

# Competing Kidney Markets

Gideon Moore  
Economics 284

Spring 2020

## Abstract

It is well documented that kidney exchanges which match patiently are more efficient than their greedy counterparts. However, in reality we still see several exchanges coexisting with heterogeneous match frequencies. I suggest that a kidney market which matches infrequently may unravel as fast exchanges “cream skin” the most desirable patients away from slower exchanges, leading to a less efficient equilibrium.

## 1 Introduction

I study the problem of matching patients for paired kidney donation in a dynamic market with two exchanges who differ only in their matching algorithm’s frequency. As documented in Agarwal et al. (2019), the kidney exchange market is highly fragmented, with many hospital-level exchanges operating significantly below critical capacity for running an efficient exchange. Moreover, despite recent literature on the virtues of patient algorithms, there is not yet a consensus wait time for periodic matching: the Alliance for Paired Donation matches daily, the United Network for Organ Sharing matches weekly, the South Korean national exchange matches monthly, and the Dutch national exchange matches quarterly. This heterogeneity suggests our understanding of the dynamics of when exchanges choose to run their match is still lacking.

As will be outlined in section 2, the consensus among economists is that waiting as long as possible is the most efficient algorithm for maximizing matches. Why, then, do some exchanges still run daily and weekly matches? I propose that in markets with waiting costs, patients who are easier to match will prefer a “greedy” exchange to a more patient option. This prevents these more efficient, slower exchanges from reaching critical mass, thereby reducing the total number of matches achieved. Moreover, exchanges are incentivized to reduce their wait time, as this will disproportionately draw in the most desirable patients.

To make this argument, I first compute a model for the utility a given patient receives from an exchange when observing its size, match frequency, and average patient. Using this model, I

construct a simulation where exchanges with fixed match frequencies compete over the course of a year to attract and match patients. I find that single exchanges are more efficient in a vacuum than two competing exchanges when generating matches. Moreover, in a market with two exchanges, fast exchanges seem to be favored by individual myopic decision makers despite being socially inferior. Finally, the patients who select into fast exchanges and are matched appear to be disproportionately easy-to-match relative to those matched in either the corresponding slow exchange or the fast exchange operating in a vacuum. As far as I am aware, this is the first paper to examine two competing kidney markets with endogenous entry by patients.

## 2 Literature

This paper fits neatly in the literature on the economics of kidney exchange precipitated by Roth, Sönmez, and Ünver (2004) as well as the follow-up paper Roth, Sönmez, et al. (2005). More specifically, this paper closely mirrors the work regarding the optimal choice of matching algorithm in a dynamic setting outlined in Akbarpour, Li, and Gharan (2020), which shows that “patient” algorithms are significantly more effective in generating matches than “greedy” algorithms for homogeneous patients. In a similar vein, Monteiro et al. (2020) find that there exists a trade-off between number of matches and average wait time, and that wait time can be rather substantially reduced with only minor compromises in match efficiency.

Moreover, this paper follows in the tradition of Agarwal et al. (2019) regarding market failures and adverse selection in the kidney exchange market. The authors highlight that while patients benefit greatly from entering exchanges, hospitals do not internalize this benefit, and so do not enroll some patients who would otherwise benefit. In addition, hospitals are not compensated for submitting their most desirable patients, leading to adverse selection within kidney exchanges and overall losses in efficiency. These two characteristics of the market lead to highly fragmented kidney exchange programs run at the hospital level rather than the national level, damaging market thickness and therefore overall efficiency.

As far as I am aware, the only other paper which examines algorithmic competition between kidney markets is Das et al. (2015). In this paper, the economy is composed of two kidney exchanges, one running a greedy algorithm and the other running a patient algorithm. Patients are assigned exogenously to the greedy exchange, the patient exchange, or both. Under these constraints, the economy is less efficient than even the greedy exchange in isolation, reflecting the outsize role of thickness in market efficiency as well as the difficulty in maintaining patients in a slow market who are also eligible for a greedy market. I hope to build on this paper by endogenizing the choice of exchange in order to better cement our understanding of market competition.

This paper is also related to the work of Ashlagi, Tennenholtz, and Zohar (2010) examining markets for server time which compete on batching algorithms. If there exist two compute platforms,

each run by a selfish server administrator who attempts to maximize the amount of compute time utilized on their cluster, the administrators compete on scheduling policy in order to force customers onto their platform. Moreover, the two administrators’ policies must be in equilibrium with each other. This can lead to inefficiencies, as rather than balancing the load across all available resources, market administrators are incentivized to find ways to clog their own machine while their competitor’s lies idle. The authors do, however, find the existence of equilibrium strategies among both pure and randomized job scheduling algorithms. This problem is an interesting mirror of the kidney exchange: in a duopoly problem, job scheduling is most efficient when divided but market forces lead to excess concentration, while kidney markets are most efficient when concentrated and appear to be excessively divided in the status quo.

Lastly, this paper contributes to the study of market unravelling. Niederle and Roth (2003) discuss the unravelling of the Gastroenterology fellowship market, where hospitals pushed offer dates earlier and earlier, to the point that fellows were accepting offers multiple years before their anticipated graduation. Haruvy, Roth, and Ünver (2006) tells a similar story for judicial clerkships, with the most promising students signing contracts in their second and third years of law school. I believe the “cream skimming” story I outline in section 5 has significant precedent in these other unravelling markets—much as the “best” students are pulled out of the pool early by eager employers, the easiest to match patients are pulled out of the kidney match by greedy exchanges before slower exchanges have a chance to match them at all, leading to an overall less efficient market.

## 3 Modelling

### 3.1 Defining the Economy

Let each kidney transplant patient  $i$  have some “match propensity”  $p_i$  distributed over some distribution  $F$ . The probability two patients  $i$  and  $j$  will match is the product of their match propensities,  $p_i p_j$ . A patient’s utility is defined based on whether they match, and how long a match takes. Normalize a patient’s utility of matching this period to 1, and have them discount that utility by a factor of  $1 - r$  every period they must wait.

