

# Efficient Use of Immunosuppressants for Kidney Transplants\*

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## Abstract

The recent development of immunosuppressive protocols (or simply, suppressants) offers a new option to patients suffering from end-stage renal disease: transplants from biologically *incompatible* donors. Suppressants are currently being used for direct transplants within patient-donor pairs, but they can be utilized more effectively when combined with kidney exchanges. To assess welfare gain from doing so, we introduce the “minimum chains algorithms” for different lengths of feasible exchanges. We calculate the minimum number of suppressants needed for transplants of a group of patient-donor pairs. Our simulation results show that it is enough to arrange *pairwise* exchanges to take the most advantage of suppressants. We also assess how much a patient-donor pair contributes to facilitating exchanges, by applying the algorithm to the pools *with* and *without* the pair. Lastly, we show that there is a significant difference in the gains of utilizing suppressants in Korea and the United States: Due to the different blood-type distribution of the two countries, the gain in Korea appears to be larger than that in the States.

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## 1. Introduction

Patients suffering from end-stage renal disease need to receive kidney transplants, unless they continue using dialysis. If a patient has a paired donor who is immunologically compatible with her, a direct transplant can be performed within the pair.<sup>1</sup> Otherwise, the patient has to register on a waiting list

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<sup>1</sup>Immunological compatibility is determined by biological characteristics of patients and donors, such as ABO blood-types, tissue (Human Leukocyte Antigen; HLA) types, and the crossmatch. The ABO blood-type is determined by the inherited antigenic substances on the surface of red blood cells. For example, if a patient has type A antigens on her red blood cells, then her blood-type is A and her antibody is of type B; if a patient has type B antigens, then her blood-type is B and her antibody is of type A; if a patient has both type A and type B antigens, then her blood-type is AB and she has no antibodies of type A or B; if a patient has no antigen of type A or B, then her blood-type is O and she

Year	Patients in waitlists	Total transplants	Transplants from deceased donors	Transplants from living donors
2009	4,769	1,238	488	750
2010	5,857	1,287	491	796
2011	7,426	1,639	680	959
2012	9,245	1,788	768	1,020
2013	11,381	1,761	750	1,011
2014	14,477	1,808	808	1,000
2015	16,011	1,892	901	990
2016	18,912	2,236	1,059	1,177
2017	21,048	2,163	903	1,260
2018	23,427	2,108	807	1,301

Table 1: Kidney transplants in Korea (the Annual Reports of KONOS)

for a deceased donor or should participate in a kidney exchange program, if available, where patients swap their donors to form compatible pairs (Roth et al., 2004). Unfortunately, these possibilities are quite limited and the number of patients in the waiting list has been increasing. In Korea, for instance, there was a fivefold increase in the number of patients in the waiting list, but the total transplants only doubled during 2009-2018 according to the Annual Reports of the Korean Network for Organ Sharing (KONOS), as shown in Table 1.

Recently, immunosuppressive protocols have been developed to offer a new option of *transplants from incompatible donors*, or simply *incompatible transplants*. This option is also referred to as “desensitization” and consists of the administration of immunosuppressive medications and a plasmapheresis treatment. For this, a patient takes rituximab that inactivates a certain part of white blood cells and undergoes a plasmapheresis treatment to remove some antibodies from blood. Intravenous immunoglobulin (IVIG) is also added to protect the patient from potential infections. A kidney transplant is then performed and the patient waits for her immune system to regenerate while keeping it from attacking the new organ.<sup>2</sup> With this procedure, the patient can receive a transplant from any donor, either compatible or blood-type/tissue-type incompatible. We simply say that the patient *uses a suppressant* when she chooses this option.

Although it is ideal for a patient to receive a compatible transplant with minor suppressive treatment, incompatible transplants can be a good alternative when compatible transplants are not available: the effectiveness of desensitization is confirmed by a number of clinical and laboratory investigations. The long-term survival rate of ABO-incompatible transplants is shown almost equivalent to that of compatible transplants: according to the KONOS Annual Report in 2018, the five-year sur-

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has types A and B antibodies. A patient with type X antibody cannot receive a transplant from a donor with type X antigens. The tissue-type is determined by a person’s HLAs, which are antigens on the surface of white blood cells that are responsible for immunological responses. If the patient and the donor have the same HLAs, they are called an *identical match*, which is rare between biologically unrelated persons since the number of possible combinations of HLAs is very large. For more information, see the Genetics Home Reference website, provided by the U.S. National Library of Medicine, at <http://ghr.nlm.nih.gov/geneFamily/hla>. A patient’s antibodies and a donor’s HLAs also determine the “crossmatch”. If the crossmatch is positive, then the patient’s antibodies react to the donor’s HLAs, thereby making a transplant difficult.

<sup>2</sup>To go through this procedure and get prepared for operation, it takes a couple of weeks, but this option is still incomparably superior to other options available from the national organ transplant program: the average waiting time is 3 to 5 years according to the National Kidney Foundation (<https://www.kidney.org/atoz/content/transplant-waitlist>).

Year	Transplants from living donors	Direct transplants of ABOc pairs	Direct transplants of ABOi pairs	Exchange transplants
2009	750	675 (90.0%)	35 (4.7%)	40 (5.3%)
2010	796	689 (86.6%)	78 (9.8%)	29 (3.6%)
2011	959	828 (86.3%)	113 (11.8%)	18 (1.9%)
2012	1,020	827 (81.1%)	193 (18.9%)	0 (0.0%)
2013	1,011	795 (78.6%)	212 (21.0%)	4 (0.4%)
2014	1,000	783 (78.3%)	212 (21.2%)	5 (0.5%)
2015	990	772 (78.0%)	208 (21.0%)	10 (1.0%)
2016	1,177	901 (76.6%)	272 (23.1%)	4 (0.3%)
2017	1,260	932 (74.0%)	322 (25.6%)	6 (0.5%)
2018	1,301	959 (73.7%)	342 (26.3%)	0 (0.0%)

(ABOc: ABO-compatible; ABOi: ABO-incompatible)

Table 2: Three types of living-donor kidney transplants in Korea

vival rate of ABO-incompatible living-donor kidney transplants is 95.3% and that of ABO-compatible living-donor kidney transplants is 96.3%.<sup>3</sup> The performance of tissue-type incompatible transplants and transplants with positive crossmatch are also reported quite satisfactory.<sup>4</sup>

As a consequence, the number of patients using suppressants is growing fast. As shown in Table 2, for instance, the proportion of blood-type incompatible kidney transplants in Korea increased from 4.7% to 26.3% of the total living-donor transplants during 2009-2018. Suppressants are being widely used in many other countries too – such as Japan and the European countries including Germany, France and Sweden, as noted by Biró et al. (2019).

The recent change presented in Table 2 draws our attention in two respects. We first note that kidney exchange has almost disappeared in Korea and all transplants from living donors are operated directly within patient-donor pairs. This implies that every patient with an incompatible donor has to use a suppressant for transplant under the current practice in Korea. However, Heo et al. (2020a) point out that suppressants can be used more effectively when combined with kidney exchanges. The following example illustrates this proposal.

**Example 1.** Suppose that compatibility is determined by ABO blood-type and denote by (X-Y) the pair whose patient has blood-type X and donor has blood-type Y. Consider a pool of three pairs: (A-B), (B-AB), and (O-AB). As well-known, a patient of blood-type A can receive a transplant only

<sup>3</sup>Clinical study reports in many other countries provide a similar result confirming the effectiveness of incompatible transplants: for instance, see Montgomery et al. (2012) for the United States, Takahashi and Saito (2013) for Japan, and Opelz et al. (2015) for European countries.

<sup>4</sup>For studies on tissue-type incompatible (i.e., HLA-incompatible) transplants, see Montgomery et al. (2011), Laging et al. (2014), and Orandi et al. (2016). For transplants with positive crossmatch, see Thielke et al. (2009), Morath et al. (2012), and Bentall et al. (2013). Suppressants have been initially used to relax minor immunological constraints for compatible transplants for long. Since 1980’s, however, they have been developed and used to eliminate blood-type compatibility constraints and then they have been further developed to eliminate almost all immunological compatibility constraints (blood-type, tissue-type, and positive crossmatch). Even hyper-sensitized patients with positive crossmatch can also make use of this option, as the outcomes of such cases are reported quite successful with various suppressive medications. For instance, Montgomery et al. (2018) show that the desensitization protocols with imlifidase (IdeS) are successfully used for patients who are broadly sensitized to HLAs. Jordan et al. (2017) also show that IdeS is effective in reducing or eliminating donor-specific antibodies, enabling HLA-incompatible transplantation for almost all patients in the sample of highly sensitized patients (24 out of 25). Also, Orandi et al. (2016) show that the survival benefit after HLA-incompatible transplants is shown significant at 8 years across all levels of donor-specific antibody.

from a donor of blood-type A or O, a patient of blood-type B from a donor of blood-type B or O, and a patient of blood-type O from a donor of blood-type O. Therefore, each patient is incompatible with her own donor in this example. Moreover, these patients cannot swap their donors for kidney exchanges either, because no trading cycle is formed among them.

Suppose that suppressants are available for this pool. If each patient is to receive a transplant from her own donor, all three patients should use suppressants. This is exactly how suppressants are currently used in Korea. However, note that the pairs (A-B) and (B-AB) form a “chain” in a sense that the donor in the (A-B) pair is compatible with the patient in the (B-AB) pair, while the remaining patient of blood-type A and the remaining donor of blood-type AB are not compatible. Such a chain can be viewed as a trading cycle with a “missing link”: If the donor in the (B-AB) pair and the patient in the (A-B) pair were compatible, these pairs would have formed a cycle along which they could swap the donors and form compatible pairs. Providing a suppressant to the patient of blood-type A fills in this missing link and transforms the chain into a trading cycle between (A-B) and (B-AB). Then, the patient of blood-type B receives a compatible transplant from the donor of blood-type B and the patient of blood-type A receives an incompatible transplant from the donor of blood-type AB, with the latter transplant being made possible by the use of a suppressant. The remaining patient in the (O-AB) pair would receive an incompatible transplant from her own donor by using a suppressant. In this case, all patients receive transplants and the patient in the B-AB pair now receives a *compatible* transplant.  $\square$

That is, when suppressants are used to transform *chains* to cycles, some incompatible transplants can be replaced by compatible transplants, as shown in this example. For an effective use of suppressants, therefore, a set of exchange cycles and *exchange chains* should be carefully selected. The patients at the head of the chain(s) will then use suppressants, facilitating compatible transplants of other pairs. All patients who do not belong to any cycle or chain should also use suppressants for direct transplants within own pairs.

To complement the axiomatic analyses of Heo et al. (2020a) and to derive further policy implications, we ask the following question: Can we numerically assess welfare gain as per this proposal under various arrangements of exchange? We introduce a computational algorithm, which we call “the minimum chains algorithm”, to calculate the minimum number of suppressants needed for transplants of a pool of patient-donor pairs. By using this algorithm, we calculate the reduction of suppressants from the current practice given different lengths of feasible cycles and chains. From these outcomes, we also suggest a “right” length of exchanges in a centralized transplant system. We find that it is sufficient to arrange *pairwise* exchanges to take the most advantage of introducing suppressants. For certain blood-type combinations of patient-donor pair, in addition, we apply the algorithm to the pools *with* and *without* a pair of each type. By comparing the resulting outcomes, we assess the *contribution* of the pair in the reduction of suppressants.

We next note from Table 2 that the transplant practice in Korea is significantly different from that in the United States: the national kidney exchange programs are running successfully in the US, making a substantial welfare improvement and promoting compatible transplants. However, desensitization has not been utilized as much as in Korea. What causes such a difference in the

transplant system? Can we tell how the system would evolve? Because a medical system is jointly affected by a number of social and institutional factors, it is hard to provide a clear answer to these questions, but we show that one possible fundamental difference of the patient-donor pool may affect the development of transplant system: the ABO blood-type distribution. By using the minimum chains algorithm, we measure the gains from utilizing suppressants in the two countries and show that the gain in Korea is larger than that in the States.

The literature on kidney exchange stems from the seminal work by Roth et al. (2004) and most papers on the subject have taken the compatibility profiles as a fixed primitive of the problem. More recently, however, newly developed technologies for transplant are being used to modify the compatibility profiles of a pool. Andersson and Kratz (2020) consider suppressants used for blood-type incompatible transplants and introduce a priority-based algorithm for pairwise exchanges. For suppressants used for blood-type and tissue-type incompatible transplants, on the other hand, Heo et al. (2020a,b) provide an axiomatic foundation of constructing a centralized transplant system. A “blood-subtyping” technology in Sönmez et al. (2018) also enables transplants between certain types of ABO-incompatible blood-types. It is shown, however, that this technology may have a negative externality on kidney exchanges.

In constructing a centralized transplant system, Roth et al. (2004) initially impose no restriction on the length of trading cycles. However, *pairwise exchanges*, where only two pairs swap their donors to form a cycle, have been widely studied in the literature to accommodate potential physical and geographical limitations in operating simultaneous transplants.<sup>5</sup> Roth et al. (2007) precisely calculate efficiency loss incurred by imposing this type of restrictions on the standard kidney exchange problem and show that it is enough to arrange 4-way exchanges at most to achieve the maximum number of transplants. In this paper, we further generalize the problem by introducing suppressants and identify the efficiency loss/gain as feasible lengths of cycles and chains get larger. We prove that for this problem, *pairwise* exchanges are sufficient and there is no gain at all of going beyond 3-way exchanges, in contrast to Roth et al. (2007).

A key feature of combining suppressants with kidney exchanges is that patient-donor pairs, who *become* compatible through the use of suppressants, still participate in the kidney exchanges. An incompatible pair has a good incentive to participate in the centralized transplant system with suppressants, as the patient of the pair has to use a suppressant anyway to receive a transplant. By joining the exchange system, there is a chance to find a compatible donor, either in a cycle or in a chain. Provided that it does not make a significant difference from which donor a patient receives a kidney when using a suppressant, she is willing to stay in the pool so as to facilitate exchanges, even if she is chosen to use a suppressant. In the standard kidney exchange context, such an “altruistic” motivation has also been studied (Sönmez and Ünver 2014, Roth et al. 2005, and Gentry et al. 2007).<sup>6</sup>

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<sup>5</sup>Pairwise exchanges are extensively studied in the literature: see Bogomolnaia and Moulin (2004) and Roth et al. (2005). Weighted graphs can also be used to identify these matchings by taking priorities into account: Okumura (2014) and Andersson and Kratz (2020). There are other attempts, on the other hand, to go without such a restriction on the size of exchange cycles: for instance, Ausubel and Morrill (2014) propose sequential exchanges where each donor undergoes an operation no later than her paired patient receives a transplant.

<sup>6</sup>The term “altruistic pairs” in Sönmez and Ünver (2014) refers to compatible pairs who participate in a kidney exchange program even though a direct transplant between themselves is possible. Since participation is voluntary, our

The rest of this paper is organized as follows. In Section 2, we formulate a model of kidney exchange with suppressants. In Section 3, we introduce 2- and 3-way minimum chains algorithm and prove that these algorithms calculate the minimum suppressants needed for transplants of each pool. In Section 4, we apply these algorithms to the pools that we construct for Korea and the United States and present the simulation results. Concluding remarks are included in Section 5.

## 2. A Model of Kidney Exchange

Let  $N = \{1, \dots, n\}$  be a finite set of of patient-donor pairs with  $|N| = n$ . Each pair  $i \in N$  consists of a patient and a donor which is represented by  $(X-Y)$  where  $X$  and  $Y$  are patient's and donor's (ABO) blood types, respectively. An exchange pool, or simply a pool, is the set of all pairs participating in a kidney exchange program. For each pool, let  $\#(X-Y)$  be the number of  $(X-Y)$  pairs.

For each patient-donor pair, a patient is either ABO-compatible (ABOc) or ABO-incompatible (ABOi) with her donor. Precisely, a patient of blood type A is ABOc with a donor of blood type A or O, but ABOi with a donor of blood type B or AB. A patient of blood type B is ABOc with a donor of blood type B or O, but ABOi with a donor of blood type A or AB. A patient of blood type O is ABOc with a donor of blood type O, but ABOi with a donor of blood type A, B, or AB. A patient of blood type AB is ABOc with a donor of any blood type.

A pair is ABO-compatible (ABOc) if the patient is ABOc with her own donor, that is, (A-A), (A-O), (B-B), (B-O), (O-O), (AB-A), (AB-B), (AB-O), and (AB-AB). On the other hand, a pair is ABO-incompatible (ABOi) if the patient is ABOi with her own donor, that is, (A-B), (A-AB), (B-A), (B-AB), (O-A), (O-B), and (O-AB).

If a patient is ABOc with the donor and in addition, there are no other immunological barriers, such as HLA (Human Leukocyte Antigen) mismatch and positive crossmatch, then the patient can receive a kidney transplant from the donor. If a patient is ABOi with the donor or other immunological barriers exist between the patient and the donor, then the patient needs to use an immunosuppressant, or simply a suppressant, to receive a kidney transplant from the donor. When a patient uses a suppressant, the patient can overcome any immunological barriers and receive a kidney transplant from any donor.

