

Computing Balanced Solutions for Large International Kidney Exchange Schemes

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ABSTRACT

To overcome incompatibility issues, kidney patients may swap their donors. In international kidney exchange programmes (IKEPs), countries merge their national patient-donor pools. We consider a recent credit system where in each round, countries are given an initial kidney transplant allocation which is adjusted by a credit function yielding a target allocation. The goal is to find a solution in the patient-donor compatibility graph that approaches the target allocation as closely as possible, to ensure long-term stability of the international pool. As solutions, we use maximum matchings that lexicographically minimize the country deviations from the target allocation. We first give a polynomial-time algorithm for computing such matchings. We then perform, for the first time, a computational study for a *large* number of countries. For the initial allocations we use, besides two easy-to-compute solution concepts, two classical concepts: the Shapley value and the nucleolus. These are hard to compute, but by using state-of-the-art software we show that they are now within reach for IKEPs of up to fifteen countries. Our experiments show that using lexicographically minimal maximum matchings instead of ones that only minimize the largest deviation from the target allocation (as previously done) may make an IKEP up to 52% more balanced.

KEYWORDS

kidney exchanges; matching game; core; compensation scheme; computer simulation

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1 INTRODUCTION

For kidney patients, kidney transplantation is still the most effective treatment. However, a kidney transplantation might not be possible due to blood-type or tissue-type incompatibilities between a patient and a willing donor. The solution is to place all patient-donor pairs

in one pool such that donors can be swapped. A *kidney exchange programme* (KEP) is a centralized program where the goal is to find an optimal kidney exchange scheme in a given pool of patient-donor pairs.

Recently, national KEPs started to collaborate, leading to a number of *international* KEPs. In 2016, the first international kidney exchange took place, between Austria and Czech Republic [17]. In 2018, Italy, Spain and Portugal started to collaborate. In 2019, Scandiatransplant, an organization for sharing deceased organs among six Scandinavian countries, started an international KEP involving Swedish and Danish transplant centers. Even though overall solutions will improve, *individual rationality* might not be guaranteed, that is, individual countries could be worse off. To improve the stability of an international KEP, the following question is therefore highly relevant: *What kind of fairness must we guarantee to ensure that all countries in an international KEP place all their patient-donor pairs in an international pool?*

Individual rationality [4, 5] and fairness versus optimality [3, 15, 25, 35] were initially studied for national KEPs, in particular in the US. However, the US situation is different from many other countries. The US has three nationwide KEPs (UNOS, APD, NKR) [2], and US hospitals work independently and compete with each other. Hence, US hospitals tend to register only the hard-to-match pairs to the national KEPs. As a consequence, the aforementioned papers focused on mechanisms that give incentives for hospitals to register all their patient-donor pairs at the KEP.

Our Setting. We consider the setting of European KEPs which are scheduled in rounds, typically once in every three months [11]. Unlike the US setting, this setting allows a search for optimal exchange schemes. The search can be done in polynomial time for 2-way exchanges (*matchings*), but is NP-hard if 3-way exchanges are permitted [1]. Below we discuss existing work for this setting.

Known Results. Carvalho and Lodi [18] used a 2-round system for ensuring stability of international KEPs with 2-way exchanges only: in the first round each country selects an internal matching, and in the second round a maximum matching is selected for the international exchanges. They gave a polynomial-time algorithm for computing a Nash-equilibrium that maximizes the total number of transplants, improving the previously known result of [19] for two countries.

Sun et al. [34] also considered 2-way exchanges only. They defined so-called selection ratios using various lower and upper target

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numbers of kidney transplants for each country. In their setting, a solution is considered to be fair if the minimal ratio across all countries is maximized. They also required a solution to be a maximum matching and individually rational. They gave theoretical results specifying which models admit solutions with all three properties and they provided polynomial-time algorithms for computing such solutions, if they exist.

Klimentova et al. [29] introduced a credit system, where the number of kidney transplants for a country is specified by a “fair” target number for that country. The differences between the actual number of transplants for a country and its target number are used as *credits* for the next round. In their simulations, they allowed 3-way exchanges for four countries and considered the potential and benefit values as target allocations, the latter yielding slightly more balanced solutions. Biró et al. [10] compared the benefit value with the Shapley value. In their simulations, for three countries allowing 3-way exchanges, they found that the Shapley value produced smaller deviations from the targets on average. Biró et al. [12] considered credit-based compensation systems from a theoretical point of view. They only allowed for 2-way exchanges but unlike [10, 29], with the possibility of having weights for representing transplant utilities. They gave a polynomial-time algorithm for finding a maximum matching that minimizes the largest deviation from a target allocation. They also showed that the introduction of weights makes the problem NP-hard.

Our Contribution. In Section 2 we explain the credit system of [10, 12, 29] and our settings. We only allow 2-way exchanges (just as [18, 19, 34], but unlike [10, 29]) and do not consider weights (just as [10, 29]). In Section 3, we generalize the above polynomial-time result of [12] by giving a polynomial-time algorithm for computing a maximum matching that *lexicographically minimizes* the country deviations from a given target allocation. In Section 4 we complement this result with a simulation for up to even *fifteen* countries in contrast to the previous studies [10, 29] for 3–4 countries, and we do this both for equal and varying country sizes. Our motivation is twofold. Firstly, international KEPs have a growing number of countries. Secondly, we aim to measure the effect of using maximum matchings that are lexicographically minimal, which requires a large number of countries. Motivated by the promising results for the Shapley value [10], we also considered the effect of using more widely accepted solution concepts from Cooperative Game Theory. Hence, we chose to take as target allocation the Shapley value and the nucleolus and compare these against the benefit value and the contribution value, a natural variant of the benefit value (see Section 2).

As mentioned, we only allow 2-way exchanges and do not consider weights: if 3-way exchanges [1] or weights [12] are allowed, the problem becomes NP-hard, and with the current technology it is not possible to perform a study on such a large scale as ours. We note that some countries, such as France and Hungary, are legally bound to using only 2-way exchanges.

