthful strategy has expected loss in a non-IR mechanism

It is straightforward to generalize to encompass multiple hospitals and show that, on average, deviating strategies not only yield benefits but also incur costs to truthful ones.

4.2.2 In mechanism `xCM`

We proceed to characterize the equilibrium strategies for mechanism `xCM`.

LEMMA 9. *Strategy profiles under idealized* **xCM** *in which, either hospitals are truthful or all hospitals are canonically deviating, are Bayes-Nash equilibria.*

Intuitively, given an edge (u, v) in a maximum matching, a hospital decides how to report u and v. If it reports both of

them then xCM, by construction, will match them (or some other two of similar types). If it reports none, then they will be matched internally, otherwise If it reports only one, then there is some small probability that one pair will remain unmatched which is clearly undesirable. By induction, the first two cases can generate the truthful strategy and the canonical deviations and these are BNE.

Observe that the selfish strategy profile is also a BNE. However, we believe that the truthful equilibrium (or some form of canonical deviation) is much more likely in practice. A good reason is that the non-reporting BNE is not robust against pairwise deviations by hospitals and so would likely be unstable given the ability of hospitals to reach mutually advantageous agreements.

THEOREM 3. *The idealized mechanism* xCM *is individually rational and efficient in the truthful Bayes-Nash equilibrium, and also in every canonical deviation Bayes-Nash equilibrium.*

PROOF. We know that under truthful strategies the total welfare is $\mu(n \cdot m)$. By Lemma 9, in equilibrium, $\forall h \in H$, $\forall (w, M(w)) \in \widetilde{M_n}$ of that hospital, h will either report both w and $M(w)$ or none. In either case, these pairs will be matched before the second stage of xCM, which is equivalent in terms of efficiency to the case of all hospitals being truthful. However, by Lemma 8 the idealized xCM is efficient under truthful strategies and therefore it is efficient in all BNE with truthful or canonical deviation strategies. □

The average case analysis concluded with Theorem 3, proves that individual rationality enables efficiency under reasonable assumptions. Ashlagi & Roth [2] get a similar result for their "Bonus" mechanism. In fact, the first steps of their algorithm are similar to the first step of xCM, in the way that matches in the S and R subgraphs are implemented. From that point, their algorithm diverges since in 3-way kidney exchanges, matches between O, U and R pairs become available.

5. EXPERIMENTAL RESULTS

We used Perl to implement the $\widetilde{G_n}$ random graph model and test the theoretical results. In particular, maximum matchings were determined by an implementation of the Galil algorithm [7] that runs in $O(|V|^3)$ time, which proved faster than open-source LP libraries. Currently, on a dual-core PC with 2.4 Ghz/CPU, the donor-patient graph of $1,000$ pairs is cleared in approximately 10 seconds.[3]

In our first experiments we generate random graphs $\widetilde{G_n}$ through the process defined in Section 2.1. The first two tables refer to the matching properties of the S and R subgraphs, in which we report the number of matched patients compared to the individual sizes of the subgraphs averaged over $1,000$ samples.

The expected values for optimal matchings of the subgraph S (Table 3) are given by Lemma 5 and for the expected matchings in R by Lemma 6. The realized values are very close to what our analysis predicts. Notice also the increasing standard deviation for matchings in R, which stems from the properties of the folded binomial.

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[3]The Perl source code is available for download from http://www.eecs.harvard.edu/econcs/code/rgke.zip Detailed instructions on how to reproduce the results of this section can be found in the package.

#pairs	#matches	$(|S| - \beta)$	sd
20	18.12	18.0	1.15
40	38.1	38.0	1.06
60	57.91	58.0	1.14
80	77.93	78.0	1.11
100	97.92	98.0	1.07

Table 3: Maximum matching in S

#pairs	#matches	$(|R| - \sqrt{\frac{2}{\pi} \cdot |R|})$	sd
20	16.64	16.43	2.64
40	34.94	34.95	3.73
60	54.16	53.82	4.79
80	72.97	72.86	5.67
100	91.76	92.02	6.12

Table 4: Maximum matching in R

For Theorem 2, which computes the expected cardinality of the maximum matchings of $\widetilde{G_n}$, we simply take $1,000$ samples of $M(\widetilde{G_n})$ for various values of n. The results are shown in Table 5, and validate the analysis.