A 2-cycle involves two pairs such that each patient is incompatible with her own donor, but compatible with the other donor. A 3-cycle involves three pairs,  $(X_i-Y_i)$ ,  $(X_j-Y_j)$ , and  $(X_k-Y_k)$ , such that each patient is incompatible with her own donor, but donor  $Y_i$  is compatible with patient  $X_j$ , donor  $Y_j$  is compatible with patient  $X_k$ , and donor  $Y_k$  is compatible with patient  $X_i$ . In the 2- and 3-cycles, each patient involved in the exchange receives a compatible transplant as a result of the kidney exchange. On the other hand, a 1-chain involves one pair whose patient is incompatible with her own

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proposal further prevents a negative externality that tissue-type suppressants may have on kidney exchange programs. As Sönmez and Ünver (2013) have observed, when tissue-type suppressants become available, the shortage of donors of a particular blood-type – usually, blood type O – can get even worse. This is because type O donors are blood-type compatible with all patients and therefore, appear in the exchange pool only when they are tissue-type incompatible with their own patients. Therefore, as tissue-type suppressants become available, these donors can be crowded out from the exchange program. In our proposal, on the other hand, we assume that all donors in incompatible pairs stay in the pool even after their patients use any types of suppressants.

donor. A 2-chain involves two pairs,  $(X_i-Y_i)$  and  $(X_j-Y_j)$ , such that each patient is incompatible with her own donor, donor  $Y_i$  compatible with patient  $X_j$ , but donor  $Y_j$  is incompatible with patient  $X_i$ . A 3-chain involves three pairs,  $(X_i-Y_i)$ ,  $(X_j-Y_j)$ , and  $(X_k-Y_k)$ , such that each patient is incompatible with her own donor, donor  $Y_i$  is compatible with patient  $X_j$ , donor  $Y_j$  is compatible with patient  $X_k$ , but donor  $Y_k$  is incompatible with patient  $X_i$ . In the 1-chain, the patient receives an incompatible transplant from her donor by using a suppressant. In the 2- and 3-chains, patient  $X_j$  and  $X_k$  receive compatible transplants as a result of the kidney exchange, but patient  $X_i$  receives an incompatible transplant by using a suppressant.

### 3. Minimum Chains Algorithms

As explained in the Introduction, all patients receive kidney transplants – either compatible or incompatible – when suppressants are available. We therefore aim to minimize the use of suppressants so as to maximize the number of compatible transplants. This problem can be solved by finding a matching at which the number of chains is minimal. A matching is *optimal* if it attains this minimum in each problem. Since the pool is finite, there always exists an optimal matching. In what follows, we propose an algorithm which gives an optimal matching (1) in a “2-way problem” where only 2-way exchanges are feasible, and (2) in a “2- and 3-way problem” where both 2- and 3-way exchanges are feasible. Denote the minimum number of chains by  $H_2$  for the 2-way problem and by  $H_3$  for the 2- and 3-way problem.

For a kidney transplant, we assume that the tissue-type compatibility matters in addition to the blood type compatibility. Therefore, ABOc pairs may participate in kidney exchanges if the patient and the donor are tissue-type incompatible. Next are the assumptions on the pool that we adapt from Roth et al. (2007).

Assumption 1. (Upper-bound assumption) No patient is tissue-type incompatible with another patient’s donor.

Assumption 2. (Large population of blood type incompatible patient-donor pairs) Pairs of types (O-A), (O-B), (O-AB), (A-AB), and (B-AB) are on the “long-side” of exchange in the sense that at least one pair of each type belongs to a chain at every optimal matching.<sup>7</sup>

Assumption 3.  $\#(A-B) > \#(B-A)$ .

Assumption 1 says that each patient is tissue-type compatible with any other donors even though the patient might have tissue-type incompatibility with her own donor. It is imposed to identify an upper bound on the number of possible compatible transplants. Assumption 2 says that it is impossible that all (O-A), (O-B), (O-AB), (A-AB), and (B-AB) pairs form cycles, receiving compatible

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<sup>7</sup>Assumption 2 is based on the fact that ABOi pairs are more likely to join a pool than the pairs with the reverse blood-types of patients and donors. For instance, (O-A) pairs appear more often than (A-O) pairs in the pool, because (A-O) pairs join the pool only if they are tissue-type incompatible, but (O-A) pairs always join the pool, independently of tissue-type incompatibility, because they are already ABOi.

transplants. However, the pairs with the reverse patient-donor types, (A-O), (B-O), (AB-O), (AB-A), and (AB-B) pairs, are called the pairs on the “short-side” for exchange. These short-side pairs are ABO-compatible, so they participate in a pool only when they are tissue-type incompatible. Assumption 3 is consistent with the data that we observe both in the U.S. and Korea, which also simplifies the construction of the algorithm and the subsequent analysis. We may also consider, however, more general cases without Assumption 3: when this inequality is reversed, a symmetric argument applies by switching A and B in these results; when the equality holds, the analysis simplifies significantly.

### 3.1. The 2-way minimum chains algorithm

First, we assume that only 2-way exchanges are feasible and propose the 2-way minimum chains algorithm which minimizes the use of suppressants.

#### The 2-way minimum chains algorithm:

- Step 0. At the end of each step, we exclude all cycles and chains formed at that step from the pool and move on to the next step.
- Step 1. Form each of the following 2-cycles as many as possible: (A-O)-(O-A), (B-O)-(O-B), (AB-O)-(O-AB), (AB-A)-(A-AB), (AB-B)-(B-AB), (B-A)-(A-B), (O-O)-(O-O), (A-A)-(A-A), (B-B)-(B-B), (AB-AB)-(AB-AB).<sup>8</sup>
- Step 2. Form 2-chains (O-O)-(O-AB) and (O-AB)-(AB-AB). If there are any remaining (O-AB)’s, keep them as 1-chains. If there is any remaining (O-O) or (AB-AB), set it aside for Step 8.<sup>9</sup>
- Step 3. Form 2-chains (O-B)-(B-AB) and (O-A)-(A-AB) as many as possible.
- Step 4. Form 2-chains (O-B)-(B-B) and (A-A)-(A-AB). If there are any remaining (O-B)’s or (A-AB)’s, keep them as 1-chains.
- Step 5. If the total number of remaining (O-A) and (B-AB) is at least as large as that of (A-B), form a 2-chain (O-A)-(A-A) and then, a 2-chain (A-A)-(A-B). If the total number of remaining (O-A) and (B-AB) is smaller than that of (A-B), form a 2-chain (A-A)-(A-B) and then, a 2-chain (A-B)-(B-B).
- Step 6. Form 2-chains (O-A)-(A-B) and (A-B)-(B-AB) as many as possible.
- Step 7. Form a 2-chain (A-B)-(B-B) or (B-B)-(B-AB).
- Step 8. If either (O-O) or (AB-AB) remains, form 2-chains with any remaining pairs.
- Step 9. Leave all remaining pairs as 1-chains.

<sup>8</sup>After Step 1, at least one of each (O-A), (O-B), (O-AB), (A-AB), (B-AB), (A-B) types by Assumption 2 and at most one of each (O-O), (A-A), (B-B), (AB-AB) types remain in the pool.

<sup>9</sup>Note that either (O-O) or (AB-AB) (but not both) remains after Step 2 only if there are exactly one (O-O), one (AB-AB), and one (O-AB) after Step 1.



As we see in the proofs of Theorems 1 and 2, there is an optimal matching at which (A-O)-(O-A), (B-O)-(O-B), (AB-O)-(O-AB), (AB-A)-(A-AB), and (AB-B)-(B-AB) cycles are formed as many as possible.<sup>10</sup> By Assumption 2, all short-side pairs are exhausted after this step.

**Theorem 1.** The 2-way minimum chains algorithm attains the minimum number of chains among all 2-way algorithms.

*Proof.* The proof is given in Appendix A. □

We calculate the number of chains obtained from the 2-way minimum chains algorithm. Let  $\mathcal{I}(\cdot)$  be an indicator function such that for a certain statement  $x$ ,  $\mathcal{I}(x) = 1$  if  $x$  holds and  $\mathcal{I}(x) = 0$  otherwise. Let

$$\begin{aligned}
I_A &\equiv \mathcal{I}(\#(\text{A-A}) \text{ is odd}), & I_B &\equiv \mathcal{I}(\#(\text{B-B}) \text{ is odd}), \\
I_O &\equiv \mathcal{I}(\#(\text{O-O}) \text{ is odd}), & I_{AB} &\equiv \mathcal{I}(\#(\text{AB-AB}) \text{ is odd}), \\
\Delta(\text{O-A}) &\equiv \#(\text{O-A}) - \#(\text{A-O}), & \Delta(\text{O-B}) &\equiv \#(\text{O-B}) - \#(\text{B-O}), \\
\Delta(\text{O-AB}) &\equiv \#(\text{O-AB}) - \#(\text{AB-O}), & \Delta(\text{A-B}) &\equiv \#(\text{A-B}) - \#(\text{B-A}), \\
\Delta(\text{A-AB}) &\equiv \#(\text{A-AB}) - \#(\text{AB-A}), & \Delta(\text{B-AB}) &\equiv \#(\text{B-AB}) - \#(\text{AB-B}). \\
c &\equiv 2\{\#(\text{A-O}) + \#(\text{B-O}) + \#(\text{AB-O}) + \#(\text{AB-A}) + \#(\text{AB-B}) + \#(\text{B-A})\} \\
&\quad + \#(\text{O-O}) + \#(\text{A-A}) + \#(\text{B-B}) + \#(\text{AB-AB}) - I_O - I_A - I_B - I_{AB}, \\
k &\equiv \Delta(\text{O-A}) + \Delta(\text{O-B}) + \Delta(\text{O-AB}) + \Delta(\text{A-AB}) + \Delta(\text{B-AB}) + \Delta(\text{A-B}) + I_A + I_B. \\
c_1 &\equiv \min\{\Delta(\text{O-AB}), I_{AB} + I_O\}, & c_2 &\equiv \min\{\Delta(\text{O-A}), \Delta(\text{A-AB})\}, \\
c_3 &\equiv \min\{\Delta(\text{O-B}), \Delta(\text{B-AB})\}, & c_4 &\equiv \min\{I_B, \Delta(\text{O-B}) - c_3\}, \\
c_5 &\equiv \min\{I_A, \Delta(\text{A-AB}) - c_2\}, \\
c_6 &\equiv \min\{I_A - c_5, \Delta(\text{O-A}) - c_2\}, \\
c_7 &\equiv \min\{I_A - c_5 - c_6, \Delta(\text{A-B})\}, \\
c_8 &\equiv \min\{\Delta(\text{O-A}) - c_2 - c_6, \Delta(\text{A-B}) - c_7\}, \\
c_9 &\equiv \min\{\Delta(\text{A-B}) - c_7 - c_8, \Delta(\text{B-AB}) - c_3\}, \\
c_{10} &\equiv \min\{\Delta(\text{A-B}) + \Delta(\text{B-AB}) - c_3 - c_7 - c_8 - 2c_9, I_B - c_4\}. \\
k_6 &\equiv \min\{I_A - c_5, \Delta(\text{A-B})\}, \\
k_7 &\equiv \min\{\Delta(\text{A-B}) - k_6, I_B - c_4\}, \\
k_8 &\equiv \min\{\Delta(\text{O-A}) - c_2, \Delta(\text{A-B}) - k_6 - k_7\}, \\
k_9 &\equiv \min\{\Delta(\text{A-B}) - k_6 - k_7 - k_8, \Delta(\text{B-AB}) - c_3\}, \\
k_{10} &\equiv \min\{\Delta(\text{A-B}) + \Delta(\text{B-AB}) - c_3 - k_6 - k_7 - k_8 - 2k_9, I_B - c_4 - k_7\}.
\end{aligned}$$

Note that  $c$  is the total number of pairs that form 2-cycles in the 2-way minimum chains algorithm and  $k$  is the number of pairs, except for (O-O) and (AB-AB), which still remain in the pool after Step 1. In what follows, we show that  $c_1, \dots, c_{10}$  and  $k_6, \dots, k_{10}$  are the numbers of certain 2-chains that are formed by the algorithm.

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<sup>10</sup>For details, see Claims 2, 12, 13, and 14 in the Appendix.

**Theorem 2.**

(1) Let  $H^*$  be the number of chains formed in Steps 1 to 7 of the 2-way minimum chains algorithm.

$$\text{Then, } H^* = \begin{cases} k - \sum_{i=2}^{10} c_i & \text{if } \Delta(\text{A-B}) \leq \Delta(\text{O-A}) - c_2 + \Delta(\text{B-AB}) - c_3, \\ k - \sum_{i=2}^5 c_i - \sum_{i=6}^{10} k_i & \text{if } \Delta(\text{A-B}) > \Delta(\text{O-A}) - c_2 + \Delta(\text{B-AB}) - c_3. \end{cases}$$

(2) The total number of chains obtained by the 2-way minimum chains algorithm is

$$H_2 = \begin{cases} H^* + 1 & \text{if } I_O + I_{AB} > \Delta(\text{O-AB}) \text{ and } 2H^* + c = n - 1, \\ H^* & \text{otherwise.} \end{cases}$$

*Proof.* (1) *Step 1.* Note that no chain is formed in Step 1. The number of remaining pairs after Step 1 is  $k + I_O + I_{AB}$ .

*Step 2.* Since  $\Delta(\text{O-AB})$  number of (O-AB) and  $(I_O + I_{AB})$  number of (O-O) and (AB-AB) remain, the number of (O-O)-(O-AB) and (O-AB)-(AB-AB) chains is  $c_1 \equiv \min\{\Delta(\text{O-AB}), I_O + I_{AB}\}$ . The remaining (O-AB)'s become 1-chains, whose number is  $(\Delta(\text{O-AB}) - c_1)$ .

*Step 3.* Since  $\Delta(\text{O-A})$  number of (O-A) and  $\Delta(\text{A-AB})$  number of (A-AB) remain, the number of (O-A)-(A-AB) chains is  $c_2 \equiv \min\{\Delta(\text{O-A}), \Delta(\text{A-AB})\}$ . Similarly, since  $\Delta(\text{O-B})$  number of (O-B) and  $\Delta(\text{B-AB})$  number of (B-AB) remain, the number of (O-B)-(B-AB) chains is  $c_3 \equiv \min\{\Delta(\text{O-B}), \Delta(\text{B-AB})\}$ .

*Step 4.* Since  $(\Delta(\text{O-B}) - c_3)$  number of (O-B) and  $I_B$  number of (B-B) remain, the number of (O-B)-(B-B) chain is  $c_4 \equiv \min\{I_B, \Delta(\text{O-B}) - c_3\}$ . Since  $I_A$  number of (A-A) and  $(\Delta(\text{A-AB}) - c_2)$  number of (A-AB) remain, the number of (A-A)-(A-AB) chain is  $c_5 \equiv \min\{I_A, \Delta(\text{A-AB}) - c_2\}$ . The remaining (O-B)'s become 1-chains, whose number is  $(\Delta(\text{O-B}) - c_3 - c_4)$ . Also, the remaining (A-AB)'s become 1-chains, whose number is  $(\Delta(\text{A-AB}) - c_2 - c_5)$ .

We divide into two cases.

**Case 1:**  $\Delta(\text{A-B}) \leq \Delta(\text{O-A}) - c_2 + \Delta(\text{B-AB}) - c_3$ .

*Step 5.* Since  $(\Delta(\text{O-A}) - c_2)$  number of (O-A) and  $(I_A - c_5)$  number of (A-A) remain, the number of (O-A)-(A-A) chain is  $c_6 \equiv \min\{I_A - c_5, \Delta(\text{O-A}) - c_2\}$ . Since  $(I_A - c_5 - c_6)$  number of (A-A) and  $\Delta(\text{A-B})$  number of (A-B) remain, the number of (A-A)-(A-B) chain is  $c_7 \equiv \min\{I_A - c_5 - c_6, \Delta(\text{A-B})\}$ . The remaining number of (A-A) is  $(I_A - c_5 - c_6 - c_7)$ .

*Step 6.* Since  $(\Delta(\text{O-A}) - c_2 - c_6)$  number of (O-A) and  $(\Delta(\text{A-B}) - c_7)$  number of (A-B) remain, the number of (O-A)-(A-B) chains is  $c_8 \equiv \min\{\Delta(\text{O-A}) - c_2 - c_6, \Delta(\text{A-B}) - c_7\}$ . The remaining (O-A)'s become 1-chains, whose number is  $(\Delta(\text{O-A}) - c_2 - c_6 - c_8)$ . Next, since  $(\Delta(\text{A-B}) - c_7 - c_8)$  number of (A-B) and  $(\Delta(\text{B-AB}) - c_3)$  number of (B-AB) remain, the number of (A-B)-(B-AB) chains is  $c_9 \equiv \min\{\Delta(\text{A-B}) - c_7 - c_8, \Delta(\text{B-AB}) - c_3\}$ .

*Step 7.* Since  $(\Delta(\text{A-B}) - c_7 - c_8 - c_9)$  number of (A-B),  $(I_B - c_4)$  number of (B-B), and  $(\Delta(\text{B-AB}) - c_3 - c_9)$  number of (B-AB) remain, the number of (A-B)-(B-B) and (B-B)-(B-AB) chains is  $c_{10} \equiv \min\{\Delta(\text{A-B}) + \Delta(\text{B-AB}) - c_3 - c_7 - c_8 - 2c_9, I_B - c_4\}$ . The remaining (A-B), (B-AB), and (B-B) become 1-chains. The number of (A-B) and (B-AB) is  $(\Delta(\text{A-B}) + \Delta(\text{B-AB}) - c_3 - c_7 - c_8 - 2c_9 - c_{10})$  and that of (B-B) is  $(I_B - c_4 - c_{10})$ .

Summing up the numbers of all 1- and 2-chains, we obtain  $k - \sum_{i=2}^{10} c_i$ .

**Case 2:**  $\Delta(\text{A-B}) > \Delta(\text{O-A}) - c_2 + \Delta(\text{B-AB}) - c_3$ .

*Step 5.* Since  $(I_A - c_5)$  number of (A-A) and  $\Delta(\text{A-B})$  number of (A-B) remain, the number of (A-A)-(A-B) chain is  $k_6 \equiv \min\{I_A - c_5, \Delta(\text{A-B})\}$ . The remaining number of (A-A) is  $(I_A - c_5 - k_6)$ . Next, since  $(\Delta(\text{A-B}) - k_6)$  number of (A-B) and  $(I_B - c_4)$  number of (B-B) remain, the number of (A-B)-(B-B) chain is  $k_7 \equiv \min\{\Delta(\text{A-B}) - k_6, I_B - c_4\}$ .

*Step 6.* Since  $(\Delta(\text{O-A}) - c_2)$  number of (O-A) and  $(\Delta(\text{A-B}) - k_6 - k_7)$  number of (A-B) remain, the number of (O-A)-(A-B) chain is  $k_8 \equiv \min\{\Delta(\text{O-A}) - c_2, \Delta(\text{A-B}) - k_6 - k_7\}$ . The remaining (O-A) become 1-chains, whose number is  $(\Delta(\text{O-A}) - c_2 - k_8)$ . Next, since  $(\Delta(\text{A-B}) - k_6 - k_7 - k_8)$  number of (A-B) and  $(\Delta(\text{B-AB}) - c_3)$  number of (B-AB) remain, the number of (A-B)-(B-AB) chain is  $k_9 \equiv \min\{\Delta(\text{A-B}) - k_6 - k_7 - k_8, \Delta(\text{B-AB}) - c_3\}$ .

