Lung Exchange*

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Abstract

Due to the worldwide shortage of deceased donor organs for transplantation, tissue/organ donations from living donors became a significant source of transplant organs for various organs including kidneys, livers, and lungs. However, not all willing living donors can donate to their intended patients due to medical incompatibility between the donor and the patient. For any organ with living donor transplantation, such incompatibilities can be overcome by an exchange (of donors) between patients with incompatible donors. Such exchanges became widespread in the last decade for kidneys with the introduction of optimization and market design techniques to kidney exchange. Following the success of kidney exchange, a small but growing number of liver exchanges are also conducted. However, even though living donor lung transplantation is introduced more than two decades ago, lung exchange is neither practiced nor introduced. From an organizational perspective living donation is more involved for lungs than kidneys or livers for it often requires two donors. While this makes living donation more difficult for the lungs, it also means that the role of exchange might be more prominent for living donor lung transplantation. We introduce lung exchange as a novel transplantation modality, develop an analytical lung exchange model, and introduce optimal lung exchange mechanisms under various logistical constraints. Our simulations suggest that the number of living donor lung transplants can be doubled by allowing 2-way and 3-way exchanges alone, and can be tripled in the absence of logistical constraints.

Keywords: Market Design, Matching, Complementarities, Lung Exchange, Organ Exchange
JEL Codes: D47, C78

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1 Introduction

Kidney Exchange, originally proposed by Rapaport (1986), has become a major source of kidney transplantations with the introduction of optimization and market design techniques by Roth, Sönmez, and Ünver (2004, 2005, 2007). A handful of transplants from kidney exchanges in the US prior to 2004, increased to 93 in 2006 and to 553 in 2010 (Massie et al., 2013). Currently transplants from kidney exchanges in the US accounts for about 10% of all living donor kidney transplants. While kidney is the most common organ donated by living donors, it is not the only one. Liver and lung are two other organs for which living donor transplantation is practiced. For the case of living donor liver transplantation, a compatible donor donates a lobe of her liver to the patient. Liver is the second most common organ for living donation and in 2013 transplants from living donors account for about 5% of all liver transplants in the US.[1] From an organizational perspective *living-donor lobar lung transplantation* is a more elaborate procedure for it often requires two compatible donors for each patient. If available for donation, both donors donate a lung lobe to the patient in need of transplantation.

For any organ with living donor transplantation, an exchange (of donors) between patients with incompatible donors is a medical possibility to overcome the incompatibility. Indeed, a small but growing number of liver exchanges have been conducted so far with the introduction of this transplant modality in South Korea in 2003 (Hwang et al., 2010).[2] On the other hand, while living donor lobar lung transplantation was introduced more than two decades ago in 1990 (Starnes, Barr, and Cohen, 1994) and it has been especially common in Japan (Sato et al., 2014), *living donor lobar lung exchange* has not been introduced so far. In this paper we

1. introduce living donor lobar lung exchange (or simply *lung exchange*) as a potential transplantation modality,

2. develop a lung exchange model,

3. introduce optimal lung exchange mechanisms under various logistical constraints, and

4. simulate the gains from lung exchange based on lung transplantation data from the US.

As in the case of kidneys and livers, deceased donor lung donations have not been able to meet the demand for lungs. As a result, hundreds of patients die each year in US alone while waiting for lung transplantation. Living donor lobar lung transplantation was initially introduced by Dr. Vaughn Starnes and his colleagues for patients who are too critically ill to survive the waiting list for deceased donor lungs. Since then, eligibility for this novel transplantation modality has been

[1]In contrast to US, living donor liver transplantation is considerably more common than deceased donor liver transplantation in East Asian countries due to cultural reasons (Tanaka et al., 2004; Chen et al., 2013).

[2]There is only one paper on liver exchange published outside of transplantation literature. Dickerson and Sandholm (2014) show that there would be efficiency gains from combining liver and kidney exchanges.

expanded to cystic fibrosis and other end-stage lung disease patients. Sato et al. (2014) report that there is no significant difference in patient survival between living donor and deceased donor lung transplantations.

A healthy human has five lung lobes: Three lobes in the right lung and two in the left. In a living donor lobar lung transplantation two donors each donate a lower lobe to the patient to replace patient's dysfunctional lungs. Each donor shall not only be blood-type compatible with the patient, but donating only a lobe he should also be as heavy. That makes living donation much harder to arrange for lungs than for kidneys or livers, even if a patient is able to find two willing donors. Based on our simulations reported in Table 2, more than 80% of the patients with two willing donors can be incompatible with at least one of their donors. In contrast, only about a third of the willing donors are incompatible with their intended patients for kidneys (Segev et al., 2005). This observation suggests that the marginal benefit of lung exchange to living donor lobar lung transplantation can be considerably higher than the marginal benefit of kidney exchange to living donor kidney transplantation. Our simulations in Table 2 confirm that this is indeed the case: For a pool of 50 patients with willing donors, the availability of lung exchange has the potential to increase the number of living donor lobar lung transplantations

- by 60% with 2-way exchanges alone,
- by about 100% when only 2-way and 3-way exchanges are allowed, and
- by almost 200% when exchanges are not restricted by size.

As in the case of kidney exchange, all operations in a lung exchange will have to be carried out simultaneously. This practice assures that no donor donates a lung lobe unless his intended recipient receives a transplant. As such, organizing these exchanges is not an easy task: A two-way lung exchange involves six simultaneous operations, a three-way lung exchange involves nine simultaneous operations, and so on. As shown in Roth, Sönmez, and Ünver (2007), most of the gains from kidney exchange can be obtained by exchanges no larger than three-way. In this paper we show that this will not be the case for lung exchange, and the marginal benefit will be considerable at least until 6-way lung exchange (cf Table 2 and Theorem 3). This observation suggests that exploring the structure of optimal lung exchange mechanisms is important under various constraints on size of feasible exchanges.

Our lung exchange model builds on the kidney exchange model of Roth, Sönmez, and Ünver (2004, 2007). Medical literature suggests that a donor can donate a lung lobe to a patient if he is

1. blood-type compatible with the patient, and
2. size-compatible (in the sense that the donor is at least as tall as the patient).

For our simulations reported in Section 5, we take both blood-type compatibility and size-compatibility into consideration in order to assess welfare gains from lung exchange under various constraints. For our analytical results on optimal lung exchange mechanisms we consider a simplified model with only blood-type compatibility as a first step. This allows us to define each patient as a triple of blood types (one for the patient and two for her incompatible donors), and we use this structure to introduce optimal mechanisms for (i) two-way exchange alone, (ii) two-way and three-way exchange, and (iii) unrestricted exchange. This simplified model has a second interpretation where there are two blood types (A and O) and two patient/donor sizes (large and small). This interpretation is also of some interest since about 85% of the US population is of blood-types A and O.

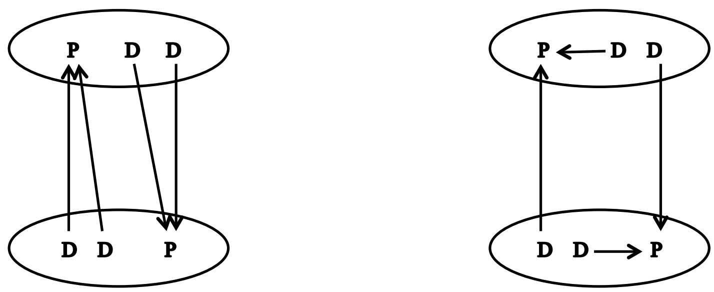

Figure 1: Possible two-way exchanges. Each patient (denoted by **P**) and her paired donors (each denoted by **D**) are represented in an ellipse. Carried donations in each exchange are represented by directed line segments. *At the left*, each patient swaps both of her donors with the other patient. *At the right*, each patient swaps a single donor with the other patient and receives a graft from her other donor.

While there are important similarities between kidney exchange and lung exchange, there are also important differences. From an analytical perspective the most important difference between lung exchange and kidney exchange is the presence of two donors for each patient for the case of lung rather than only one as in the case of kidney. For each patient, the two donors (i.e., lung lobes) are perfect complements.[3] This difference makes the lung exchange model analytically more demanding than the kidney exchange model. Even organizing an individual exchange is a richer problem for lung exchange than for kidney exchange. For kidney exchange, each exchange (regardless of the size of the exchange) is in a *cycle* configuration where the donor of each patient donates a kidney to the next patient in a cycle. For the lung exchange there are two exchange configurations for two-way exchange (see Figure 1), five exchange configurations for three-way exchange, (see Figure 2) and so on. The richness of exchange configurations in lung exchange also means, optimal organization of these exchanges will be more challenging for lung exchange than for kidney exchange. Despite this technical challenge we provide optimal lung exchange mechanisms for the cases of (i) 2-way

[3]In matching literature there are not many models that can incorporate complementarities and find positive results. Most of the matching literature focuses on various substitutability conditions and shows negative results even in the existence of slightest complementarities in preferences. For example see Hatfield and Milgrom (2005), Hatfield and Kojima (2008), and Hatfield and Kominers (2015).