Our experiments show that a credit system using lexicographically minimal maximum matchings instead of ones that minimize the largest deviation make an international KEP up to 52% more balanced, without decreasing the overall number of transplants. The exact improvement depends on the solution concept used. Choosing the latter is up to the policy makers of the international KEP. From

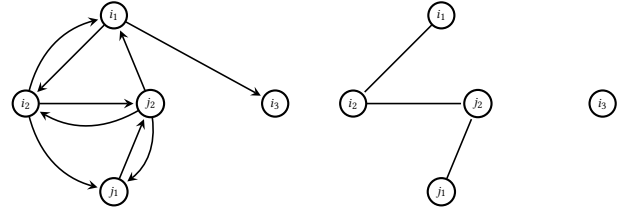


Figure 1: A directed compatibility graph (left) which we make undirected (right). Here, $M = \{M\}$, where $M = \{i_1 i_2, j_1 j_2\}$. If $V_1 = \{i_1, i_2, i_3\}$ and $V_2 = \{j_1, j_2\}$, then $s_1(M) = s_2(M) = 2$.

our experiments, however, the Shapley value turned out, again, to yield the best results, namely on average a (relative) deviation of up to 0.52% from the target allocation (whereas the other three solution concept stay within 1.23%).

2 OUR MODEL

We model a KEP as follows. A *compatibility graph* is a directed graph $D = (V, E)$ with an arc weighting w . Each vertex in V is a patient-donor pair, and there is an arc from patient-donor pair i to patient-donor pair j if the donor of pair i is compatible with the patient of pair j . The associated weight w_{ij} indicates the utility of the transplantation. An *exchange cycle* is a directed cycle C in D . The *weight* of a cycle C is the sum of the weights of its arcs. An *exchange scheme* X is a union of pairwise vertex-disjoint exchange cycles in D . The weight of X is the sum of the weights of its cycles. The goal is to find an exchange scheme of maximum weight, subject to a fixed *exchange bound* ℓ , which is an upper bound on the length of the exchange cycles that may be used.

We obtain an international KEP by partitioning V into sets V_1, \dots, V_n , where n is the number of countries involved and V_p is the set of patient-donor pairs of country p . The objective is still to find an exchange scheme of D that has maximum weight subject to the exchange bound ℓ . In this setting, we must now in addition ensure that the countries accept the proposed exchange schemes. **Assumptions.** We set $\ell = 2$ and $w \equiv 1$. As $\ell = 2$, we can make D undirected by adding an edge between two vertices i and j if and only if (i, j) and (j, i) are in A (see Figure 1). So, from now on, compatibility graphs are undirected.

We now explain the recent credit system from [12, 29] for international KEPs, which run in rounds. Let $N = \{1, \dots, n\}$ be the set of countries and for some $h \geq 1$, let D_h be the compatibility graph in round h with vertex set of countries V_1^h, \dots, V_n^h . Let μ_h be the size of a maximum matching in D_h , so $2\mu_h$ is the maximum number of kidney transplants possible in round h . As we optimize social welfare, we define an *allocation* for round h as a vector $x^h \in \mathbb{R}^N$ with $x^h(N) = 2\mu_h$, where we write $x^h(S) = \sum_{p \in S} x_p^h$ for a subset $S \subseteq N$. Thus, x_p^h describes the share of $x^h(N) = 2\mu_h$ that is allocated to country p . We can only allocate integer numbers (kidneys), but nevertheless we do allow allocations x^h to be non-integer, as we will explain later.

Assume that we are given a “fair” allocation y^h for round $h \geq 1$, together with a *credit function* $c^h : N \rightarrow \mathbb{R}$, which satisfies $\sum_{p \in N} c_p^h = 0$; we let $c^1 \equiv 0$ and define c^h for $h \geq 2$ below. For

$p = 1, \dots, n$, we set $x_p^h = y_p^h + c_p^h$. Then x^h is an allocation, as y^h is an allocation and $\sum_{p \in N} c_p^h = 0$. We call x^h the *target allocation* and y^h the *initial allocation* for round h .

We now define c^h for $h \geq 2$. Let \mathcal{M}^h be the set of all maximum matchings of D_h . As we optimize social welfare, we choose a matching $M^h \in \mathcal{M}^h$. The set $\{(i, j) \in E \mid ij \in M^h, j \in V_p^h\}$ consists of all kidney transplants in round h that involve patients in country p (with donors both from country p and other countries). We let $s_p(M^h)$ denote the size of this set, or equivalently, $s_p(M^h) = |\{j \in V_p^h \mid ij \in M^h\}|$ (see Figure 1). We now compute a new credit function c^{h+1} by setting $c_p^{h+1} = x_p^h - s_p(M^h)$ and note that $\sum_{p \in N} c_p^{h+1} = 0$, as required. For round $h + 1$, a new initial allocation y^{h+1} is given. For $p = 1, \dots, n$, we set $x_p^{h+1} = y_p^{h+1} + c_p^{h+1}$ and repeat the process. Note that $c_p^h = \sum_{t=1}^{h-1} (y_p^t - s_p(M^t))$ for a country p and round $h \geq 2$, so credits are in fact the accumulation of the deviations from the initial allocations.

We now specify our choices for the initial allocations y^h and maximum matchings $M^h \in \mathcal{M}^h$.

Choosing the initial allocation y . As mentioned, we use a cooperative game-theoretic perspective. A (*cooperative*) *game* is a pair (N, v) , where N is a set $\{1, \dots, n\}$ of *players* and $v : 2^N \rightarrow \mathbb{R}_+$ is a *value function* with $v(\emptyset) = 0$. A *coalition* is a subset $S \subseteq N$. If $v(N)$ is maximum over all partitions of N , then the players have an incentive to form the *grand coalition* N . The central problem is then how to distribute $v(N)$ amongst the players in such a way that players are not inclined to leave the grand coalition. In this context, an *allocation* is a vector $x \in \mathbb{R}^N$ with $x(N) = v(N)$. A *solution concept* prescribes a set of “fair” allocations for cooperative games, where the notion of fairness depends on context. The *core* of a game (N, v) consists of all allocations $x \in \mathbb{R}^N$ with $x(S) \geq v(S)$ for every $S \subseteq N$. Core allocations offer no incentive for a group of players to leave the grand coalition N and form a coalition on their own, so they ensure that N is stable. However, games may have an empty core.

