Computerized Platform for Optimal Organ Allocations in Kidney Exchanges

Yanhua Chen, Jack D. Kalbfleisch, Yijiang Li, Peter X.-K. Song and Yan Zhou
Department of Biostatistics, University of Michigan, Ann Arbor, MI 48109, USA
E-mail: {chenyanh, jdkalbfl, yijiang, pxsong, zhouyan}@umich.edu

Abstract— *Kidney transplantation has emerged as the treatment for the most serious forms of kidney disease, but the supply of kidneys from deceased donors cannot meet the fast-growing demand. Recently, Kidney Paired Donation (KPD) program, a modality which enables willing but incompatible live donor-candidate pairs to swap donors, offers a promising solution for closing the gap between kidney supply and demand. Most of current KPD programs focus mainly on organ allocations strategies achieving the maximum number of transplants or matches. However, patients' quality of life after transplants can be more important for kidney candidates. In this paper, we propose a novel algorithmic platform to optimize cross-matches with the maximum benefits for donor-candidate pairs. Utilizing the power of integer programming, our platform implements a recently proposed method that takes probabilistic-based utility as the objective function, so that the overall expected utility, instead of the number of matches, is maximized. Moreover, involving altruistic donors in the allocations lead to a significant improvement in successful transplants. Empirically, we demonstrate the computerized platform for optimal organ allocations in kidney exchanges through extensive simulation experiments.*

Keywords: Kidney exchange; Optimal matching; Integer programming; Computerized platform

1. Introduction

Kidney transplantation has emerged as the treatment for the most serious forms of kidney disease. However, there is a considerable shortage of donor kidneys in the U.S.: more than $80,000$ patients are on the waiting list for transplants by the end of 2010 [9]. In the real world clinical application, deceased donation and living donation are the two resources of organs for kidney transplantation, and living-donor transplant has a higher chance of success. Unfortunately, about one-third of patients with willing live donors will be excluded from kidney transplantation because of ABO blood type mismatch or HLA incompatibility [8]. ABO blood type mismatch infers to: type O people are universal donors for any candidates; people who have type AB blood can donate to only the same blood type patients; and a type A or B donor can donate to the same type or a type AB candidate. HLA incompatibility occurs when a recipient candidate is sensitized to some of the Human Leukocyte Antigens (HLA) of his/her willing donor. Therefore, KPD program is established as a promising clinical solution to overcome the shortage of donors. The essential idea of such program is to exchange living kidney donors between two willing but incompatible donor-candidate pairs. The fundamental question in the KPD program is how to make an optimal decision of kidney exchanges that benefit patients the best.

An Integer Programming (IP) approach is widely used to tackle the optimization problem of selecting the optimal matches among incompatible donor-candidate pairs. Unfortunately, most of all current methods focus on determining the optimal two-way and/or three-way cycle exchanges through the means of graphic representation. Such constraint on the length of cycles to be less than 3 is imposed due to logistic consideration [1]. In this setting, many articles have considered to maximize the total number of transplants; see for examples, [11], [12], [14], [13], [1], [3]. In the real kidney exchanges, it is not only necessary to consider how to increase the number of transplants, but also needs to improve the quality of life for recipients after their transplants so that the transplants can make them live better. Therefore, we consider an expected-utility-based algorithm proposed by [6], which takes account of the medical-outcome-based utility (e.g., the life years gained from real transplants (LYFT) [16]) as well as the probability of successful actual transplants. In addition, most of the KPD exchanges only consider the paired donor-candidates to swap donors between them. Recently, these swaps also include chains triggered by altruistic donors (ADs) because chains offer more advantages [10], [4], [2]. On the one hand, it relaxes the reciprocality requirement of KPD, so pairs can find a donor from other pairs or ADs, rather than matching both the donor and candidate of another pair. More importantly, the simultaneity requirement of KPD is relaxed, even if one donor of chain reneges, the candidate has some opportunity to get transplants. Therefore, we integrate ADs into the expected-utility-based algorithm to improve the kidney exchanges. The idea is to define a virtual recipient for an AD and carry out the similar optimization using the algorithm of paired exchanges. A complete review of KPD program is presented in [15].

In summary, we implement an innovative method that

takes account of utility and uncertainty into the optimization of graph matching and further integrates ADs into the traditional KPD program. Through simulation experiments, we demonstrate the superiority of the expected-utility-based approach in comparison to the existing allocation strategies. Thus, our algorithmic platform brings more benefits for a greater number of kidney patients. In addition, we develop a general KPD graphic user interface (GUI) software that allows to model, visualize, and monitor the real world kidney exchanges. The remainder of the paper is organized as follows. We first present the mathematical formulation, optimization algorithm and theoretical work of kidney exchange problem in details in Section 2. In Section 3, we provide thorough computerized platform, experimental results and GUI software. Finally, we give a conclusion and discuss some future work in Section 4.