*Step 7.* Since  $(\Delta(\text{A-B}) - k_6 - k_7 - k_8 - k_9)$  number of (A-B),  $(I_B - c_4 - k_7)$  number of (B-B), and  $(\Delta(\text{B-AB}) - c_3 - k_9)$  number of (B-AB) remain, the number of (A-B)-(B-B) and (B-B)-(B-AB) chains is  $k_{10} \equiv \min\{\Delta(\text{A-B}) + \Delta(\text{B-AB}) - c_3 - k_6 - k_7 - k_8 - 2k_9, I_B - c_4 - k_7\}$ . The remaining (A-B), (B-AB), and (B-B) become 1-chains. The number of (A-B) and (B-AB) is  $(\Delta(\text{A-B}) + \Delta(\text{B-AB}) - c_3 - k_6 - k_7 - k_8 - 2k_9 - k_{10})$  and that of (B-B) is  $(I_B - c_4 - k_7 - k_{10})$ .

Summing up the numbers of all 1- and 2-chains, we obtain  $k - \sum_{i=2}^5 c_i - \sum_{i=6}^{10} k_i$ .

(2) Recall that in Step 2, if  $I_O + I_{AB} > \Delta(\text{O-AB})$  (or equivalently,  $I_O = I_{AB} = \Delta(\text{O-AB}) = 1$ ), exactly one of (O-O) or (AB-AB) has been set aside for Step 8. Since both (O-O) and (AB-AB) can form a 2-chain with any other pair, it will eventually be a 1-chain in Step 8 if no 1-chain is formed in Steps 2 to 7. It happens when all the other pairs belong to either 2-cycles or 2-chains, which implies that  $2H^* + c = n - 1$ . In all other cases, there is at least one 1-chain formed in Steps 2 to 7, and therefore, this 1-chain can form a 2-chain with the remaining (O-O) or (AB-AB) in Step 8, without changing the total number of chains formed in the previous steps.  $\square$

### 3.2. The 3-way minimum chains algorithm

Now we consider the case when 3-way exchanges are feasible in addition to 2-way exchanges. We modify the 2-way minimum chains algorithm to the 3-way minimum chains algorithm by allowing both 2- and 3-way exchanges.

#### The 3-way minimum chains algorithm

**Step 0.** At the end of each step, we exclude all cycles and chains formed at that step from the pool and move on to the next step.

**Step 1.** Form 2-cycles (O-O)-(O-O) as many as possible if there are more than one (O-O) pairs in the pool. If one (O-O) pair remains, form a 3-cycle (O-O)-(O-O)-(O-O) with this pair and the two pairs from a (O-O)-(O-O) cycle. If the pool begins with only one (O-O) pair, set it aside from the pool for Steps 2 and 5. Repeat this process for (AB-AB), (A-A), and (B-B) pairs.

- Step 2. Form a 2-cycle (AB-O)-(O-AB) as many as possible. Next, using the (O-O) and (AB-AB) pairs set aside in Step 1, form a 3-chain (O-O)-(O-AB)-(AB-AB), if any. Then, form a 2-chain (O-O)-(O-AB) or (O-AB)-(AB-AB), if any.
- Step 3. Form 2-cycles (A-O)-(O-A), (B-O)-(O-B), (AB-A)-(A-AB), and (AB-B)-(B-AB) as many as possible.
- Step 4. Form a 2-cycle (B-A)-(A-B) as many as possible.
- Step 5. Form 2-chains (O-A)-(A-AB) and (O-B)-(B-AB) as many as possible. Next, if there is an (A-A) pair set aside in Step 1, form a 3-chains (O-A)-(A-A)-(A-AB) with this pair and the two pairs from a 2-chain (O-A)-(A-AB). Similarly, if there is a (B-B) pair set aside in Step 1, form a 3-chains (O-B)-(B-B)-(B-AB) with this pair and the two pairs from a 2-chain (O-B)-(B-AB).
- Step 6. Form a 3-chain (O-A)-(A-B)-(B-AB) as many as possible.
- Step 7. Form a 2-chain (O-A)-(A-B) and then, a 2-chain (A-B)-(B-AB) as many as possible.
- Step 8. Leave all remaining pairs as 1-chains.

**Theorem 3.** The 3-way minimum chains algorithm attains the minimum number of chains among all 3-way algorithms.

*Proof.* The proof is given in Appendix A. □

Now, we calculate the number of chains  $H_3$  obtained from the 3-way minimum chains algorithm. Let

$$\begin{aligned}
\bar{k} &\equiv \Delta(\text{O-A}) + \Delta(\text{O-B}) + \Delta(\text{A-AB}) + \Delta(\text{B-AB}) + \Delta(\text{A-B}), \\
m_1 &\equiv \min\{\Delta(\text{O-A}), \Delta(\text{A-AB})\}, \\
m_2 &\equiv \min\{\Delta(\text{O-B}), \Delta(\text{B-AB})\}, \\
m_3 &\equiv \min\{\Delta(\text{O-A}) - m_1, \Delta(\text{A-B}), \Delta(\text{B-AB}) - m_2\}, \\
m_4 &\equiv \min\{\Delta(\text{O-A}) - m_1 - m_3, \Delta(\text{A-B}) - m_3\}, \\
m_5 &\equiv \min\{\Delta(\text{A-B}) - m_3 - m_4, \Delta(\text{B-AB}) - m_2 - m_3\}.
\end{aligned}$$

**Theorem 4.** The total number of chains obtained by the 3-way minimum chains algorithm is

$$H_3 = \Delta(\text{O-AB}) + \Delta(\text{O-A}) + \Delta(\text{O-B}) + \Delta(\text{A-B}) + \Delta(\text{A-AB}) + \Delta(\text{B-AB}) - m_1 - m_2 - 2m_3 - m_4 - m_5.$$

*Proof.* By assumption 2, at least one (O-AB) pair remains after forming 2-cycles (O-AB)-(AB-O) in Step 2. Similarly, at least one (O-A)-(A-AB) chain and at least one (O-B)-(B-AB) chain are formed in Step 5. Therefore, if there exists any pair of the same blood-types after Step 1, the pair is added to other chains in Step 2 or 5, without changing the total number of chains. We proceed without these pairs of the same blood-types in what follows.

*Steps 1 to 4.* No chain is formed in Steps 1 to 4 except the 1-chains of (O-AB), whose number is  $\Delta(\text{O-AB})$ . The number of remaining pairs after Step 4 is  $\bar{k}$ .

*Step 5.* The number of (O-A)-(A-AB) chains is  $m_1 \equiv \min\{\Delta(\text{O-A}), \Delta(\text{A-AB})\}$ . The number of (O-B)-(B-AB) chains is  $m_2 \equiv \min\{\Delta(\text{O-B}), \Delta(\text{B-AB})\}$ . The remaining (A-AB) and (O-B) become 1-chains, whose numbers are  $(\Delta(\text{A-AB}) - m_1)$  and  $(\Delta(\text{O-B}) - m_2)$ , respectively.

*Step 6.* Since  $(\Delta(\text{O-A}) - m_1)$  number of (O-A),  $\Delta(\text{A-B})$  number of (A-B), and  $(\Delta(\text{B-AB}) - m_2)$  number of (B-AB) remain, the number of (O-A)-(A-B)-(B-AB) chains is  $m_3 \equiv \min\{\Delta(\text{O-A}) - m_1, \Delta(\text{A-B}), \Delta(\text{B-AB}) - m_2\}$ .

*Step 7.* Since  $(\Delta(\text{O-A}) - m_1 - m_3)$  number of (O-A) and  $(\Delta(\text{A-B}) - m_3)$  number of (A-B) remain, the number of (O-A)-(A-B) chain is  $m_4 \equiv \min\{\Delta(\text{O-A}) - m_1 - m_3, \Delta(\text{A-B}) - m_3\}$ . Since  $(\Delta(\text{A-B}) - m_3 - m_4)$  number of (A-B) and  $(\Delta(\text{B-AB}) - m_2 - m_3)$  number of (B-AB) remain, the number of (A-B)-(B-AB) chain is  $m_5 \equiv \min\{\Delta(\text{A-B}) - m_3 - m_4, \Delta(\text{B-AB}) - m_2 - m_3\}$ . The remaining (O-A), (A-B), and (B-AB) become 1-chains, whose numbers are  $(\Delta(\text{O-A}) - m_1 - m_3 - m_4)$ ,  $(\Delta(\text{A-B}) - m_3 - m_4 - m_5)$ , and  $(\Delta(\text{B-AB}) - m_2 - m_3 - m_5)$ , respectively.

Summing up the numbers of all chains, we obtain  $H_3 = \Delta(\text{O-AB}) + \Delta(\text{O-A}) + \Delta(\text{O-B}) + \Delta(\text{A-B}) + \Delta(\text{A-AB}) + \Delta(\text{B-AB}) - m_1 - m_2 - 2m_3 - m_4 - m_5$ .  $\square$

### 3.3. The minimum chains algorithm allowing more than 3-way exchanges

Lastly, we consider an environment without any restriction on the size of exchanges.<sup>11</sup> In the standard kidney exchange model without suppressants, Roth et al. (2007) also ask this question and calculate the marginal improvement in kidney exchanges as feasible size of exchanges gets larger. We further generalize this analysis by incorporating suppressants into the standard model. We assess efficiency loss/gain as feasible size of cycles and chains gets larger.

**Proposition 1.** The 3-way minimum chains algorithm attains the minimum number of chains when there is no restriction in the size of exchanges. The minimum number of chains is calculated as  $H_3$  in Theorem 4.

*Proof.* The proof is given in Appendix A.  $\square$

Proposition 1 states that the number of minimum chains does not change *at all* by introducing 4-way exchanges or more in this problem. That is, it is enough to arrange 2- and 3-way exchanges to achieve full efficiency. This result is similar to the conclusion of Roth et al. (2007) that there is no improvement by introducing 5-way exchanges or more to the standard kidney exchange setup. Proposition 1 sharpens this result and shows that, when chains can also be formed with cycles, there is no need to go beyond 3-way exchanges. To be more precise about the reduction of suppressants, we next conduct a quantitative analysis by running simulations in Section 4.

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<sup>11</sup>It is ideal to arrange all operations simultaneously, but if it is unavailable, non-simultaneous operations can also be considered so as to relax size restrictions on exchanges. There are recent proposals and case reports about such non-simultaneous exchanges: see Ausubel and Morrill (2014) and Rees et al. (2009) for instance.

## 4. Simulations: Using Patient-Donor Characteristics

We now measure the reduction of suppressants in simulations. We start with the process of generating patient-donor pools.

### 4.1. Generating patient-donor pools

To generate a Korean transplant pool, we use biological characteristics of patients and donors provided by Joo et al. (2009), the Blood Services Statistics (2014-2018) of the Korean Red Cross, and the Annual Reports (2014-2018) of the Korean Network for Organ Sharing (KONOS). Those characteristics include the ABO blood types of patients and donors, the gender of patients, the spousal relationship between patient-donor, and the PRA (panel reactive antibody) distribution of patients. Their distributions are presented in Table 3. In this analysis, we consider all possible populations with/without Assumption 3,  $\#(A-B) > \#(B-A)$ , that we impose in deriving the formulae in Theorems 2 and 4. For the pools with  $\#(A-B) > \#(B-A)$ , Theorems 2 and 4 directly apply; for the pools with  $\#(A-B) < \#(B-A)$ , the formulae are derived by switching the roles of type A and type B in Theorems 2 and 4; and for the pools with  $\#(A-B) = \#(B-A)$ , the computation formulae take a very simple form.

The ABO blood-type of each patient or each donor is randomly chosen by using the blood-type frequency of Korea: A patient (or a donor) is given blood type O with the probability of 27.41%, type A with the probability of 34.25%, type B with the probability of 26.84%, and type AB with the probability of 11.50%. The gender of a patient is similarly chosen by the gender distribution in Table 3. According to Joo et al. (2009), on the other hand, a patient is given a low PRA type with the probability of 78.13%, a medium type with the probability of 16.47%, and a high type with the probability of 5.40%. According to Roth et al. (2007), a low PRA patient has a positive crossmatch probability 5%, a medium PRA patient 45%, and a high PRA patient 90%.<sup>12</sup> The spousal relation between a patient and a donor is also chosen from the corresponding distribution in Table 3. If a patient with her spousal donor is female, then it is more likely to have a positive crossmatch due to pregnancies. According to Roth et al. (2007), we adjust the probability of having positive crossmatch of such pairs so that a low PRA type patient has the probability of 28.75%, a medium PRA type patient 58.75%, and a high PRA type patient 92.50%.

We generate each patient-donor pair whose biological characteristics are specified as above and decide whether to include it in the pool or not. If a patient-donor pair is ABO-compatible (ABOc) with no positive crossmatch (PCM), we dispose the pair, because the patient can receive a transplant directly from his or her own donor. However, if a pair is ABOi or ABOc with PCM, we add the pair to the pool. We replicate this process until we form a pool of size 25, 50, and 100. For each pool size, we construct 500 pools, to which we apply the minimum chains algorithms.

Table 4, on the other hand, represents the distributions of these biological characteristics of the United States, which we borrow from Roth et al. (2007). It is notable that the blood-type distribution differs significantly in the two countries: the frequency of type O is much higher in the States than

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<sup>12</sup>A low PRA patient has less than 10 PRA percentage, a medium PRA patient greater than or equal to 10 and less than 80 PRA percentage, and a high PRA patient greater than or equal to 80 PRA percentage.

ABO blood types	Frequency (%)
O	27.41
A	34.25
B	26.84
AB	11.50

Patient gender	Frequency (%)
Female	40.38
Male	59.62

Unrelated living donors	Frequency (%)
Spouse	34.57
Other	65.43

PRA types	Frequency (%)
Low PRA	78.13
Medium PRA	16.47
High PRA	5.40

Table 3: Patient-donor characteristics in Korea

ABO blood types	Frequency (%)
O	48.14
A	33.73
B	14.28
AB	3.85

Patient gender	Frequency (%)
Female	40.90
Male	59.10

Unrelated living donors	Frequency (%)
Spouse	48.97
Other	51.03

PRA types	Frequency (%)
Low PRA	70.19
Medium PRA	20.00
High PRA	9.81

Table 4: Patient-donor characteristics in the U.S. (Roth et al., 2007)

in Korea and that of type B and AB are much lower in the States than in Korea. The distributions of other characteristics, such as PRA and gender, are relatively similar in the two countries though. Using Table 4, we also generate 500 pools of each pool size, to which we apply the minimum chains algorithms. We then compare the outcomes of Korea and the States.

## 4.2. Minimum number of incompatible transplants

Note that each pair in every pool is either tissue-type incompatible or ABO incompatible (or both), so every patient in the pool should use a suppressant under the current practice in Korea, as discussed in Introduction. Therefore, for a pool of size  $k$  (where  $k \in \{25, 50, 100\}$ ), the number of suppressants needed for the pool is exactly  $k$ . We therefore regard  $k$  as the maximum number of incompatible transplants and set it to be the baseline value. In what follows, we assess the reduction of incompatible transplants from  $k$  as we allow forming cycles or/and chains for exchanges. Tables 5 and 6 respectively show the outcomes of Korea and the United States. Each column corresponds to the result for a given length of exchange cycles and/or chains.

### Columns (1) to (3): Standard kidney exchanges with trading cycles only

If kidney exchanges are arranged in the standard model, then the pairs will swap their donors for compatible transplants. The remaining pairs that do not belong to any cycle will then have to use suppressants for transplants and the patients of these pairs will receive direct transplants from own paired donors. As some patients now receive compatible transplants along the exchange cycles, the number of *incompatible* transplants will be smaller than the baseline  $k$ . For this problem, Roth et al. (2007) calculate the number of compatible transplants along exchange cycles, given that a feasible size of exchange cycle is 2, 3, 4 or more, respectively. We apply their computation formulae to the pools that we generate. The number of incompatible transplants is then  $k$  minus the resulting number of compatible transplants. Columns (1) to (3) present the average numbers of incompatible transplants in this setup, as the size of feasible cycles gets larger.

### Columns (4) to (6): Minimum chains algorithm forming cycles and chains

If chains and cycles are formed jointly, then we can directly apply the minimum chains algorithms to calculate the number of incompatible transplants. Columns (4) to (6) present the outcomes of the algorithms as the size of feasible cycles and chains gets larger. By Proposition 1, the numbers of incompatible transplants in Columns (5) and (6) are the same, as the 3-way minimum chains algorithm attains  $H_3$  even when there is no restriction on the size of exchanges.

Now, here are our findings from the simulation analyses summarized in Tables 5 and 6.