Each patient enrolled in an exchange will become “critical” with probability  $\lambda$  each period. Whether or not a patient is critical is visible to the market administrator. If a critical patient is not matched at the end of that period, they will “expire” and be removed from the exchange.

### 3.2 The Utility of an Exchange

Per Akbarpour, Li, and Gharan (2020), waiting until a patient becomes critical to attempt to match them is a significant improvement over matching them earlier. Therefore, under our model, a critical patient will either match or expire in the following period, leaving the exchange. Further,

a patient who is not critical will only leave the exchange if matched to a critical patient. If a patient is not critical and does not match with a critical patient, they will re-enroll in the exchange the following period.

Given the above, a patient with match propensity  $p_i$  will have utility recursively defined as follows:

$$U_i(\lambda) = \mathbb{P}(\text{match}|p_i) \cdot 1 + \mathbb{P}(\neg\text{match} \cap \neg\text{critical}|p_i) \cdot (1 - r) \cdot U_i(\lambda)$$

By isolating the utility term to the left hand side, I generate a closed-form function of the utility of a given exchange:

$$U_i(\lambda) = \frac{\mathbb{P}(\text{match}|p_i)}{1 - (1 - r) \cdot \mathbb{P}(\neg\text{match} \cap \neg\text{critical}|p_i)}$$

In order to reduce this further to the bare parameters of our economy, I must now find both the  $\mathbb{P}(\text{match}|p_i)$ , the probability of matching in a given period, and  $\mathbb{P}(\neg\text{match} \cap \neg\text{critical}|p_i)$ , the probability of continuing to the next period. For the remainder of the calculations, “given  $p_i$ ” will be omitted for concision; know all expressions are given an individual’s fixed  $p_i$ .

### 3.3 The Probability of a Match

By partition, we know

$$\mathbb{P}(\text{match}) = \mathbb{P}(\text{match} \cap \neg\text{critical}) + \mathbb{P}(\text{match} \cap \text{critical})$$

Using Bayes’ Rule, this can be rewritten as

$$\mathbb{P}(\text{match}) = \mathbb{P}(\text{match}|\neg\text{critical}) \cdot \mathbb{P}(\neg\text{critical}) + \mathbb{P}(\text{match}|\text{critical}) \cdot \mathbb{P}(\text{critical})$$

Note that  $\mathbb{P}(\text{critical})$  is the parameter  $\lambda$  axiomatically defined as part of our economy. Thus, the above can be further simplified to

$$\mathbb{P}(\text{match}) = \mathbb{P}(\text{match}|\neg\text{critical}) \cdot (1 - \lambda) + \mathbb{P}(\text{match}|\text{critical}) \cdot \lambda$$

To continue, then, we must derive both  $\mathbb{P}(\text{match}|\neg\text{critical})$  and  $\mathbb{P}(\text{match}|\text{critical})$ .

### 3.3.1 The Probability of Matching When Not Critical

$$\begin{aligned}
\mathbb{P}(\text{match}|\neg\text{critical}) &= \mathbb{P}(\text{chosen by someone critical}) \\
&= 1 - \mathbb{P}(\text{chosen by no one critical}) \\
&= 1 - \prod_j^{N\lambda} \mathbb{P}(\neg\text{chosen by a given critical patient}) \\
&= 1 - \prod_j^{N\lambda} (1 - \mathbb{P}(\text{chosen by a given critical patient})) \\
&= 1 - \prod_j^{N\lambda} (1 - \mathbb{P}(\text{chosen} \cap \text{compatible})) \\
&= 1 - \prod_j^{N\lambda} (1 - \mathbb{P}(\text{chosen}|\text{compatible})\mathbb{P}(\text{compatible}))
\end{aligned}$$

As defined in our model, the probability  $i$  and  $j$  are compatible is simply  $p_i p_j$ .

On the other hand,  $\mathbb{P}(\text{chosen}|\text{compatible})$  is a very difficult term to break down further, as it would essentially require integrating over all possible graphs and their probabilities of occurrence. Here, I will make a naive approximation: if each compatible patient is equally likely to be chosen, the probability of any individual patient being chosen is one over the expected number of matches. I believe this is a fair first-order approximation; a worthwhile step moving forward would likely be to test this via simulation. For now, however, we will take it as acceptable.

If this is accepted, we must then find the expected number of compatible partners. Fortunately, this is a significantly simpler question. Let  $\mathbb{I}_{ij}$  be an indicator variable for patients  $i$  and  $j$  being compatible.

$$\begin{aligned}
\mathbb{E}(\# \text{ of matches for } j) &= \mathbb{E}\left(\sum_{i \neq j} \mathbb{I}_{ij}\right) \\
&= \sum_{i \neq j} \mathbb{E}(\mathbb{I}_{ij}) \\
&= \sum_{i \neq j} \mathbb{P}(i \text{ compatible with } j) \\
&= \sum_{i \neq j} p_i p_j
\end{aligned}$$

Progressing with the proof from above:

$$\begin{aligned}
\mathbb{P}(\text{match}|\neg\text{critical}) &= 1 - \prod_j^{N\lambda} (1 - \mathbb{P}(\text{chosen}|\text{compatible})\mathbb{P}(\text{compatible})) \\
&= 1 - \prod_j^{N\lambda} (1 - \mathbb{E}(\# \text{ of matches})^{-1} p_i p_j) \\
&= 1 - \prod_j^{N\lambda} \left( 1 - \frac{p_i p_j}{\sum_{k \neq j} p_j p_k} \right) \\
&= 1 - \prod_j^{N\lambda} \left( 1 - \frac{p_i}{\sum_{k \neq j}^N p_k} \right) \\
&= 1 - \prod_j^{N\lambda} \left( 1 - \frac{p_i}{p_i + \sum_{k \neq i, j}^N p_k} \right)
\end{aligned}$$