2. Optimization Algorithm

2.1 Graph-based Formulation

A kidney exchange problem can be represented as a directed graph $G = (V, E)$. Let $|V|$ be the number of vertices (nodes) and $|E|$ be the number of edges in a KPD graph, where $|.|$ denotes cardinality. Figure 1 shows an example. Each vertex in graph G represents an incompatible donor-candidate pair (e.g., vertex 1) or an altruistic donor (e.g., vertex 7). Each edge from vertex i to vertex j indicates that the donor kidney in vertex i is compatible with the candidate in vertex j (e.g., $7 \rightarrow 1$). In this directed graph, each edge is assigned a weight representing *edge utility* e_{ij} of the kidney transplant from the donor in vertex i to the candidate in vertex j (e.g., $e_{71} = 9$). In addition, an *edge probability* p_{ij} is considered for each edge to reflect the chance of an actual successful kidney transplant from i to j (e.g., $p_{71} = 0.6$). All the directed edges are established for compatibility of ABO blood types and HLA sensitization.

The goal of optimization for kidney exchange program is to find a collection of mutually disjoint cycles or chains that attain the maximum overall expected utility of graph G. This task of optimizing matches on graph G can be realized by the following setup of an integer programming [6]:

$$\max \sum_{c \in C} y_c u_c, \tag{1}$$

$$\text{s.t.} \begin{array}{c} y_c \in \{0,1\}, \forall c \in C, \\ \sum_{c \in C(i)} y_c \leq 1, 1 \leq i \leq |V|. \end{array}$$

where C is the exchange set of all cycles or chains with length 2 and/or 3 in graph G. $C(i)$ is the exchange set of cycles or chains in C that contain vertex i and y_c is a vector of indicators representing if cycle or chain exchange set c is to be executed for transplant ($y_c = 1$) or not ($y_c = 0$). Notice that u_c is the expected utility of cycle or chain exchange set c, which has been fully discussed in [6]. According to [6], where $u_c = \sum U_c P_c$.

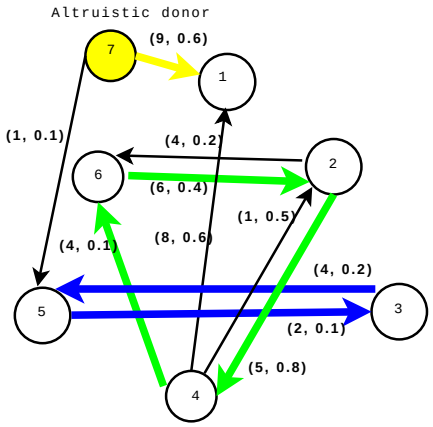


Fig. 1: A toy kidney exchange program including an altruistic donor and six incompatible pairs. It contains 3 two-way cycles ({2,4}, {2,6}, {3,5}), 1 three-way cycle ({6,2,4}) and 3 chains beginning with an altruistic donor ({7,1}, {7,5} {7,5,3}). The optimal matches selected by IP are: {7,1}, {6,2,4}, and {3,5}, which represent the optimal exchanges $7 \rightarrow 1$, $6 \rightarrow 2 \rightarrow 4 \rightarrow 6$ and $3 \rightarrow 5 \rightarrow 3$.

U_c is the maximum utility of the possible exchange sets in c, while $P_c = \prod_{\substack{i,j \in c \\ e_{ij} \in E_s}} p_{ij} \prod_{\substack{i,j \in c \\ e_{ij} \in (1-E_s)}} (1 - p_{ij})$ for the corresponding exchange sets c, where E_s indicates a set of edges e_{ij} leading to actual transplants. Therefore, the calculation of expected utility is based on all possible configurations in exchange set corresponding to each edge either resulting in an actual successful transplant or not in the real lab match run. And for each such configuration, we aim to choose the available cycle that yields the highest expected utility. In addition, the expected utility of a chain initiated by an AD can be computed in a similar way except creating a dummy cycle from the ending vertex of chain. For example, add a dummy edge from vertex 1 to vertex 7 with edge utility $e_{17} = 0$ and edge probability $p_{17} = 1$, which results in a 2-way cycle $\{7, 1\}$. In Figure 1, using the above formula, we compute the expected utilities of cycles as $u_{\{2,4\}} = 2.4$, $u_{\{2,6\}} = 0.8$, $u_{\{6,2,4\}} = 3.35$, $u_{\{3,5\}} = 0.12$. Also, the expected utilities of chains are calculated as $u_{\{7,1\}} = 5.4$, $u_{\{7,5\}} = 0.1$, $u_{\{7,5,3\}} = 0.156$. Then, plugging the expected utilities u_c into Equation (1), we use IP to find the optimal solution of the virtual matches: $7 \rightarrow 1$, $6 \rightarrow 2 \rightarrow 4 \rightarrow 6$ and $3 \rightarrow 5 \rightarrow 3$. Finally, not all the optimal virtual matches lead to actual operations. For instance, some higher order cycles (e.g, three-way cycles) are less likely to be chosen because such cycles tend to be more difficult to successful carry out [1]. If lab match run suggests one transplant fails (e.g., edge e_{62} is broken), then the entire three-way exchange $6 \rightarrow 2 \rightarrow 4 \rightarrow 6$ is labeled as a failure in the existing methods. However, [6] suggests a method with fall-back option; that is, we can choose the kidney exchange between 2 and 4 as a sub-cycle. As a result, the transplants now include $7 \rightarrow 1$, $2 \rightarrow 4 \rightarrow 2$, and $3 \rightarrow 5 \rightarrow 3$.