**A significant reduction suppressants by introducing chains:** In Columns (1) and (4), we find that the use of suppressants are significantly reduced by forming 2-chains in addition to 2-cycles. Specifically, for a pool of 100 pairs, if only 2-cycles are feasible, then 45.568 patients need to use suppressants on average. However, if 2-chains are additionally feasible, 30.576 patients need to use suppressants. That is, from the baseline  $k = 100$ , exchange cycles lead to a reduction of 54.3% and chains lead to a further reduction of 69.4% in total. Columns (2) and (5) and Columns (3) and (6) also provide a similar observation: when 3- and 2-cycles are feasible, 40.152 patients need to use



Pool size	(1) 2-cycles and 1-chains	(2) 3-, 2-cycles, and 1-chains	(3) 4-, 3-, 2-cycles, and 1-chains	(4) 2-cycles, 2- and 1-chains	(5) 3-, 2-cycles, 3-, 2- and 1-chains	(6) 4-, 3-, 2-cycles, 4-, 3-, 2- and 1-chains
25	15.284 (2.919)	13.424 (3.125)	13.356 (3.144)	9.914 (2.258)	9.722 (2.317)	9.722 (2.317)
50	25.656 (4.577)	22.196 (4.921)	21.990 (4.984)	16.818 (3.468)	16.640 (3.554)	16.640 (3.554)
100	45.568 (6.938)	40.152 (7.234)	39.752 (7.189)	30.576 (5.356)	30.458 (5.469)	30.458 (5.469)

Table 5: Average numbers of incompatible transplants in Korea (standard errors in parentheses)

Pool size	(1) 2-cycles and 1-chains	(2) 3-, 2-cycles, and 1-chains	(3) 4-, 3-, 2-cycles, and 1-chains	(4) 2-cycles, 2- and 1-chains	(5) 3-, 2-cycles, 3-, 2- and 1-chains	(6) 4-, 3-, 2-cycles, 4-, 3-, 2- and 1-chains
25	14.948 (2.978)	13.048 (2.978)	13.026 (2.974)	10.292 (2.437)	10.196 (2.496)	10.196 (2.496)
50	24.764 (5.066)	21.670 (5.098)	21.566 (5.103)	18.558 (4.395)	18.494 (4.434)	18.494 (4.434)
100	44.744 (7.315)	39.788 (7.447)	39.644 (7.382)	35.858 (6.651)	35.850 (6.653)	35.850 (6.653)

Table 6: Average numbers of incompatible transplants in U.S. (standard errors in parentheses)

suppressants, but the number decreases to 30.458 if 3- and 2-chains are additionally feasible, which results in the decrease of 9.694 suppressants. When 4-, 3- and 2-cycles are feasible, 39.752 patients need to use suppressants, but the number decreases to 30.458 if 4-, 3- and 2-chains are additionally feasible, which results in the decrease of 9.294 suppressants.

**Economies of scale in the reduction:** Each column presents the outcomes with  $k = 25, 50,$  and  $100$  in Table 5. These outcomes show that economies of scale exist in exchanges when cycles and/or chains are formed among the pairs. For instance, consider Column (1) of Table 5. When  $k = 25$ , the reduction is 38.9% (namely, from 25 to 15.284); when  $k = 50$ , the reduction is 48.7% (namely, from 50 to 25.656); and when  $k = 100$ , the reduction is 54.4% (namely, from 100 to 45.568). We see that the reduction increases as the size of the pool increases. Similarly, Column (4) provides a similar observation when chains can also be formed. As  $k$  increases, the percentage reduction increases from 60.3% to 66.4%, and again to 69.4% (namely, from 25 to 9.914, from 50 to 16.818, and from 100 to 30.576). A similar observation from other columns is obtained when 3-chains or/and 4-chains become feasible. This result implies that it is important to organize a “thick” market for exchanges, because the gains from trade increase as the market size increases.

**Marginal improvement by increasing the size of exchanges:** Although there is a significant reduction of suppressants by introducing 2-chains, as discussed above, the benefit of introducing 3-chains or more appears insignificant. Columns (4) and (5) present the marginal improvement by increasing the size of exchanges, from 2-way to 3-way. For the pool of  $k = 100$  in Column (4), for instance, the use of suppressants changes from 30.576 to 30.458 only. Introducing 4-chains, on the

other hand, does not improve it at all, as proven in Proposition 1, and thus, Columns (5) and (6) present the same number of incompatible transplants. This observation implies that it is enough to arrange 2-way exchanges in the presence of suppressants to take the most advantage of forming cycles and chains. This implication is quite useful in constructing a centralized transplant system, because there has been a concern of efficiency loss from restricting the size of exchanges. Our observation shows that it is possible to achieve almost full efficiency with the smallest size of exchanges.

This result, on the other hand, is quite similar to the conclusion of Roth et al. (2007) which also measure the marginal improvements with exchange cycles only, as presented in Columns (1) to (3). For the standard kidney exchange setup, however, the marginal improvement by introducing 3-way exchanges is sufficiently large, in contrast to what we find in the setup with suppressants. For the pool of  $k = 100$  in Columns (1) and (2), for instance, the use of suppressants changes from 45.568 to 40.152, which is a significant reduction. The marginal improvement by introducing 4-cycles, however, becomes quite negligible: the use of suppressants changes from 40.152 to 39.752 for the pool of  $k = 100$ .

**Different outcomes in the two countries, Korea and the United States:** We replicate this analysis for the United States by using the biological characteristics presented in Table 2 and provide the results in Table 6. The aforementioned observations persist in the United States, but there is one major difference in the outcome that is worth noting: the gain from introducing 2-chains to 2-cycles in the States is not as large as in Korea, as can be seen in Columns (1) and (4) of Table 6. In Korea, for the pool of  $k = 100$ , the reduction from forming 2-chains is 14.992 (namely, from 45.568 to 30.576 in Columns (1) and (4) of Table 5); in the States, however, the reduction is 8.886 (namely, from 44.744 to 35.858), which is significantly smaller than that of Korea. From Columns (2) and (5) in Tables 5 and 6, we have a similar observation.

The substantial difference in the gain of using chains originates from different ABO blood-type distributions. Although the frequency of blood-type O is quite high in the States, the frequency of blood type AB in the States is so low that the number of 3- and 2-chains formed in a U.S. pool is much smaller than that in Korea. There will be more pairs forming 1-chains, increasing the number of incompatible transplants in the United States. The gain from introducing 3-cycles to 2-cycles, however, is similar in both countries, as shown in Columns (1) and (2) of Tables 5 and 6. From these observations, we conclude that Korea has a comparative advantage in incorporating suppressants to the transplant system, while the United States has it in enlarging the size of exchanges in the standard kidney exchange setup. This would be one factor that affects different development of transplant systems in the two countries.

### 4.3. The effect of removing each short-side pair

In this section, we measure the value of each pair on the short-side in exchanges. Under Assumption 2, there are five pairs on the short-side, (A-O), (B-O), (AB-O), (AB-A), and (AB-B). If a short-side pair is removed from a pool, then the minimum number of chains increases and more patients need to use suppressants to receive kidney transplants, because these pairs are those who facilitate compatible transplants in the exchange cycles. The contribution of each type of short-sided pairs may differ, as can be seen in the following example.

Consider a pool when 2-chains and 2-cycles can only be formed and apply the 2-way minimum chains algorithm to the pool first. Now, suppose that an (AB-O) pair is removed from the pool. At the initial outcome of the 2-way minimum chains algorithm, this (AB-O) pair forms a 2-cycle with (O-AB) pair. Removing the (AB-O) pair will release one (O-AB) pair, who would seek forming a cycle or a chain. Note that an (O-AB) pair can only form a cycle with an (AB-O) pair and a chain with an (O-O) or (AB-AB) pair, but these pairs are exhausted in the minimum chains algorithm to form 2-cycles or 2-chains. Therefore, the released (O-AB) pair will form a 1-chain, increasing the number of incompatible transplant by one.

Suppose that an (A-O) pair is removed from the pool in the same setup instead of the (AB-O) pair. At the initial outcome of the algorithm, this (A-O) pair forms a 2-cycle with (O-A) pair. Removing the (A-O) pair will release one (O-A) pair, who would seek forming a cycle or a chain. When there exists a 1-chain (A-AB), then the released (O-A) pair can form a 2-chain, without increasing the number of chains (or equivalently, the number of incompatible transplants). If there is no such 1-chain, then the released (O-A) pair will remain as a 1-chain, increasing the number of incompatible transplants, by 1.

As can be seen, the extent to which incompatible transplants increase varies, depending on the set of initial chains and cycles formed along the minimum chains algorithm. We quantitatively measure the extent by applying the minimum chains algorithm to the pools *with* and *without* the pair.

To do so, we first construct a pool of 100 pairs with at least one of each short-side pair and apply the algorithm. Next, we remove one short-side pair and compute the minimum number of chains for the remaining 99 pairs. We then take the difference between the two minimum numbers to measure the effect of removing the short-side pair from the pool. Tables 7 and 8 present differences in the average minimum numbers of incompatible transplants when each short-side pair is removed from a Korean pool, and from a U.S. pool, respectively. This analysis enables us to assess the value of each short-side pair in our algorithms.

### **Columns (1) to (3): Standard kidney exchanges with trading cycles only**

We start with Columns (1) to (3) for the standard kidney exchanges with trading cycles only. First, when only 2-cycles are allowed to form, when a short-side pair is removed, then the released long-sided pair remains as 1-chain, increasing the use of suppressants by 1, as can be seen in Column (1) of these tables. If 3-cycles are additionally allowed to form as in Column (2), the values of each pair differ across their types. For instance, since (AB-O) is always used to form 3-cycles such as (AB-O)-(O-A)-(A-AB), (AB-O)-(O-B)-(B-AB), etc, the removal of (AB-O) results in an increase of the number of chains by two. Unlike (AB-O) pair, for other types of short-sided pairs, the number of chains may not increase as much when they are removed from the pool. For instance, if an (A-O) pair is removed from a 3-cycle (A-O)-(O-B)-(B-A), for instance, then one (O-B) and one (B-A) pair will be released. When there exists a 1-chain (A-B), then the released (B-A) pair can form a 2-cycle with the (A-B) pair. The released (O-B) pair would form a 1-chain then, increasing the number of incompatible transplants by one only, not two. If there is no 1-chain (A-B), however, the number will increase by two. Counting all possible cases, the increase of incompatible transplants on average is 1.257 as presented in the first row of Column (2) in Table 7. The results on other pairs are summarized in Tables 7 and 8. For (AB-A), for instance, the number increases by 1.213 and for (AB-B), by 1.232. A similar argument

applies to Column (3) of Table 7 when 4-cycles can also be formed: if an (AB-O) pair is removed, for instance, from a 4-cycle, such as (AB-O)-(O-A)-(A-B)-(B-AB), the number of chains increases by more than two, as shown in the third row of Column (3) in Table 7. Table 8 is for the United States and we have similar results: For (A-O), the number increases by 1.068 and for (B-O), by 1.263; for (AB-A), the number increases by 1.262 and for (AB-B), by 1.062.

**Columns (4) to (6): Minimum chains algorithm forming cycles and chains**

Next, let us consider the environment where chains are formed together with cycles. Columns (4) to (6) summarizes the results for different lengths of exchanges. First, in Column (4) of Table 7, we find the following results: for (A-O), the number of chains increases by .857, that is, the separated (O-A) remains as a 1-chain with the probability of .857, but forms a 2-chain, (O-A)-(A-B) or (O-A)-(A-AB), with the probability of .143. For (B-O), the number increases by .801, that is, the separated (O-B) remains as a 1-chain with the probability of .801, but forms a 2-chain, (O-B)-(B-A) or (O-B)-(B-AB), with the probability of .199. For (AB-O), the number increases by one since the separated (O-AB) cannot form a 2-chain with any pair remaining as a 1-chain. For (AB-A), the number increases by .152, that is, the separated (A-AB) remains as a 1-chain with the probability of .152, but forms a 2-chain, (O-A)-(A-AB) or (B-A)-(A-AB), with the probability of .848. For (AB-B), the number increases by .235, that is, the separated (B-AB) remains as a 1-chain with the probability of .235, but forms a 2-chain, (O-B)-(B-AB) or (A-B)-(B-AB), with the probability of .765.

Column (4) of Table 8 presents the same analysis made for the U.S. pools: for (A-O), the number of chains increases by .998, that is, the separated (O-A) remains as a 1-chain with the probability of .998. For (B-O), the number increases by .927, that is, the separated (O-B) remains as a 1-chain with the probability of .927. When (A-O) or (B-O) is removed, the separated pair, (O-A) or (O-B), is less likely to form 2-chains, such as (O-A)-(A-AB) and (O-B)-(B-AB), in the U.S. than in Korea, because the frequencies of blood types B and AB are lower in the U.S. As the separated pair remains as a 1-chain more frequently in the U.S. than in Korea, the removed pair becomes more valuable in the U.S. For (AB-A), the number increases by .005, that is, the separated (A-AB) remains as a 1-chain with the probability of .005. For (AB-B), the number increases by .092, that is, the separated (B-AB) remains as a 1-chain with the probability of .092. When (AB-A) or (AB-B) is removed, the separated pair, (A-AB) or (B-AB), is more likely to form 2-chains in the U.S. than in Korea, because the frequency of blood type O is higher in the U.S. As the separated pair forms 2-chains more frequently in the U.S. than in Korea, the removed pair becomes less valuable in the U.S.

When 3-chains can also be formed, we apply the 3-way minimum chains algorithm, which generates a similar impact to those from the 2-way minimum chains algorithm, as can be seen in Columns (5) of Tables 7 and 8. A difference from the analysis with the 2-way minimum chains algorithm is that the released pairs can form 3-chains as well as 2-chains. In Column (5) of Table 7, for instance, for (A-O), the number of chains increases by .867, that is, the separated (O-A) remains as a 1-chain with the probability of .867 and forms a 2- or 3-chain, (O-A)-(A-B), (O-A)-(A-AB), or (O-A)-(A-B)-(B-AB), with the probability of .133. For (B-O), the number increases by .812, that is, the separated (O-B) remains as a 1-chain with the probability of .812 and forms a 2- or 3-chain, (O-B)-(B-A), (O-B)-(B-AB), or (O-B)-(B-A)-(A-AB), with the probability of .188. Column (5) of Table 8 for the U.S. pools

	(1) 2-cycles and 1-chains	(2) 3-, 2-cycles, and 1-chains	(3) 4-, 3-, 2-cycles, and 1-chains	(4) 2-cycles, 2- and 1-chains	(5) 3-, 2-cycles, 3-, 2- and 1-chains	(6) 4-, 3-, 2-cycles, 4-, 3-, 2- and 1-chains
(A-O)	1.000 (0.000)	1.257 (0.438)	1.201 (0.401)	0.857 (0.351)	0.867 (0.340)	0.867 (0.340)
(B-O)	1.000 (0.000)	1.245 (0.430)	1.205 (0.404)	0.801 (0.399)	0.812 (0.391)	0.812 (0.391)
(AB-O)	1.000 (0.000)	2.000 (0.000)	2.388 (0.488)	1.000 (0.000)	1.000 (0.000)	1.000 (0.000)
(AB-A)	1.000 (0.000)	1.213 (0.410)	1.176 (0.381)	0.152 (0.360)	0.152 (0.360)	0.152 (0.360)
(AB-B)	1.000 (0.000)	1.232 (0.423)	1.177 (0.382)	0.235 (0.424)	0.189 (0.392)	0.189 (0.392)

Table 7: Changes in average numbers of incompatible transplants when each short-side pair is removed from a Korean pool (standard errors in parentheses)

	(1) 2-cycles and 1-chains	(2) 3-, 2-cycles, and 1-chains	(3) 4-, 3-, 2-cycles, and 1-chains	(4) 2-cycles, 2- and 1-chains	(5) 3-, 2-cycles, 3-, 2- and 1-chains	(6) 4-, 3-, 2-cycles, 4-, 3-, 2- and 1-chains
(A-O)	1.000 (0.000)	1.068 (0.252)	1.048 (0.214)	0.998 (0.045)	0.996 (0.063)	0.996 (0.063)
(B-O)	1.000 (0.000)	1.263 (0.441)	1.213 (0.410)	0.927 (0.261)	0.921 (0.271)	0.921 (0.271)
(AB-O)	1.000 (0.000)	2.000 (0.000)	2.206 (0.405)	1.000 (0.000)	1.000 (0.000)	1.000 (0.000)
(AB-A)	1.000 (0.000)	1.262 (0.441)	1.224 (0.418)	0.005 (0.074)	0.005 (0.074)	0.005 (0.074)
(AB-B)	1.000 (0.000)	1.062 (0.242)	1.015 (0.124)	0.092 (0.292)	0.092 (0.292)	0.092 (0.292)

Table 8: Changes in average numbers of incompatible transplants when each short-side pair is removed from a U.S. pool (standard errors in parentheses)

also presents a similar result, so we omit the detailed discussion.

From these outcomes, we conclude that the (AB-A) and (AB-B) pairs contribute to the reduction much more in Korea than in the States; the (A-O) and (B-O) pairs do so much more in the States than in Korea. This difference originates from the blood-type distribution of the two countries. For instance, if (AB-A) pair is removed, it will release one (A-AB) pair; in the United States, the frequency of type O is so high that it is more likely that there exists a 1-chain (O-A), which can form a 2-chain with the released (A-AB) pair; in Korea, however, the frequency of type O is not as high as in the States, so the probability of forming a 2-chain will be lower than in the States. A similar argument applies for (A-O) pair, given that the frequency of type AB is extremely low in the States.

Finally, we compare the outcomes presented in Columns (1) and (4). By allowing 2-chains in addition to 2-cycles, the increase in the number of chains becomes smaller for all short-sided pairs except for (AB-O). This result indicates that the possibility of using suppressants makes the role of short-side pairs less important. Note that there is always a shortage of short-side pairs, as assumed in Assumption 2. If the value of these pairs is too large, the resulting number of incompatible transplants will be greater in the shortage of these pairs. By forming chains together with cycles, however, the shortage of these pairs becomes a less important issue, as shown above. The same conclusion can be obtained by comparing Columns (2) and (5).

## 5. Conclusion

In this paper, we propose the minimum chains algorithms to compute the minimum use of suppressants needed for transplants of a pool of patient-donor pairs. From the simulation analyses using these algorithms, we quantitatively measure the reduction of suppressants from the baseline value  $k$ .

These results provide several policy implications in constructing a centralized transplant system. First, this proposal lead to a significant improvement from the baseline and to make the largest improvement, it is important to construct a thick market for exchanges, because of economies of scale. Second, forming chains in addition to cycles allows us to achieve full efficiency even with pairwise exchanges, because going beyond 2-way exchanges brings in a very marginal improvement. Lastly, the gain from doing so is different across countries and it is affected by the fundamental difference in biological characteristics of patient-donor pairs. So, in constructing a transplant system, the blood-type distribution and other biological traits should be carefully considered. The value of each type of short-side pairs, on the other hand, is also dependent on the blood-type distribution. The estimated values of these pairs can be utilized in providing them incentives to participate in the pool, facilitating compatible transplants.