Note that as  $N$ , the size of the exchange, grows, the impact of any single patient's match propensity on the average match propensity of the pool approaches zero. For large enough  $N$ , then,  $\sum_{k \neq i, j}^N p_k \approx (N-2)\bar{p}$ , where  $\bar{p}$  is the average propensity of the pool. Using this approximation, we can simplify the above further:

$$\begin{aligned}
\mathbb{P}(\text{match}|\neg\text{critical}) &= 1 - \prod_j^{N\lambda} \left( 1 - \frac{p_i}{p_i + \sum_{k \neq i, j}^N p_k} \right) \\
&\approx 1 - \prod_j^{N\lambda} \left( 1 - \frac{p_i}{p_i + (N-2)\bar{p}} \right) \text{ for large } N \\
&\approx 1 - \left( 1 - \frac{p_i}{(N-2)\bar{p} + p_i} \right)^{N\lambda} \text{ for large } N
\end{aligned}$$

While a small approximation, this adjustment yields major computational benefits. For a given  $p_i$ , the unadjusted formula requires  $O(N^2)$  computations: summing  $N-1$  terms in the denominator of the fraction, then multiplying all  $N\lambda$  results. With this minor change, however, I have transformed this  $O(N^2)$  time complexity equation into one which is  $O(1)$ , significantly reducing computational burden down the line.

### 3.3.2 The Probability of Matching When Critical

$$\begin{aligned}
\mathbb{P}(match|critical) &= \mathbb{P}(\text{chosen by someone}) \\
&= 1 - \mathbb{P}(\text{chosen by no one}) \\
&= 1 - \prod_{j \neq i}^N \mathbb{P}(\text{-chosen by a given patient}) \\
&= 1 - \prod_{j \neq i}^N (1 - \mathbb{P}(\text{chosen by a given patient})) \\
&= 1 - \prod_{j \neq i}^{\lambda N} (1 - \mathbb{P}(\text{chosen by a critical patient})) \\
&\quad * \prod_{j \neq i}^{(1-\lambda)N} (1 - \mathbb{P}(\text{chosen by a non-critical patient}))
\end{aligned}$$

From the proof above, we already know that

$$\prod_{j \neq i}^{\lambda N} (1 - \mathbb{P}(\text{chosen by a critical patient})) \approx \left( 1 - \frac{p_i}{(N-2)\bar{p} + p_i} \right)^{N\lambda-1}$$

Note here we must subtract one from the exponent; this is because the patient herself is critical, and so is deducted from the critical patient pool.

However, we must still determine the value of  $\prod_{j \neq i}^{(1-\lambda)N} (1 - \mathbb{P}(\text{chosen by a non-critical patient}))$ .

$$\begin{aligned}
\prod_{j \neq i}^{(1-\lambda)N} (1 - \mathbb{P}(\text{chosen by a non-critical patient})) &= \prod_{j \neq i}^{(1-\lambda)N} (1 - \mathbb{P}(\text{chosen} \cap \text{compatible})) \\
&= \prod_{j \neq i}^{(1-\lambda)N} (1 - \mathbb{P}(\text{chosen} | \text{compatible}) \cdot \mathbb{P}(\text{Compatible})) \\
&= \prod_{j \neq i}^{(1-\lambda)N} (1 - \mathbb{E}(\# \text{ of Matches})^{-1} \cdot p_i p_j) \\
&= \prod_{j \neq i}^{(1-\lambda)N} \left( 1 - \frac{p_i p_j}{\sum_{k \neq j}^{N\lambda} p_j p_k} \right) \\
&= \prod_{j \neq i}^{(1-\lambda)N} \left( 1 - \frac{p_i}{p_i + \sum_{k \neq j}^{N\lambda-1} p_k} \right)
\end{aligned}$$

By an analogous limit argument to that outlined in section 3.3.1, I argue that for large enough  $N$ , any single patient will have minimal impact on the sum of match propensities in the denominator. Moreover, as each patient becomes critical independently, we can expect that the average match propensity among critical patients should be equal to the match propensity of the population, allowing a substitution for  $\bar{p}$  and significant reduction in computational complexity.

$$\begin{aligned}
\prod_{j \neq i}^{(1-\lambda)N} (1 - \mathbb{P}(\text{chosen by a non-critical patient})) &= \prod_{j \neq i}^{(1-\lambda)N} \left( 1 - \frac{p_i}{p_i + \sum_{k \neq j}^{N\lambda-1} p_k} \right) \\
&\approx \prod_{j \neq i}^{(1-\lambda)N} \left( 1 - \frac{p_i}{p_i + (N\lambda - 1)\bar{p}} \right) \\
&\approx \left( 1 - \frac{p_i}{(N\lambda - 1)\bar{p} + p_i} \right)^{N(1-\lambda)}
\end{aligned}$$

Combining this with the above results, our final formula for the probability of matching when critical is:

$$\mathbb{P}(\text{match} | \text{critical}) \approx 1 - \left( 1 - \frac{p_i}{(N-2)\bar{p} + p_i} \right)^{N\lambda-1} \left( 1 - \frac{p_i}{(N\lambda-1)\bar{p} + p_i} \right)^{N(1-\lambda)}$$



### 3.3.3 Total Probability of a Match

Recalling again the formula from the beginning of the subsection, we know that

$$\mathbb{P}(\text{match}) = (1 - \lambda) \cdot \mathbb{P}(\text{match}|\neg\text{critical}) + \lambda \cdot \mathbb{P}(\text{match}|\text{critical})$$

With the above results, we have solved for both of the remaining unknown terms. Therefore, our final formula for  $\mathbb{P}(\text{match})$  is:

$$\mathbb{P}(\text{match}) \approx (1-\lambda) \cdot \left(1 - \left(1 - \frac{p_i}{(N-2)\bar{p} + p_i}\right)^{N\lambda}\right) + \lambda \cdot \left(1 - \left(1 - \frac{p_i}{(N-2)\bar{p} + p_i}\right)^{N\lambda-1} \left(1 - \frac{p_i}{(N\lambda-1)\bar{p} + p_i}\right)^{N(1-\lambda)}\right)$$