For an allocation x and a coalition $\emptyset \neq S \neq N$ in a game (N, v) , we define the *excess* $e(S, x) := x(S) - v(S)$ and obtain the *excess vector* $e(x) \in \mathbb{R}^{2^n - 2}$ by ordering the $2^n - 2$ in a non-decreasing sequence. The *nucleolus* of a game (N, v) is the unique allocation [33] that lexicographically maximizes $e(x)$ over the set of allocations x with $x_p \geq v(\{p\})$ for every $p \in N$ (note that the latter set of allocations is nonempty for generalized matching games). The nucleolus is a core allocation if the core is nonempty. The *Shapley value* $\phi(N, v)$ of a game (N, v) , which does not necessarily belong to the core, is defined by setting for every $p \in N$,

$$\phi_p(N, v) = \sum_{S \subseteq N \setminus \{p\}} \frac{|S|!(n - |S| - 1)!}{n!} \left(v(S \cup \{p\}) - v(S) \right). \quad (1)$$

The *surplus* of a game (N, v) is $\text{surp} = v(N) - \sum_{p \in N} v(\{p\})$. For $p \in N$ we can allocate $v(\{p\}) + \alpha_p \cdot \text{surp}$ for some α with $\sum_{p \in N} \alpha_p = 1$. We obtain the *benefit value* [29] if for each $p \in N$,

$$\alpha_p = \frac{v(N) - v(N \setminus \{p\}) - v(\{p\})}{\sum_{p \in N} (v(N) - v(N \setminus \{p\}) - v(\{p\}))}.$$



Figure 2: A compatibility graph with a set $N = \{1, 2, 3\}$ of three countries. Suppose in round 1 (left) $V_1 = \{i_1\}$, $V_2 = \{i_2, i_3\}$ and $V_3 = \{i_4\}$ and in round 2 (right) $V_1 = \{i_1\}$, $V_2 = \{i_2\}$ and $V_3 = \{i_3\}$. Using the Shapley value yields in round 1, in the notation of the credit system, $x^1 = y^1 = (\frac{2}{3}, \frac{8}{3}, \frac{2}{3})$, $M^1 = \{(i_1, i_2), (i_3, i_4)\}$ (the thick edges in the left graph), $s(M^1) = (1, 2, 1)$ and $c^2 = y^1 - s(M^1) = (-\frac{1}{3}, \frac{2}{3}, -\frac{1}{3})$, and in round 2, $y^2 = (\frac{4}{3}, \frac{1}{3}, \frac{1}{3})$, $x^2 = y^2 + c^2 = (1, 1, 0)$, $M^2 = \{(i_1, i_2)\}$ (the thick edge in the right graph) and $c^3 = x^2 - s(M^2) = (0, 0, 0)$. Using the nucleolus yields the same for round 1, but in round 2, $y^2 = (2, 0, 0)$, and hence $x^2 = y^2 + c^2 = (\frac{5}{3}, \frac{2}{3}, -\frac{1}{3})$, $M^2 = \{(i_1, i_2)\}$ and $c^3 = x^2 - s(M^2) = (\frac{2}{3}, -\frac{1}{3}, -\frac{1}{3})$.

We obtain the *contribution value* by setting for each $p \in N$,

$$\alpha_p = \frac{v(N) - v(N \setminus \{p\})}{\sum_{p \in N} (v(N) - v(N \setminus \{p\}))}.$$

A *generalized matching game* [12] is a game (N, v) on an undirected graph $D = (V, E)$ with an edge weighting w and a partition (V_1, \dots, V_n) of V . For $S \subseteq N$, we let $V(S) = \bigcup_{p \in S} V_p$. The value $v(S)$ of coalition S is the maximum weight of a matching in the subgraph of D induced by $V(S)$. If $w \equiv 1$, then $v(S)$ is the maximum size of a matching in the subgraph of D induced by $V(S)$. In particular $v(N) = \mu$, where μ is the size of a maximum matching in D . If $V_p = \{p\}$ for $p = 1, \dots, n$, then we obtain the classical *matching game* (see, for example, [13, 22, 26, 27, 30]).

In our setting, N is a set of countries. So, player $p \in N$ represents country p , which has set of patient-donor pairs V_p and size $|V_p|$. Recall also that we set $w \equiv 1$. For the initial allocation y in a round we consider four solution concepts of the corresponding generalized matching game: two *computationally involved* ones, namely the nucleolus and the Shapley value and two *easy-to-compute* ones, namely the benefit value and the contribution value. Recall that $x(N) = 2\mu$ for an allocation x , as we count the number of kidney transplants instead of the number of patient-donor swaps. To resolve this incompatibility, we simply multiply the allocations prescribed by the above four solution concepts by two.

Choosing the solution M . Recall that in order to optimize social welfare we choose a maximum matching in each round. Ideally, each country p should receive a number of kidney transplantations for its patients that is close to its target allocation x for the round under consideration. In [12] a polynomial-time algorithm was given for finding a maximum matching M that minimizes

$$d_1 := \max_{p \in N} \{|x_p - s_p(M)|\}.$$

Let $\delta(M) = (|x_{p_1} - s_{p_1}(M)|, \dots, |x_{p_n} - s_{p_n}(M)|)$ be the vector obtained by reordering the components $|x_p - s_p(M)|$ non-increasingly. We say that M is *lexicographically minimal* for an allocation x if $\delta(M)$ is lexicographically minimal over all matchings $M \in \mathcal{M}$. Note

that every lexicographically minimal matching in \mathcal{M} is a matching that minimizes $\max_{p \in N} \{x_p - s_p(M)\}$, but the reverse might not be true. In each round of our credit-based model we propose to take a maximum matching that is lexicographically minimal; see Figure 2 for an example. In the next section, we show how to compute such a matching in polynomial time.

Remark. Recall that $c_p^h = \sum_{t=1}^{h-1} (y_p^t - s_p(M^t))$ for a country p and round $h \geq 2$. Hence, credits for a country can build up over time even with our choice of fair target allocations. For instance, consider the example in Figure 2. Suppose every future round looks the same as round 2 and the nucleolus is used as the target allocation. Then, $c_{i_1}^h = c_{i_1}^{h-1} + 1$ for $h \geq 3$. However, these situations did not occur in any of our experiments where we used the credit function.