2.2 Algorithm

The computerized platform for kidney exchanges is based on a graphic optimization algorithm, described in detail as the following steps:

1) Given incompatible donor-candidate pairs and ADs at time $t = 0$, build a directed graph $G = (V, E)$ with each vertex representing a donor-candidate pair or an AD and each edge from vertex i to j denoting compatibility, so that there is a possibility match between the donor in vertex i to the candidate in vertex j.
2) Assign edge utility e_{ij} and edge probability p_{ij} to each match pair of donor i and candidate j. e_{ij} is derived from medical-outcome-based utility or some existing KPD scoring systems [11], and p_{ij} is derived from a statistical model for probability of successful transplants.
3) Find chains beginning at vertices of ADs with length size equal to 2 and/or 3.
4) Add dummy edges from the end vertices of chains to ADs, on which assign the edge utility $e_{ij} = 0$ and the edge probability $p_{ij} = 1$.
5) Find all cycles with length size 2 and/or 3 in graph G using the depth-first search algorithm.
6) Compute the expected utility u_c according to the configuration of each cycle exchange set.
7) Solve Equation (1) to get indicators y_c representing the optimal virtual donor-candidate matches.
8) Determine the final optimal kidney transplants according to Bernoulli trails with a certain success probability in the real lab match run. If such a Bernoulli trial is realized, the transplant will lead to an successful operation; otherwise, it fails.
9) Compute the number of completed transplants and associated utility of optimal kidney transplants.
10) Remove the vertices of donor-candidate pairs and ADs that finish successful transplants from graph G, and those end vertices of chains are “bridge donors" [10] as new ADs.
11) At time $t = t + 1$, form the new incompatible donor-candidate pairs and ADs based on pair arrival rate λ according to a Poisson process, then go to step 1).

2.3 Theoretical Analysis

In this section, we show that the decision version of our algorithm for kidney exchange program is NP-complete given in Equation (1).

***Theorem** 1:* Given a graph $G = (V, E)$ and an integer n ($n \geq 3$), the problem of deciding if G admits a perfect cycle/chain cover containing cycles/chains of length at most n is NP-complete.

Our proof of Theorem 1 follows that in [1]. First, it is easy to demonstrate this problem is in NP. Second, we can prove that it is NP-hard through a reduction from a 3D-Matching problem. Due to the space limitation, we omit detail of the proof.

3. Experiments

3.1 Computerized Platform and Evaluation Measurement

We tested the algorithm on a computerized platform by mimicking a general kidney exchange simulation system proposed in [6], which appropriately reflects the real world clinical application. In this computerized platform, we hope to evaluate different kidney allocation strategies. The flowchart for the computerized platform is illustrated in Figure 2. First, we generated data of candidates and donors separately. Candidates are sampled at random from the University of Michigan kidney paired donation database, which currently has 187 incompatible donor-candidate pairs. This database provides us the important information of ABO blood type and HLA useful to characterized each sampled candidate. Donors, on the other hand, are generated by the population distributions of ABO and HLA. In particular, the distribution of ABO blood types for the US population is: $O(44\%)$, $A(42\%)$, $B(10\%)$, and $AB(4\%)$, according to Stanford Blood Center (2010) [1], and the distribution of HLA is derived from HLA haplotypes frequencies of the US population [7]. Through random sampling, we can appoint ADs directly from the set of drawn donors or construct an incompatible donor-candidate pair if either their ABO blood types mismatch or HLA incompatibility. In this way, simulated donors and candidates reflect real-world of data. Second, KPD parameters needed for data generation, including an initial pair number n and percentage of ADs, are specified for the first match run. Third, a directed graph $G = (V, E)$ involving edge utilities and edge probabilities is created by using characteristics of candidates and donors. In this paper, for illustration, we assign values of edge utilities and edge probabilities according to uniform random distributions on interval denoted by $[\min, \max] = [a, b]$, such as $U[10, 20]$ and $P[0.1, 0.5]$, respectively. Fourth, for a given KPD graph, we find all cycles and chains with length size equal to 2 and/or 3 by the depth-first search algorithm. Furthermore, using IP optimization algorithm discussed in Section 2, we search for the optimal solution regarding the maximum potential matches (transplants) under each allocation strategy applying Gurobi optimization software [5]. Fifth, the ready transplant matches are finalized as actual successful transplants in the real lab match run according to Bernoulli trails with a certain success probability. At the end, the actual successful transplants are output from the platform. Moreover, in an evolving KPD program, successful donor-candidate matches will leave the database and some