### 3.4 The Probability of Continuation

To compute the utility of an exchange, recall the denominator also contains the probability of continuation,  $\mathbb{P}(\neg\text{match} \cap \neg\text{critical})$ .

$$\begin{aligned} \mathbb{P}(\neg\text{match} \cap \neg\text{critical}) &= \mathbb{P}(\neg\text{critical}) \cdot \mathbb{P}(\neg\text{match}|\neg\text{critical}) \\ &= (1 - \lambda) \cdot \mathbb{P}(\neg\text{match}|\neg\text{critical}) \\ &= (1 - \lambda) \cdot (1 - \mathbb{P}(\text{match}|\neg\text{critical})) \end{aligned}$$

Recall that I have already show  $\mathbb{P}(\text{match}|\neg\text{critical}) \approx 1 - \left(1 - \frac{p_i}{p_i + (N-2)\bar{p}}\right)^{N\lambda-1}$  in section 3.3.1. Inserting this into the equation above, I show that

$$\mathbb{P}(\neg\text{match} \cap \neg\text{critical}) \approx (1 - \lambda) \left(1 - \frac{p_i}{p_i + (N-2)\bar{p}}\right)^{N\lambda-1}$$

### 3.5 Tying it All Together

Recall our formula for the utility from an exchange as derived in 3.2:

$$U_i(\lambda) = \frac{\mathbb{P}(\text{match})}{1 - (1 - r) \cdot \mathbb{P}(\neg\text{match} \cap \neg\text{critical})}$$

Using the above results, I can substitute for both  $\mathbb{P}(\text{match})$  and  $\mathbb{P}(\neg\text{match} \cap \neg\text{critical})$ , yielding my final formula for the utility of an exchange, dependant only on the parameters of the economy

and the current state of the exchange:

$$U_i(\lambda) \approx \frac{(1 - \lambda) \cdot \left(1 - \left(1 - \frac{p_i}{(N-2)\bar{p} + p_i}\right)^{N\lambda}\right) + \lambda \cdot \left(1 - \left(1 - \frac{p_i}{(N-2)\bar{p} + p_i}\right)^{N\lambda-1} \left(1 - \frac{p_i}{(N\lambda-1)\bar{p} + p_i}\right)^{N(1-\lambda)}\right)}{1 - (1 - r) \cdot (1 - \lambda) \cdot \left(1 - \frac{p_i}{p_i + (N-2)\bar{p}}\right)^{N\lambda-1}}$$

## 4 Simulation

### 4.1 Simulating a Single Exchange

I use the `networkx` package in Python to simulate running kidney exchanges over the course of a year. The complete source code is available in a repository on my GitHub, [https://github.com/gmoore016/Competing\\_Kidney\\_Exchange](https://github.com/gmoore016/Competing_Kidney_Exchange).

In the simulation, when patient  $i$  enters an exchange, she is randomly linked to each existing member  $j$  with probability  $p_i p_j$ , where  $p_i$  is patient  $i$ 's match propensity. These match propensities are drawn on entry from a uniform distribution.

Each period, `inflow` patients enter the market one at a time. Then, each patient in the market becomes critical with probability `expiry_rate`. The exchange runs a match every `freq` periods. At this point, I attempt to match as many critical patients as possible; any remaining critical patients then expire.

To calculate the optimal matching, I use the `networkx` builtin method `match_weight_matching`. Based on the blossom algorithm developed in Edmonds (1965), this method finds a matching which maximizes the total *edge* weights within a graph. I therefore must transform the maximal node weight matching problem into a maximal edge weight matching problem. Fortunately, this is simple in the context of matching: each edge has weight equal to the number of critical patients it is connected to. From there, I run the algorithm on the subgraph of edges with positive weight; otherwise, the maximal matching may include edges with zero weight.

It is worth noting a single run of the algorithm is  $O(N^3)$ , where  $N$  is the number of patients in the exchange at the time of the match. This match is run `360 / freq` times over the course of the simulation, yielding a total simulation complexity of  $O(N^3 \text{freq}^{-1})$  per run. In general, the  $N$  term dominates, meaning that the simulations which run fewer matches take longer due to the increased number of patients present in those matches.

Each parameterization is run ten times, in order to understand the underlying structure of the results. The complete simulation results are available in appendix B.

In general, the exchange which waits the maximum quantity of time before matching is the most effective, with the number of matches generally increasing in the length of the thickening period, as visible in table 1. This aligns with expectations from Akbarpour, Li, and Gharan (2020); however, while their results use homogeneous patients with equal match probabilities, here I have shown the

result also holds empirically when patients are heterogeneous. However, the length of time waiting in the exchange also increases linearly, visible in table 2. Thus, if there is some cost to waiting, some patients may instead choose a fast but less effective exchange.

## 4.2 Simulating Dual Exchanges

The above simulation results largely confirm existing findings in the literature. However, the novel utility formulation developed in section 3 allows for a more interesting breed of simulation: when presented with two exchanges, which will a patient choose?

The simulation runs largely as in the single-exchange case above. However, after a patient is assigned a match propensity, she is then offered the choice of two exchanges, and enrolls in the one which will provide her greater expected utility.

When examining the standard deviations on the number of matches for each exchange as listed in table 4, it is worth noting that there is significant dispersion around the number of matches a given exchange can expect. This is because the distribution is largely bimodal—after an initial competition phase, one exchange will gain critical mass while the other withers due to a lack of new patients.

In general, it appears the fast exchange has a greater expected number of matches than the slow exchange, suggesting it is more likely to dominate. Note that generally, the sum of the matches in the two exchanges is less than the matches made under the same parameters in the single exchange case; therefore, as suggested by Das et al. (2015), the two exchange case is less effective at maximizing matches than either single exchange case. Across nearly all specifications, the average match propensity in the fast exchange is significantly higher than in the slow exchange as visible in table 6.