We finally note that the computations with the minimum chains algorithms and the corresponding simulations provide lower bounds of suppressants needed for transplants of a given pool. This is because of Assumption 1 saying that there is no tissue-type incompatibility between any distinct two pairs. If a patient of one pair and a donor of another pair may also be tissue-type incompatible, as often observed in practice, the number of suppressants needed for a pool will be larger than that we calculate. A natural question arises: is our lower bound tight enough? To answer to this question,

we use integer programming so as to calculate the actual number of suppressants without imposing Assumption 1. The corresponding results, deferred to Appendix B, show that the outcomes presented in Tables 5 and 6 are very close to the outcomes of the integer programming. This implies that the lower bounds that the minimum chains algorithms calculate are tight enough and are good approximations of the actual use of suppressants in the absence of Assumption 1.

## Appendix A: Proofs of Theorems 1 and 3

We start with a remark and two lemmas.

**Remark 1. Transitivity of the donor-patient relation:** For each  $X, Y, Z \in \{O, A, B, AB\}$ , if type  $X$  donor is compatible with type  $Y$  patient, and type  $Y$  donor is compatible with type  $Z$  patient, then type  $X$  donor is also compatible with type  $Z$  patient.

For each exchange pool, choose an optimal matching for the 2-way (or 2- and 3-way) problem and let  $H_2$  (or  $H_3$ ) be the corresponding number of chains. We refer to this matching as the initial one in the following. For each  $X, Y \in \{O, A, B, AB\}$ , (X-Y)-cycle (or (X-Y)-chain) means the cycle (or the chain, respectively) to which (X-Y) belongs before the reorganization begins.

**Lemma 1.** It is possible to preserve the number of chains  $H_2$  (or  $H_3$ ) by reorganizing the cycles and chains of the initial matching so that no chain includes any pair on the short side.

*Proof.* Note that the initial matching is optimal, so that the minimum number of chains is attained. Suppose that there is a chain including a pair on the short side at the initial matching, for instance (A-O). We show that it is possible to reorganize the initial matching so that no chain includes any pair on the short side. By Assumption 2, there is at least one (O-A) that belongs to a chain at the initial matching.

(1) Suppose that (A-O) belongs to a 1-chain. If (O-A) belongs to a 1-chain, forming a 2-cycle (A-O)-(O-A) reduces the number of chains by two, a contradiction. If (O-A) belongs to a 2-chain, forming a 2-cycle (A-O)-(O-A) and leaving the remaining pair as a 1-chain reduce the number of chains by one, a contradiction. If (O-A) belongs to a 3-chain, forming (A-O)-(O-A) and leaving the remaining pairs as two 1-chains preserve the same number of chains. The remaining two pairs cannot form a 2-chain or a 2-cycle because it reduces the number of chains below the minimum.

(2) Suppose that (A-O) belongs to a 2-chain. If (O-A) belongs to a 1-chain, forming a 2-cycle (A-O)-(O-A) and leaving the remaining pair as a 1-chain reduce the number of chains by one, a contradiction. If (O-A) belongs to a 2-chain, forming (A-O)-(O-A) and leaving the remaining pairs as two 1-chains preserve the same number of chains. The remaining pairs cannot form a 2-chain or a 2-cycle because it reduces the number of chains below the minimum. If (O-A) belongs to a 3-chain, forming (A-O)-(O-A) and leaving the remaining pairs as one 1-chain and one 2-chain preserve the same number of chains.<sup>13</sup>

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<sup>13</sup>The existence of the 2-chain can be shown as follows. If (O-A) is the middle pair of the (O-A)-chain, the donor of the first pair (type O) and the patient of the last pair (either type A or AB) are compatible and therefore, the remaining two pairs form a 2-chain. If (O-A) is either the first or the last pair of the (O-A)-chain, then it is obvious that the remaining two pairs form a 2-chain.

(3) Suppose that (A-O) belongs to a 3-chain. If (O-A) belongs to a 1-chain, forming a 2-cycle (A-O)-(O-A) and leaving the remaining pairs as two 1-chains preserve the same number of chains. If the remaining two pairs form a 2-chain, then it reduces the number of chains by one, a contradiction. If (O-A) belongs to a 2-chain, we divide into two subcases. First, if (A-O) is the middle pair of the 3-chain, then after forming (A-O)-(O-A), by Remark 1, the remaining pair of the (O-A)-chain can form a 2-chain with a remaining pair of the (A-O)-chain. Another remaining pair of the (O-A)-chain will be a 1-chain, preserving the same number of chains. Second, if (A-O) is either the first or the last pair of the (A-O)-chain, then the remaining two pairs of the (A-O)-chain form a 2-chain. The remaining pair of the (O-A)-chain will be a 1-chain, preserving the same number of chains. If (O-A) belongs to a 3-chain, by Remark 1, we can show that the remaining pairs can form either two 2-chains or one 1-chain and one 3-chain, preserving the same number of chains. If the remaining pairs form any cycle, it reduces the number of chains below the minimum, a contradiction.

We repeat this process until is no pair on the short-side belongs to a chain.  $\square$

Let  $X, Y \in \{A, B, AB, O\}$  where  $X \neq Y$ . In the proofs of Theorems 1 and 3, we show that it is possible to preserve  $H_2$  (or  $H_3$ ) by forming a 2-cycle (X-Y)-(Y-X) as many as possible and reorganizing the remaining pairs from the initial matching. Note that to form a 2-cycle (X-Y)-(Y-X), we need to take (X-Y) and (Y-X) from some cycles or chains of the initial matching. Since there are various cycles and chains to which (X-Y) and (Y-X) initially belong, in principle, we need to show how to reorganize the remaining pairs by considering all possibilities. Our next lemma shows, however, that we do not need to check all cases.

**Lemma 2.** To show that the minimum number of chains is preserved by forming a 2-cycle (X-Y)-(Y-X) and reorganizing the remaining pairs, it is sufficient to check the case that (X-Y) belongs to a 3-cycle and (Y-X) belongs to either a 3-chain or a 3-cycle.

*Proof.* Let (X-Y) and (Y-X) be pairs that do not belong to a 2-cycle (X-Y)-(Y-X). We show that if it is not the case that (X-Y) belongs to a 3-cycle and (Y-X) belongs to either a 3-chain or a 3-cycle, then the minimum number of chains can always be preserved by forming a 2-cycle (X-Y)-(Y-X) and reorganizing the remaining pairs.

(1) Suppose that (X-Y) belongs to a 1-chain. If (Y-X) belongs to a 1-chain, forming (X-Y)-(Y-X) reduces the number of chains by two, a contradiction. If (Y-X) belongs to a 2-chain,<sup>14</sup> forming (X-Y)-(Y-X) and leaving the remaining pair as a 1-chain reduce the number of chains by one, a contradiction. If (Y-X) belongs to a 3-chain, forming (X-Y)-(Y-X) and leaving the remaining two pairs as two 1-chains preserve the same number of chains. If (Y-X) belongs to a 2-cycle, forming (X-Y)-(Y-X) and leaving the remaining pair as a 1-chain preserve the same number of chains. If (Y-X) belongs to a 3-cycle, forming (X-Y)-(Y-X) and leaving the remaining two pairs as a 2-chain preserve the same number of chains.

(2) Suppose that (X-Y) belongs to a 2-chain. If (Y-X) belongs to a 2-chain, forming (X-Y)-(Y-X) and leaving the remaining two pairs as two 1-chains preserve the same number of chains. If (Y-X)

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<sup>14</sup>Since the choice of (X-Y) is arbitrary, the proof for this case applies to the reverse case when (X-Y) belongs to a 2-chain and (Y-X) belongs to a 1-chain. Similar remarks can be made to all other cases.



belongs to the first or the last pair of a 3-chain, then the remaining two pairs of this chain form a 2-chain. If (Y-X) is the middle pair of the 3-chain, then by Remark 1, the remaining three pairs can form one 1-chain and one 2-chain. If (Y-X) belongs to a 2-cycle, forming (X-Y)-(Y-X) releases two pairs from the (X-Y)-chain and the (Y-X)-cycle. By Remark 1, these two pairs form either a 2-cycle or a 2-chain. Forming a 2-cycle reduces the number of chains by one, a contradiction. If they form a 2-chain, the same number of chains can be preserved. If (Y-X) belongs to a 3-cycle, forming (X-Y)-(Y-X) releases three pairs from the (X-Y)-chain and the (Y-X)-cycle. By Remark 1, these three pairs can form a 3-chain, which preserves the same number of chains.

(3) Suppose that (X-Y) belongs to a 3-chain. If (Y-X) belongs to a 3-chain, forming a (X-Y)-(Y-X) cycle releases four pairs from the two 3-chains. If at least one of the (X-Y) and (Y-X) is the middle pair of the 3-chain, Remark 1 applies and these four remaining pairs can form either [two 2-chains] or [one 1-chain and one 3-chain]. If both (X-Y) and (Y-X) are not the second pair in the 3-chains, then the remaining two pairs of each 3-chain can form a 2-chain. Therefore, forming a (X-Y)-(Y-X) cycle and two chains with the remaining pairs preserves the same number of chains.

(4) Suppose that (X-Y) belongs to a 2-cycle other than (X-Y)-(Y-X). If (Y-X) belongs to a 2-cycle, forming (X-Y)-(Y-X) releases two pairs from the two 2-cycles. By Remark 1, the remaining two pairs form a 2-cycle. Therefore, forming a 2-cycle (X-Y)-(Y-X) and another 2-cycle with the remaining pairs preserves the same number of chains.  $\square$

Now we are ready to prove our first main theorem.

*Proof of Theorem 1.* Choose any optimal matching with the number of chains  $H_2$  that satisfies the statement of Lemma 1 to which we refer as the initial matching. At each claim we repeat the process as many times as possible to form cycles or chains proposed. We exclude all these cycles and chains from the pool at the end of the claim and reorganize any remaining pairs in the next claim.

**Claim 1.** It is possible to preserve the same number of chains  $H_2$  by reorganizing the cycles and chains from the initial matching so that any cycle does not contain more than one pair on the short side.

*Proof.* Suppose that there is a cycle composed of two pairs on the short side, for instance, (A-O)-(B-O). By Assumption 2, there is at least one (O-A) that belongs to a chain. Suppose that (O-A) belongs to a 1-chain. Then, forming a new 2-cycle (A-O)-(O-A) and a 1-chain (B-O) preserves the same number of chains.<sup>15</sup>

Suppose that (O-A) belongs to a 2-chain. We have four pairs, (A-O), (B-O), (O-A), and the remaining pair of the (O-A)-chain. Forming a new 2-cycle (A-O)-(O-A) and a new 2-chain with (B-O) and the remaining pair of the (O-A)-chain preserves the same number of chains. Note that the donor of (B-O) can give her kidney to any other pair. If (B-O) and the remaining pair form a cycle, then it reduces the number of chains by one, a contradiction.<sup>16</sup> Note that the newly formed cycle (A-O)-(O-A) includes only one pair on the short side and it is the only new cycle formed in the process.

<sup>15</sup>Of course, by using the same argument as in the proof of Lemma 1, we need to reorganize (B-O) to be included in some cycle.

<sup>16</sup>Once again, footnote 18 applies to this chain.

Repeat this process until all (A-O)-(B-O) cycles are exhausted. A similar argument applies to any other 2-cycles composed of two pairs on the short side. ■

From now on, we assume that each cycle of our initial matching does not have more than one pair on the short side.

**Claim 2.** It is possible to preserve the same number of chains  $H_2$  by forming an additional 2-cycle (A-O)-(O-A).

*Proof.* This claim follows from Lemma 2. ■

The same argument applies to other 2-cycles (B-O)-(O-B), (AB-O)-(O-AB), (AB-A)-(A-AB), (AB-B)-(B-AB), and (A-B)-(B-A) until all pairs on the short-side and (B-A)'s are exhausted.

**Claim 3.** If there are more than one (O-O) that do not belong to the (O-O)-(O-O) cycle, then it is possible to preserve the same number of chains  $H_2$  by forming an additional 2-cycle (O-O)-(O-O).

*Proof.* This claim follows from Lemma 2. ■

We apply the same argument to (A-A), (B-B), and (AB-AB) and form 2-cycles (A-A)-(A-A), (B-B)-(B-B), and (AB-AB)-(AB-AB) until at most one of each pair remains. Note that there exist at least one of each (O-A), (O-B), (O-AB), (A-AB), (B-AB) and (A-B) and at most one of each (A-A), (B-B), (O-O) and (AB-AB) among the remaining pairs. Note that no remaining pairs can form a 2-cycle.

**Remark 2.** Let  $X, Y, Z \in \{O, A, B, AB\}$ . Suppose that we form a 2-chain with (X-Y) and (Y-Z) and check whether we can preserve the same number of chains by reorganizing these pairs in the 2-way problem. We claim that it is sufficient to consider the cases where both (X-Y) and (Y-Z) initially belong to 2-chains. If both of them belong to 1-chains, forming (X-Y)-(Y-Z) reduces the number of chains by one, a contradiction. If one of them belongs to a 1-chain and another a 2-chain, then forming (X-Y)-(Y-Z) and leaving the remaining pair as a 1-chain preserve the same number of chains. Therefore, it is sufficient to consider the case that both (X-Y) and (Y-Z) belong to 2-chains.

**Claim 4.** If there is any remaining (O-O) or (AB-AB), then it is possible to preserve the same number of chains by forming an additional 2-chain (O-O)-(O-AB) or (O-AB)-(AB-AB).

*Proof.* Since there exist at most one (O-O), at most one (AB-AB), and no pair on the short side, (O-O) and (AB-AB) cannot form a 2-cycle with any remaining pairs. Moreover, (O-AB) can form a 2-chain only with (O-O) or (AB-AB). Therefore, (O-AB) belongs to a 1-chain and the claim follows from Remark 2. ■

Since a remaining (O-AB) cannot form a 2-chain or a 2-cycle with any remaining pair in the pool, we keep it as a 1-chain. On the other hand, if either (O-O) or (AB-AB) still remains after forming 2-chains (O-O)-(O-AB) and (O-AB)-(AB-AB), then all (O-AB)'s should be exhausted. Since there is at least one (O-AB), at most one (O-O), and at most one (AB-AB), at most one of (O-O) or (AB-AB)

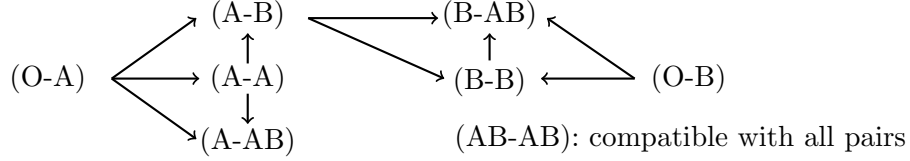


Figure 1: The compatibility relations among the remaining pairs.

remains in the pool. For simplicity of our proof, we assume that at most one  $(AB-AB)$  remains in the pool.<sup>17</sup> Figure 1 describes the compatibility relation between all the remaining pairs.

**Claim 5.** If there exist  $[(O-B) \text{ and } (B-AB)]$  or  $[(O-A) \text{ and } (A-AB)]$ , then it is possible to preserve the same number of chains  $H_2$  by forming an additional 2-chain  $(O-B)-(B-AB)$  or  $(O-A)-(A-AB)$ .

*Proof.* Suppose that there exist  $(O-B)$  and  $(B-AB)$  (other than  $(O-B)-(B-AB)$ ). By Remark 2, we only need to check the case that both of them belong to 2-chains. For  $(O-B)$ , the 2-chain must be  $(O-B)-(B-B)$  or  $(O-B)-(AB-AB)$ . For  $(B-AB)$ , the 2-chain must be  $(A-B)-(B-AB)$ ,  $(B-B)-(B-AB)$ , or  $(B-AB)-(AB-AB)$ . Since at most one  $(B-B)$  and at most one  $(AB-AB)$  remain, all possible cases are:

$$\begin{aligned} & [(O-B)-(B-B) \text{ and } (A-B)-(B-AB)], [(O-B)-(B-B) \text{ and } (B-AB)-(AB-AB)], \\ & [(O-B)-(AB-AB) \text{ and } (A-B)-(B-AB)], \text{ and } [(O-B)-(AB-AB) \text{ and } (B-B)-(B-AB)]. \end{aligned}$$

In all cases, forming a 2-chain  $(O-B)-(B-AB)$  and another 2-chain with the remaining pairs preserve the same number of chains. ■

A similar argument applies to a 2-chain  $(O-A)-(A-AB)$ . For  $(O-A)$ , the 2-chain must be  $(O-A)-(A-B)$ ,  $(O-A)-(A-A)$ , or  $(O-A)-(AB-AB)$ . For  $(A-AB)$ , the 2-chain must be either  $(A-A)-(A-AB)$  or  $(A-AB)-(AB-AB)$ . Since at most one  $(A-A)$  and at most one  $(AB-AB)$  remain, all possible cases are:

$$\begin{aligned} & [(O-A)-(A-B) \text{ and } (A-A)-(A-AB)], [(O-A)-(A-B) \text{ and } (A-AB)-(AB-AB)], \\ & [(O-A)-(A-A) \text{ and } (A-AB)-(AB-AB)], \text{ and } [(O-A)-(AB-AB) \text{ and } (A-A)-(A-AB)]. \end{aligned}$$

In all cases, forming  $(O-A)-(A-AB)$  and another 2-chain with the remaining pairs preserve the same number of chains. ■

After Claim 5, note that either one of  $[(O-B) \text{ or } (B-AB)]$  and either one of  $[(O-A) \text{ and } (A-AB)]$  are exhausted.

**Claim 6.** If there exist either  $[(O-B) \text{ and } (B-B)]$  or  $[(A-A) \text{ and } (A-AB)]$ , then it is possible to preserve the same number of chains  $H_2$  by forming an additional 2-chain  $(O-B)-(B-B)$  or  $(A-A)-(A-AB)$ .