#pairs	#matches	$\mu(n)$	sd
20	7.83	7.57	3.16
40	18.12	18.04	4.46
60	28.56	28.66	5.66
80	39.2	39.35	6.69
100	49.51	50.09	7.33
200	104.75	104.18	11.22

Table 5: Maximum matching in $\widetilde{G_n}$

5.1 Experiments with incentives

We will put our theory to test on mechanism xCM, since irCM is not easy to implement efficiently and also lacks a thorough incentives analysis. We start by examining the welfare surplus of rCM with 3 truthful hospitals, each reporting some $\widetilde{G_n}$. Again, we take $1,000$ samples for various sizes of n.

n	H-1	H-2	H-3	Total	Selfish	$W(s, G)$
20	9.63	9.36	9.45	28.44	22.77	5.94
40	20.26	20.05	20.31	60.62	54.24	6.74
60	31.05	31.22	31.23	93.49	86.14	7.36
80	41.99	41.97	42.31	126.26	118.27	7.88
100	52.97	52.37	52.59	157.93	150.55	8.33

Table 6: Surplus from rCM with truthful hospitals

The left part of Table 6 refers to the simulation results and the right one gives the theoretical predictions. The column titled "Selfish" gives the welfare when hospitals are not reporting anything to the centralized mechanism. Our theory predicts with high accuracy the expected welfare surplus. For example, for $n = 60$ we have that $W = 7.36$ using Corollary 2, when the real value is $93.49 - 86.14 = 7.35$. Last, notice that the surplus is distributed evenly among all

hospitals with values that are very close to $\mu(n) + W/3$, as predicted in Corollary 2. For example, if $n = 60$, the predicted utility is $28.71 + 2.45 = 31.16$, which is very close to what all hospitals receive (see H-1,2,3 for $n = 60$)

Next, we proceed to study cases in which not all hospitals are truthful. Here we will consider only full deviations and for brevity we will refer to this as simply a deviation. Our analysis in Section 4 showed that deviating strategies are provably hurtful to the utility of truthful hospitals under a non-IR centralized mechanism. To validate the truthfulness of xCM, we modify our simulation so that H-1 deviates fully. We first run on the non-IR centralized mechanism we defined as rCM. See Table 7.

n	H-1$_d$	H-2	H-3	Total
20	10.67	8.60	8.65	27.92
40	23.08	18.39	18.52	59.99
60	35.45	28.68	28.81	92.93
80	47.71	38.62	38.55	124.88
100	60.68	49.18	48.94	158.8

Table 7: H-1 deviates in rCM

We again take 1,000 samples for each value of the hospital size n, and report the average values. First, notice that H-1 matches consistently more pairs any other truthful hospital. Second, it is interesting to see that total welfare is not hurt by the deviation (if we compare it to the one reported in Table 5). This should not come as a surprise, since Theorem 3 actually builds upon this property to deliver a mechanism that is IR and efficient on average. Next, we run xCM under the same setting to get the results in Table 8.

n	H-1$_d$	H-2	H-3	Total
20	9.28	9.46	9.27	28.01
40	19.74	19.79	20.03	59.57
60	30.65	30.51	30.54	91.69
80	41.66	41.91	41.13	124.7
100	52.02	52.39	52.36	156.76

Table 8: H-1 deviates under xCM

There are two important remarks. First, imposing IR is effective against incentives if one looks at the individual utilities received by each hospital (also compare with Table 6). Furthermore, the mechanism produces on average efficient outcomes if we compare with Table 6, as predicted by Theorem 3.

5.2 Robustness of results

The $\widetilde{G}_n$ model makes several simplifying assumptions, by using a specific blood type distribution and treating the tissue-type compatibilities as independent random events with probability $p_c = 0.2$. Here we test how relevant our model remains with the introduction of nuisance parameters.