## 5 Discussion

I believe the above results are suggestive of a “cream skimming” phenomenon, where the most easy-to-match patients place less emphasis on thickness than do those who are difficult to match, and so are peeled away from the efficient slower exchange via competition from a faster exchange.

The first element that suggests this trend is visible in table 4: fast exchanges typically match significantly more patients than competing slow exchanges. Given the single-exchange results from table 1, we know that slower exchanges perform better in a vacuum; therefore, this advantage during competition must stem from a disproportionate number of patients entering the fast exchange.

Further examination of table 6 can shed light on what draws patients to the fast exchange over the slow exchange. Across most specifications, the patients matched in the fast exchange have significantly higher match propensities than their slow-exchange counterparts. They also have a

significantly higher match propensity than those from the single exchange case. This suggests that high-propensity patients are selecting themselves into the exchange which matches more frequently.

Note that patients with high match propensity can provide a positive externality to an exchange: relative to a harder-to-match patient, high-propensity patients are more likely to match with someone who is currently unmatched and about to expire. In this case, that expiring patient is made significantly better off, as they are matched when they otherwise would not be. Moreover, as high-propensity patients are likely to have many matches, it is rare they will “take” someone else’s match when they become critical, as they are likely to have many partners available to them.

The above two results—that patients with high match propensities prefer exchanges which match frequently and are also more desirable—suggest that in a market with two competing exchanges, the faster exchange is likely to “cream skim” the slower exchange. This leaves the slow exchange with only the least desirable patients, causing it to eventually collapse due to lack of critical mass. Given Akbarpour, Li, and Gharan (2020) shows that a more patient matching algorithm generates significantly more matches than a greedy alternative, this selection into the inefficient match could have significant consequences in terms of total kidney exchanges performed.

Worth noting is that my simulation has patients choose a single exchange, while in reality patients can enter multiple exchanges at once. I do not believe this changes my argument. Suppose patients can enter a daily exchange, a monthly exchange, or both. In this case, any patients which enter both have functionally entered the daily exchange, as by the time the monthly exchange runs anybody who matches in the daily exchange will already be removed from the pool, again leaving the monthly exchange with only the most difficult-to-match patients.

I also wish to highlight a special case: when a patient is compatible with their donor and does not have to enter an exchange at all. This situation is analogous to a patient deciding between a very large but somewhat slow exchange and a fast exchange where they are guaranteed to match. According to National Kidney Foundation (2016), 5,537 kidneys were provided by living donors in 2014. Per Agarwal et al. (2019), kidney exchanges facilitate approximately 800 operations each year. This means that more than 80% of living kidney transplants do not pass through an exchange. Consider that many of those self-matching pairs could have matched with and saved a patient who instead went unmatched, especially given that the patients who are compatible with their donor are also likely highly-compatible. A mechanism which corrects the distortions outlined in this paper could not only boost matches among patients who already entered kidney exchange, but also induce people to enter kidney exchanges who would not otherwise do so, significantly expanding the universe of potential matches.

## 6 Next Steps

### 6.1 Derivatives of Utility

Recall the equation for total utility of an exchange derived in section 3.5. At some level, the fundamental questions this paper pursues boil down to questions about the derivatives of this utility function. The equation is far too complex to be reasonably differentiated by hand; however, using symbolic algebra, mathematical computing languages such as Mathematica and MATLAB can make analytic differentiation straightforward. MATLAB output of  $\frac{\partial U}{\partial N}$  and  $\frac{\partial^2 U}{\partial N \partial p}$  are visible in appendix A.\*

#### 6.1.1 The Derivative in $N$

I will admit to having a somewhat strong prior on the derivative of  $N$ -if thickness is desirable for all patients, we would expect this to be positive at all points. However, as it stands the formulation of the derivative returned by MATLAB is of ambiguous sign. This is because

$$\text{substitution \#1} = \lambda \log \left( 1 - \frac{p}{\bar{p}(N-1)} \right) \cdot \left( 1 - \frac{p}{\bar{p}(N-1)} \right)^{N\lambda-1} + \frac{p \cdot \left( 1 - \frac{p}{\bar{p}(N-1)} \right)^{N\lambda-2} (N\lambda - 1)}{\bar{p}(N-1)^2}$$

Note that the first term of the above equation is negative due to taking the log of a number between 0 and 1, while the second term is positive, as it is the product of exclusively positive numbers. This is then divided by a positive number and added to the rest of the terms in the equation. Thus, if this term is significantly positive or negative, it could pull the entire derivative up or down. One further avenue of exploration would be to examine under what conditions the above equation is positive or negative, and see if there exist reasonable bounds under which it is always positive.

Note, I believe the remaining terms in the formula for  $\frac{\partial U}{\partial N}$  are positive. Therefore, if I am able to prove that substitution #1 is positive under some bounds, the whole derivative should be unambiguously positive under those same bounds.

#### 6.1.2 The Derivative in $N$ and $p_i$

One claim of my argument is that “easy to match” patients gain less from thickness than those who are “hard to match,” leading them to be more willing to defect from a slow match. It is reasonable to frame this as an argument about the second derivative:  $\frac{\partial^2 U}{\partial N \partial p_i}$  could be negative, which would mean that as  $p_i$  increases the gains from thickness decline.

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\*Many thanks to Derek Gaines for MATLAB assistance.

As is visible in A.2, the second partial derivative of  $U_i$  is quite complex, involving many terms and a full eighteen substitutions from MATLAB output. I am optimistic, however, that if I can place conditions as described above to reign in the first derivative, it could also make the second derivative tractable.