*Proof.* Suppose that there exist  $(O-B)$  and  $(B-B)$  (other than  $(O-B)-(B-B)$ ). Since  $(O-B)$  exists, all  $(B-AB)$ 's are exhausted by Claim 5. By Remark 2, we only need to check the case that both  $(O-B)$

<sup>17</sup>A similar argument can be given if at most one  $(O-O)$  remains in the pool.

and (B-B) belong to 2-chains which must be (O-B)-(AB-AB) and (A-B)-(B-B). The same number of chains is preserved by forming two 2-chains of (O-B)-(B-B) and (A-B)-(AB-AB). Similarly, suppose that there exist (A-A) and (A-AB). Since (A-AB) exists, all (O-A)'s are exhausted by Claim 5 and the 2-chains must be (A-AB)-(AB-AB) and (A-A)-(A-B). The same number of chains is preserved by forming two 2-chains of (A-A)-(A-AB) and (A-B)-(AB-AB). ■

Let  $n_{OA}$ ,  $n_{AB}$ , and  $n_{BAB}$  be the numbers of the *remaining* (O-A), (A-B), and (B-AB), respectively.

**Claim 7.** (1) Suppose that  $n_{OA} + n_{BAB} \geq n_{AB}$  among the remaining pairs. If there exist [(O-A) and (A-A)], then it is possible to preserve the same number of chains  $H_2$  by forming a 2-chain (O-A)-(A-A). Next, if there still exist [(A-A) and (A-B)], then it is possible to preserve the same number of chains  $H_2$  by forming a 2-chain (A-A)-(A-B).

(2) Suppose that  $n_{OA} + n_{BAB} < n_{AB}$  among the remaining pairs. If there exist [(A-A) and (A-B)], then it is possible to preserve the same number of chains  $H_2$  by forming a 2-chain (A-A)-(A-B). Next, if there still exist [(A-B) and (B-B)], then it is possible to preserve the same number of chains  $H_2$  by forming a 2-chain (A-B)-(B-B).

*Proof.* (1) Suppose that  $n_{OA} + n_{BAB} \geq n_{AB}$  and [(O-A) and (A-A)] exist. Since (O-A) still exist, all (A-AB)'s are exhausted by Claim 5. By Remark 2, we only need to check the case that both (O-A) and (A-A) belong to 2-chains. For (O-A), the 2-chain must be either (O-A)-(A-B) or (O-A)-(AB-AB). For (A-A), the 2-chain must be either (A-A)-(A-B) or (A-A)-(AB-AB). Since at most one (AB-AB) remains, all possible cases are:

$$\begin{aligned} & [(O-A)-(A-B) \text{ and } (A-A)-(A-B)], [(O-A)-(A-B) \text{ and } (A-A)-(AB-AB)], \\ & \text{and } [(O-A)-(AB-AB) \text{ and } (A-A)-(A-B)]. \end{aligned}$$

In the latter two cases, forming two 2-chains (O-A)-(A-A) and (A-B)-(AB-AB) preserves the same number of chains. On the other hand, in the first case, forming (O-A)-(A-A) releases two (A-B)'s. Since  $n_{OA} + n_{BAB} \geq n_{AB}$  and (A-A)-(A-B) has one (A-B), there exists either an (O-A) that belongs to a chain other than (O-A)-(A-B) or a (B-AB) that belongs to a chain other than (A-B)-(B-AB). Denote this pair by  $p^*$ . If  $p^*$  is (O-A), then the (O-A)-chain must be either a 1-chain [(O-A)] or a 2-chain [(O-A)-(AB-AB)]. If  $p^*$  is (B-AB), then all (O-B)'s are exhausted by Claims 5 and the (B-AB)-chain must be a 1-chain [(B-AB)], a 2-chain [(B-B)-(B-AB)], or a 2-chain [(B-AB)-(AB-AB)]. In any case, it is possible to form two chains with these pairs, in addition to (O-A)-(A-A), preserving the same number of chains.

Next, suppose that [(A-A) and (A-B)] still exist. It implies that (O-A)-(A-A) is not formed in Claim 7(1) and (O-A) does not remain. Since (A-A) exists, all (A-AB)'s are exhausted by Claim 6. By Remark 2, we only need to check the case that both (A-A) and (A-B) belong to 2-chains, which must be one of

$$[(A-A)-(AB-AB) \text{ and } (A-B)-(B-B)] \text{ and } [(A-A)-(AB-AB) \text{ and } (A-B)-(B-AB)].$$

In any case, forming a 2-chain (A-A)-(A-B) and another 2-chain with the remaining pairs preserves the same number of chains.

(2) Suppose that  $n_{OA} + n_{BAB} < n_{AB}$  and that [(A-A) and (A-B)] still exist. Since (A-A) exists, all (A-AB)'s are exhausted by Claim 6. By Remark 2, we only need to check the case that both (A-A) and (A-B) pairs belong to 2-chains. For (A-A), the 2-chain must be (O-A)-(A-A) or (A-A)-(AB-AB). For (A-B), the 2-chain must be (A-B)-(B-B), (A-B)-(B-AB), (O-A)-(A-B), or (A-B)-(AB-AB). Since at most one (AB-AB) remains, all possible cases are:

$$\begin{aligned} & [(O-A)-(A-A) \text{ and } (A-B)-(B-B) ], [(O-A)-(A-A) \text{ and } (A-B)-(B-AB) ], \\ & [(O-A)-(A-A) \text{ and } (O-A)-(A-B) ], [(O-A)-(A-A) \text{ and } (A-B)-(AB-AB) ], \\ & [(A-A)-(AB-AB) \text{ and } (A-B)-(B-B) ], [(A-A)-(AB-AB) \text{ and } (A-B)-(B-AB) ], \\ & \text{and } [(A-A)-(AB-AB) \text{ and } (O-A)-(A-B) ]. \end{aligned}$$

In the last four cases, forming (A-A)-(A-B) and another 2-chain with the remaining pairs preserves the same number of chains. In the first case, forming (A-A)-(A-B) releases [(O-A) and (B-B)]. Since  $n_{OA} + n_{BAB} < n_{AB}$ , (O-A)-(A-A) has one (O-A), and (A-B)-(B-B) has one (A-B), there exists at least one (A-B) that belongs to a chain other than (O-A)-(A-B) and (A-B)-(B-AB), which must be either [(A-B)] or [(A-B)-(AB-AB)]. In any case, it is possible to form a 2-chain (A-A)-(A-B) and two additional chains with the remaining pairs, preserving the same number of chains. In the second and third cases, forming (A-A)-(A-B) releases [(O-A) and (B-AB)] or [two (O-A)'s]. Since  $n_{OA} + n_{BAB} < n_{AB}$  and (O-A)-(A-A) has one (O-A), there exist at least two (A-B)'s that belong to chains other than (O-A)-(A-B) and (A-B)-(B-AB). Since at most one (AB-AB) and at most (B-B) remain, the two (A-B)-chains must be [(A-B) and (A-B)], [(A-B) and (A-B)-(AB-AB)], [(A-B) and (A-B)-(B-B)], or [(A-B)-(B-B) and (A-B)-(AB-AB)]. If the two (A-B)'s are 1-chains [(A-B) and (A-B)], forming (A-A)-(A-B) and two 2-chains (O-A)-(A-B) reduces the number of chains by one, a contradiction. In any other cases, it is possible to form (A-A)-(A-B) and three additional chains with the remaining pairs, preserving the same number of chains.

Now, suppose that [(A-B) and (B-B)] still exist. Since (B-B) exists, all (O-B)'s are exhausted by Claim 6. By Remark 2, we only need to check the case that both (B-B) and (A-B) belong to 2-chains. For (B-B), the 2-chain must be either (B-B)-(B-AB) or (B-B)-(AB-AB). For (A-B), the 2-chain must be (O-A)-(A-B), (A-B)-(B-AB), or (A-B)-(AB-AB). Since at most one (AB-AB) remains, all possible cases are:

$$\begin{aligned} & [(B-B)-(B-AB) \text{ and } (O-A)-(A-B) ], [(B-B)-(B-AB) \text{ and } (A-B)-(B-AB) ], \\ & [(B-B)-(B-AB) \text{ and } (A-B)-(AB-AB) ], [(B-B)-(AB-AB) \text{ and } (O-A)-(A-B) ], \\ & [(B-B)-(AB-AB) \text{ and } (A-B)-(B-AB) ] \end{aligned}$$

In the last three cases, forming (A-B)-(B-B) and another 2-chain with the remaining pairs preserves the same number of chains. In the first case, forming (A-B)-(B-B) releases (O-A) and (B-AB). In the second case, forming (A-B)-(B-B) releases two (B-AB)'s. Since  $n_{OA} + n_{BAB} < n_{AB}$  and (B-B)-(B-AB) has one (B-AB), there exist at least two (A-B)'s that belong to chains other than (O-A)-(A-B) and (A-B)-(B-AB). These chains must be either [(A-B) and (A-B)] or [(A-B) and (A-B)-(AB-AB)]. If they are [(A-B) and (A-B)], forming (A-B)-(B-B) and two additional 2-chains with the remaining pairs reduces the number of chains by one, a contradiction. If they are [(A-B) and (A-B)-(AB-AB)],

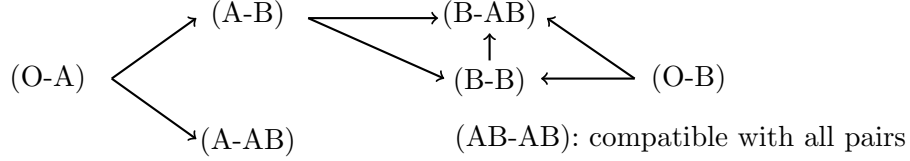


Figure 2: The compatibility relations among the remaining pairs after Claim 7.

forming (A-B)-(B-B) and two 2-chains and one 1-chain with the remaining pairs preserves the same number of chains. ■

Since by Assumption 3,  $\#(A-B) - \#(B-A) \geq 1$  or  $n_{AB} \geq 1$ , all (A-A)'s are exhausted after applying Claim 7. Figure 2 describes the compatibility relation between all the remaining pairs at this stage.

**Claim 8.** (1) If there exist [(O-A) and (A-B)], then it is possible to preserve the same number of chains  $H_2$  by forming (O-A)-(A-B). (2) Next, if there exist [(A-B) and (B-AB)], then it is possible to preserve the same number of chains  $H_2$  by forming (A-B)-(B-AB).

*Proof.* (1) Suppose that there exist [(O-A) and (A-B)]. Since (O-A) exists, all (A-AB)'s are exhausted by Claim 5. By Remark 2, we only need to check the case that both of these pairs belong to 2-chains. For (O-A), the 2-chain must be (O-A)-(AB-AB) and for (A-B), the 2-chain must be (A-B)-(B-AB), (A-B)-(B-B), or (A-B)-(AB-AB). Since at most one (AB-AB) remains, all possible cases are:

$$[(O-A)-(AB-AB) \text{ and } (A-B)-(B-AB)] \text{ and } [(O-A)-(AB-AB) \text{ and } (A-B)-(B-B)].$$

In any case, forming (O-A)-(A-B) and another 2-chain with the remaining pairs preserves the same number of chains.

(2) Suppose that there exist [(A-B) and (B-AB)]. By Claim 8(1), all (O-A)'s are exhausted. Since (B-AB) exists, all (O-B)'s are exhausted by Claim 5. By Remark 2, we only need to check the case that both of these pairs belong to 2-chains. For (A-B), the 2-chain must be either (A-B)-(B-B) or (A-B)-(AB-AB) and for (B-AB), the 2-chain must be either (B-B)-(B-AB) or (B-AB)-(AB-AB). Since at most one (B-B) and at most one (AB-AB) remain, all possible cases are:

$$[(A-B)-(B-B) \text{ and } (B-AB)-(AB-AB)] \text{ and } [(A-B)-(AB-AB) \text{ and } (B-B)-(B-AB)].$$

In any case, forming (A-B)-(B-AB) and another 2-chain (B-B)-(AB-AB) preserves the same number of chains. ■

Note that the only 2-chains possibly formed after this stage are (B-B)-(B-AB) and (A-B)-(B-B) together with a chain involved with (AB-AB).

**Claim 9.** If there exist [(A-B) and (B-B)] or [(B-B) and (B-AB)], then it is possible to preserve the same number of chains  $H_2$  by forming an additional 2-chain (A-B)-(B-B) or (B-B)-(B-AB).

*Proof.* Once again, by Remark 2, we only need to consider the case that these pairs belong to 2-chains. Suppose that [(A-B) and (B-B)] pairs exist. Since (A-B) exists, all (O-A)'s and (B-AB)'s are exhausted by Claim 8. Since (B-B) exists, all (O-B)'s are exhausted by Claim 6. Note that (A-B) and (B-B) can form a 2-chain only with (AB-AB), but at most one (AB-AB) remains. Next, suppose that [(B-B) and (B-AB)] exist. Since (B-AB) exists, all (O-B)'s and (A-B)'s are exhausted by Claims 5 and 8. Therefore, (B-B) and (B-AB) can form a 2-chain only with (AB-AB), but at most one (AB-AB) remains. ■

If (AB-AB) does not exist, then all the remaining pairs can form 1-chains only. If an (AB-AB) still remains, then it is compatible with any remaining pair. Therefore, either (AB-AB) belongs to a 2-chain at the initial matching or (AB-AB) is the only remaining pair, completing the proof. □

Next we prove our second main theorem.

*Proof of Theorem 3.* Choose any optimal matching that satisfies the statement of Lemma 1 with the number of chains  $H_3$  to which we refer as the initial matching. At each claim we repeat the process as many times as possible to form cycles or chains proposed. We exclude all these cycles and chains from the pool at the end of the claim and reorganize any remaining pairs in the next claim.

**Claim 10.** It is possible to preserve the same number of chains  $H_3$  by (1) forming 2-cycles (O-O)-(O-O) as many as possible when  $\#(\text{O-O})$  is even and (2) forming one 3-cycle (O-O)-(O-O)-(O-O) and 2-cycles (O-O)-(O-O) as many as possible when  $\#(\text{O-O})$  is odd.

*Proof.* Suppose that there are two (O-O)'s. By Lemma 2, we only need to consider the case that one (O-O) belongs to a 3-cycle and another (O-O) belongs to either a 3-cycle or a 3-chain. Note that for the 3-cycle with the first (O-O), the remaining two pairs of the (O-O)-cycle form a 2-cycle. Let  $C^*$  be this 2-cycle.

(1) Suppose that another (O-O) belongs to a 3-chain. By Lemma 1, the first pair of the (O-O)-chain should be (O-O) and the remaining pairs of the (O-O)-chain can form a 2-chain. Therefore, forming (O-O)-(O-O), the 2-cycle  $C^*$ , and a 2-chain with the remaining pairs of the (O-O)-chain preserves the same number of chains.

(2) Suppose that another (O-O) belongs to a 3-cycle. Since the remaining two pairs of this (O-O)-cycle can form a 2-cycle, forming (O-O)-(O-O), the 2-cycle  $C^*$ , and another 2-cycle with the remaining pairs of the second (O-O)-cycle preserves the same number of chains.

If  $\#(\text{O-O})$  is even, then we are done. If  $\#(\text{O-O})$  is odd, then we keep one remaining (O-O) as 1-chain (which increases the number of chains above the minimum by one). Obviously, we can make the (O-O) as a 1-chain without affecting other cycles or chains when it belongs to a 2-chain, a 3-chain, or a 3-cycle. Note that the (O-O) cannot be a 1-chain, since it will reduce the number of chains below the minimum. Now suppose that the (O-O) belongs to a 2-cycle. Then, the other pair of this (O-O)-cycle is (A-O), (B-O), or (AB-O), which we denote by (X-O). By Assumption 2, there is at least one (O-X) that belongs to a chain. If (O-X) belongs to a 1-chain, then forming (X-O)-(O-X) and keeping (O-O) as a 1-chain do not change the number of chains, a contradiction. If (O-X) belongs to a 2-or 3-chain, then by Lemma 1, the (O-X) should be the first pair of the (O-X)-chain and the

remaining pair(s) forms a chain. Therefore, forming (O-X)-(X-O), a chain with the remaining pair(s) of the (O-X)-chain, and the 1-chain (O-O) increases the number of chains by one. Finally, if  $\#(\text{O-O}) > 1$ , then this (O-O) is used to make (O-O)-(O-O)-(O-O). On the other hand, if  $\#(\text{O-O}) = 1$ , then this (O-O) is used to make a chain with (O-AB) at Step 2. In any case, the number of chains decreases by one, keeping the minimum. ■

We apply a similar argument to (A-A), (B-B), and (AB-AB) and form 2- and 3-cycles until all these pairs are exhausted. However, if the pool begins with one (O-O), one (A-A), one (B-B), or one (AB-AB), then these pairs remain as 1-chains.

**Claim 11.** It is possible to preserve the same number of chains  $H_3$  by reorganizing the cycles and chains of the initial matching so that any cycle does not contain more than one pair on the short side.

*Proof.* The proof is divide into three cases.

**Case 1.** A 2-cycle composed of two pairs on the short side. for instance, (A-O)-(AB-A). By Assumption 2, there are at least one (O-A) and at least one (A-AB) that belong to some chains. By Lemma 1, (O-A) should be the first pair in the (O-A)-chain and (A-AB) should be the last pair in the (A-AB)-chain. Therefore, even though either one of these chains is a 3-chain, the remaining pairs of the 3-chain can form a 2-chain. Forming two 2-cycles of (A-O)-(O-A) and (AB-A)-(A-AB) and two chains with the remaining pairs preserves the same number of chains.<sup>18</sup>

**Case 2.** A 3-cycle composed of exactly two pairs on the short side.

Case 2.1. Suppose that the two pairs on the short side are of the same type, for instance, (A-O)-(A-O)-(X-Y). Since (A-O)-(X-Y) is a 2-cycle, it is sufficient to consider how to reorganize (A-O). By Assumption 2, there is at least one (O-A) that belongs to some chain. By Lemma 1, this (O-A) must be the first pair of the (O-A)-chain and the remaining pair(s) of the (O-A)-chain can be kept as one chain. Altogether, forming two 2-cycles (A-O)-(X-Y) and (A-O)-(O-A) and a chain with the remaining pair(s) preserves the same number of chains.

From now on, we assume that the two pairs on the short side are of different types.