3 COMPUTING A LEXICOGRAPHICALLY MINIMAL MAXIMUM MATCHING

Let (N, v) be a generalized matching game with a set V of patient-donor pairs. Let \mathcal{M} be the set of maximum matchings in the corresponding compatibility graph D , and let x be an allocation. We will show how to compute a maximum matching from \mathcal{M} that is lexicographically minimal for x . We need the $O(|V|^3)$ -time algorithm from [12] which computes for a set of closed intervals I_1, \dots, I_n , a maximum matching $M \in \mathcal{M}$ with $s_p(M) \in I_p$ for $p = 1, \dots, n$ or finds that such a matching does not exist (the algorithm constructs in linear time an auxiliary graph G' on $O(|V|)$ vertices and then finds a maximum weight perfect matching of G' in $O(|V|^3)$ time by using Edmonds' algorithm [24]). Now suppose we are given a set of intervals I_1, \dots, I_n , some of which are open instead of closed. Let I_p be an open interval. Recall that the s -values are sizes of subsets of matching edges and thus are integers. Hence, we may replace I_p by the largest closed interval with integer end-points contained in I_p if this closed interval exists. If not, then a matching $M \in \mathcal{M}$ with $s_p(M) \in I_p$ does not exist. In other words, we found the following:

COROLLARY 3.1. *For a generalized matching game (N, v) with set V of patient-donor pairs and (not necessarily closed) intervals I_1, \dots, I_n , we can find in $O(|V|^3)$ time a matching $M \in \mathcal{M}$ with $s_p(M) \in I_p$ for each $p \in \{1, \dots, n\}$ or find that such a matching does not exist.*

Using Corollary 3.1, our algorithm Lex-Min computes for a generalized matching game (N, v) and allocation x , values d_1, \dots, d_t with $d_1 > \dots > d_t$ for some integer $t \geq 1$, and returns a matching $M \in \mathcal{M}$ that is lexicographically minimal for x .

Lex-Min

input : a generalized matching game (N, v) and allocation x
output : a lexicographically minimal matching $M \in \mathcal{M}$ for x .

Step 1. Compute the smallest number $d_1 \geq 0$ such that there exists a matching $M \in \mathcal{M}$ with $|x_p - s_p(M)| \leq d_1$ for all $p \in N$.

Step 2. Compute a minimal set $N_1 \subseteq N$ (with respect to set inclusion) such that there exists a matching $M \in \mathcal{M}$ with

$$\begin{aligned} |x_p - s_p(M)| &= d_1 && \text{for all } p \in N_1 \\ |x_p - s_p(M)| &< d_1 && \text{for all } p \in N \setminus N_1. \end{aligned}$$

Step 3. Proceed in a similar way for $t \geq 1$:

- **while** $N_1 \cup \dots \cup N_t \neq N$ **do**
- $t \leftarrow t + 1$.

- $d_t \leftarrow$ smallest d such that there exists a matching $M \in \mathcal{M}$ with

$$\begin{aligned} |x_p - s_p(M)| &= d_j && \text{for all } p \in N_j, j \leq t-1 \\ |x_p - s_p(M)| &\leq d_t && \text{for all } p \in N \setminus (N_1 \cup \dots \cup N_{t-1}). \end{aligned}$$

- $N_t \leftarrow$ inclusion minimal subset of $N \setminus (N_1 \cup \dots \cup N_{t-1})$ such that there exists a matching $M \in \mathcal{M}$ with

$$\begin{aligned} |x_p - s_p(M)| &= d_j && \text{for all } p \in N_j, j \leq t-1 \\ |x_p - s_p(M)| &= d_t && \text{for all } p \in N_t \\ |x_p - s_p(M)| &< d_t && \text{for all } p \in N \setminus (N_1 \cup \dots \cup N_t). \end{aligned}$$

Step 4. Return a matching $M \in \mathcal{M}$ with $|x_p - s_p(M)| = d_j$ for all $p \in N_j$ and all $j \in \{1, \dots, t\}$.

We say that the countries in a set $N \setminus (N_1 \cup \dots \cup N_{t-1})$ are *unfinished* and that a country is *finished* when it is placed in some N_t . Note that Lex-Min terminates as soon as all countries are finished. We can now prove our theoretical result.

THEOREM 3.2. *The Lex-Min algorithm computes a lexicographically minimal matching in $O(n|V|^3 \log |V|)$ time for a generalized matching game (N, v) with an allocation x .*

PROOF. We first prove the correctness of Lex-Min. Let (N, v) be a generalized matching game and let x be an allocation. Let \bar{M} be the matching from \mathcal{M} that is returned by Lex-Min. We claim that \bar{M} is a lexicographically minimal matching for x . In order to prove this, let $M^* \in \mathcal{M}$ be a lexicographically minimal matching. Since both \bar{M} and M^* are maximum matchings, we have $M^* = \bar{M} \oplus \mathcal{P} \oplus C$, where \mathcal{P} and C are sets of even alternating paths and (even) alternating cycles, respectively. We make the additional assumption that among all the lexicographically minimal matchings in \mathcal{M} , M^* is chosen as *closest* to \bar{M} in the sense that $|\mathcal{P}| + |C|$ is as small as possible.

We claim that $C = \emptyset$. Otherwise, we would switch M^* to another maximum matching along an alternating cycle $C \in C$. This yields a new matching $M^* \oplus C \in \mathcal{M}$ which is again lexicographically minimal, as the switch does not affect any $s_p(M^*)$. Moreover, $M^* \oplus C$ is closer to \bar{M} , contradicting our choice of M^* . Hence, there exists a disjoint union of paths P_1, \dots, P_k such that $M^* = \bar{M} \oplus P_1 \oplus \dots \oplus P_k$. We claim that each P_j has endpoints in different countries; otherwise switching from M^* to \bar{M} along P_j would not affect any $s_p(M^*)$ and so again would lead to a new lexicographically minimal matching closer to \bar{M} .

Let $d_1^* > d_2^* > \dots$ denote the different values of $|x_p - s_p(M^*)|$ and let $N_j^* \subseteq N$ denote the corresponding sets of players $p \in N$ with $|x_p - s_p(M^*)| = d_j^*$. We prove by induction on t that for every t , it holds that $d_t^* = d_t$ and $N_t^* = N_t$, which implies that $M^* = \bar{M}$ and thus \bar{M} is lexicographically minimal. Let $t = 1$. In Claims 1 and 2, we prove that $d_1^* = d_1$ and $N_1^* = N_1$.

Claim 1: $d_1^* = d_1$.

Proof: As M^* is lexicographically minimal, $d_1^* \leq d_1$. If $d_1^* < d_1$, then d_1 was not chosen as small as possible, since $M = M^*$ satisfies $|x_p - s_p(M)| \leq d_1^*$ for every $p \in N$. Hence $d_1^* = d_1$. \square

Claim 2: $N_1^* = N_1$.

Proof: If $N_1^* \subsetneq N_1$, then N_1 is not minimal, as $|x_p - s_p(M^*)| \leq d_1^* = d_1$ for $p \in N_1^*$ and $|x_p - s_p(M^*)| < d_1^* = d_1$ for $p \in N \setminus N_1^*$. This

contradicts Step 2 of Lex-Min. Hence, $N_1^* \not\subseteq N_1$. Let $p_0 \in N_1^* \setminus N_1$. So, $|x_{p_0} - s_{p_0}(M^*)| = d_1^* = d_1 > |x_{p_0} - s_{p_0}(\overline{M})|$. There are two cases.