## 6.2 Simulate with Machine Learning

Rather than bothering with the utility calculations from section 3, another avenue could be to use machine learning to train using the simulator from section 4. Given it is simple to calculate a patient's utility ex-post, we have a clear feedback function with which to train our algorithm. Moreover, the set of parameters— $\lambda$ ,  $p_i$ , and  $r$ , as well as an  $N$  and  $\bar{p}$  for each exchange—is bounded enough to hopefully keep the problem tractable.

This has some significant benefits—it allows us to forego our current large sample approximations, as well as the estimate of the probability of matching given compatibility. However, it would likely require significant computation time. Moreover, it may be difficult to interpret “optimal” play in a way that is reasonable to humans, potentially leaving us with an answer but no rationale.

## 7 Conclusion

The above evidence suggests that when faced with competition, slow exchanges are liable to unravel despite their efficiency gains. Hopefully this goes at least some way toward explaining the fragmented, heterogeneous kidney exchanges we see in reality. However, having identified the problem, I am far from providing a solution. Fundamentally, easy-to-match patients provide a positive externality which they must be compensated for lest they defect. Given this problem, there are two options: subsidize easy-to-match patients or prevent defection. Beyond general objections towards paying people for organs, subsidizing high-propensity patients has problematic distributional consequences: a patient who is simple to match is both likely to match quickly and gains a subsidy, while a hard to match patient is liable to get nothing. An alternative solution would be to nationalize kidney exchange, and require kidney transplants to register with the national registry. However, many would likely feel this solution involves significant government overreach, and may vitalize a black market for kidney exchanges.

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## A Derivatives

Below find the output of MATLAB’s symbolic differentiation algorithm when run on my equation for  $U_i$ . Here,  $\text{lam}=\lambda$ ,  $\text{q}=\bar{p}$ , and  $\text{p}=p_i$ .

## A.1 Derivative in $N$

$$\begin{aligned}
 & \frac{\frac{1}{(\lambda - 1) \sqrt{(\lambda - 1) \left( \frac{N \lambda}{\#7} - 1 \right) + \frac{\lambda \#6}{\#2} (r - 1)}}}{\#3} \\
 & - \frac{\frac{1}{\lambda \log(\#7) \sqrt{\lambda}} \frac{N \lambda}{\#7} + \frac{N \lambda p \#6}{\#4} \sqrt{(\lambda - 1)} + \frac{\lambda \#1}{\#2}}{\frac{1}{\lambda \#6} \sqrt{\log(\#5) (\lambda - 1)} + \frac{N \lambda p (\lambda - 1)}{q (N \lambda - 1) \#5} \sqrt{N (\lambda - 1) + 1}} \sqrt{\#3}
 \end{aligned}$$

where

$$\begin{aligned}
 \#1 &== \lambda \log(\#7) \#6 + \frac{N \lambda - 2}{p \#7 (N \lambda - 1)} \\
 \#2 &== \#5 \\
 \#3 &== \#6 (\lambda - 1) (r - 1) - 1 \\
 \#4 &== q (N - 1) \\
 \#5 &== 1 - \frac{p}{q (N \lambda - 1)} \\
 \#6 &== \#7 \\
 \#7 &== 1 - \frac{p}{q (N - 1)}
 \end{aligned}$$



## A.2 Derivative in $N$ and $p_i$

$$\begin{aligned}
 & \frac{\#5 (lam - 1) (r - 1) \#1}{\#6} - \frac{(lam - 1)}{\#7} + \frac{N lam \#14}{\#10} \\
 & - \frac{N lam \log(1 - \#18) \#14}{q (N - 1)} - \frac{N lam p \#15 (N lam - 1)}{\#8} \\
 & - lam \frac{\#1}{\#12} - \frac{\#14}{q (N lam - 1)} + \frac{lam - 1}{(\#17 - 1) \#12} + \frac{N lam (lam - 1)}{\#11} \\
 & + \frac{N \log(1 - \#17) (lam - 1)^2}{\#4} + \frac{N lam p (lam - 1) \#16}{q (N lam - 1) (1 - \#17)} \\
 & + \frac{\#15 (N lam - 1) \#3}{q (N - 1)} + \frac{N \#2 (lam - 1)}{\#4} \frac{\#6}{\#6} \\
 & + \frac{\#2}{\#12} \frac{lam}{q (N - 1) \#12} - \frac{\#9}{\#4} \frac{N \#14 (lam - 1)}{q (N - 1)} - \frac{N lam \#14 (lam - 1)}{q (N - 1)} \\
 & (lam - 1) (r - 1) \frac{\#6}{\#6} - \frac{\#15 (N lam - 1)}{\#6} \\
 & \frac{N lam p \#14}{\#10} \frac{(lam - 1)}{\#10} \\
 & - lam \frac{\#2}{\#12} - \frac{\#14 \#3}{\#6} \frac{(lam - 1) (r - 1)}{\#6} \frac{1}{(q \#6 (N - 1))^2} \\
 & + \frac{\#15 (N lam - 1) \#5 \#2 (lam - 1) (r - 1)^2}{q \#6 (N - 1)^3}
 \end{aligned}$$

where

$$\begin{aligned}
 \#1 &= \frac{\#10 (N \text{ lam} - 1)}{\#11} + \frac{\text{lam} \#15}{\#8} - \frac{\text{lam} \log(1 - \#18) \#10 (N \text{ lam} - 1)}{q (N - 1)} \\
 \#2 &= \frac{p (1 - \#18)}{N \text{ lam} - 3} - \frac{(N \text{ lam} - 1) (N \text{ lam} - 2)}{\#9} \\
 \#3 &= \text{lam} \log(1 - \#18) \#15 + \frac{p \#10 (N \text{ lam} - 1)}{\#11} \\
 \#4 &= q (N \text{ lam} - 1) (1 - \#17) \\
 \#5 &= \#15 (\text{lam} - 1) (r - 1) - 1 \\
 \#6 &= (\text{lam} - 1) (\#14 - 1) + \frac{\text{lam} \#15}{\#13} \\
 \#7 &= N \text{ lam} \#15 (\text{lam} - 1) \\
 \#8 &= q (\#18 - 1) (N - 1) \\
 \#9 &= q (N - 1)^2 \\
 \#10 &= (1 - \#18)^{N \text{ lam} - 2} \\
 \#11 &= q (N - 1)^2 \\
 \#12 &= q (N \text{ lam} - 1)^2 (1 - \#17)^{\#16} \\
 \#13 &= (1 - \#17)^{N (\text{lam} - 1)} \\
 \#14 &= (1 - \#18)^{N \text{ lam}} \\
 \#15 &= (1 - \#18)^{N \text{ lam} - 1} \\
 \#16 &= N (\text{lam} - 1) + 1 \\
 \#17 &= \frac{p}{q (N \text{ lam} - 1)} \\
 \#18 &= \frac{p}{q (N - 1)}
 \end{aligned}$$