Case 2.2. We begin with a 3-cycle with (AB-O) which must be either (X-Y)-(AB-O)-(Z-W) or (AB-O)-(X-Y)-(Z-W) where (X-Y) is a pair on the short side different from (AB-O) and (Z-W) is not a pair on the short side. By Assumption 2, there exists an (O-AB) that belongs to a chain, which has to be a 1-chain by Lemma 1. Similarly, by Assumption 2, there exists a long-side pair (Y-X) that belongs to a chain. By Lemma 1, it has to be the first or the last pair of the chain, and therefore, the remaining pair(s) of the chain can form one chain even though (Y-X) is removed. Altogether, forming (AB-O)-(O-AB), (X-Y)-(Y-X), one 1-chain (Z-W), and another chain with the remaining pair(s) of (Y-X)-chain preserves the same number of chains.

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<sup>18</sup>Suppose that the two pairs are of the same type, for instance, (A-O)-(A-O), and less than two (O-A)'s belong to a chain which implies that all other (O-A)'s belong to cycles. Since there are two (A-O)'s from (A-O)-(A-O), forming an additional (A-O)-(O-A) and a chain with (A-O) and the remaining pair(s) of the (O-A)-chain preserves the number of chains. This matching is optimal but all (O-A)'s belong to cycles, a violation of Assumption 2.



Case 2.3. We consider a 3-cycle of the form  $(AB-X)-(X-O)-(Y-Z)$  where  $X = A$  or  $B$  and  $(Y-Z)$  is not a pair on the short side. Suppose that  $(Y-Z)$  is  $(X-AB)$  or  $(O-X)$ . Since  $(AB-X)-(X-AB)$  or  $(X-O)-(O-X)$  is a 2-cycle, it is sufficient to show how to reorganize a remaining pair  $(X-O)$  or  $(AB-X)$  by using the same argument as in Case 2.1.

Next, suppose that  $(Y-Z)$  is neither  $(X-AB)$  nor  $(O-X)$ . By Assumption 2, there exist at least one  $(X-AB)$  and at least one  $(O-X)$  that belong to some chains. By Lemma 1,  $(X-AB)$  must be the last pair of the  $(X-AB)$ -chain and  $(O-X)$  must be the first pair of the  $(O-X)$ -chain. Note that these long-side pairs share the same type  $X$ , so that the donor of the pair preceding  $(X-AB)$  in the  $(X-AB)$ -chain is compatible with the patient of the pair following  $(O-X)$  in the  $(O-X)$ -chain. If both the  $(X-AB)$ -chain and the  $(O-X)$ -chain are 3-chains, then they must be  $[(O-W)-(W-X)-(X-AB)$  and  $(O-X)-(X-W)-(W-AB)]$  where  $X, W \in \{A, B\}$  and  $X \neq W$ . Therefore, forming  $(AB-X)-(X-AB)$ ,  $(X-O)-(O-X)$ ,  $(X-W)-(W-X)$ , one 2-chain  $(O-W)-(W-AB)$ , and one 1-chain  $(Y-Z)$  preserves the same number of chains. If at least one of the two chains is not a 3-chain, then the remaining pairs of the  $(X-AB)$ -chain and the  $(O-X)$ -chain can form one chain. Therefore, forming  $(AB-X)-(X-AB)$ ,  $(X-O)-(O-X)$ , one 1-chain  $(Y-Z)$ , and another chain with the remaining pairs preserves the same number of chains.

A similar argument applies when  $(AB-X)-(X-Y)-(Y-O)$  where  $X, Y \in \{A, B\}$ ,  $X \neq Y$ , and  $(X-Y)$  is not a pair on the short side.

Case 2.4. Lastly, we consider a 3-cycle composed of  $(A-O)$ ,  $(B-O)$ , and  $(X-Y)$  where  $(X-Y)$  is not a pair on the short side, which must be one of the following:  $(A-O)-(B-O)-(O-A)$ ,  $(A-O)-(B-O)-(B-A)$ ,  $(B-O)-(A-O)-(O-B)$ , and  $(B-O)-(A-O)-(A-B)$ . Note that each 3-cycle has a 2-cycle,  $(A-O)-(O-A)$ ,  $(A-O)-(B-A)$ ,  $(B-O)-(O-B)$ , and  $(B-O)-(A-B)$ . Therefore, it is sufficient to show how to reorganize a remaining pair by using the same argument as in Case 2.1. A similar argument applies to a 3-cycle composed of  $(AB-A)$ ,  $(AB-B)$ , and  $(X-Y)$  where  $(X-Y)$  is not a pair on the short side.

**Case 3.** A 3-cycle composed of three pairs on the short side. Note that this 3-cycle can be decomposed into a 2-cycle and a 1-chain. The 2-cycle can be handled by Case 1 and the remaining 1-chain can be reorganized by using the same argument as in Case 2.1. ■

**Claim 12.** If there exist  $[(AB-O)$  and  $(O-AB)]$ , then it is possible to preserve the same number of chains  $H_3$  by forming an additional 2-cycle  $(AB-O)-(O-AB)$ .

*Proof.* By Lemma 1, each  $(AB-O)$  belongs to a cycle. Suppose that there is an  $(AB-O)$  that belongs to a cycle other than  $(AB-O)-(O-AB)$ . By Assumption 2, there is at least one  $(O-AB)$  that does not belong to an  $(AB-O)-(O-AB)$  cycle. By Lemma 2, we only need to consider the case that  $(AB-O)$  belongs to a 3-cycle and  $(O-AB)$  belongs to a 3-cycle or a 3-chain. Note that if  $(O-AB)$  belongs to a chain, then by Lemma 1, it must be a 1-chain. On the other hand, if  $(O-AB)$  belongs to a cycle other than  $(AB-O)-(O-AB)$ , then it must be a 3-cycle of the form  $(X-O)-(O-AB)-(AB-Y)$  where  $X \in \{A, B, AB\}$  and  $Y \in \{A, B, O\}$ . Since both  $(X-O)$  and  $(AB-Y)$  are on the short side, it contradicts to Claim 11. ■

**Claim 13.** If there exist [(A-O) and (O-A)] or [(B-O) and (O-B)], then it is possible to preserve the same number of chains  $H_3$  by forming an additional 2-cycle (A-O)-(O-A) or (B-O)-(O-B).

*Proof.* By Lemma 1, each (A-O) belongs to a cycle. Suppose that there is an (A-O) that belongs to a cycle other than (A-O)-(O-A). By Assumption 2, there is at least one (O-A) that does not belong to the (A-O)-(O-A) cycle. By Lemma 2, we only need to consider the case that (A-O) belongs to a 3-cycle and (O-A) belongs to a 3-cycle or a 3-chain. By Claim 11, the (A-O)-cycle can include only one pair on the short side, and therefore, it must be either (A-O)-(A-B)-(B-A) or (A-O)-(O-B)-(B-A). Since the remaining two pairs of (A-O)-(A-B)-(B-A) can form a 2-cycle, we only consider (A-O)-(O-B)-(B-A).

(1) Suppose that (O-A) belongs to a 3-chain. By Lemma 1, (O-A) must be the first pair in the (O-A)-chain, which must be either (O-A)-(A-B)-(B-A) or (O-A)-(A-B)-(B-AB). Since the remaining two pairs of (O-A)-(A-B)-(B-A) can form a 2-cycle, we only consider (O-A)-(A-B)-(B-AB). By forming two 2-cycles (A-O)-(O-A) and (B-A)-(A-B) and a 2-chain (O-B)-(B-AB), the same number of chains is preserved.

(2) Suppose that (O-A) belongs to a 3-cycle, which must be (O-A)-(A-B)-(B-O). By forming three 2-cycles (A-O)-(O-A), (B-O)-(O-B), and (B-A)-(A-B), the same number of chains is preserved.

A similar argument can be developed for (B-O)-(O-B). ■

**Claim 14.** If there exist [(AB-A) and (A-AB)] or [(AB-B) and (B-AB)], then it is possible to preserve the same number of chains  $H_3$  by forming an additional 2-cycle (AB-A)-(A-AB) or (AB-B)-(B-AB).

*Proof.* By Lemma 1, each (AB-A) belongs to a cycle. Suppose that there is an (AB-A) that belongs to a cycle other than (AB-A)-(A-AB). By Lemma 2, we only need to consider the case that (AB-A) belongs to a 3-cycle and (A-AB) belongs to a 3-cycle or a 3-chain. By Claim 11, the (AB-A)-cycle can include only one pair on the short side, and therefore, it must be either (AB-A)-(A-B)-(B-A) or (AB-A)-(A-B)-(B-AB). Since the remaining two pairs of (AB-A)-(A-B)-(B-A) can form a 2-cycle, we only consider (AB-A)-(A-B)-(B-AB).

(1) Suppose that (A-AB) belongs to a 3-chain. By Lemma 1, (A-AB) must be the last pair in the (A-AB)-chain, which must be either (A-B)-(B-A)-(A-AB) or (O-B)-(B-A)-(A-AB). Since the remaining two pairs of (A-B)-(B-A)-(A-AB) can form a 2-cycle, we only consider (O-B)-(B-A)-(A-AB). After forming (AB-A)-(A-AB), the remaining pairs (A-B), (B-AB), (O-B), and (B-A), can form a 2-cycle (B-A)-(A-B) and a 2-chain (O-B)-(B-AB), which preserves the same number of chains.

(2) Suppose that (A-AB) belongs to a 3-cycle, which must be (A-AB)-(AB-B)-(B-A). Forming three 2-cycles, (AB-A)-(A-AB), (B-A)-(A-B), and (B-AB)-(AB-B), preserves the same number of chains.

A similar argument can be developed for (AB-B)-(B-AB). ■

Note that by Claims 10, all pairs with the same patient-donor type are exhausted from the pool. Also, by Claims 12 to 14 and by Assumption 2, no pair on the short side remains in the pool.

**Claim 15.** If there exist [(B-A) and (A-B)], then it is possible to preserve the same number of chains  $H_3$  after forming an additional 2-cycle (B-A)-(A-B).

*Proof.* By Lemma 2, it is enough to show that both (B-A) and (A-B) cannot belong to a 3-cycle. In fact, it is not difficult to check that neither (B-A) nor (A-B) can form a 3-cycle with the remaining pairs. ■

By Assumption 3, all (B-A)'s are exhausted at this stage. Therefore, the only remaining pairs are (O-A), (O-B), (O-AB), (A-AB), (B-AB), and (A-B).

**Claim 16.** If there exist [(O-A) and (A-AB) ] or [(O-B)-(B-AB) ], then it is possible to preserve the same number of chains  $H_3$  after forming an additional 2-chain (O-A)-(A-AB) or (O-B)-(B-AB).

*Proof.* Suppose that there exist (O-A) and (A-AB). For (O-A), the chain must be a 1-chain (O-A), 2-chain (O-A)-(A-B), or 3-chain (O-A)-(A-B)-(B-AB). For (A-AB), the chain must be a 1-chain (A-AB). Therefore, all possible cases are:

$$[(O-A) \text{ and } (A-AB) ], [(O-A)-(A-B) \text{ and } (A-AB) ], \text{ and } [(O-A)-(A-B)-(B-AB) \text{ and } (A-AB) ]$$

In the first case, forming (O-A)-(A-AB) reduces the number of chains by one, a contradiction. In the second and the third cases, forming (O-A)-(A-AB) and a chain with the remaining pair(s) preserves the same number of chains. A similar argument can be developed for (O-B)-(B-AB). ■

Now suppose that a 2-chain (O-A)-(A-AB) is formed and (A-A) remains as a 1-chain. Then, it is possible to form a 3-chain (O-A)-(A-A)-(A-AB) which reduces the number of chains by one, as explained when (A-A) is obtained after Claim 10. A similar observation can be made for a 3-chain (O-B)-(B-B)-(B-AB).

**Claim 17.** If there exist [(O-A), (A-B), and (B-AB) ], then it is possible to preserve the same number of chains  $H_3$  after forming an additional 3-chain (O-A)-(A-B)-(B-AB) and reorganizing the remaining pairs.

*Proof.* Suppose that there exist (O-A), (A-B), and (B-AB). By Claim 16, all (A-AB)'s and (O-B)'s are exhausted. Therefore, (O-A) must belong to a 1-chain or a 2-chain (O-A)-(A-B), (A-B) must belong to a 1-chain or a 2-chain (O-A)-(A-B) or (A-B)-(B-AB), and (B-AB) must belong to a 1-chain or 2-chain (A-B)-(B-AB). In each case, we end up with the desired conclusion either by obtaining a contradiction to the assumption that the initial matching is optimal, or by forming a 3-chain (O-A)-(A-B)-(B-AB) and two additional chains with the remaining pairs which preserves the same number of chains. ■

**Claim 18.** If there exist [(O-A) and (A-B) ], then it is possible to preserve the same number of chains  $H_3$  after forming an additional 2-chain (O-A)-(A-B).

*Proof.* Suppose that there exist (O-A) and (A-B). By Claims 16 and 17, all (A-AB)'s and (B-AB)'s are exhausted and (O-A) and (A-B) must be 1-chains. Therefore, forming a 2-chain (O-A)-(A-B) reduces the number of chains by one, a contradiction. ■

**Claim 19.** If there exist [(A-B) and (B-AB) ], then it is possible to preserve the same number of chains  $H_3$  after forming an additional 2-chain (A-B)-(B-AB).

*Proof.* Suppose that there exist (A-B) and (B-AB). By Claims 16 and 17, since all (O-B)'s and (O-A)'s are exhausted, (A-B) and (B-AB) must be 1-chains. Therefore, forming a 2-chain (A-B)-(B-AB) reduces the number of chains by one, a contradiction. ■

The number of chains formed by the 3-way minimum chains algorithm is exactly  $H_3$ , which is the smallest number of chains among all 3-way algorithms. □

*Proof of Proposition 1.* Choose an optimal matching without any restriction on the size of exchanges to which we refer as the initial matching. Let  $H_0$  be the corresponding number of chains. For each  $X, Y \in \{O, A, B, AB\}$ , (X-Y)-cycle (or (X-Y)-chain) means the cycle (or the chain) to which (X-Y) belongs before the reorganization begins.

**Lemma 3.** It is possible to preserve the number of chains at  $H_0$  by reorganizing the cycles and chains of the initial matching so that no chain includes any pair on the short side.

*Proof.* Suppose that there is a chain including a pair on the short side at the initial matching, for instance (A-O). By Assumption 2, there exists an (O-A) that belongs to a chain. We show that it is possible to reorganize the initial matching so that no chain includes any pair on the short side.

(1) Suppose that (A-O) is the first pair of the (A-O)-chain. If (O-A) is either the first or the last pair of the (O-A)-chain, then the remaining pairs of the (O-A)-chain and the (A-O)-chain can form two chains by themselves. If (O-A) is a middle pair of the (O-A)-chain, then by Remark 1, the pairs ahead of the (O-A) can form a chain with the remaining pairs of the (A-O)-chain. The pairs behind the (O-A) form a chain by themselves. Forming (A-O)-(O-A) and the two chains preserves the same number of chains. A similar argument applies if (A-O) is the last pair of the (A-O)-chain.

(2) Suppose that (A-O) is a middle pair of the (A-O)-chain. The proof is obvious if (O-A) is either the first or the last pair of the (O-A)-chain. If (O-A) is a middle pair in the (O-A)-chain, once again, by Remark 1, the pairs behind the (O-A) and the pairs ahead of the (A-O) can form a chain. Also, the pairs ahead of the (O-A) and the pairs behind the (A-O) can form a chain. Altogether, forming (A-O)-(O-A) and two chains with the remaining pairs preserves the same number of chains.

A similar argument can be developed for all other pairs on the short-side so that no chain includes any short-side pair. □

Choose any optimal matching that satisfies the statement of Lemma 3 with the number of chains  $H_0$  to which we refer as the initial matching. At each claim, we repeat the process as many times as possible to form cycles or chains proposed. We exclude these cycles and chains from the pool at the end of the claim and reorganize the remaining pairs in the next claim.

**Claim 20.** Suppose that  $X \in \{O, A, B, AB\}$ . It is possible to preserve the same number of chains  $H_0$  by (1) forming 2-cycles (X-X)-(X-X) as many as possible when  $\#(X-X)$  is even and (2) forming one 3-cycle (X-X)-(X-X)-(X-X) and 2-cycles (X-X)-(X-X) as many as possible when  $\#(X-X)$  is odd.

*Proof.* Suppose that there exist two (X-X)'s. If a (X-X) belongs to a cycle greater than size 2, then the remaining pairs of the cycle can form a cycle. If a (X-X) belongs to a chain, then there are two cases. If the pair is the first or the last pair of the chain, then the remaining pairs can still form

a chain without the (X-X). If the pair is neither the first nor the last pair of the chain, then the pairs ahead of the (X-X) and the pairs behind the (X-X) can form a chain. Therefore, by forming (X-X)-(X-X) and keeping the other pairs in chains or cycles, the same number of chains is preserved. If there exists one (X-X) pair after forming (X-X)-(X-X) as many as possible, we can form a 3-cycle (X-X)-(X-X)-(X-X) by combining the remaining (X-X) and an (X-X)-(X-X). If  $\#(X-X) = 1$ , then we apply the same argument as in Claim 10.  $\square$

After applying Claim 20, all (O-O), (A-A), (B-B), (AB-AB) pairs are excluded from the pool.

**Claim 21.** Suppose that  $X, Y \in \{O, A, B, AB\}$  and  $X \neq Y$ . If there exist [(X-Y) and (Y-X)], then it is possible to preserve the same number of chains  $H_0$  by forming an additional 2-cycle (X-Y)-(Y-X).

*Proof.* Suppose that there exist (X-Y) and (Y-X) pairs in the pool. The proof is divided into 5 cases.

(1) Suppose that (X-Y) and (Y-X) belong to two different cycles. By Remark 1, the remaining pairs can form one cycle jointly. Therefore, forming (X-Y)-(Y-X) and another cycle with the remaining pairs preserves the same number of chains.

(2) Suppose that (X-Y) belongs to a cycle, but (Y-X) belongs to a chain. By Remark 1, the pairs ahead of the (X-Y) can form a chain with the pairs behind the (Y-X). Similarly, the pairs behind the (X-Y) can form a chain with the pairs ahead of the (Y-X). Altogether, forming (X-Y)-(Y-X) and a chain with the remaining pairs preserves the same number of chains.