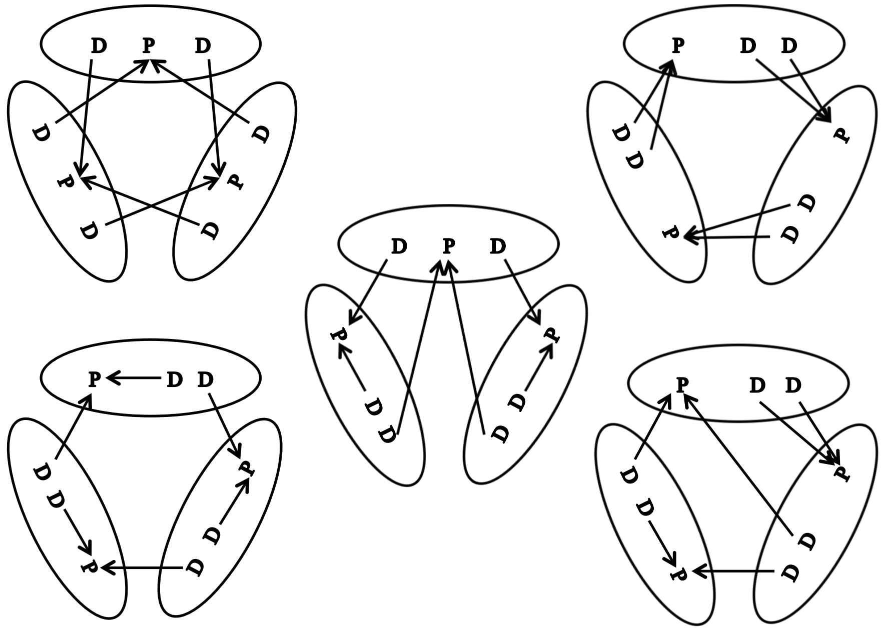

Figure 2: Possible three-way exchanges. *At the upper-left*, each patient trades one donor in a clock-wise trade and the other donor in a counter-clock-wise trade. *At the upper-right*, each patient trades both of her donors in clock-wise trades. *At the lower-left*, each patient trades one donor in a clock-wise exchange and receives a graft from her other donor. *At the middle*, one patient is treated asymmetrically with respect to the other two: one patient trades both of her donors in 2 two-way trades, one with one patient, the other with the other patient; while each of the other patients receives a graft from her remaining donor. *At the lower-right*, all patients are treated asymmetrically, one patient receives from one of her own donors, one patient's both donors donate to a single patient, while the last patient's both donors donate to the other two patients.

exchange, (ii) 2-way and 3-way exchange, and (iii) unconstrained exchange.

Increasingly, economists are taking advantage of advances in technology to design new or improved allocation mechanisms in applications as diverse as entry-level labor markets (Roth and Peranson, 1999), spectrum auctions (Milgrom, 2000), internet auctions (Edelman, Ostrovsky, and Schwarz, 2007; Varian, 2007), school choice (Abdulkadiroğlu and Sönmez, 2003), kidney exchanges (Roth, Sönmez, and Ünver, 2004, 2005, 2007), course allocation (Sönmez and Ünver, 2010; Budish and Cantillon, 2012), affirmative action (Kojima, 2012; Hafalir, Yenmez, and Yildirim, 2013; Echenique and Yenmez, 2012; Kominers and Sönmez, 2013), cadet-branch matching (Sönmez and Switzer, 2013; Sönmez, 2013), and assignment of arrival slots (Schummer and Vohra, 2013; Abizada and Schummer, 2013). Our paper not only contributes to the emerging field of market design by introducing a novel application in lung exchange, but also contributes to transplantation literature by introducing a novel transplantation modality.

2 A Model of Lung Exchange

We assume that each patient, who has two live willing donors, can receive from his own donors if and only of both of them are blood-type compatible with the patient. That is, the two lung lobes are perfect complements for the patient. There are four human blood types, O, A, B, and AB denoting existence or absence of the two blood proteins A or B in the human blood. A patient can receive from a donor a lobe of the lung, unless the donor carries a blood protein that the patient does not have. Thus, O donors can donate to all patients, A can donate to only A and AB, B can donate to B and AB, and AB can only donate to AB.

In our benchmark model, we assume that there is no requirement of size compatibility and the only requirement of compatibility regards blood types. This assumption helps us to focus exclusively on the effects of the two-donor requirement on organ exchange (which is only one parameter separation from the widely studied kidney exchange model). Moreover, as we illustrate at the end of this section, it has an equivalent interpretation including both size and blood-type compatibility requirements when only the patients and donors with the two most common blood types are considered.

Let $\mathcal{B} = \{O, A, B, AB\}$ be the set of blood types. We denote generic elements by $X, Y, Z \in \mathcal{B}$. Let $\trianglerighteq$ be the partial order on blood types defined by $X \trianglerighteq Y$ if and only blood type X can donate to blood type Y. Figure 3 illustrates the partial order $\trianglerighteq$.[4] Let $\triangleright$ denote the asymmetric part of $\trianglerighteq$.

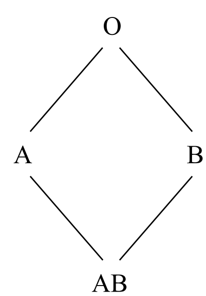

Figure 3: The Partial Order $\trianglerighteq$ on the Set of Blood Types $\mathcal{B} = \{O, A, B, AB\}$.

Each patient participates in the lung exchange with two donors, which we refer to as a **triple**. The relevant information concerning the patient and her two donors can be summarized in the form of a triple of blood types $X - Y - Z \in \mathcal{B}^3$, where X is the blood type of the patient, and Y and Z are the blood types of the donors. We will refer to each element in $\mathcal{B}^3$ as a **triple type** such that the order of the donors has no relevance, i.e., types $X - Y - Z$ and $X - Z - Y$ refer to the same triple type.

[4] For any $X, Y \in \mathcal{B}$, $X \trianglerighteq Y$ if and only if there is a downward path from blood type X to blood type Y in Figure 3.

Definition 1 *A* **lung exchange pool** *is a vector of nonnegative integers* $\mathcal{E} = \{n(X-Y-Z) : X-Y-Z \in \mathcal{B}^3\}$ *such that:*

1. $n(X-Y-Z) = n(X-Z-Y)$ *for all* $X-Y-Z \in \mathcal{B}^3$.
2. $n(X-Y-Z) = 0$ *for all* $X-Y-Z \in \mathcal{B}^3$ *such that* $Y \trianglerighteq X$ *and* $Z \trianglerighteq X$.

The number $n(X-Y-Z)$ *stands for the number of participating* $X-Y-Z$ *type triples.*

The first condition in the definition of a lung exchange pool corresponds to the assumption that the order of the donors does not matter, i.e., $X-Y-Z$ and $X-Z-Y$ represent the same type. The second condition corresponds to the assumption that compatible patient-donor triples do not participate in the lung exchange.

The model (and the results we present in the following sections) have an alternative interpretation with size compatibility on donation. Consider the following alternative model. There are only two blood types O or A,[5] and two sizes large (l) or small (s) for each individual. A donor can donate to a patient if: (i) the patient is blood type compatible with the donor and (ii) the donor is not strictly smaller than the patient. Figure 4 illustrates the partial order $\tilde{\trianglerighteq}$ on the set of individual types $\{O, A\} \times \{l, s\}$. Note that the donation partial order in Figure 4 is order isomorphic to the donation partial order of the original model in Figure 3 if we identify Ol with O, Al with A, Os and B and As with AB. Therefore, all the results of the section also apply to the model with size compatibility constraints on donation after appropriately relabeling individuals' types. From now

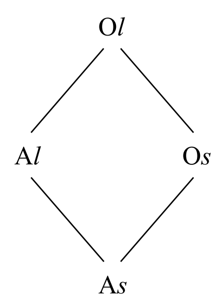

Figure 4: The Partial Order $\tilde{\trianglerighteq}$ on $\{O, A\} \times \{l, s\}$.

on, we will use the blood-type interpretation of the compatibility relation. But each result can be stated in terms of the alternative model with two sizes and only O and A blood types.

[5] O and A are the most common blood types in the world. Close to 80% of the world population belong to one of these two types. Moreover, in the US, these two types cover around 85% of the population.

3 Two-Way Lung Exchange

In this section, we will assume that only two-way exchanges are allowed. We will characterize the maximum number of patients receiving transplants for any given exchange pool $\mathcal{E}$. We will also describe a matching that achieves this maximum.

A two-way exchange is the simplest form of lung exchange, including two triples exchanging one or both of their donors' grafts, and the easiest to coordinate. Since a donor cannot be forced into signing a contract of donation, she can change her mind any time. Therefore, if all transplants in an exchange are not carried simultaneously, it may cause some patients not to receive a transplant in spite of one or both of his donors donating to somebody else. Because of logistical constraints regarding the availability of several transplant teams at the same time and coordination regarding patient donor triples, organizing two-way exchanges are easier than more complex exchanges. Thus, as a first step in our analysis, it is important to understand the structure and size of optimal matchings with only two-way exchanges.

There are 40 types of triples accounting for repetitions due to reordering of donors. The following Lemma simplifies the problem substantially by showing that only six of these types may take part in two-way exchanges.

Lemma 1 *In any given exchange pool $\mathcal{E}$, the only types that could be part of a two-way exchange are $A-Y-B$ and $B-Y-A$ where $Y \in \{O, A, B\}$.*

Proof of Lemma 1: Since AB blood-type patients are compatible with their donors, there are no AB blood-type patients in the market. This implies that no triple with an AB blood-type donor can be part of a two-way exchange, since AB blood-type donors can only donate to AB blood-type patients.