## B Simulation Tables

Table 1: The number of matches given a single exchange under the specified parameters. Standard deviation of sample (*not* of sample mean) is in parentheses below.

Expiry rate==0.1					
Inflow\Frequency	1.00	7.00	30.00	87.00	350.00
3.00	918.60	980.80	946.40	1012.20	1020.80
(SD)	(7.12)	(8.39)	(6.79)	(4.76)	(3.55)
10.00	3335.80	3369.80	3191.80	3381.00	3410.40
(SD)	(13.18)	(11.87)	(7.45)	(7.01)	(7.59)
25.00	8471.60	8484.80	8007.60	8469.00	8519.20
(SD)	(13.29)	(6.55)	(9.56)	(12.87)	(6.41)
Expiry rate==0.5					
Inflow\Frequency	1.00	7.00	30.00	87.00	350.00
3.00	632.80	940.00	965.80	1033.60	1046.40
(SD)	(18.02)	(15.32)	(3.33)	(3.24)	(2.07)
10.00	3043.20	3395.60	3270.80	3463.40	3488.80
(SD)	(26.20)	(11.65)	(4.24)	(5.34)	(2.70)
25.00	8342.00	8634.20	8205.60	8671.00	8725.00
(SD)	(22.35)	(8.19)	(5.15)	(3.80)	(5.68)
Expiry rate==0.9					
Inflow\Frequency	1.00	7.00	30.00	87.00	350.00
3.00	422.40	908.80	961.80	1034.80	1047.40
(SD)	(19.11)	(12.76)	(3.33)	(2.35)	(1.90)
10.00	2615.80	3390.40	3277.40	3471.80	3497.40
(SD)	(48.15)	(10.74)	(4.99)	(2.39)	(2.50)
25.00	8036.20	8648.00	8221.00	8689.80	8744.80
(SD)	(25.88)	(9.04)	(4.35)	(3.05)	(2.53)

Table 2: The average age of a matched patient given a single exchange under the specified parameters. Standard deviation of sample (*not* of sample mean) is in parentheses below.

Expiry rate==0.1					
Inflow\Frequency	1.00	7.00	30.00	87.00	350.00
3.00	5.02	10.30	22.63	50.71	178.75
(SD)	(5.67)	(8.08)	(12.24)	(26.19)	(98.74)
10.00	6.09	11.39	23.01	50.77	178.79
(SD)	(6.30)	(8.93)	(12.42)	(26.13)	(98.70)
25.00	7.57	11.64	22.94	50.81	178.93
(SD)	(7.71)	(9.21)	(12.52)	(26.13)	(98.63)
Expiry rate==0.5					
Inflow\Frequency	1.00	7.00	30.00	87.00	350.00
3.00	0.61	3.71	15.30	43.68	174.81
(SD)	(0.98)	(2.37)	(8.73)	(25.09)	(100.87)
10.00	0.63	3.90	15.42	43.78	174.94
(SD)	(0.97)	(2.40)	(8.74)	(25.09)	(100.76)
25.00	0.84	3.95	15.42	43.84	174.96
(SD)	(1.18)	(2.41)	(8.73)	(25.08)	(100.77)
Expiry rate==0.9					
Inflow\Frequency	1.00	7.00	30.00	87.00	350.00
3.00	0.08	3.02	14.51	42.98	174.56
(SD)	(0.28)	(2.03)	(8.66)	(25.11)	(101.03)
10.00	0.06	3.07	14.58	43.06	174.56
(SD)	(0.25)	(2.02)	(8.66)	(25.11)	(101.00)
25.00	0.08	3.09	14.59	43.08	174.56
(SD)	(0.28)	(2.02)	(8.66)	(25.11)	(101.01)

Table 3: The average match propensity of a matched patient given a single exchange under the specified parameters. Standard deviation of sample (*not* of sample mean) is in parentheses below.

Expiry rate==0.1					
Inflow\Frequency	1.00	7.00	30.00	87.00	350.00
3.00	0.55	0.52	0.51	0.51	0.51
(SD)	(0.27)	(0.28)	(0.28)	(0.29)	(0.29)
10.00	0.51	0.51	0.50	0.50	0.50
(SD)	(0.28)	(0.29)	(0.29)	(0.29)	(0.29)
25.00	0.50	0.50	0.50	0.50	0.50
(SD)	(0.29)	(0.29)	(0.29)	(0.29)	(0.29)
Expiry rate==0.5					
Inflow\Frequency	1.00	7.00	30.00	87.00	350.00
3.00	0.61	0.54	0.51	0.50	0.51
(SD)	(0.25)	(0.27)	(0.28)	(0.29)	(0.29)
10.00	0.55	0.51	0.50	0.50	0.50
(SD)	(0.26)	(0.28)	(0.29)	(0.29)	(0.29)
25.00	0.52	0.51	0.50	0.50	0.50
(SD)	(0.29)	(0.29)	(0.29)	(0.29)	(0.29)
Expiry rate==0.9					
Inflow\Frequency	1.00	7.00	30.00	87.00	350.00
3.00	0.65	0.55	0.52	0.51	0.50
(SD)	(0.24)	(0.27)	(0.28)	(0.29)	(0.29)
10.00	0.59	0.51	0.50	0.50	0.50
(SD)	(0.25)	(0.28)	(0.29)	(0.29)	(0.29)
25.00	0.54	0.50	0.50	0.50	0.50
(SD)	(0.27)	(0.29)	(0.29)	(0.29)	(0.29)

Table 4: The average number of matches given competing fast and slow exchanges under the specified parameters.