[1] http://bloodcenter.stanford.edu/about_blood/blood_types.html

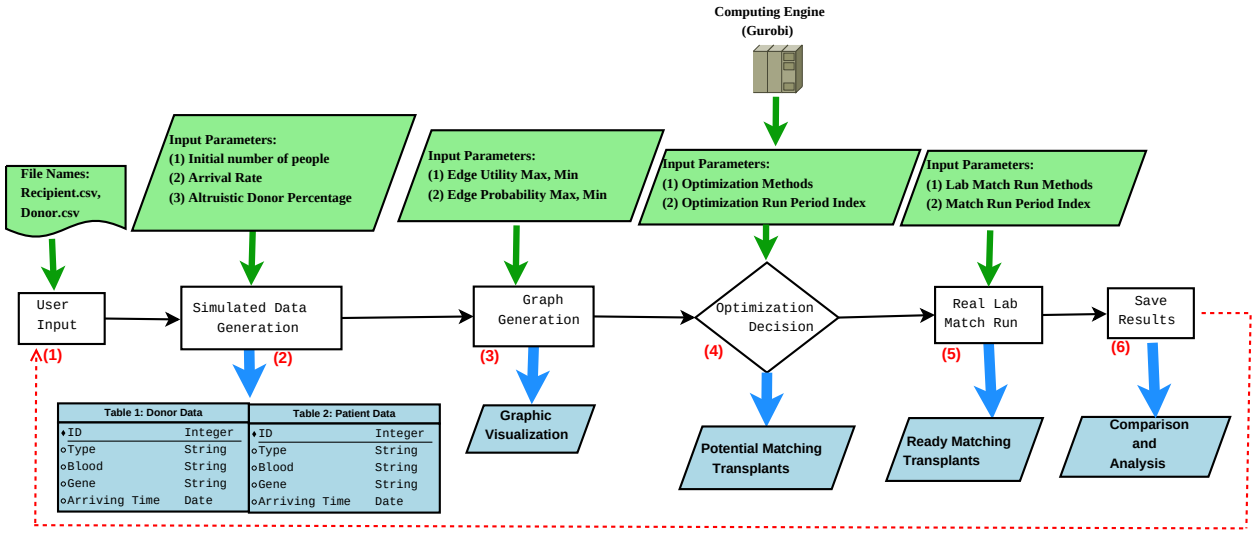


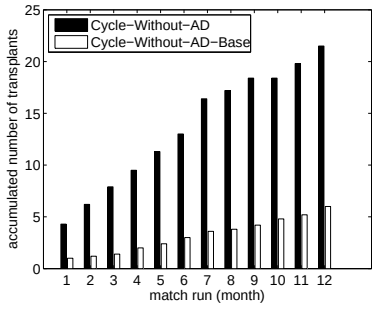
Fig. 2: A flowchart of computerized platform for kidney exchanges.

new pairs will enter into the pool according to a Poisson process with an arrival rate λ. Thus, a new match run will be performed at another time (see the dot line in Figure 2). In order to make a better comparison, we fixed the number of match runs as $k = 12$, mimicking the reality that there is one match run each month within a year. In the following simulation experiments, we evaluated the kidney exchange results based on two criteria: the accumulated number of transplants and accumulated utility. The higher the number of transplants or the utility is, the higher mutual benefits for the kidney transplant patients. For each allocation strategy, we conducted 100 test runs, and reported the averaged accumulated number of transplants and averaged accumulated utility.

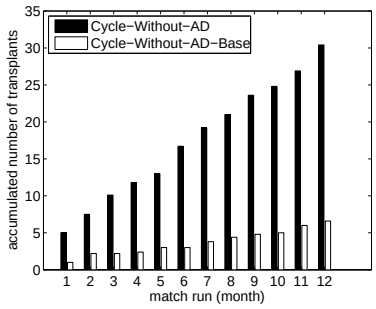
3.2 Results

We began by creating a KPD pool of by specifying three input parameters: the initial number of pairs $n = 200$, the arrival rate of pairs $\lambda = 10$ or $\lambda = 20$, and the percentage of ADs 5%. Then we generated a directed graph by assigning edge utility and edge probability as $U[10, 10]$ and $P[0.1, 0.5]$, respectively. First, we aimed to compare two allocation strategies in terms of accumulated number of transplants, in the settings where the KPD only involved donor-candidate pairs (namely no ADs). The two strategies to be compared are (1) *Cycle-Without-AD-Base*: a traditional method that does not consider the expected utility in the optimization and fall-back option in the real lab match run; (2) *Cycle-Without-AD*: a new method [6] that uses the expected utility in the optimization and accounts for the fall-back option in the real lab match run. The accumulated number of transplants obtained by the two approaches with different arrival rates λ are shown in Figure 3. Generally, the accumulated number of transplants appears higher for a larger number of arrival rate (e.g., $\lambda = 20$ in Figure 3(b) versus $\lambda = 10$ in Figure 3(a)). This implies that the more pairs participate in the kidney exchange program, the higher number of achieving matches in the KPD pool. Moreover, the accumulated number of transplants gained by the new approach (i.e., *Cycle-Without-AD*) is significantly higher than the traditional method (i.e., *Cycle-Without-AD-Base*) in the magnitude of $2-4$ folds. These results indicate that the new approach is clearly advantageous to increase the number of transplants in kidney exchanges.