We next argue that no triple with an O blood-type patient can be part of a two-way exchange. To see this, suppose that $X-Y-Z$ and $O-Y'-Z'$ take part in a two-way exchange. If X exchanges her Y donor, then Y can donate to O so $Y = O$. If X does not exchange her Y donor, then Y can donate to X. In either case, $Y \trianglerighteq X$. Similarly $Z \trianglerighteq X$, implying that $X-Y-Z$ is a compatible triple, a contradiction.

From what is shown above, the only triples that can be part of a two-way exchange are those where the patient blood type is in $\{A, B\}$, and the donors' blood types are in $\{O, A, B\}$. If we further exclude the compatible combinations and repetitions due to reordering the donors, we are left with the six triple types stated in the Lemma. It is easy to verify that triples of these types can indeed participate in two-way exchanges (see Figure 5). ■

The six types of triples in Lemma 1, are such that every A blood-type patient has at least one B blood-type donor, and every B blood-type patient has at least one A blood-type donor. Therefore,

A blood-type patients can only take part in a two-way exchange with B blood-type patients, and vice versa. Furthermore if they participate in a two-way exchange, the $A-A-B$ and $B-B-A$ types must exchange exactly one donor; the $A-B-B$ and $B-A-A$ types must exchange both donors; and the $A-O-B$ and $B-O-A$ types might exchange one or two donors. We summarize the possible two-way exchanges as the edges of the graph in Figure 5. We will show that

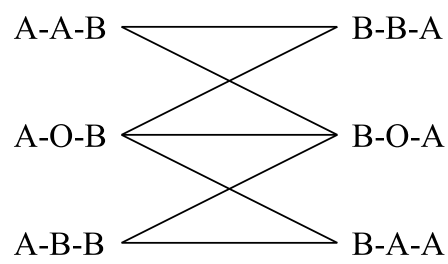

Figure 5: Possible Two-Way Exchanges

the following matching algorithm maximizes the number of transplants through two-way exchanges. The algorithm sequentially maximizes three subsets of two-way exchanges:

Algorithm 1 (Sequential Matching Algorithm for Two-Way Exchanges)

Step 1: Match the maximum number of $A-A-B$ and $B-B-A$ types.[6] Match the maximum number of $A-B-B$ and $B-A-A$ types.

Step 2: Match the maximum number of $A-O-B$ types with any subset of the remaining $B-B-A$ and $B-A-A$ types. Match the maximum number of $B-O-A$ types with any subset of the remaining $A-A-B$ and $A-B-B$ types.

Step 3: Match the maximum number of the remaining $A-O-B$ and $B-O-A$ types.

Figure 6 graphically illustrates the pairwise exchanges that are carried out at each step of the sequential matching algorithm. The next Theorem shows the optimality of this algorithm and characterizes the maximum number of transplants through two-way exchanges.

Theorem 1 *Given an exchange pool $\mathcal{E}$, the above sequential matching algorithm maximizes the number of two-way exchanges. The maximum number of patients receiving transplants through two-way exchanges is* $2\min\{N_1, N_2, N_3, N_4\}$ *where:*

$$\begin{aligned}
N_1 &= n(A-A-B) + n(A-O-B) + n(A-B-B) \\
N_2 &= n(A-O-B) + n(A-B-B) + n(B-B-A) + n(B-O-A) \\
N_3 &= n(A-A-B) + n(A-O-B) + n(B-O-A) + n(B-A-A) \\
N_4 &= n(B-B-A) + n(B-O-A) + n(B-A-A)
\end{aligned}$$

[6] I.e., match $\min\{n(A-A-B), n(B-B-A)\}$ type $A-A-B$ triples with $\min\{n(A-A-B), n(B-B-A)\}$ type $B-B-A$ triples.

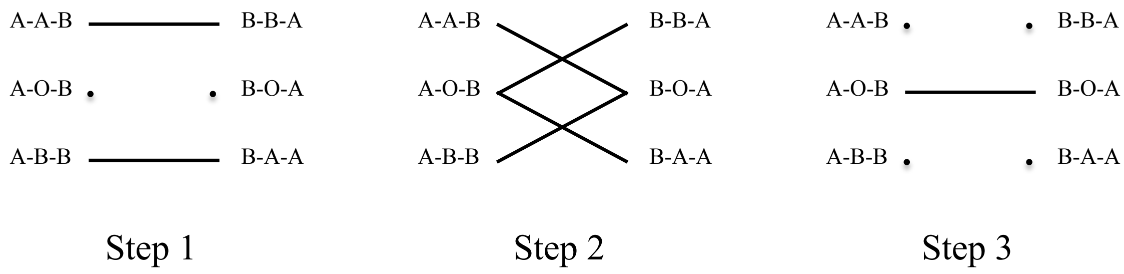

Figure 6: The Optimal Two-Way Sequential Matching Algorithm

Figure 7 depicts the sets of triple types whose market populations are N_1, N_2, N_3, and N_4.

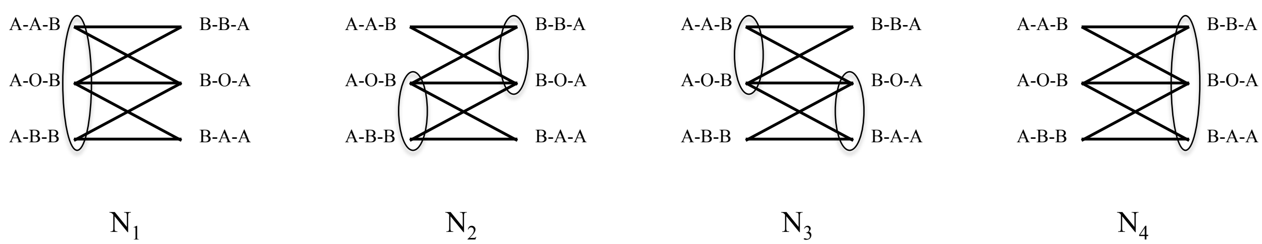

Figure 7: The Maximum Number of Transplants through Two-Way Exchanges

Proof of Theorem 1: Let N denote the maximum number of two-way exchanges. Since each such exchange results in two transplants, the maximum number of transplants through two way exchanges is $2N$. We will prove the Theorem in two parts

Proof of "$N \leq \min\{N_1, N_2, N_3, N_4\}$": Since each two-way exchange involves an A blood-type patient, we have that $N \leq N_1$. Since $A-A-B$ types can only be part of a two-way exchange with $B-B-A$ or $B-O-A$ types, the number of two-way exchanges that involve an $A-A-B$ type is bounded above by $n(B-B-A)+n(B-O-A)$. Therefore, the number of two-way exchanges involving an A blood-type patient is less than or equal to this upper bound plus the number of $A-O-B$ and $A-B-B$ types, i.e., $N \leq N_2$. The inequalities $N \leq N_3$ and $N \leq N_4$ follow from symmetric arguments switching the roles of A and B blood types.

Proof of "$N \geq \min\{N_1, N_2, N_3, N_4\}$": We will next show that the matching algorithm achieves $\min\{N_1, N_2, N_3, N_4\}$ exchanges. This implies $N \geq \min\{N_1, N_2, N_3, N_4\}$. Since $N \leq \min\{N_1, N_2, N_3, N_4\}$, we conclude that $N = \min\{N_1, N_2, N_3, N_4\}$ and hence the matching algorithm is optimal.

Case 1. "$N_1 = \min\{N_1, N_2, N_3, N_4\}$": The inequalities $N_1 \leq N_2$, $N_1 \leq N_3$, and $N_1 \leq N_4$ imply that:

$$\begin{aligned} n(A-A-B) &\leq n(B-B-A)+n(B-O-A) \\ n(A-B-B) &\leq n(B-A-A)+n(B-O-A) \\ n(A-A-B)+n(A-B-B) &\leq n(B-B-A)+n(B-A-A)+n(B-O-A) \end{aligned}$$

Therefore, after the maximum number of $A-A-B$ and $B-B-A$ types and the maximum number of $A-B-B$ and $B-A-A$ types are matched in the first step, there are enough $B-O-A$ types to accommodate any remaining $A-A-B$ and $A-B-B$ types in the second step.

Since $N_1 \leq N_4$, there are at least $n(A-O-B)$ triples with B blood-type patients who are not matched to $A-A-B$ and $A-B-B$ types in the first two steps. Therefore, all $A-O-B$ type triples are matched to triples with B blood-type patients in the second and third steps. The resulting matching involves N_1 exchanges, since all A blood-type patients take part in a two-way exchange.

Case 2."$N_2 = \min\{N_1, N_2, N_3, N_4\}$": Since $N_2 \leq N_1$, we have $n(A-A-B) \geq n(B-B-A) + n(B-O-A)$. Therefore, all $B-B-A$ types are matched to $A-A-B$ types in the first step. Similarly, $N_2 \leq N_4$ implies that $n(A-O-B)+n(A-B-B) \leq n(B-A-A)$. Therefore, all $A-B-B$ types are matched to $B-A-A$ types in the first step. In the second step, there is no remaining $B-B-A$ types, but enough $B-A-A$ types to accommodate all $A-O-B$ types. Similarly, in the second step, there is no remaining $A-B-B$ types, but enough $A-A-B$ types to accommodate all $B-O-A$ types. There are no more exchanges in the third step. The resulting matching involves N_2 two-way exchanges.

The cases where N_3 and N_4 are the minimizers follow from symmetric arguments exchanging the roles of A and B blood types. ■

4 Larger Size Exchanges

We have seen in Section 3 that if only two-way exchanges are allowed for, then every two-way exchange must involve exactly one A and one B blood-type patient. The following Lemma generalizes these observations to K-way exchanges for arbitrary $K \geq 2$. In particular, every K-way exchange must involve an A and a B blood-type patient, but if $K \geq 3$, then it might also involve O blood-type patients.