(3) Suppose that (X-Y) and (Y-X) belong to two different chains. By Lemma 3, (X-Y) should be either (A-B) or (B-A). By Remark 1, the pairs ahead of the (X-Y) can form a chain with the pairs behind the (Y-X). Also, the pairs behind the (X-Y) can form a chain with the pairs ahead of the (Y-X). If the (X-Y) or the (Y-X) is either the first or the last pair of the chain, then the remaining pairs can form a chain. Altogether, forming (X-Y)-(Y-X) and the two chains with the remaining pairs preserves the same number of chains.

(4) Suppose that (X-Y) and (Y-X) belong to the same cycle. If there are more than one pair between (X-Y) and (Y-X), then these pairs can form a cycle. If there is only one pair between (X-Y) and (Y-X), then it must be a pair on the short side because no (X-X)-type pair remains in the pool. Denote this short-side pair by (Z-W). By Assumption 2, there exists a (W-Z) in a chain. By Lemma 3, this (W-Z) should be either the first pair or the last pair of the chain and therefore, the remaining pairs of the chain can form a chain without (Z-W). Altogether, forming (X-Y)-(Y-X), (Z-W)-(W-Z), and a chain with the remaining pairs of the (Z-W)-chain (if applicable), and any additional cycles (if any) preserves the same number of chains.

(5) Suppose that (X-Y) and (Y-X) belong to the same chain. By Lemma 3, again, (X-Y) should be either (A-B) or (B-A). If there is only one pair between (X-Y) and (Y-X), then the pair should be a pair on the short side, which is infeasible by Lemma 3. If there are more than one pairs between (X-Y) and (Y-X) pairs, then these pairs can form a cycle. Lastly, the pairs that are not located between (X-Y) and (Y-X) in the chain can form a chain. Altogether, the same number of chains is preserved.  $\square$

The remaining pairs after applying Claim 21 are (O-A), (O-B), (O-AB), (A-B), (A-AB), and (B-AB). Then, Claims 16 to 19 apply to complete the proof. This process of reorganizing the pairs exactly

describes the 3-way minimum chains algorithm defined in Section 3.2. Therefore, we obtain  $H_0 = H_3$  and Proposition 1.

## Appendix B. Integer Programming Formulation

In this appendix, we use integer programming (IP) to compute the minimum number of chains (or incompatible transplants) in an exchange pool when a patient may have a positive crossmatch with another pair's donor according to the patient's PRA type. Even if the patient is ABO-compatible with the other pair's donor, if a positive crossmatch occurs between them, the patient cannot receive a kidney transplant from the donor without using immunosuppressants. Because we consider additional incompatibility constraints in IP formulations, their results cannot be smaller than those predicted by the formulae in Section 4. In other words, the minimum numbers of incompatible transplants predicted by the formulae can be viewed as lower bounds of incompatible transplants in more realistic situations. We want to check whether these lower bounds are good approximations for the minimum numbers of incompatible transplants.

We use the same pools generated for the computation in Section 4 but additionally consider ABO compatibility and positive crossmatch between two distinct pairs to generate a compatibility matrix  $[c_{ij}]$  for each pool. We determine the compatibility between the patient of pair  $i$  and the donor of pair  $j$  as follows: First, determine ABO compatibility between patient  $i$  and donor  $j$ , according to their ABO blood types. Second, determine whether patient  $i$  has a positive crossmatch with donor  $j$ , according to the patient's PRA type. If patient  $i$  has a low, medium, or high PRA type, patient  $i$  has a positive crossmatch with donor  $j$  with probability 5%, 45%, or 90%, respectively. Finally, if patient  $i$  is ABO-compatible with donor  $j$ , and if patient  $i$  has no positive crossmatch with donor  $j$ , let  $c_{ij} = 1$ . Otherwise, let  $c_{ij} = 0$ .

Let  $N$  denote the set of patient-donor pairs. Let  $c_{ij} = 1$  if patient  $i$  is ABO-compatible with donor  $j$ , and has no positive crossmatch. Otherwise, let  $c_{ij} = 0$ . Let  $x_{ij} = 1$  if patient  $i$  receives a transplant from donor  $j$  and let  $x_{ij} = 0$  otherwise. Let  $x = (x_{ij})_{i,j \in N}$ . Let  $k$  be a positive integer with  $k \leq |N|$ . Each cycle or chain can consist of at most  $k$  pairs.

To compute the minimum number of 1-chains, we modify the IP formulation in Roth et al. (2007, p.849) as follows:

$$\begin{aligned} \min_x |N| - \sum_{i,j \in N} x_{ij} \quad \text{s.t.} \quad & (1) \ x_{ij} \in \{0, 1\}, \ \forall i, j \in N; \\ & (2) \ x_{ij} \leq c_{ij}, \ \forall i, j \in N; \\ & (3) \ \sum_{j \in N} x_{ij} \leq 1, \ \forall i \in N; \\ & (4) \ \sum_{j \in N} x_{ij} = \sum_{j \in N} x_{ji}, \ \forall i \in N; \\ & (5) \ x_{i_1 i_2} + x_{i_2 i_3} + \cdots + x_{i_k i_{k+1}} \leq k - 1, \ \forall \{i_1, i_2, \dots, i_k, i_{k+1}\} \subseteq N. \end{aligned}$$

The objective function minimizes the total number of 1-chains, i.e., pairs left after all feasible cycles are formed. Constraints (2) require that patient  $i$  receive a transplant from donor  $j$  only when patient  $i$  is compatible with donor  $j$ . Constraints (3) require that patient  $i$  receive at most one transplant. Constraints (4) require that patient  $i$  receive a transplant only when a patient receives a transplant from donor  $i$ . Constraints (5) require that each cycle consist of at most  $k$  pairs.

	(1) 2-cycles and 1-chains	(2) All cycles and 1-chains	(3) 2-cycles, 2- and 1-chains	(4) All cycles and all chains
25	16.664 (2.904)	14.676 (3.293)	10.584 (2.186)	10.108 (2.330)
50	28.468 (4.356)	23.426 (4.941)	17.666 (3.325)	16.940 (3.525)
100	49.964 (6.970)	40.796 (7.215)	31.452 (5.117)	30.572 (5.463)

**Table B.1.** Integer programming: Average numbers of incompatible transplants in Korea (standard errors in parentheses)

We build IP formulations for kidney exchange models with immunosuppressants, or suppressants, for short. Let  $s_i = 1$  if patient  $i$  uses suppressants and let  $s_i = 0$  otherwise. Let  $s = (s_i)_{i \in N}$ .

Given that every patient receives a transplant, we want to minimize the total number of patients who use suppressants as follows:

$$\min_s \sum_{i \in N} s_i \quad \text{s.t.} \quad \begin{aligned} (1) & \quad x_{ij} \in \{0, 1\}, \quad \forall i, j \in N; \\ (2) & \quad s_i \in \{0, 1\}, \quad \forall i \in N; \\ (3) & \quad x_{ij} \leq c_{ij} + s_i, \quad \forall i, j \in N; \\ (4) & \quad \sum_{j \in N} x_{ij} = 1, \quad \forall i \in N; \\ (5) & \quad \sum_{i \in N} x_{ij} = 1, \quad \forall j \in N; \\ (6) & \quad x_{i_1 i_2} + x_{i_2 i_3} + \dots + x_{i_k i_{k+1}} \leq k - 1, \quad \forall \{i_1, i_2, \dots, i_k, i_{k+1}\} \subseteq N. \end{aligned}$$

Constraints (3) require that patient  $i$  receive a transplant from donor  $j$  only when patient  $i$  is compatible with donor  $j$  or when patient  $i$  uses suppressants. Constraints (4) require that each patient  $i$  receive one transplant. Constraints (5) require that each donor  $j$  give a kidney to one patient. Constraints (6) require that each cycle or chain consist of at most  $k$  pairs.

Tables B.1 and B.2 show average numbers of incompatible transplants in Korea and in the United States, respectively, based on the integer programming formulations. In each table, Column (1) shows the average minimum numbers of 1-chains when only 2-cycles are feasible. Column (2) shows the average minimum numbers of 1-chains when all cycles are feasible. Column (3) shows the average minimum numbers of 2- and 1-chains when only 2-cycles are feasible. Column (4) shows the average minimum numbers of all chains when all cycles are feasible.

By comparing the results in Table B.1 with those in Table 5, for the case in Korea, we find that our 2-way formula can provide good (lower bound) approximations for the minimum numbers of incompatible transplants. In Column (4) of Table 5, when the size of a pool is 100, our 2-way formula predicts that the average minimum number of incompatible transplants is about 30.576. In Column (3) of Table B.1, given the same pool size, the integer programming formulation predicts the average minimum number to be about 31.452.

By comparing Column (3) of Table B.2 with Column (4) of Table 6, for the case in the United States when the pool size is 100, we also find that our 2-way formula can provide good lower bounds.

	(1) 2-cycles and 1-chains	(2) All cycles and 1-chains	(3) 2-cycles, 2- and 1-chains	(4) All cycles and all chains
25	17.964 (2.894)	15.428 (3.486)	11.458 (2.217)	10.938 (2.455)
50	29.912 (4.975)	23.758 (5.223)	19.968 (4.080)	19.160 (4.347)
100	51.792 (7.317)	41.070 (7.500)	36.958 (6.394)	36.132 (6.617)

**Table B.2.** Integer programming: Average numbers of incompatible transplants in U.S. (standard errors in parentheses)

Our 2-way formula predicts the average minimum number of incompatible transplants to be about 35.858 and the integer programming formulation predicts it to be about 36.958.

### Appendix C. Simulations under Assumption 3

In this appendix, for each pool size, we randomly generate 500 pools according to the frequencies of patient-donor characteristics in Korea and in the United States, as shown in Tables 3 and 4, when each pool satisfies Assumption 3, which requires that  $\#(A-B) > \#(B-A)$ . We then use the formulae or integer programming to compute the minimum number of chains (or incompatible transplants) for each pool. Tables C.1 and C.2 present average minimum numbers of incompatible transplants based on the formulae of Roth et al. (2007) and our minimum chains algorithms in Korea, and in the United States, respectively. Tables C.3 and C.4 show changes in average minimum numbers of incompatible transplants when each short-side pair is removed from a Korean pool, or from a U.S. pool. Tables C.5 and C.6 present average minimum numbers of incompatible transplants based on the integer programming formulations in Korea, and in the United States, respectively.

First of all, whether we require pools to satisfy Assumption 3 does not appear to change the overall results (i.e., average numbers of incompatible transplants based on the formulae) in Tables C.1 and C.2, as compared with those in Tables 5 and 6. Neither it qualitatively affects the results (i.e., average numbers of incompatible transplants based on the integer programming formulations) in Tables C.5 and C.6, as compared with those in Tables B.1 and B.2.

Secondly, regardless of whether we require pools to satisfy Assumption 3, our 2-way formula appears to provide good lower bounds. When each pool consists of 100 pairs in Korea, our 2-way formula predicts the average minimum number of incompatible transplants to be about 30.512, as in Column (4) of Table C.1. The integer programming formulation predicts it to be about 31.426, as in Column (3) of Table C.5. When each pool consists of 100 pairs in the United States, our 2-way formula predicts the average minimum number of incompatible transplants to be about 36.068, as in Column (4) of Table C.2. The integer programming formulation predicts it to be about 37.058, as in Column (3) of Table C.6.

Thirdly, we observe differential effects of removing a short-side pair when we require pools to



	(1) 2-cycles and 1-chains	(2) 3-, 2-cycles, and 1-chains	(3) 4-, 3-, 2-cycles, and 1-chains	(4) 2-cycles, 2- and 1-chains	(5) 3-, 2-cycles, 3-, 2- and 1-chains	(6) 4-, 3-, 2-cycles, 4-, 3-, 2- and 1-chains
25	15.800 (2.948)	13.878 (3.108)	13.788 (3.163)	10.164 (2.266)	9.976 (2.352)	9.976 (2.352)
50	26.088 (4.627)	22.588 (4.871)	22.340 (4.908)	16.916 (3.488)	16.716 (3.591)	16.716 (3.591)
100	46.436 (7.182)	40.890 (7.432)	40.396 (7.370)	30.512 (5.351)	30.372 (5.481)	30.372 (5.481)

**Table C.1.** Average numbers of incompatible transplants in Korea (standard errors in parentheses)

	(1) 2-cycles and 1-chains	(2) 3-, 2-cycles, and 1-chains	(3) 4-, 3-, 2-cycles, and 1-chains	(4) 2-cycles, 2- and 1-chains	(5) 3-, 2-cycles, 3-, 2- and 1-chains	(6) 4-, 3-, 2-cycles, 4-, 3-, 2- and 1-chains
25	15.260 (3.045)	13.604 (3.263)	13.536 (3.308)	10.224 (2.572)	10.120 (2.604)	10.120 (2.604)
50	25.280 (4.703)	22.498 (4.969)	22.380 (4.993)	18.490 (4.156)	18.450 (4.176)	18.450 (4.176)
100	45.320 (7.095)	40.702 (7.319)	40.458 (7.280)	36.068 (6.325)	36.054 (6.340)	36.054 (6.340)

**Table C.2.** Average numbers of incompatible transplants in U.S. (standard errors in parentheses)

satisfy Assumption 3. For Korean pools, removing one pair of type (B-O) or (AB-A) increases the average minimum number of incompatible transplants more greatly in Table C.3 with Assumption 3 than in Table 7 without the assumption. However, removing one pair of type (A-O) or (AB-B) induces a smaller effect on the number of incompatible transplants in Table C.3 than in Table 7. If each pool satisfies Assumption 3, i.e., if  $\#(A-B) > \#(B-A)$ , there is no  $\#(B-A)$  left after 2-cycle (B-A)-(A-B) is formed. When (B-O) is removed, the separated (O-B) is more likely to form a 1-chain, because it cannot form a 2-chain (O-B)-(B-A) or a 3-cycle (O-B)-(B-A)-(A-O). When (AB-A) is removed, the separated (A-AB) is more likely to form a 1-chain, because it cannot form a 2-chain (B-A)-(A-AB) or a 3-cycle (AB-B)-(B-A)-(A-AB). For U.S. pools, similarly, removing (B-O) or (AB-A) makes a greater effect on the number of incompatible transplants in Table C.4 than in Table 8. Removing (A-O) or (AB-B) makes a smaller effect with Assumption 3 than without it.

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	(1) 2-cycles and 1-chains	(2) 3-, 2-cycles, and 1-chains	(3) 4-, 3-, 2-cycles, and 1-chains	(4) 2-cycles, 2- and 1-chains	(5) 3-, 2-cycles, 3-, 2- and 1-chains	(6) 4-, 3-, 2-cycles, 4-, 3-, 2- and 1-chains
(A-O)	1.000 (0.000)	1.000 (0.000)	1.000 (0.000)	0.683 (0.466)	0.687 (0.464)	0.687 (0.464)
(B-O)	1.000 (0.000)	1.618 (0.486)	1.512 (0.500)	0.935 (0.246)	0.978 (0.146)	0.978 (0.146)
(AB-O)	1.000 (0.000)	2.000 (0.000)	2.503 (0.501)	1.000 (0.000)	1.000 (0.000)	1.000 (0.000)
(AB-A)	1.000 (0.000)	1.595 (0.492)	1.504 (0.501)	0.340 (0.474)	0.337 (0.473)	0.337 (0.473)
(AB-B)	1.000 (0.000)	1.000 (0.000)	1.000 (0.000)	0.089 (0.285)	0.015 (0.123)	0.015 (0.123)

**Table C.3.** Changes in average numbers of incompatible transplants when each short-side pair is removed from a Korean pool (standard errors in parentheses)

	(1) 2-cycles and 1-chains	(2) 3-, 2-cycles, and 1-chains	(3) 4-, 3-, 2-cycles, and 1-chains	(4) 2-cycles, 2- and 1-chains	(5) 3-, 2-cycles, 3-, 2- and 1-chains	(6) 4-, 3-, 2-cycles, 4-, 3-, 2- and 1-chains
(A-O)	1.000 (0.000)	1.000 (0.000)	1.000 (0.000)	0.994 (0.077)	0.994 (0.077)	0.994 (0.077)
(B-O)	1.000 (0.000)	1.507 (0.500)	1.413 (0.493)	0.990 (0.102)	1.000 (0.000)	1.000 (0.000)
(AB-O)	1.000 (0.000)	2.000 (0.000)	2.369 (0.483)	1.000 (0.000)	1.000 (0.000)	1.000 (0.000)
(AB-A)	1.000 (0.000)	1.360 (0.482)	1.291 (0.455)	0.006 (0.076)	0.006 (0.076)	0.006 (0.076)
(AB-B)	1.000 (0.000)	1.000 (0.000)	1.000 (0.000)	0.020 (0.140)	0.000 (0.000)	0.000 (0.000)

**Table C.4.** Changes in average numbers of incompatible transplants when each short-side pair is removed from a U.S. pool (standard errors in parentheses)

	(1) 2-cycles and 1-chains	(2) All cycles and 1-chains	(3) 2-cycles, 2- and 1-chains	(4) All cycles and all chains
25	17.144 (2.873)	15.176 (3.271)	10.770 (2.184)	10.324 (2.344)
50	28.892 (4.667)	23.826 (5.033)	17.812 (3.358)	17.084 (3.581)
100	50.560 (7.181)	41.332 (7.471)	31.426 (5.155)	30.488 (5.481)

**Table C.5.** Integer programming: Average numbers of incompatible transplants in Korea (standard errors in parentheses)

	(1) 2-cycles and 1-chains	(2) All cycles and 1-chains	(3) 2-cycles, 2- and 1-chains	(4) All cycles and all chains
25	18.076 (2.945)	15.690 (3.586)	11.342 (2.393)	10.814 (2.600)
50	30.168 (4.824)	24.410 (5.206)	19.798 (3.934)	19.084 (4.128)
100	51.948 (7.271)	41.934 (7.563)	37.058 (6.205)	36.352 (6.341)

**Table C.6.** Integer programming: Average numbers of incompatible transplants in U.S. (standard errors in parentheses)

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