Next, we integrated the ADs into the new allocation strategy and investigated the role of ADs in the kidney exchanges. As discussed in Section 2, method *Cycle-With-AD* is modified by simply adding dummy edges from each donor-candidate vertex to the ADs with cycle-length size 2 and/or 3. Then we utilized the same optimization procedure as that of the *Cycle-Without-AD* method to find the optimal exchanges. Figures 4(a)-(c) display the accumulated number of transplants obtained by two strategies: (1) *Cycle-Without-AD* and (2) *Cycle-With-AD*, where the edge utility is generated by $U[10, 10]$, $U[10, 20]$, and $U[10, 30]$, and the arrival rate is assigned by $\lambda = 10$. In these panels, based on the accumulated number of transplants over 12 match runs, method *Cycle-With-AD* gives at least 10% more matches than the method without using ADs. Moreover, we plotted the results for the case of $\lambda = 20$ in Figures 4(d)-(f). Again, when more people enters, method with ADs clearly performed better than the one without ADs. In the meanwhile, we also compared accumulated utility of these two methods when the edge utility distribution changes from $U[10, 10]$ to $U[10, 30]$ in the cases of $\lambda = 10$ and $\lambda = 20$. From Figures 5(a)-(c), we noticed that the accumulated utility of the *Cycle-With-AD* method enjoys a gain between 15% to 30% over the *Cycle-Without-AD* method if $\lambda = 10$.



(a)



(b)

Fig. 3: Comparison of accumulated number of transplants versus month (number of match run) for *Cycle-Without-AD-Base* and *Cycle-Without-AD* methods with different arrival rate of pairs: (a) $\lambda = 10$, (b) $\lambda = 20$.

Likewise, Figures 5(d)-(f) report the accumulated utility of the method using ADs is about at least 10% higher than that of the method not using ADs if $\lambda = 20$. Therefore, it is obvious that on average the method without using ADs is consistently outperformed by the method using ADs over all match runs in terms of accumulated number of transplants and accumulated utility. As a result, using ADs in the kidney exchanges would help clinicians to achieve more number and better quality of transplants.

3.3 Software

In this paper, one of our new contributions is the development of a graphic user interface (GUI) software to visualize inputs and outputs in a kidney exchange program. Our simulation experiments above were carried out by using our GUI software developed by C++ language on a machine with Quad 3GHz Intel Core2 processors and 4GB RAM. The software offers a range of functions to create a user-friendly interface and builds appropriate configurations to support communications between inputs and outputs essential in the kidney exchanges. It includes six types of functional components associated with inputs and outputs, which are displayed in the middle panel of Figure 2: (1) reader of original data from internal and external files; (2) KPD data simulator; (3) KPD graph generator; (4) Optimizer of KPD kidney donation; (5) KPD lab match run; (6) output of graph matching results. In addition, the input data or parameters are showed in the upper panel of Figure 2, while the output data or results are showed in the lower panel of Figure 2.

For instance, Figure 6 shows a slapshot of GUI software of kidney exchanges for five match runs by the *Cycle-With-AD* method. Revelent information is displayed in multiple-windows. *Recipient* (right-top) and *Donor* (right-middle) windows in Figure 6 show the randomly drawn kidney experimental data when the initial number of pairs, arrival rate and percentage of ADs are fixed as 50, 10 and 5% respectively. The display of data includes period (i.e., number of match run), ID, type of vertex (i.e., pair or AD), blood type or HLA type. If ID number is the same between recipient candidate and donor, it indicates a pair of originally incompatible donor-candidate, otherwise it denotes an AD. In the *Graph Builder* window (right-bottom), the corresponding directed graph is created with the edge utility and edge probability generated by $U[10, 10]$ and $P[0.1, 0.5]$, respectively. After selecting an optimization method, such as *Cycle-Without-AD-Base*, *Cycle-Without-AD*, or *Cycle-With-AD*, the center window will report the optimal graph matches between donors and recipients, including donor ID, donor type, recipient ID, recipient type, number of transplants and associated utility at each match run. Also, if desired, a further match run can be performed, leading to an evolving kidney exchange data exploration. In summary, the GUI provides a very powerful tool to help clinicians, donors and patients more easily analyze and assess the kidney exchange program.