Lemma 2 *Let $\mathcal{E}$ and $K \geq 2$ be given. Then, the only types that could be part of a K-way exchange are $O-Y-A$, $O-Y-B$, $A-Y-B$, and $B-Y-A$ where $Y \in \{O, A, B\}$. Furthermore, every K-way exchange must involve an A and a B blood-type patient.*

Proof of Lemma 2: As argued in the proof of Lemma 1, no AB blood-type patient nor donor can be part of a K-way exchange. Therefore, the only triples that can be part of a K-way exchange are those where its patient's and its donors' blood types are in $\{O, A, B\}$. After excluding the compatible combinations, we are left with the triple types listed above.

Take any K-way exchange. Since every triple type listed above has at least an A or a B blood-type donor, the K-way exchange involves an A or a B blood-type patient. If it involves an A blood-type patient, then that patient brings in a B blood-type donor, so it must also involve a B blood-type patient. If it involves a B blood-type patient, then that patient brings in an A blood-type donor, so it must also involve an A blood-type patient. It is trivial to see that all types in the hypothesis can feasibly participate in exchange in a suitable exchange pool.[7] ■

In kidney exchange pools, O patients with A donors are much more than any other type and in particular their opposite type pairs, A patients with O donors. That is because, O patients with A donors arrive for exchange all the time, while A patients with O donors only arrive if there is tissue type incompatibility between them (as otherwise the donor is compatible and directly donates to the patient). This is an empirical observation caused by the structure of partial-order-based blood-type compatibility structure. In general, patients with "less sought after" blood type donors relative to their own blood type are in excess and plenty when the exchange pool reaches a relatively large volume. A similar situation will also occur in lung exchange pools in the long run.[8] For kidney exchange models, Roth, Sönmez, and Ünver (2007) makes an explicit long-run assumption regarding this asymmetry. We will make a corresponding assumption for lung exchange below. However, our assumption will be much milder; we will assume this only for two types of triples rather than all triple types with "less sought after" donor blood types relative to their patients.

Definition 2 *A lung exchange pool $\mathcal{E}$ satisfies the* **long-run** *assumption if for every matching composed of arbitrary size exchanges, there is at least one $O-O-A$ and one $O-O-B$ type that do not take part in any exchange.*

Suppose that the exchange pool $\mathcal{E}$ satisfies the long-run assumption and μ is a matching composed of arbitrary size exchanges. The long-run assumption ensures that we can create a new matching μ' from μ by replacing every $O-A-A$ and $O-B-A$ type taking part in an exchange by an unmatched $O-O-A$ type, and every $O-B-B$ type taking part in an exchange by an unmatched $O-O-B$ type. Then, the new matching μ' is composed of the same size exchanges

[7] We already demonstrated the possibility of exchanges regarding triples (of the types in the hypothesis of the lemma) with A and B blood type patients in Lemma 1. An $O-A-A$ type triple can be matched in a four-way exchange with $A-O-B$, $A-O-B$, $B-A-A$ type triples (symmetric argument holds for $O-B-B$). On the other hand, an $O-A-B$ type triple can be matched in a three-way exchange with $A-O-B$ and $B-O-A$ type triples. An $O-O-A$ or an $O-O-B$ type can be used instead of $O-A-B$ in the previous above example.

[8] Actually, this asymmetry is expected to be more severe for lungs, as tissue type incompatibility is not an issue for lungs unlike kidneys.

as μ, and it induces the same number of transplants as μ. Furthermore, the only O blood-type patients matched under μ' belong to the triples of types $O-O-A$ or $O-O-B$.

Let $\bar{K} \geq 2$ be the maximum allowable exchange size. Consider the problem of finding an **optimal** matching, i.e., one that maximizes the number of transplants when only $1, \ldots, \bar{K}$-way exchanges are allowed. By the above paragraph, for any optimal matching μ, we can construct another optimal matching μ' in which the only triples with O blood-type patients matched under μ' belong to the types $O-O-A$ or $O-O-B$. Since by the long-run assumption, the numbers of $O-O-A$ and $O-O-B$ participants in the market is non-binding, an optimal matching can be characterized just in terms of the numbers of the six participating types in Lemma 2 that have A and B blood-type patients.

First, we use this approach to describe a matching that achieves the maximum number of transplants when $\bar{K} = 3$. Two- and three-way exchanges are logistically the most realistic ones to organize. Therefore, it is important to get insights for them besides two-way exchanges.

4.1 Two- and Three-way Exchanges

We start the analysis of optimal matchings under two- and three-way exchanges by describing a collection of two and three-way exchanges. We show in Lemma 3 in Appendix A that one can restrict attention to these exchanges in constructing an optimal matching.

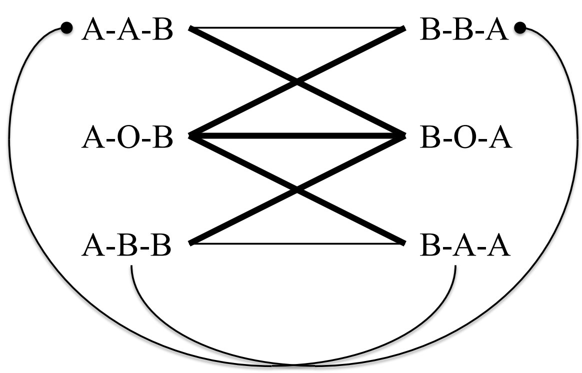

Figure 8: A Subset of Two- and Three-Way Exchanges

Definition 3 *Given a lung exchange pool $\mathcal{E}$, consider the two and three-way exchanges in Figure 8 where:*

1. *A regular (i.e. non-bold/no dotted end) edge between two types represents a two-way exchange involving those two types.*
2. *A bold edge between two types represents a three-way exchange involving those two types and a $O-O-A$ or $O-O-B$ type.*

3. *An edge with a dotted end represents a three-way exchange involving two types from the dotted end, and one type from the non-dotted end.*

We will show that when the long-run assumption is satisfied, the following matching algorithm maximizes the number of transplants through two and three-way exchanges. The algorithm sequentially maximizes three subsets of exchanges:

Algorithm 2 (Sequential Matching Algorithm for Two-&Three-way Exchanges)

Step 1: Carry out the two and three way exchanges in Figure 8 among $A-A-B$, $A-B-B$, $B-B-A$, and $B-A-A$ types to maximize the number of transplants subject to the following constraints $(*)$:

1. Leave at least a total $\min\{n(A-A-B)+n(A-B-B), n(B-O-A)\}$ of $A-A-B$ and $A-B-B$ types unmatched.
2. Leave at least a total $\min\{n(B-B-A)+n(B-A-A), n(A-O-B)\}$ of $B-B-A$ and $B-A-A$ types unmatched.

Step 2: Carry out the maximum number of three-way exchanges in Figure 8 involving $A-O-B$ types and the remaining $B-B-A$ or $B-A-A$ types. Carry out the maximum number of three-way exchanges in Figure 8 involving $B-O-A$ types and the remaining $A-A-B$ or $A-B-B$ types.

Step 3: Carry out the maximum number of three-way exchanges in Figure 8 involving the remaining $A-O-B$ and $B-O-A$ types.

Figure 9 graphically illustrates the two and three-way exchanges that are carried out at each step of the sequential matching algorithm. For expositional purposes, we present the sub-algorithm that solves the constrained optimization in Step 1 in Appendix B. The following Theorem shows the optimality of the above algorithm.

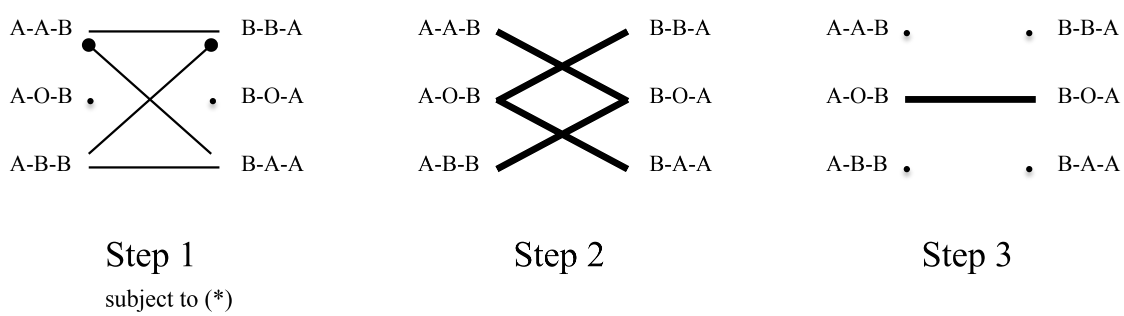

Figure 9: The Optimal Two and Three-Way Sequential Matching Algorithm

Theorem 2 *Given a lung exchange pool $\mathcal{E}$ satisfying the long-run assumption, the above sequential matching algorithm maximizes the number of transplants through two and three-way exchanges.*

Proof: See Appendix A. ■

4.2 Unrestricted Exchange Size

Although larger exchanges could be logistically more difficult to organize, it is important to understand the theoretical upper bounds of benefits from exchange. In this subsection, we inspect optimal matchings when there are no exchange size restrictions. In particular, we answer the following question: what is the smallest exchange size we can always use to find an optimal matching when there are no exchange size constraints. While addressing this question, we also answer (1) what is the maximum number of patients that can be matched in an exchange pool, and (2) whether there is a straightforward intuitive algorithm to find an optimal matching.[9].