Case 1. $s_{p_0}(M^*) = x_{p_0} + d_1^*$.

Then $s_{p_0}(M^*) > s_{p_0}(\overline{M}) \geq 0$, so there exists an even path, say, P_1 starting in V_{p_0} with an M^* -edge and ending in some V_{p_1} with an \overline{M} -edge. Recall that the endpoints of P_1 are in different countries, hence $p_1 \neq p_0$. Note that replacing M^* by $M^* \oplus P_1$ would decrease $s_{p_0}(M^*)$ and increase $s_{p_1}(M^*)$.

Assume first that $s_{p_1}(M^*) \geq s_{p_1}(\overline{M})$. As P_1 ends in V_{p_1} , we have $s_{p_1}(\overline{M}) \geq 1$. Hence, there exists an alternating path, say P_2 , that starts with an M^* -edge in V_{p_1} and ends with an \overline{M} -edge in some V_{p_2} , $p_2 \neq p_1$. If $p_2 = p_0$, then $M^* \oplus P_1 \oplus P_2$ would be lexicographically minimal and closer to \overline{M} , a contradiction. Hence $p_2 \notin \{p_0, p_1\}$ and in case $s_{p_2}(M^*) \geq s_{p_2}(\overline{M})$, we may continue to construct a sequence p_0, p_1, p_2, \dots in this way. Note that whenever we run into a cycle, that is, when $p_s = p_r$ for some $r > s$, then we get a contradiction by observing that $M^* \oplus P_{r+1} \oplus \dots \oplus P_s$ is also lexicographically minimal (indeed switching M^* to \overline{M} along P_{r+1}, \dots, P_s does not affect any $s_p(M^*)$) and closer to \overline{M} . Hence, eventually, our sequence p_0, p_1, \dots, p_r must end up with $s_{p_r}(M^*) < s_{p_r}(\overline{M})$. We then derive that $s_{p_r}(M^* \oplus P_1 \oplus \dots \oplus P_r) \leq s_{p_r}(\overline{M}) \leq x_{p_r} + d_1$. If $p_r \notin N_1$, then we even get $s_{p_r}(M^* \oplus P_1 \oplus \dots \oplus P_r) \leq s_{p_r}(\overline{M}) < x_{p_r} + d_1$. We now define the matching $M' := M^* \oplus P_1 \oplus \dots \oplus P_r$. Note that M' is a maximum matching closer to \overline{M} . To obtain a contradiction with our choice of M^* we show that M' is lexicographically minimal.

We first consider $p = p_r$. We have $s_{p_r}(M') = s_{p_r}(M^*) + 1 \geq x_{p_r} - d_1 + 1 > x_{p_r} - d_1$. Combining this with the upper bound found above, we obtain

$$\begin{aligned} x_{p_r} - d_1 < s_{p_r}(M') &\leq x_{p_r} + d_1 \text{ if } p_r \in N_1 \\ x_{p_r} - d_1 < s_{p_r}(M') &< x_{p_r} + d_1 \text{ if } p_r \notin N_1. \end{aligned} \quad (2)$$

For $p = p_0$, we have that $s_{p_0}(M') = s_{p_0}(M^*) - 1 = x_{p_0} + d_1 - 1$, where the last equality holds because $p_0 \in N_1^*$. Hence, we have

$$|s_{p_0}(M') - x_{p_0}| = d_1 - 1. \quad (3)$$

From (2) and (3) and the fact that $|s_p(M') - x_p| = |s_p(M^*) - x_p|$ if $p \notin \{p_0, p_r\}$, we conclude that either M' is lexicographically minimal, which yields our contradiction, or $p_r \in N_1$ and $s_{p_r}(M') = x_{p_r} + d_1$. Assume that the latter case holds. Then we have $s_{p_r}(M^*) = s_{p_r}(M') - 1 = x_{p_r} + d_1 - 1$. However, then M^* and M' are symmetric with respect to p_0 and p_r , namely, $|s_{p_0}(M^*) - x_{p_0}| = d_1 = |s_{p_r}(M') - x_{p_r}|$ and $|s_{p_r}(M^*) - x_{p_r}| = |d_1 - 1| = |s_{p_0}(M') - x_{p_0}|$. Combining these equalities with the fact that $|s_p(M') - x_p| = |s_p(M^*) - x_p|$ if $p \notin \{p_0, p_r\}$ implies that M' is lexicographically minimal, the contradiction. Hence, $N_1^* \setminus N_1 = \emptyset$. As $N_1^* \not\subseteq N_1$, we obtain $N_1^* = N_1$.

Case 2. $s_{p_0}(M^*) = x_{p_0} - d_1^*$.

In this case we have $s_{p_0}(M^*) < s_{p_0}(\overline{M})$. Hence, there must exist an alternating path P_1 that starts in V_{p_0} with an \overline{M} -edge and that ends in some V_{p_1} with an M^* -edge. Just as in Case 1, it holds that $p_1 \neq p_0$. If $s_{p_1}(M^*) \leq s_{p_1}(\overline{M})$, we may continue with an alternating path P_2 starting from V_{p_1} and ending in some V_{p_2} with $p_2 \notin \{p_0, p_1\}$, and continuing in this way we eventually end up with a sequence p_0, p_1, \dots, p_r such that $s_{p_r}(M^*) > s_{p_r}(\overline{M})$. Then $M' := M^* \oplus P_1 \oplus \dots \oplus P_r$ has $s_{p_0}(M') = s_{p_0}(M^*) + 1$ and $s_{p_r}(M') = s_{p_r}(M^*) - 1$. By the same arguments as in Case 1, we prove that

M' is a maximum matching that is lexicographically minimal and that is closer to \overline{M} than M^* is. This contradicts our choice of M^* , proving Claim 2. \diamond

Now let $t \geq 2$. Assume that $d_1^* = d_1, \dots, d_{t-1}^* = d_{t-1}$ and $N_1^* = N_1, \dots, N_{t-1}^* = N_{t-1}$. By using the same arguments as in the proof of Claim 1, we find that $d_t^* = d_t$. By using the same arguments as in the proof of Claim 2, we find that $N_t^* \not\subseteq N_t$. We will now show that $N_t^* = N_t$. We consider a country $p_0 \in N_t^* \setminus N_t$ and split the proof into two cases similar to Cases 1 and 2 for the case $t = 1$, namely when $s_{p_0}(M^*) = x_{p_0} + d_t^*$ and $s_{p_0}(M^*) = x_{p_0} - d_t^*$. We will only show the first case in detail, as the proof of the other case is similar. Hence, from now on we assume that $s_{p_0}(M^*) = x_{p_0} + d_t^*$.