4. Conclusions and Future Work

In this paper, we investigated a new kidney allocation strategy based on expected-utility to maximize the mutual benefits for kidney exchanges. The problem is formulated as to search for the maximum disjoint vertex sets in a weighted directed graph. First, a depth-first search algorithm is implemented to identify all cycles/chains with length size 2 and/or 3. Then, an optimal solution of maximum expected utility can be obtained by an IP. Finally, ADs are added to increase the possibility of exchanges. Through simulation studies that closely imitate the real application on computerized platform, we demonstrated that the expected-utility-based allocation strategy provides the higher quantity and quality of life than the current practising methods in the kidney exchanges. This will result in thousands of kidney patients for life-saving each year in USA.

All algorithms discussed in this paper have been fully integrated into a GUI software package, which will be released publicly through the necessary Institutional Review Board (IRB) regulations. In the future, we plan to conduct practical studies to solicit feedbacks so that the software can be improved with more user-friendly features for clinical convenience. We also intend to incorporate interaction tools for input data process, integration, and modeling, as well as

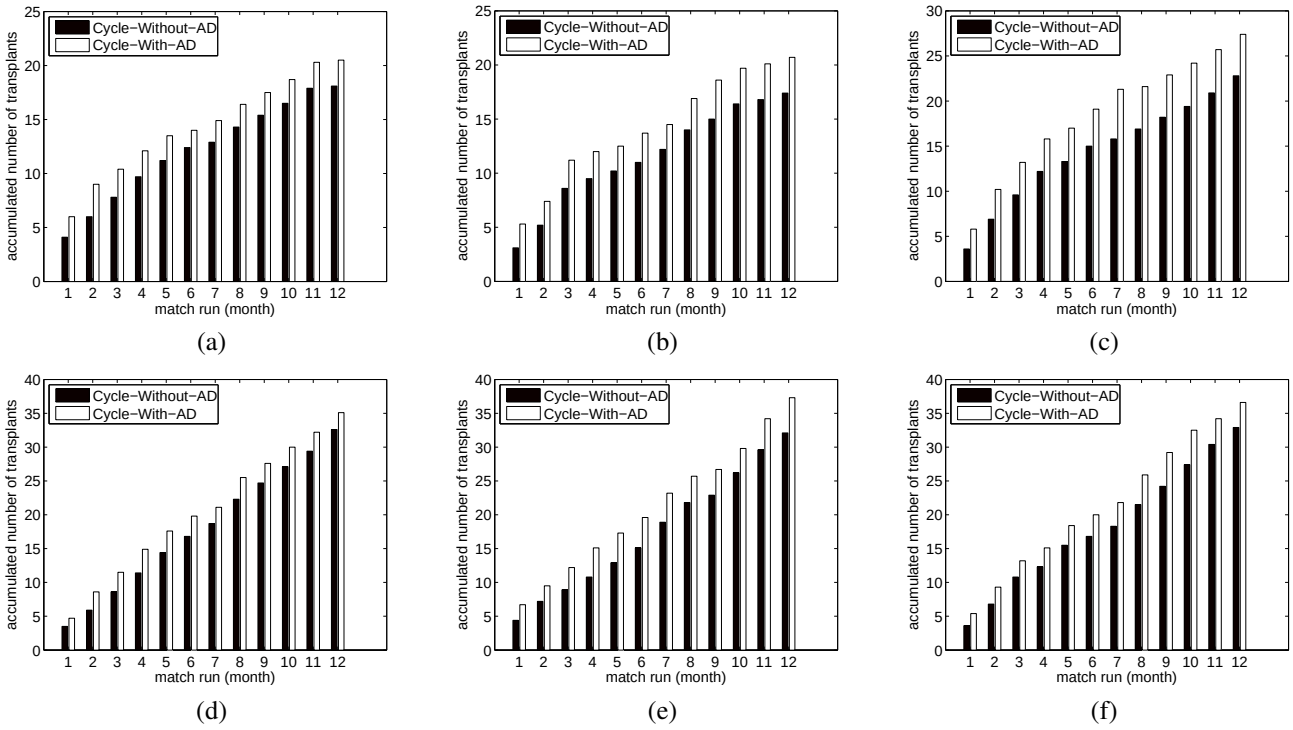


Fig. 4: Comparison of accumulated number of transplants versus month (number of match run) for *Cycle-Without-AD* and *Cycle-With-AD* methods with different arrival rate of pairs (λ) and different edge utility distributions (U): (a) $\lambda = 10$ and $U[10, 10]$, (b) $\lambda = 10$ and $U[10, 20]$,(c) $\lambda = 10$ and $U[10, 30]$, (d) $\lambda = 20$ and $U[10, 10]$,(e) $\lambda = 20$ and $U[10, 20]$, (f) $\lambda = 20$ and $U[10, 30]$.

output data graphical visualization into our existing system for its maximum flexibility of clinical practice.

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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*, pp. 295–304, 2007.

[2] G. Ashlagi, A. Roth, and M. Rees. "Nonsimultaneous Chains and Dominos in Kidney Paired Donation – Revisited," *American Journal of Transplant*, vol. 11, pp. 1–11, 2011.