Using the intermediate results in this Appendix, we state the main theorem of this section about the sufficiency of 2–6-way exchanges:

Theorem 3 *Suppose that the lung exchange pool $\mathcal{E}$ satisfies the long-run assumption and exchange sizes are unrestricted. Then there exists an optimal matching such that none of the exchanges in this matching are larger than 6-way.*[10]

Proof: See Appendix C. ■

The next example shows that using 6-way exchanges is not only sufficient, but also necessary to find an optimal matching in some exchange pools.

Example 1 Consider an exchange pool $\mathcal{E}$ with

- 3 blood type O patients and 6 blood type O donors,
- 2 blood type B patients and 4 blood type B donors, and
- 1 blood type A patient and 2 blood type A donors.

Hence, for optimality, each patients receives a lung lobe from two donors of exactly her own blood type, and all are matched. $(^{\varkappa})$

Triple types are:

[9] These two results are stated and proven in Appendix C as Theorem 4.

[10] Moreover, for finding an optimal matching without exchange size constraints we propose an algorithm in Appendix C, Algorithm 3. The optimality of this algorithm is proven through the proof of Theorem 4, also in this Appendix, which also proves the above theorem.

1. $A - O - B$ needs to be in the same exchange as both Patients 2 & 3
2. $B - O - A$
3. $B - O - A$
4. $O - O - B$ needs to be in the same exchange as one of Patients 1, 2, 3
5. $O - O - B$ needs to be in the same exchange as one of Patients 1, 2, 3
6. $O - O - B$ needs to be in the same exchange as one of Patients 1, 2, 3

Hence, Argument ($^{\varkappa}$) along with the arguments in the enumerated list above imply that a 6-way exchange is necessary to match all patients and obtain an optimal matching.

5 Simulations

In this section, we conduct calibrated simulations to quantify potential gains from an organized lung exchange.

We start with explaining the calibration parameters we used in the simulations. We use aggregate data statistics from lung transplantation (deceased or live) patient population from the US (see Table 1).[11] Live donor lobar transplantation is especially common for two classes of patients in the world: those who suffer from cystic fibrosis or pulmonary hypertension. Therefore we assume that all live transplant lung patients come from these two classes. Among all lung transplants (from deceased or live), these classes of patients constitute 14.57% and 5.47% of all transplant patient additions in the US, respectively. We use this cystic fibrosis to pulmonary hypertension patient ratio of 2.66 to 1 in generating our random patients. New patient additions to the lung exchange pool are assumed to have the same age distribution as the respective deceased donor list additions reported in Table 1. Cystic fibrosis patients are relatively much younger. We only consider adult patients in our analysis. Patients' blood type distribution is also given in the same table from the same US sample. Moreover, the weight of each patient is also randomly determined. The distribution of weights of female and male American adults were obtained the National Health and Nutrition Examination Survey 2007-2008.[12] Using these distributions we randomly generate each patient: disease, gender, age, blood type, and weight.

We assume that each patient is randomly matched with two US adults as directed donors. Donor gender is determined as 50% male–50% female; donor blood-type distribution is matched that of the

[11] Although live donor lobar lung transplantation is not as common in the US as eastern Asian countries, the US data statistics are obtained from the largest transplant patient population in the world, very detailed, and readily available on the internet. That is the reason we use the data statistics from the US to calibrate our simulations.

[12] Retrieved on May 27, 2014 from `https://www.census.gov/compendia/statab/2012/tables/12s0209.pdf`.

Data for Lung Transplant Patients with Respect to Diagnosis				
	Cystic Fibrosis		**Pulm. Hypertension**	
Percentage	14.57%		5.47%	
Gender Distribution				
Female	48.74%		76.18%	
Male	51.26%		23.82%	
Age Distribution				
Adult Ages	**Female**	**Male**	**Female**	**Male**
18-34	76.24%	70.30%	30.30%	29.38%
35-49	20.78%	25.97%	43.76%	46.13%
50-64	2.98%	3.73%	25.95%	24.48%
Blood Type Distribution				
O	45.35%		46.96%	
A	41.78%		36.69%	
B	9.77%		12.49%	
AB	3.14%		3.97%	

Table 1: Data Statistics for Lung Transplant Patients. This table reflects the US OPTN national data obtained on May 27-31, 2014 from `http://www.optn.org` for lung transplant recepient candidates added to the deceased donor wait list to date. "Percentage" row reflects the percentage of patients with cyclic fibrosis and primary pulmonary hypertension among all 35,420 new additions to date. The rest of the data is for adult patients between ages 18-64 only that constitute about 84% of all new additions for either diagnosis type.

US general population: 44% O, 42% A, 10% B, and 4% AB.[13] For their age distribution, we use the US census data for gender age composition of the US population in 2010[14] and weight distribution that we used. Donor weights are also assumed to be distributed with the same distribution used for the patients. Using these distributions, we randomly generate the characteristics of each donor of the triple: gender, age, blood type, and weight.

After generating $n = 10, 20,$ or 50 patient-donor triples, we check which triples are compatible, i.e., which of the patients can receive a lung lobe from each of her donors. Compatibility test has two components:

- blood-type compatibility: we use $\trianglerighteq$ relation we always used throughout the paper; and
- size compatibility: we assume that a patient can only receive a transplant from a donor as *heavy* as herself.[15]

Patients that are incompatible with at least one of their own donors participate in the exchange. Others receive two lobes directly from their own donors. In this way we form an exchange pool.

[13]For example see `http://www.bloodbook.com/world-abo.html`. We retrieved it on May 27, 2014.
[14]Retrieved on May 27, 2014 from `http://www.census.gov/prod/cen2010/briefs/c2010br-03.pdf`.
[15]Height could have been used as an alternative size compatibility measure.

Then we find optimal 2-way, 2&3-way, 2–4-way, 2–5-way, and unrestricted matchings. We generate $S = 500$ such patient samples and take the averages and sample standard errors of the numbers of patients matched through direct donation and optimal exchanges under and exchange-matched patients in Table 2. We also run a control group of simulations in which size compatibility is not required.

Lung Exchange Simulations Average Numbers of Patients Matched								
Sample	**Donor Size**	**Direct**	**Exchange Technology**					
Size	**Constraint?**	**Donation**	**2-way**	**2&3-way**	**2–4-way**	**2–5-way**	**Unrestrict**
10	**No**	4.364	0.492	0.66	0.71	0.734	0.738
		(1.5724)	(0.90751)	(1.2163)	(1.3272)	(1.394)	(1.4076)
	Yes	1.564	0.356	0.476	0.552	0.574	0.576
		(1.1422)	(0.81645)	(1.0899)	(1.2691)	(1.3357)	(1.3431)
20	**No**	8.852	1.472	2.072	2.328	2.434	2.462
		(2.2884)	(1.5537)	(2.1363)	(2.3916)	(2.5048)	(2.5419)
	Yes	3.156	1.148	1.7	2.058	2.254	2.472
		(1.6313)	(1.422)	(1.9844)	(2.4113)	(2.6668)	(3.0285)
50	**No**	22.42	4.688	6.862	7.836	8.31	8.446
		(3.6538)	(2.59)	(3.669)	(4.041)	(4.1613)	(4.184)
	Yes	8.092	4.936	8.028	10.286	11.858	15.534
		(2.64)	(2.9863)	(4.3865)	(5.5112)	(6.144)	(7.2278)

Table 2: Lung Exchange Simulations. Here each patient needs double lobar transplants and has two donors. She has either pulmonary hypertension or cystic fibrosis as the main reason of her disease. Standard errors reported under averages in parentheses belong to the sample; for the standard errors of the averages, these need to be divided by the square root of the simulation number, $\sqrt{500} = 22.361$.

Potential gains from exchange increase significantly with the relaxation of restrictions on feasible exchange size. When $n = 50$ with donor size compatibility requirement(the last two lines), only 16% of the patients can receive direct donation and the rest, 84% participate in exchange. Using only 2-way exchange 10% of the patients can be matched (i.e., an overall 60% increase in the patients receiving live transplantation). As we increase the largest permissible exchange sizes, the gains continue to significantly increase. Using 2&3-way exchanges, we can double the number of patients receiving live transplant with respect to direct donation only (16% of all patients can additionally be matched). Of course, larger exchange sizes require more transplant teams to be simultaneously available, and can force the limits of logistical constraints. For example, a 5-way exchange requires 15 simultaneous surgeries. Even so, using 2–5-way exchanges, we can match 23.5% of all patients in lung exchange, an almost 150% increase above direct donation, an almost 50% increase over 2&3-way exchanges. Hence, the tradeoff of not conducting larger exchanges can be considerable in terms of life loss. Most remarkably, without any restrictions on exchange sizes, more than 190% patients who receive direct donation can be matched, almost tripling the number of patients receiving transplants to 47% of all patients in the population.

The effect of sample size on marginal contribution of exchanges is also very significant: when $n = 10$, the contribution of 2&3-way and unrestricted are only 30% and 37% of patients matched through direct donation (instead of 100% and 190% for $n = 50$), respectively (and those refer to 4.75% and 5.75% of all patients).

6 Conclusion

For any organ with possible living donor transplantation, living donor organ exchange is also a medically feasible. Despite the introduction and practice of living donor lung transplantation since 1990, living donor lung exchange is neither introduced in the literature nor implemented in practice. In this paper we propose lung exchange as a new transplantation modality, formulate an analytical model for lung exchange, introduce optimal lung exchange mechanisms for a simplified version of the model under various logistical constraints, and finally simulate the potential gains from lung exchange.