Fast Exchange:				
Expiry rate==0.1				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	1567.20	2241.20	3570.20	3363.40
(SD)	(354.15)	(260.90)	(81.67)	(87.14)
25.00	3693.00	5977.00	9246.40	8499.00
(SD)	(1303.51)	(612.93)	(342.43)	(864.69)
Expiry rate==0.5				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	1740.00	2772.60	482.20	1141.20
(SD)	(1489.81)	(932.19)	(912.10)	(1261.66)
25.00	3401.80	5917.40	1924.00	680.60
(SD)	(4024.95)	(3866.65)	(3385.59)	(597.17)
Expiry rate==0.9				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	2679.20	2584.60	2301.40	1134.00
(SD)	(35.46)	(100.27)	(247.69)	(949.89)
25.00	7999.20	6877.80	4108.60	2534.60
(SD)	(56.29)	(889.44)	(2569.87)	(2638.92)
Slow Exchange:				
Expiry rate==0.1				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	1722.40	1113.60	62.40	69.40
(SD)	(351.65)	(257.34)	(26.04)	(66.28)
25.00	4760.00	2524.40	158.20	240.80
(SD)	(1294.84)	(611.78)	(59.51)	(375.21)
Expiry rate==0.5				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	1395.40	401.40	2840.80	2261.20
(SD)	(1494.88)	(1033.44)	(987.10)	(1441.57)
25.00	5013.80	2603.80	6395.20	8056.60
(SD)	(4030.59)	(4002.27)	(3312.60)	(625.81)
Expiry rate==0.9				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	57.00	168.20	530.60	2109.40
(SD)	(7.13)	(103.50)	(319.67)	(1241.08)
25.00	114.40	1339.20	4247.60	6062.40
(SD)	(50.20)	(964.77)	(2634.34)	(2839.18)

Table 5: The average age of a matched patient given competing fast and slow exchanges under the specified parameters.

Fast Exchange:				
Expiry rate==0.1				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	5.77	5.47	6.38	6.17
(SD)	(6.13)	(5.82)	(6.63)	(6.41)
25.00	7.03	6.37	7.78	7.80
(SD)	(7.14)	(6.86)	(7.94)	(7.95)
Expiry rate==0.5				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	0.64	0.64	0.63	0.61
(SD)	(0.98)	(0.98)	(0.97)	(0.95)
25.00	0.82	0.84	0.83	0.75
(SD)	(1.17)	(1.18)	(1.18)	(1.11)
Expiry rate==0.9				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	0.06	0.06	0.06	0.06
(SD)	(0.25)	(0.25)	(0.25)	(0.26)
25.00	0.08	0.07	0.08	0.08
(SD)	(0.29)	(0.27)	(0.28)	(0.29)
Slow Exchange:				
Expiry rate==0.1				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	5.40	10.67	29.12	77.16
(SD)	(5.77)	(7.98)	(6.99)	(21.09)
25.00	6.15	11.59	27.59	58.26
(SD)	(6.64)	(8.74)	(8.52)	(28.76)
Expiry rate==0.5				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	0.64	4.18	15.44	43.07
(SD)	(0.97)	(2.34)	(8.88)	(25.68)
25.00	0.84	4.01	15.47	43.19
(SD)	(1.18)	(2.42)	(8.82)	(25.09)
Expiry rate==0.9				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	0.07	3.74	15.31	43.65
(SD)	(0.28)	(2.24)	(9.08)	(25.44)
25.00	0.07	3.15	14.57	42.97
(SD)	(0.27)	(2.07)	(8.68)	(25.08)

Table 6: The average match propensity of a matched patient given competing fast and slow exchanges under the specified parameters.

Fast Probs:				
Expiry rate==0.1				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	0.57	0.50	0.52	0.52
(SD)	(0.27)	(0.26)	(0.28)	(0.28)
25.00	0.61	0.43	0.51	0.51
(SD)	(0.28)	(0.26)	(0.28)	(0.28)
Expiry rate==0.5				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	0.55	0.55	0.56	0.56
(SD)	(0.27)	(0.27)	(0.27)	(0.26)
25.00	0.52	0.52	0.53	0.60
(SD)	(0.28)	(0.28)	(0.28)	(0.28)
Expiry rate==0.9				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	0.59	0.59	0.59	0.58
(SD)	(0.26)	(0.26)	(0.26)	(0.26)
25.00	0.54	0.54	0.54	0.54
(SD)	(0.27)	(0.27)	(0.27)	(0.27)
Slow Probs:				
Expiry rate==0.1				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	0.50	0.58	0.59	0.44
(SD)	(0.27)	(0.29)	(0.30)	(0.30)
25.00	0.44	0.70	0.71	0.28
(SD)	(0.26)	(0.26)	(0.29)	(0.32)
Expiry rate==0.5				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	0.56	0.51	0.50	0.50
(SD)	(0.26)	(0.28)	(0.29)	(0.29)
25.00	0.52	0.50	0.50	0.49
(SD)	(0.28)	(0.29)	(0.29)	(0.29)
Expiry rate==0.9				
Inflow\Frequency	1.00	7.00	30.00	87.00
10.00	0.51	0.52	0.50	0.50
(SD)	(0.28)	24(0.29)	(0.28)	(0.29)
25.00	0.52	0.50	0.50	0.50
(SD)	(0.28)	(0.28)	(0.29)	(0.29)