[3] P. Biro, D. Manlove, and R. Rizzi, "Maximum weight cycle packing in directed graphs, with application to kidney exchange programs," in *Discrete Mathematics, Algorithms and Applications*, vol. 1, no. 4, pp. 499–517, 2009.

[4] S. Gentry, R. Montgomery, B. Seihart and D. Segev, "The roles of dominos and nonsimultaneous chains in kidney paired donation," *American Journal of Transplant*, vol. 9, pp. 1330–1336, 2009.

[5] The website: http://www.gurobi.com/

[6] Y. Li, J. Kalbfleisch, P. Song, Y. Zhou, A. Leichtman and M. Rees, "Optimization and simulation of an evolving kidney paired donation (KPD) program," *Department of Biostatistics, University of Michigan, Working Paper Series, Working Paper 90, http://www.bepress.com/umichbiostat/paper90* , May 2011

[7] M. Maiers, L. Gragert, and W. Klitz, "High-resolution HLA alleles and haplotypes in the United States population," *Human Immunology*, vol. 68, no. 9, pp. 779–788, 2007.

[8] R. Montgomery. "Renal transplantation across HLA and ABO antibody barriers: integrating paired donation into desensitization protocols," *American Journal of Transplant*, vol. 10, pp. 449–457, 2010.

[9] The website: http://optn.transplant.hrsa.gov/

[10] M. Rees, J. Kopke, R. Pelletier, D. Segev, M. Rutter, A. Fabrega, J. Rogers, O. Pankewycz, J. Hiller, A. Roth, T. Sandholm, M. Unver, and R. Montgomery, "A non-simultaneous extended altruistic donor chain," *New England Journal of Medicine*, vol. 360, no. 11, pp. 1096–1101, 2009.

[11] A. Roth, T. Sonmez, and M. Unver, "Kidney exchange," *Quarterly Journal of Economics*, vol. 119, no. 2, pp. 457–488, 2004.

[12] A. Roth, T. Sonmez, and M. Unver, "A kidney exchange clearinghouse in New England," *American Economic Review*, vol. 95, no. 2, pp. 376–380, 2005.

[13] A. Roth, T. Sonmez, and M. Unver, "Efficient kidney exchange: Concidence of wants in a market with compatibility-based preferences," *American Economic Review*, vol. 97, no. 3, pp. 828–851, 2007.

[14] S. Saidman, A. Roth, T. Somez, M. Unver, and F. Delmonico, "Increasing the opportunity of live kidney donation by matching for two and three way exchanges," *Transplantation*, vol. 81, no. 5, pp. 773–782, 2006.

[15] C. Wallis, K. Samy, A. Roth and M. Rees. "Kidney paired donation," *Nephrol Dial Transplant*, vol. 0, pp. 1–9, 2011.

[16] R. Wolfe, et al., "Calculating life years from transplant (LYFT): method for kidney and kidney-pancreas candidates," *American Journal of Transplant*, vol. 8, pp. 997–1011, 2008.