Analytically lung exchange is a more challenging application of matching markets than kidney exchange since each patient is in need of two compatible donors that are perfect complements. Exploiting the structure induced by the blood-type compatibility requirement for lung transplantation, we introduce optimal lung exchange mechanisms under various logistical constraints. While we abstract away from the donor size constraint for our analytical model and results, we consider a more realistic model for our calibrated simulations taking into consideration both blood-type compatibility requirement and the donor-size requirement. In our simulations we show that the marginal contribution of exchange to living donor organ transplantation is very substantial for the case of lung transplantation as much as doubling the number of living donor transplants with two and three-way exchanges alone, and tripling it in the absence of constraints on the size of feasible exchanges.

Living donor transplantation and living donor organ exchange technologies are especially important for countries where there are barriers to deceased donor transplantation due to cultural reasons. This includes several Asian countries such as Japan, Taiwan, and South Korea. Japan in particular has one of the most prominent living-donor lung transplantation programs in the world. We started interacting with members of the Japanese transplantation community in September 2014 after a preliminary version of our paper was written and presented at Tsukuba, Japan. So far they have been receptive to the idea of lung exchange and they are in the process of organizing a database on donor specifics for living donor lung transplantation to assess the potential benefits from lung exchange. While this data is readily available in Japan for patients who received donation from their compatible donors, it is not available for a much larger fraction of patients with willing but incompatible living donors.

Appendix A Proof of Theorem 2

We first state and prove two Lemmas that will be used in proving Theorem 2. Lemma 3 below states that under the long-run assumption, one can restrict attention to the exchanges in Definition 3 to construct an optimal matching.

Definition 4 *A matching μ is* **Figure 8 consistent** *if it consists of the two and three-way exchanges described in Definition 3.*

Lemma 3 *Suppose that the lung exchange pool $\mathcal{E}$ satisfies the long-run assumption, and only two and three-way exchanges are allowed. Then, there is an optimal matching that is Figure 8 consistent.*

Proof of Lemma 3: We first show that if a matching μ includes an exchange not represented in Figure 8, then there is a matching μ' that induces at least as many transplants and includes one less exchange excluded from Figure 8. To see this, take any exchange in μ not represented as an edge in Figure 8. The exchange must be at most three-way since larger exchanges are not allowed. Furthermore by Lemma 2, the exchange includes two types $A-Y-Z$ and $B-Y'-Z'$ that are vertices of Figure 8. To create the matching μ', we first undo this exchange in μ, then create a weakly larger exchange which involves unmatched types and is represented as an edge in Figure 8.

Case 1. "There is a bold edge between the types $A-Y-Z$ and $B-Y'-Z'$ in Figure 8": Then we create the three-way exchange that corresponds to that bold edge.

If there is no bold edge between $A-Y-Z$ and $B-Y'-Z'$ in Figure 8, then these types can not be $A-A-B$ and $B-B-A$, because the only allowable exchange involving $A-A-B$ and $B-B-A$ is the two-way exchange included in Figure 8. By an analogous argument, these types can also not be $A-B-B$ and $B-A-A$. This leaves out two more cases:

Case 2. "$A-Y-Z = A-A-B$ and $B-Y'-Z = B-A-A$": The only allowable exchange involving these two types not represented in Figure 8 is the three-way exchange where the third participant is $A-O-B$. In this case, we create the three-way exchange that corresponds to the bold edge between the unmatched $A-O-B$ and $B-A-A$ types.

Case 3. "$A-Y-Z = A-B-B$ and $B-Y'-Z = B-B-A$": We omit the argument for this case, since it is symmetric to Case 2.

By the finiteness of the problem, there is an optimal matching μ that is not necessarily Figure 8 consistent. By what we have shown above, we can construct an optimal matching μ' that is Figure 8 consistent from the matching μ, by iteratively replacing the exchanges that are excluded from Figure 8 with those that are included in it. ■

Lemma 4 *Suppose that the lung exchange pool $\mathcal{E}$ satisfies the long-run assumption and $n(A-A-B)+n(A-B-B) > n(B-O-A)$. If a matching μ is Figure 8 consistent and includes at least* *one three-way exchange involving an $A-O-B$ and a $B-O-A$ type, then there is a matching μ' such that: (i) μ' is Figure 8 consistent, (ii) μ' induces at least as many transplants as μ and (iii) μ' includes one less three-way exchange involving an $A-O-B$ and a $B-O-A$ type compared to μ.*

Proof of Lemma 4: To construct μ', we first undo exactly one three-way exchange in μ that involves an $A-O-B$ and a $B-O-A$ type. In the following, we will call these $A-O-B$ and $B-O-A$ types, "the $A-O-B$ type" and "the $B-O-A$ type." To finish constructing μ', we consider five cases:

Case 1. "There is an unmatched $A-A-B$ or $A-B-B$ type under μ": Then create a three-way exchange involving that type and the $B-O-A$ type.

If we do not fall into Case 1, then all $A-A-B$ and $A-B-B$ types are matched under μ; but since $n(A-A-B)+n(A-B-B) > n(B-O-A)$, they cannot all be part of a three-way exchange with $B-O-A$ types. That leaves out four more cases:

Case 2. "An $A-A-B$ and a $B-B-A$ type are part of a two-way exchange under μ": Then undo that two-way exchange and create two new three-way exchanges, one involving the unmatched $A-A-B$ type and the $B-O-A$ type, and another involving the unmatched $B-B-A$ type and the $A-O-B$ type.

Case 3. "Two $A-A-B$ types and a $B-A-A$ type are part of a three-way exchange under μ": Then undo that three-way exchange and create two new three-way exchanges, one involving one of the two unmatched $A-A-B$ types and the $B-O-A$ type, and another involving the unmatched $B-A-A$ type and the $A-O-B$ type.

Case 4. "An $A-B-B$ and a $B-A-A$ type are part of a two-way exchange under μ": Then undo that two-way exchange and create two new three-way exchanges, one involving the unmatched $A-B-B$ type and the $B-O-A$ type, and another involving the unmatched $B-A-A$ type and the $A-O-B$ type.

Case 5. "An $A-B-B$ type and two $B-B-A$ types are part of a three-way exchange under μ": Then undo that three-way exchange and create two new three-way exchanges, one involving the unmatched $A-B-B$ type and the $B-O-A$ type, and another involving one of the two unmatched $B-B-A$ types and the $A-O-B$ type.

In each of the five cases considered above, the newly constructed matching μ' satisfies (i)–(iii) in Lemma 4. ■

Proof of Theorem 2: Define the numbers K_A and K_B by:

$$K_A := n(A-O-B) - n(B-B-A) - n(B-A-A)$$

$$K_B := n(B-O-A) - n(A-A-B) - n(A-B-B)$$

We will consider two cases depending on the signs of K_A and K_B.

Case 1. "$\max\{K_A, K_B\} \geq 0$":

Suppose without loss of generality that $K_A \leq K_B$. Then, $K_B = \max\{K_A, K_B\} \geq 0$. This implies, by the definition of K_B, that $n(B-O-A) \geq n(A-A-B) + n(A-B-B)$. Therefore, all $A-A-B$ and $A-B-B$ types participate in three-way exchanges with $B-O-A$ types in Step 2 of the algorithm.

The number of $A-O-B$ types that are not matched in Step 2 is given by:

$$\begin{aligned}
& n(A-O-B) - \min\{n(B-B-A) + n(B-A-A), n(A-O-B)\} \\
&\quad = \max\{n(A-O-B) - n(B-B-A) - n(B-A-A), 0\} \\
&\quad = \max\{K_A, 0\} \\
&\quad \leq K_B = n(B-O-A) - n(A-A-B) - n(A-B-B).
\end{aligned}$$

As a result, the number of $A-O-B$ types that are not matched in Step 2 is less than or equal to the number of $B-O-A$ types that are not matched in Step 2. Therefore, all $A-O-B$ types participate in three way exchanges in Steps 2 and 3 of the algorithm.

We have shown that the algorithm creates at least $3 \times [n(A-A-B)+n(A-B-B)+n(A-O-B)]$ transplants. Since each exchange consists of at most three participants and must involve an A blood-type patient, this is also an upper bound on the number of transplants through two and three-way exchanges. Therefore, the outcome of the algorithm must be optimal.

Case 2. "$\max\{K_A, K_B\} < 0$":

By Lemma 3, there exists an optimal matching μ_0 that is Figure 8 consistent. Since $K_B < 0$, we have $n(A-A-B) + n(A-B-B) > n(B-O-A)$. Therefore, we can iteratively apply Lemma 4 to μ_0, to obtain an optimal and Figure 8 consistent matching μ_1 that does not include a three-way exchange involving an $A-O-B$ and a $B-O-A$ type.

Let Δ_A denote the number of unmatched $A-O-B$ types in μ_1. Since $K_A < 0$, i.e., $n(B-B-A) + n(B-A-A) > n(A-O-B)$, there is more than Δ_A many participants with $B-B-A$ or $B-A-A$ types, who do not take part in an exchange with $A-O-B$ types in μ_1. Choose an arbitrary Δ_A many of these $B-B-A$ or $B-A-A$ participants, undo the exchanges they participate in under μ_1, and create Δ_A new three-way exchanges involving these participants and the unmatched $A-O-B$ types.