We know that $p_0 \in N_t^*$, so $p_0 \notin N_1^* \cup \dots \cup N_{t-1}^* = N_1 \cup \dots \cup N_{t-1}$. Hence $s_{p_0}(\overline{M}) \leq x_{p_0} + d_t$, and $p_0 \notin N_t$ implies $s_{p_0}(\overline{M}) < x_{p_0} + d_t$, so that $s_{p_0}(M^*) > s_{p_0}(\overline{M})$. So there is an alternating path P_1 starting in V_{p_0} with an M^* -edge and ending in some V_{p_1} with an \overline{M} -edge. Again, we may assume that $p_1 \neq p_0$. If $s_{p_1}(M^*) \geq s_{p_1}(\overline{M})$, then there must be some alternating path P_2 starting in V_{p_1} with an M^* -edge and leading to some V_{p_2} with $p_2 \notin \{p_0, p_1\}$ and so on, until eventually we obtain a sequence p_0, p_1, \dots, p_r with $s_{p_r}(M^*) < s_{p_r}(\overline{M})$.

As before, we let $M' := M^* \oplus P_1 \oplus \dots \oplus P_r$ and note that $M' \in \mathcal{M}$ is closer to \overline{M} than M^* is. Hence, to obtain a contradiction, it remains to show that M' is lexicographically minimal. As $p_0 \notin N_1 \cup \dots \cup N_t$, we find that $s_{p_0}(M') = s_{p_0}(M^*) - 1 \geq s_{p_0}(\overline{M}) > x_{p_0} - d_t$. On the other hand, $s_{p_0}(M') < s_{p_0}(M^*) = x_{p_0} + d_t$. Hence

$$|s_{p_0}(M') - x_{p_0}| < d_t. \quad (4)$$

Now consider $p = p_r$. We first rule out that $p_r \in N_1 \cup \dots \cup N_{t-1}$. Assume to the contrary that $p_r \in N_j$ for some $j \in \{1, \dots, t-1\}$. Then as lower bound we have $s_{p_r}(M') = s_{p_r}(M^*) + 1 \geq x_{p_r} - d_j + 1 > x_{p_r} - d_j$, and as upper bound, $s_{p_r}(M') = s_{p_r}(M^*) + 1 \leq s_{p_r}(\overline{M}) \leq x_{p_r} + d_j$. Hence,

$$|s_{p_r}(M') - x_{p_r}| \leq d_j. \quad (5)$$

Inequality (5), together with (4) and the fact that $|s_p(M') - x_p| = |s_p(M^*) - x_p|$ for $p \notin \{p_0, p_r\}$ shows that M' is lexicographically smaller than M^* , a contradiction. Hence, $p_r \notin N_1 \cup \dots \cup N_{t-1}$.

We now have $s_{p_r}(\overline{M}) \leq x_{p_r} + d_t$ if $p_r \in N_t$ and $s_{p_r}(\overline{M}) < x_{p_r} + d_t$ if $p_r \notin N_t$. Hence, we can repeat the arguments that we used for the case where $t = 1$ to obtain our contradiction. This completes the correctness proof of Lex-Min.

Running time analysis. As x_p is fixed and $s_p(M)$ is an integer between 0 and $|V|/2$, there are $O(|V|)$ values for $|x_p - s_p(M)|$. Hence, we can find d_t by binary search in $O(\log |V|)$ time. This requires $O(\log |V|)$ applications of Corollary 3.1, each of which taking time $O(|V|^3)$. Thus finding d_t takes $O(|V|^3 \log |V|)$ time. Each time we find d_t , the number of finished countries increases by at least one. Hence, the total running time of Lex-Min is $O(n|V|^3 \log |V|)$. \square

4 THE SIMULATIONS

Our goals are to examine the benefits of using Lex-Min instead of a maximum matching that minimizes the largest country deviation d_1 from the target allocation x (we find such a matching by only performing Step 1 of Lex-Min) and to test the effect of several (sophisticated) solution concepts. We therefore perform simulations for a large number of countries, as we explain below.

Simulation instances. Using the generator [32] (an updated version of [36], which was commonly used (see e.g. [16, 20, 28, 31]) but nowadays (e.g. in [21]) replaced by [32]) we obtain 100 compatibility graphs D_1, \dots, D_{100} , each with roughly 2000 vertices. We then construct 100 compatibility graphs D_1^1, \dots, D_{100}^1 for round 1, where for $i \in \{1, \dots, 100\}$, D_i^1 is a subgraph of D_i of size roughly 500. So, a quarter of the patient-donor pairs will enter the program in round 1. The remaining patient-donor pairs will be added as vertices to the compatibility graph randomly, by a uniform distribution between the remaining rounds. Our code is available in GitHub repository [7], along with the data from [32] describing the compatibility graphs and the seeds used for the randomization.

We perform simulations for n countries with $n = 4, \dots, 15$. We had set D_1, \dots, D_{100} to have size roughly 2000 to be able to go up to $n = 15$ (due to similar results for a simulation with a size of 1000 for up to $n = 10$, we believe our choice of 2000 is robust). For every n , we first divide the vertices of each D_i in an arbitrary but equal way between the countries, so countries have the same size. For $i \in \{1, \dots, 100\}$, we set $D_i^1(n) = D_i^1$. Then, for each $D_i^1(n)$ we start a 6-year international KEP with quarterly matching rounds, that is, a simulation that consists of 24 rounds in total. In this way we obtain 24 compatibility graphs $D_i^1(n), \dots, D_i^{24}(n)$ for each simulation.

Let $M_i^j(n)$ be the maximum matching that we compute for $D_i^j(n)$. If $j \leq 23$, then we construct $D_i^{j+1}(n)$ as follows. First, we remove the vertices matched by $M_i^j(n)$; the corresponding patient-donor pairs have been helped. If $j \geq 4$, we also remove those vertices from $D_i^j(n)$ that are not in $M_i^j(n)$ but that do belong to $D_i^{j-3}(n)$. This is because patients may seek for alternative treatment or may have deceased after one year in the KEP. Finally, we add the vertices that correspond to the patient-donor pairs that were assigned, in advance of the simulation, to enter the program in round $j + 1$.