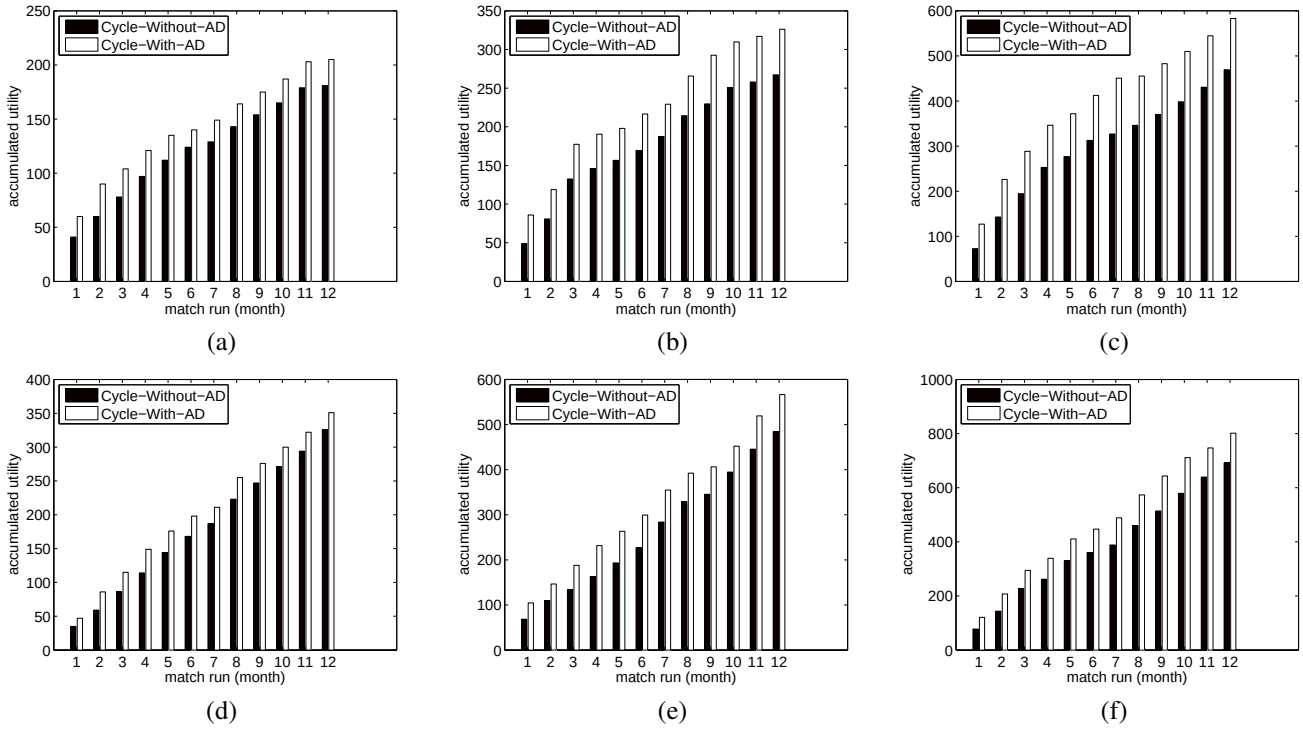

Fig. 5: Comparison of accumulated utility versus month (number of match run) for *Cycle-Without-AD* and *Cycle-With-AD* methods with different arrival rate of pairs (λ) and different edge distributions (U): (a) $\lambda = 10$ and $U[10, 10]$, (b) $\lambda = 10$ and $U[10, 20]$,(c) $\lambda = 10$ and $U[10, 30]$, (d) $\lambda = 20$ and $U[10, 10]$,(e) $\lambda = 20$ and $U[10, 20]$, (f) $\lambda = 20$ and $U[10, 30]$.

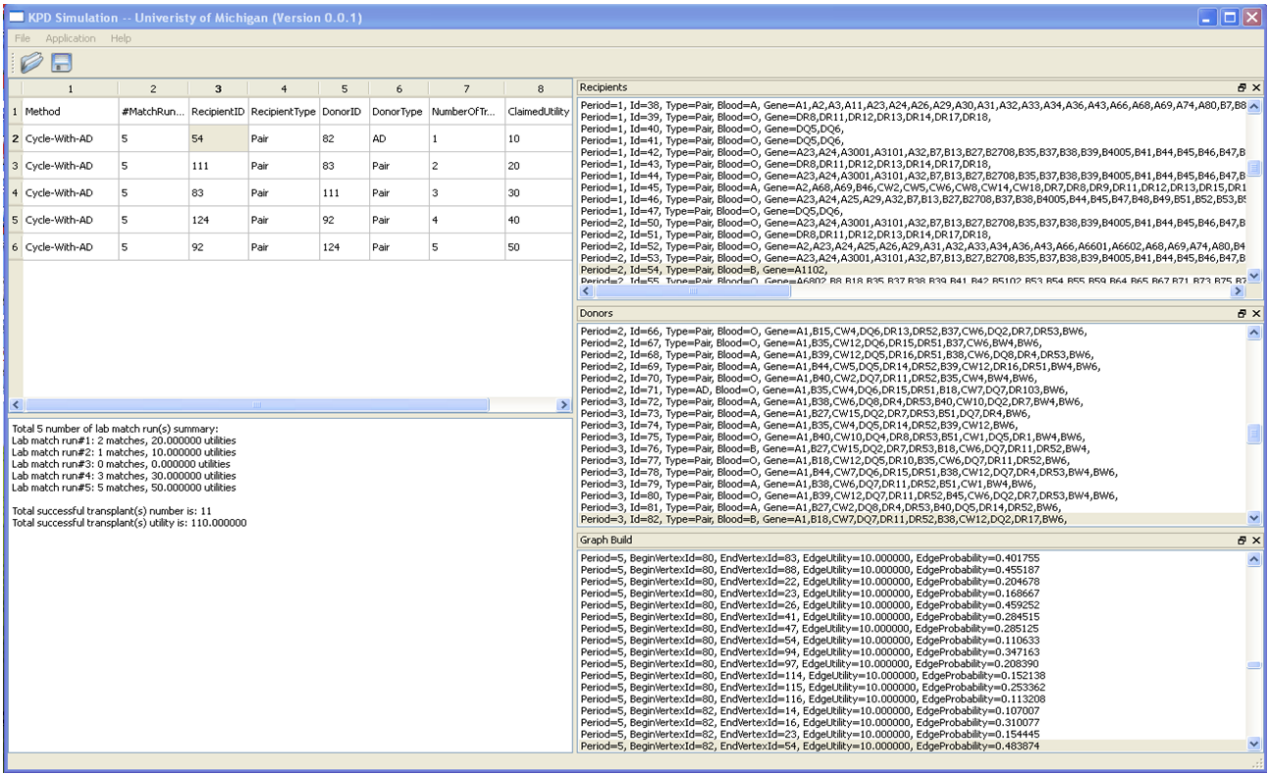

Fig. 6: A GUI example for kidney exchanges