Similarly, let Δ_B denote the number of unmatched $B-O-A$ types in μ_1. Since $K_B < 0$, i.e., $n(A-A-B) + n(A-B-B) > n(B-O-A)$, there is more than Δ_B many participants with $A-A-B$ or $A-B-B$ types, who do not take part in an exchange with $B-O-A$ types in μ_1. Choose an arbitrary Δ_B many of these $A-A-B$ or $A-B-B$ participants, undo the exchanges they participate in under μ_1, and create Δ_B new three-way exchanges involving these participants and the unmatched $B-O-A$ types.

The new matching μ_2 obtained from μ_1 in the above manner is Figure 8 consistent. Furthermore μ_2 induces at least as many transplants as μ_1, therefore it is also optimal. Note also that under μ_2, all $A-O-B$ types take part in a three-way exchange with $B-B-A$ or $B-A-A$ types, and all $B-O-A$ types take part in a three-way exchange with $A-A-B$ or $A-B-B$ types.

Let μ denote an outcome of the sequential matching algorithm described in the text. Since $K_A, K_B < 0$, the constraint $(*)$ in Step 1 becomes equivalent to:

1. Leave at least a total $n(B-O-A)$ of $A-A-B$ and $A-B-B$ types unmatched.

2. Leave at least a total $n(A-O-B)$ of $B-B-A$ and $B-A-A$ types unmatched.

Therefore in Step 2 of the algorithm, all $A-O-B$ types take part in a three-way exchange with $B-B-A$ or $B-A-A$ types, and all $B-O-A$ types take part in a three-way exchange with $A-A-B$ or $A-B-B$ types. This implies that the total number of transplants from exchanges involving $A-O-B$ or $B-O-A$ types is the same $(= 3 \times [n(A-O-B) + n(B-O-A)])$ for both matchings μ_2 and μ.

The restriction of the matching μ_2 to the two and three-way exchanges represented as edges among $A-A-B$, $A-B-B$, $B-B-A$, and $B-A-A$ types in Figure 8, respects the constraint $(*)$. Therefore, the total number of transplants in μ_2 from exchanges not involving $A-O-B$ nor $B-O-A$ types cannot exceed the total number of transplants in Step 1 of the algorithm leading to μ. As a result, the total number of transplants under μ is at least as large as the total number of transplants under μ_2, implying that μ is also optimal. ■

Appendix B The Sub-algorithm of the Sequential Matching Algorithm for Two-&Three-way Exchanges

In this section, we present a sub-algorithm that solves the constrained optimization problem in Step 1 of the matching algorithm for two-&three-way exchanges. We define:

$$\kappa_A := \min\{n(A-A-B) + n(A-B-B), n(B-O-A)\}$$
$$\kappa_B := \min\{n(B-B-A) + n(B-A-A), n(A-O-B)\}$$

We can equivalently restate Step 1 by strengthening constraint $(*)$ to be satisfied with equality:

> Carry out the two and three way exchanges in Figure 8 among $A-A-B$, $A-B-B$, $B-B-A$, and $B-A-A$ types to maximize the number of transplants subject to the

following constraints (**):

1. Leave *exactly* a total of κ_A of $A-A-B$ and $A-B-B$ types unmatched.
2. Leave *exactly* a total of κ_B of $B-B-A$ and $B-A-A$ types unmatched.

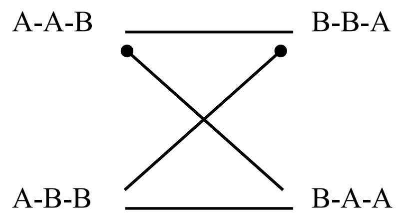

Figure 10: The Exchanges in Step 1 of the Two-&Three-Way Matching Algorithm

Figure 10 summarizes the two-and three-way exchanges that may be carried out in Step 1 above. In the following discussion, we restrict attention to the types and exchanges represented in Figure 10.

In order to satisfy the first part of constraint (**), we can set aside any combination l_A of $A-A-B$ types and m_A of $A-B-B$ types, where l_A and m_A are integers satisfying

$$0 \leq l_A \leq n(A-A-B),\ 0 \leq m_A \leq n(A-B-B), \quad \text{and } l_A + m_A = \kappa_A. \tag{1}$$

For any l_A and m_A satisfying Equation (1), the remaining number γ_A of B donors of A patients is:

$$\gamma_A = n(A-A-B) - l_A + 2[n(A-B-B) - m_A] \tag{2}$$

Let $\underline{l}_A$ and $\bar{l}_A$ [$\underline{m}_A$ and $\bar{m}_A$] be the smallest and largest values of l_A [m_A] among (l_A, m_A) pairs that satisfy Equation (1). Then, the possible numbers of remaining B donors of A patients after satisfying the first part of condition (**) is an integer interval $[\underline{\gamma}_A, \bar{\gamma}_A]$ where

$$\underline{\gamma}_A = n(A-A-B) - \underline{l}_A + 2[n(A-B-B) - \bar{m}_A]$$

$$\bar{\gamma}_A = n(A-A-B) - \bar{l}_A + 2[n(A-B-B) - \underline{m}_A]$$

We can analogously define the integers $\underline{l}_B$, $\bar{l}_B$, $\underline{m}_B$, and $\bar{m}_B$, $\underline{\gamma}_B$, and $\bar{\gamma}_B$ such that the possible numbers of remaining A donors of B patients that respect the second part of constraint (**) is an integer interval $[\underline{\gamma}_B, \bar{\gamma}_B]$.

In the first step of the sub-algorithm, we determine which combination of types to set aside to satisfy constraint (**). We will consider three cases depending on the relative positions of the intervals $[\underline{\gamma}_A, \bar{\gamma}_A]$ and $[\underline{\gamma}_B, \bar{\gamma}_B]$.

Sub-algorithm 1 (Sub-algorithm of the Sequential Matching Algorithm for Two-&Three-way Exchanges)

Step 1:

We first determine γ_A and γ_B:

Case 1. "$[\underline{\gamma}_A, \bar{\gamma}_A] \cap [\underline{\gamma}_B, \bar{\gamma}_B] \neq \emptyset$": Choose any $\gamma_A = \gamma_B \in [\underline{\gamma}_A, \bar{\gamma}_A] \cap [\underline{\gamma}_B, \bar{\gamma}_B]$.

Case 2. "$\bar{\gamma}_A < \underline{\gamma}_B$":

Case 2.1. If $n(A-A-B) - \bar{l}_A - [n(B-B-A) - \underline{l}_B]$ is positive and odd; and $\underline{\gamma}_A < \bar{\gamma}_A$, then set $\gamma_A = \bar{\gamma}_A - 1$ and $\gamma_B = \underline{\gamma}_B$.

Case 2.2. Otherwise, set $\gamma_A = \bar{\gamma}_A$ and $\gamma_B = \underline{\gamma}_B$.

Case 3. "$\bar{\gamma}_B < \underline{\gamma}_A$": Symmetric to Case 2, interchanging the roles of A and B.

Then, we set aside l_A many $A-A-B$'s and m_A many $A-B-B$'s, where the integers l_A and m_A are uniquely determined by Equations (1) and (2) to ensure that the remaining number of B donors of A patients is γ_A. The integers l_B and m_B are determined analogously.

Step 2:

In two special cases explained below, the second step of the sub-algorithm sets aside one extra triple, on top of those already set aside in Step 1.

Case 1. If $\bar{\gamma}_A < \underline{\gamma}_B$, $n(A-A-B) - \bar{l}_A - [n(B-B-A) - \underline{l}_B]$ is positive and odd; $\underline{\gamma}_A = \bar{\gamma}_A$, and $n(B-B-A) - \underline{l}_B > 0$, then set an extra $B-B-A$ triple aside.

Case 2. If $\bar{\gamma}_B < \underline{\gamma}_A$, $n(B-B-A) - \bar{l}_B - [n(A-A-B) - \underline{l}_A]$ is positive and odd; $\underline{\gamma}_B = \bar{\gamma}_B$, and $n(A-A-B) - \underline{l}_A > 0$, then set an extra $A-A-B$ triple aside.

Step 3:

After having set the triples determined in Steps 1 and 2 of the sub-algorithm aside, we sequentially maximize three subsets of exchanges among the remaining triples in Figure 10.

Step 3.1: Carry out the maximum number of two-way exchanges between the $A-A-B$ and $B-B-A$ types.

Step 3.2: Carry out the maximum number of three-way exchanges consisting of two $A-A-B$ and one $B-A-A$ triple, and those consisting of two $B-B-A$ and one $A-B-B$ triple, among the remaining types.

Step 3.3: Carry out the maximum number of two-way exchanges between the remaining $A-B-B$ and $B-A-A$ types.

Figure 11 graphically illustrates the two and three-way exchanges that are carried out at Steps 3.1–3.3 of the sub-algorithm.

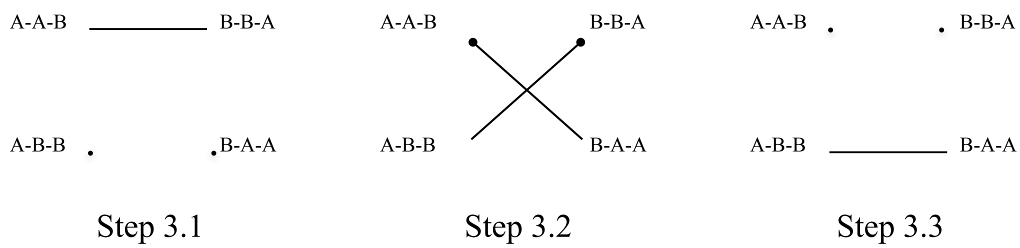

Figure 11: Steps 3.1–3.3 of the Sub-algorithm

Proposition 1 *The sub-algorithm described above solves the constrained optimization problem in Step 1 of the matching algorithm for two-&three-way exchanges.*

Proof: Constraint $(*)$ is satisfied by construction since in Step 1 of the sub-algorithm γ_i is chosen from $[\underline{\gamma}_i, \bar{\gamma}_i]$ for $i = A, B$. Below, we show optimality by considering different cases.