In particular, we test two different blood-type distributions, one O(27%), A(32%), B(31%) and AB(10%) as in Korea and one set to O(44%), A(42%), B(10%) and AB(4%) as in the USA. Note that each distribution induces different parameters for the calculation of the $\mu(n)$ formula in Lemma 2. Let us denote with $\mu_K(n)$ and $\mu_U(n)$ the formulas for Korea

and US respectively. Furthermore we endow p_c with a variability as in Table 1. In particular, every pair draws a PRA sensitivity from the distribution of Table 1 which defines its individual crossmatch probability. Two pairs i, j are then tissue-type compatible with probability $(1 - p_{c,i}) \cdot (1 - p_{c,j})$

We try to reproduce Table 5 in this more realistic scenario, since Theorem 2 is the core of our analysis. The results on 1,000 samples are shown in Table 9:

#pairs	#(Korea)	$\mu_K(n)$	#(USA)	$\mu_U(n)$
20	7.18	8.67	5.83	7.62
40	17.21	20.6	14.4	18.11
60	28.27	32.74	23.86	28.75
80	39.54	44.99	33.89	39.46
100	51.24	57.3	44.01	50.22
200	111.16	119.41	97.6	104.39

Table 9: Matches with different ABO distributions and with PRA sensitivity (see Table 1)

The theoretical predictions do become less accurate under these different assumptions due mostly to the introduction of PRA variability. However, our theoretical model remains robust, in that it shares the approximate behavior of the realized values. For example, one can observe that the ratios of simulation over theoretical values are decreasing and approaching 1 for large graph sizes.

Next, we would like to examine if xCM remains effective in mitigating the impact of strategic playing under PRA variability. To stress our analysis further, we will examine the US blood type distribution. Our baseline is again defined to be rCM. In the first scenario we wish to find out the best welfare that can be achieved and we assume this to happen when all hospitals are truthful. The results are shown in Table 10.

n	H-1	H-2	H-3	Total
20	8.05	7.88	7.75	23.67
40	18.37	18.08	18.04	54.49
60	29.15	29.13	28.99	87.27
80	39.82	39.85	39.4	119.06
100	50.99	50.71	51.21	152.92

Table 10: All truthful in rCM (PRA+US blood freqs.)

Next we let hospital H-1 deviate. The results shown in Table 11 reveal that H-1 is doing consistently better than truthful hospitals, but at the same time appears not to hurt much the overall efficiency ($\sim$ 1-2%).

n	H-1$_d$	H-2	H-3	Total
20	9.18	7.45	7.33	23.96
40	20.41	16.52	16.68	53.61
60	32.19	26.16	25.74	84.09
80	45.29	36.25	35.98	117.52
100	57.15	46.0	45.97	149.12

Table 11: H-1 deviating in rCM (PRA+US)

Next we run our simulation with H-1 deviating under mechanism xCM. The results are shown in Table 12.

n	H-1_d	H-2	H-3	Total
20	7.78	7.3	7.56	22.64
40	17.54	17.36	17.47	52.37
60	27.66	27.72	27.27	82.65
80	37.2	37.53	37.48	112.20
100	48.33	47.81	48.02	144.16

Table 12: H-1 deviating in `xCM` (PRA+US)

We conclude that `xCM` restores fairness since H-1_d receives approximately the same number of transplantations with truthful participants, while it consistently receives more than others under `rCM`. Furthermore, the cost in efficiency is small and stems mostly from the O and S subgraphs, which under the PRA model are more likely to contain highly sensitized patients. As a result, our connectivity assumptions are violated, thus leading to a noticeable loss in efficiency. For $n = 40$, that is for a *CM* with 120 total patients, this loss is $\sim 3.6\%$ of the total efficiency. Therefore, our analysis remains robust in dealing with parameters such as the PRA variability or different blood type distributions, that were not explicit parts of the model. Further improvements are expected by modeling PRA sensitivity within the $\widetilde{G_n}$ model and refactoring the analysis (Assumption 2).

6. CONCLUSIONS

We address efficiency and incentives in kidney exchanges through a quantified random graph analysis which is new on this domain. This perspective elucidates important aspects of centralized kidney exchanges which are currently in an experimental stage.

We started with the definition of a random graph model of kidney exchanges, namely the model $\widetilde{G_n}$. Subsequently, we exploited the skewed connectivity among its subgraphs to derive analytically $\mu(n)$, i.e. the expected number of patients matched in a maximum matching drawn from $\widetilde{G_n}$. This allowed us to explain much of early experimental results but more importantly to study multiple-hospital, centralized mechanisms (CM). In particular, we were able to quantify the expected individual benefit of a hospital as being $\propto \sqrt{n}$ in a CM with hospitals of size n. To the best of our knowledge, this is the first formal proof of the valuable network effect that comes from nationwide kidney exchanges.