A *simulation instance* consists of the data needed to generate a graph $D_i^1(n)$ and its successors $D_i^2(n), \dots, D_i^{24}(n)$, together with specifications for the initial allocation y and maximum matching M to be used in each round. We computed these choices as follows.

Initial allocations. Recall from Section 2 that we consider the Shapley value, nucleolus, benefit value and contribution value as initial allocations. These solution concepts are defined in terms of values $v(S)$ of the generalized matching game (N, v) on a compatibility graph $D_i^j(n)$. Recall that for a coalition of countries $S \subseteq N$, $v(S)$ is the size of a maximum matching in the subgraph of $D_i^j(n)$ induced by the vertices of the countries of S . We compute the size of a maximum matching efficiently, using the package of [23]. The contribution value and benefit value can now be efficiently computed, using their definitions. For the Shapley value, we were still able to implement a naive approach relying directly on (1). However, computing the nucleolus of a generalized matching game is highly nontrivial for the number of countries we consider: we had to use the *Lexicographical Descent* method of [9]. This is the state-of-the-art method in nucleolus computation. It breaks down the computation of the nucleolus into $O(n)$ linear programs (LPs), which still have exponential size, but can be handled easier through the solution of small dual relaxations combined with easily generated primal feasible starting points. In this way we are able to deal with significantly larger instances than in previous approaches.

Solutions. As mentioned, we aim to examine the benefits of using solutions (maximum matchings) prescribed by Lex-Min instead of those that give us a deviation of d_1 from the target allocation. For the latter it suffices to perform only the first step of Lex-Min. In both cases we apply Corollary 3.1. As explained in Section 3 (see also [12]), applying Corollary 3.1 requires solving a maximum weight perfect matching problem; we used the package of [23].

Credit system. To distinguish between the effect of Lex-min and the effect of c we run the same simulations for these four *scenarios*:

- (1) *lexmin+c*: M is the maximum matching returned by Lex-Min and $x = y + c$.
- (2) *lexmin*: M is the maximum matching returned by Lex-Min and $x = y$.
- (3) *d1+c*: M is a maximum matching minimizing d_1 and $x = y + c$.
- (4) *d1*: M is a maximum matching minimizing d_1 and $x = y$.

Computational environment and scale. We ran all simulations on a desktop PC with Intel Core i7-6700 3.4 GHz CPU and 8 GB of RAM, running on Windows 10 OS and C++ implementation in Visual Studio. Our code [7] use the open-source code [6] of the Lexicographical Descent method for computing the nucleolus. The scale of our experiments for international KEPs is *unprecedented*: the total number of simulations we ran is equal to $4 \times 4 \times 12 \times 100 = 19200$ (namely, four initial allocations y ; four scenarios; twelve country sizes n ; and 100 initial compatibility graphs D_i).

Evaluation measure. To measure balancedness we do as follows. After the 24 matching runs of a single instance, we will have a total target allocation x^* , which is defined as the sum of the 24 target allocations, and a maximum matching M^* , which is the union of the chosen matchings in each of the 24 matching runs. Note that the total number of kidney transplants is $2|M^*|$. We now define the *total relative deviation* as $\frac{\sum_{p \in N} |x_p^* - s_p(M^*)|}{2|M^*|}$. Recall that for each triple that consists of a country set size, choice of allocation and choice of scenario, we run 100 instances. We take the average of the 100 relative deviations. This gives us the *average total relative deviation*. We use this measure to take into account the scale of the international KEP. We also took the *maximum relative deviation*, which is defined as $\frac{\max_{p \in N} |x_p^* - s_p(M^*)|}{2|M^*|}$, leading to the *average maximum relative deviation*. In both cases, exactly the same conclusions can be drawn; see the arXiv version of our paper [8] for details.

Results and Evaluation. Figure 3 shows our main results. Our main conclusion from Figure 3 is that *lexmin+c* yields the lowest average total relative deviation for all four initial allocation y , with larger differences when the number of countries is growing. From Figure 3 we can also compute the *relative improvement* of *lexmin+c* over *d1+c*. For example, for $n = 15$, this percentage is $(2.54 - 1.23)/2.54 = 52\%$ for the nucleolus, whereas for the other solution concepts it is 41% (Shapley value); 48% (contribution value); and 48% (benefit value). Considering the average improvement over $n = 4, \dots, 15$ yields percentages of 48% (nucleolus); 33% (Shapley value); 44% (contribution value) and 40% (benefit value).

As mentioned, the choice for initial allocation is up to the policy makers of the international KEP. However, from Figure 4 we see that the Shapley value in the *lexmin+c* scenario consistently provides the smallest deviations from the target allocations (**0.52%** for $n = 15$), while the contribution value for $n \leq 12$ and the nucleolus for $n \geq 13$



Figure 3: Average total relative deviations where n is ranging from 4 to 15.

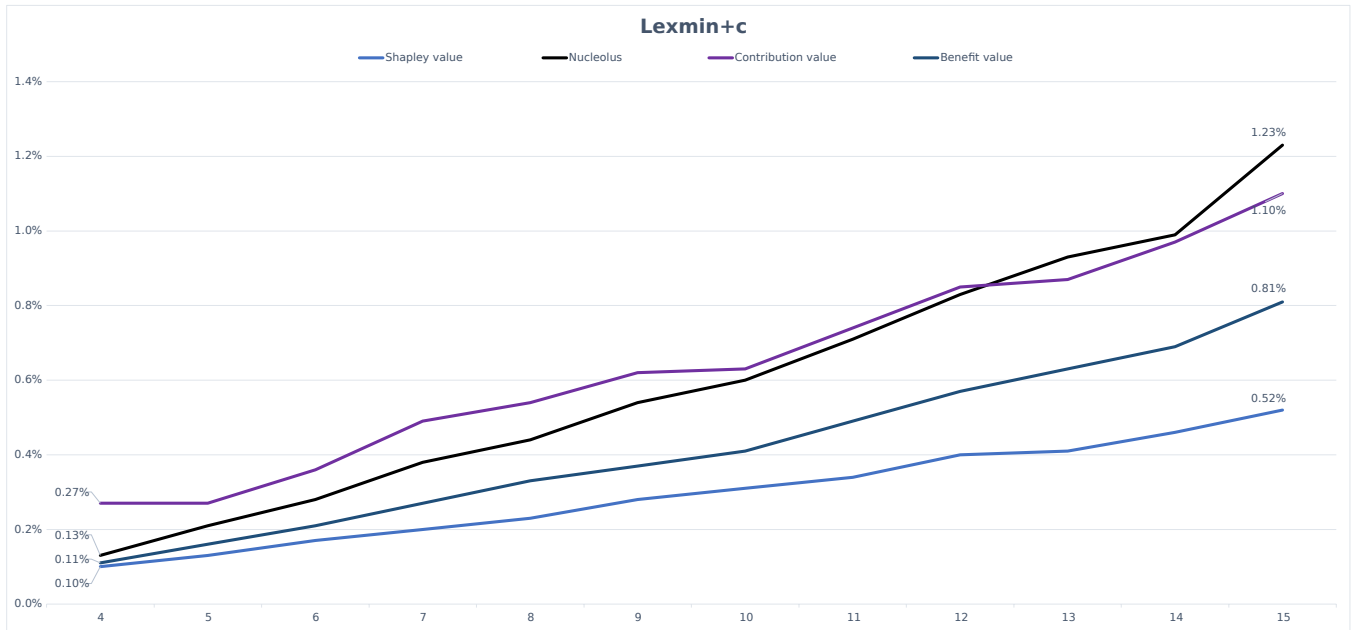


Figure 4: Displaying the four *lexmin+c* graphs of Figure 3 in one plot.

perform the worst. We now evaluate a number of other aspects of our experiments (see [8] for the details):

- (1) We also tested the scenario of using arbitrary maximum matchings. As expected, this makes the kidney exchange scheme significantly more unbalanced, with average total relative deviations above 14% for all four initial allocations y .

- (2) From Figure 3 we can compare *lexmin+c* with *lexmin*, and *d1+c* with *d1* to see that using *c* has a substantial effect. However, using *lexmin+c* is the best: whilst *lexmin* ensures that allocations stay close to the target allocations, the role of *c* is to keep the deviations small and to guarantee fairness for the participating countries over a long time period.
- (3) In Section 2, we gave an example where credits build up over time infinitely. However, this behaviour did not happen in any of our 24-round simulations (as argued above). We performed a refined analysis to verify if such behaviour could be expected if the number of rounds is larger than 24. We did not see any such indication.
- (4) The computational time saved by *d1+c* compared to *lexmin+c* is negligible. As for the other computation requirements, while the *exponential explosion* in generating the cooperative games (that is, computing the 2^n values $v(S)$) is dominating after a while, building the compatibility graph took most of the time initially (up to $n = 12$).
- (5) Cooperation between countries leads to a significantly larger number of total kidney transplants than non-cooperation, especially when more countries are participating.
- (6) In our cooperative setting, we still maximize total welfare and therefore choose maximum matchings. However, we note that a change in parameter may result in a change in maximum matching size (total number of kidney transplants). However, these differences turned out to be negligible (between 0.01% and 0.1% on average).
- (7) *Lex-min* computes at most $n - 1$ d_j -values, and in our experiments we actually found instances where d_{n-1} was computed even for $n = 10$.
- (8) We also performed a coalitional stability check to see if the initial allocations and solutions (actual allocations) are in the core of the associated generalized matching game. We found a high and similar level of stability for all four scenarios that is slightly decreasing when the number of countries is increasing. Although the Shapley value provides consistently the smallest deviations (see Figure 4), Table 1 shows that the nucleolus and the benefit values provide higher levels of coalitional stability (measured in the distance of violating a core inequality) not only at the level of initial allocations, but even with respect to the actual number of transplants.

Varying country sizes. We repeated our *whole* experimental study for varying country sizes with ratio small:medium:large=1:2:3. It turned out that we can draw exactly the same conclusions.

5 CONCLUSIONS

We extended the theoretical study of Biró et al. [12] on credit systems in international KEPs by proving that we can even compute, in polynomial time, a maximum matching that is lexicographically minimal with respect to the country deviations from target allocations. Our experiments showed that using these solutions leads to a significant improvement especially when the number of countries is large. This is relevant, as international KEPs, such as Eurotransplant, are under development and others, such as ScandiTransplant, are expected to grow.

Table 1: Average distances, over n ranging from 4 to 15, of accumulated initial allocations $y = \sum_{h=1}^{24} y^h$ and accumulated number of kidney transplants $s = \sum_{h=1}^{24} s(M^h)$ (where M^h is the chosen matching in period h) respectively, from violating a core inequality of the accumulated generalized matching games under the *lexmin+c* scenario. The accumulated generalized matching game is obtained from the generalized matching games (N, v^h) on compatibility graphs D^h for $h = 1, \dots, 24$ by setting $v = \sum_{h=1}^{24} v^h$. For example, by using the Shapley value as the initial allocation, every coalition has a minimum guaranteed surplus of 50.39 kidney transplants on average by participating in the international KEP.

Allocations	Shapley	Nucleolus	Benefit	Contribution
Initial	50.46	53.34	53.40	48.15
Transplants	50.39	53.10	53.19	48.13

We also advocate the use of lexicographically minimal matchings as we now have a polynomial-time algorithm for computing them. Moreover, our simulations show that computing them instead of maximum matchings that only minimize the maximum deviation indeed does not require any significant additional computational time (see [8]). A challenging part of our project was to compute the nucleolus of generalized matching games consisting of up to fifteen countries. For this we used the method of [9].

Future Research. All the above findings for 2-way exchange cycles are also interesting to research for a setting with ℓ -way exchange cycles for $\ell \geq 3$. The previous experimental studies [10, 29] for $\ell = 3$ only considered 3–4 countries. To do meaningful experiments for a large number of countries, a new practical approach is required to deal with the computational hardness of computing optimal solutions (recall the aforementioned NP-hard result of [1] for $\ell \geq 3$).

We also plan to consider directed compatibility graphs with weights $w(i, j)$ on the arcs (i, j) representing the utility of transplant (i, j) . Computing a maximum-weight solution that minimizes the weighted country deviation d_1 now becomes NP-hard [12]. However, we could still consider the set of maximum-size solutions as our set \mathcal{M} instead of the set of maximum-weight solutions. Then we can find a maximum-weight matching that lexicographically minimizes the original country deviations $|x_p - s_p(M)|$. The main challenge is to set weights $w(i, j)$ appropriately, since optimization policies may vary widely in national KEPs: in Europe, maximizing the number of transplants is the first objective (cf. our setting in which $w \equiv 1$) but further scores are based on different objectives, such as improving the quality of the transplants, easing the complexity of the logistics or giving priority to highly sensitized patients; see [14] for further details.

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