Next, under a quantitatively and qualitatively reasonable argument (see Assumption 2), we leveraged our analysis to study the incentives problem. First, we showed that non-truthful strategies do have negative effects on individual and overall welfare. We then analyzed an archetypal IR mechanism, namely `xCM` and proved that it is efficient and IR in equilibrium. Extensive experimental results validated our theoretical predictions and the nice properties of `xCM`. Furthermore, we checked for robustness on an augmented model $\widetilde{G_n}(PRA, F)$ which takes into account a variable PRA sensitivity for patients (given in Table 1) and any ABO blood-type distribution F.

7. ACKNOWLEDGMENTS

8. REFERENCES

[1] D. Abraham, A. Blum, and T. Sandholm. Clearing algorithms for barter exchange markets: enabling nationwide kidney exchanges. In *Proceedings of the 8th ACM conference on Electronic commerce*, page 304. ACM, 2007.

[2] I. Ashlagi and A.E. Roth. Individual rationality and participation in large scale, multi-hospital kidney exchange. In *Proceedings of the 12th ACM Conference on Electronic Commerce*, (to appear) 2011.

[3] I. Ashlagi, F. Fischer, I. Kash, and A. Procaccia. Mix and match. In *Proceedings of the 11th ACM conference on Electronic Commerce*, pages 305–314. ACM, 2010.

[4] B. Bollobás. *Modern graph theory.* Springer Verlag, 1998.

[5] B. Bollobás. *Random graphs.* Cambridge Univ Pr, 2001.

[6] J. Edmonds. Paths, trees, and flowers. *Canadian Journal of Mathematics*, 17(3):449–467, 1965.

[7] Z. Galil. Efficient algorithms for finding maximum matching in graphs. *ACM Computing Surveys (CSUR)*, 18(1):23–38, 1986.

[8] R. Montgomery, A. Zachary, L. Ratner, D. Segev, J. Hiller, J. Houp, M. Cooper, L. Kavoussi, T. Jarrett, J. Burdick, et al. Clinical results from transplanting incompatible live kidney donor/recipient pairs using kidney paired donation. *Jama*, 294(13):1655, 2005.

[9] C. Papadimitriou and K. Steiglitz. *Combinatorial optimization: algorithms and complexity.* Dover Pubns, 1998.

[10] M. Rees, J. Kopke, R. Pelletier, D. Segev, M. Rutter, A. Fabrega, J. Rogers, O. Pankewycz, J. Hiller, A.E. Roth, et al. A nonsimultaneous, extended, altruistic-donor chain. *New England Journal of Medicine*, 360(11):1096, 2009.

[11] M. Rees, R. Pelletier, S. Mulgaonkar, D. Laskow, B. Nibhanupudy, J. Kopke, A.E. Roth, U. Unver, T. Sandholm, and J. Rogers. Report From A 60 Transplant Center Multiregional Kidney Paired Donation Program: 2. *Transplantation*, 86(2S):1, 2008.

[12] A.E. Roth, T. Sönmez, and M. Ünver. Kidney Exchange*. *Quarterly Journal of Economics*, 119(2):457–488, 2004.

[13] A.E. Roth, T. Sönmez, and M. Ünver. Efficient kidney exchange: Coincidence of wants in markets with compatibility-based preferences. *The American economic review*, 97(3):828–851, 2007.

[14] S. Saidman, A.E. Roth, T. Sönmez, M. Ünver, and F. Delmonico. Increasing the opportunity of live kidney donation by matching for two-and three-way exchanges. *Transplantation*, 81(5):773, 2006.

[15] M. Ünver. Dynamic kidney exchange. *Review of Economic Studies*, 77(1):372–414, 2010.

[16] Wikipedia. Blood type, 2010. [Online; accessed 22-December-2010].

[17] S. Zenios, E. Woodle, and L. Friedman Ross. Primum non nocere: Avoiding harm to vulnerable wait list candidates in an indirect kidney exchange. *Transplantation*, 72(4):648, 2001.