Case 1. "$[\underline{\gamma}_A, \bar{\gamma}_A] \cap [\underline{\gamma}_B, \bar{\gamma}_B] \neq \emptyset$": In this case, Step 1 of the sub-algorithm sets $\gamma_A = \gamma_B$, i.e.:

$$n(A-A-B) - l_A + 2[n(A-B-B) - m_A] = n(B-B-A) - l_B + 2[n(B-A-A) - m_B]$$

and no extra triple is set aside in Step 2. Note that the above equality implies that at the end of Step 3.1 of the sub-algorithm, the numbers of remaining $A-A-B$ and $B-B-A$ triples are even (at least one being zero). So again by the above equality, all triples that are not set aside in Step 1 take part in two and three-way exchanges by the end of Step 3 of the sub-algorithm. This implies optimality.

Case 2. "$\bar{\gamma}_A < \underline{\gamma}_B$, i.e.,

$$n(A-A-B) - \bar{l}_A + 2[n(A-B-B) - \underline{m}_A] < n(B-B-A) - \underline{l}_B + 2[n(B-A-A) - \bar{m}_B]\text{"} : \quad (3)$$

We next establish an upper bound on the number of triples with B patients that can participate in two and three-way exchanges. Suppose that p_B many $B-B-A$ triples and r_B many $B-A-A$ triples can take part in two and three-way exchanges while respecting condition $(*)$. Since matching each $B-B-A$ triple requires one B donor of A patients; matching each $B-A-A$ triple requires two B donors of A patients; and the maximum number of B donors of A patients is $\bar{\gamma}_A$, we have the constraint:

$$p_B + 2r_B \leq \bar{\gamma}_A$$

Note also that $p_B \leq \bar{p}_B := n(B-B-A) - \underline{l}_B$. Therefore we can not match any more triples with B patients than the bound:

$$\begin{array}{rcll} \bar{p}_B + \frac{1}{2}(\bar{\gamma}_A - \bar{p}_B) & = & \max_{p_B, r_B \in \mathbb{R}} & p_B + r_B \\ & & \text{s.t.} & p_B + 2r_B \leq \bar{\gamma}_A \\ & & & p_B \leq \bar{p}_B \end{array} \tag{4}$$

Case 2.1. "*$n(A-A-B) - \bar{l}_A - [n(B-B-A) - \underline{l}_B]$ is positive and odd; and $\underline{\gamma}_A < \bar{\gamma}_A$*":

Note that $\gamma_A = \bar{\gamma}_A - 1$ and $\gamma_B = \underline{\gamma}_B$ imply that $l_A = \bar{l}_A - 1$, $m_A = \underline{m}_A + 1$, $l_B = \underline{l}_B$, and $m_B = \bar{m}_B$. So $n(A-A-B) - l_A - [n(B-B-A) - l_B]$ is positive and even. Furthermore, no extra triple is set aside in Step 2. Therefore, an even number of $A-A-B$ types remain unmatched at the end of Step 3.1. Also, by Equation (3),

$$n(A-A-B) - l_A + 2[n(A-B-B) - m_A] < n(B-B-A) - l_B + 2[n(B-A-A) - m_B] \tag{5}$$

So all the $A-B-B$ types available at the end of Step 3.1 take part in three-way exchanges with $B-A-A$ types in Step 3.2; and there are enough remaining $B-A-A$ types to accommodate all $A-B-B$ types in Step 3.3. Therefore, all triples with A donors that are not set aside in Step 1 take part in two and three-way exchanges in Step 3 of the sub-algorithm.

We next show that it is impossible to match more triples with B patients while respecting constraint $(*)$, which will prove optimality. Since in Case 2.1, $\bar{\gamma}_A - \bar{p}_B$ is odd and $\gamma_A = \bar{\gamma}_A - 1$, rounding down the upper bound in Equation (4) to the nearest integer gives:

$$\bar{p}_B + \frac{1}{2}(\gamma_A - \bar{p}_B).$$

Note that this is the number of triples with B patients that take part in two and three way exchanges in Step 3 of the sub-algorithm. (In Step 3.1, $\bar{p}_B \equiv n(B-B-A) - \underline{l}_B$ many $B-B-A$ triples take part in two-way exchanges; and in Steps 3.2 and 3.3, $\frac{1}{2}(\gamma_A - \bar{p}_B)$ many $B-A-A$ triples take part in two and three way exchanges.)

Case 2.2. We further break Case 2.2 into four different subcases:

Case 2.2.1. "*$n(A-A-B) - \bar{l}_A - [n(B-B-A) - \underline{l}_B]$ is positive and odd; $\underline{\gamma}_A = \bar{\gamma}_A$, and $n(B-B-A) - \underline{l}_B > 0$*":

Note that $\gamma_A = \bar{\gamma}_A$ and $\gamma_B = \underline{\gamma}_B$ imply that $l_A = \bar{l}_A$, $m_A = \underline{m}_A$, $l_B = \underline{l}_B$, and $m_B = \bar{m}_B$. So $n(A-A-B) - l_A - [n(B-B-A) - l_B]$ is positive and odd and Equation (5) holds. Since one more $B-B-A$ triple is set aside in Step 2, an even number of $A-A-B$ types remain unmatched at the end of Step 3.1. By Equation (5), all triples with A donors that are not set aside in Step 1 take part in two and three-way exchanges in Step 3 of the sub-algorithm.

We next show that it is impossible to match more triples with B patients while respecting constraint $(*)$, which will prove optimality. Since in this case, $\bar{\gamma}_A - \bar{p}_B$ is odd and $\gamma_A = \bar{\gamma}_A$, rounding down the upper bound in Equation (4) to the nearest integer gives:

$$\bar{p}_B - 1 + \frac{1}{2}[\gamma_A - (\bar{p}_B - 1)].$$

Note that this is the number of triples with B patients that take part in two and three way exchanges in Step 3 of the sub-algorithm (In Step 3.1, $\bar{p}_B - 1 \equiv n(B-B-A) - \underline{l}_B - 1$ many $B-B-A$ triples take part in two-way exchanges; and in Steps 3.2 and 3.3, $\frac{1}{2}[\gamma_A - (\bar{p}_B - 1)]$ many $B-A-A$ triples take part in two and three way exchanges.)

Case 2.2.2. "$n(A-A-B) - \bar{l}_A - [n(B-B-A) - \underline{l}_B]$ *is positive and odd,* $\underline{\gamma}_A = \bar{\gamma}_A$*, and* $n(B-B-A) - \underline{l}_B = 0$":

Since $n(B-B-A) \geq \bar{l}_B \geq \underline{l}_B$ and $n(B-B-A) - \underline{l}_B = 0$, we have $\bar{l}_B = \underline{l}_B$, which implies that $\bar{\gamma}_B = \underline{\gamma}_B$. Since $\underline{\gamma}_A = \bar{\gamma}_A$ and $\underline{\gamma}_B = \bar{\gamma}_B$, in this case, the choice of γ_A and γ_B in Step 1 of the sub-algorithm correspond to the unique way of satisfying constraint $(**)$. That is, $\gamma_A = \underline{\gamma}_A = \bar{\gamma}_A$ and $\gamma_B = \underline{\gamma}_B = \bar{\gamma}_B$, $l_A = \underline{l}_A = \bar{l}_A$, $m_A = \underline{m}_A = \bar{m}_A$, $l_B = \underline{l}_B = \bar{l}_B$, and $m_B = \underline{m}_B = \bar{m}_B$. Also, Equation (5) holds.

So $n(A-A-B) - l_A$ is positive and odd and $n(B-B-A) - l_B = 0$. Furthermore, no extra triple is set aside in Step 2. Therefore, there are no matches in Step 3.1 and all of the (odd number of) $A-A-B$ triples are available in the beginning of Step 3.2. By Equation (5), all but one of these $A-A-B$ triples take part in three-way exchanges with $B-A-A$ types in Step 3.2; and there are enough remaining $B-A-A$ types to accommodate all $A-B-B$ types in Step 3.3. Therefore, all triples with A donors, except one $A-A-B$ triple, that are not set aside in Step 1 take part in two and three-way exchanges in Step 3 of the sub-algorithm.

To see that it is not possible to match any more triples with A patients, remember that in the current case the combination of triples that are set aside in Step 1 of the algorithm is determined uniquely; and note that since there are no remaining $B-B-A$ triples, the $A-A-B$ triples can only participate in three-way exchanges with $B-A-A$ triples. Each such three-way exchange requires exactly two $A-A-B$ triples, therefore it is impossible to match all of the (odd number of) $A-A-B$ triples.

We next show that it is impossible to match more triples with B patients while respecting constraint $(*)$ which will prove optimality. Since in Case 2.2.2, $\bar{\gamma}_A - \bar{p}_B$ is odd and $\gamma_A = \bar{\gamma}_A$, rounding down the upper bound in Equation (4) to the nearest integer gives:

$$\bar{p}_B + \frac{1}{2}[(\gamma_A - 1) - \bar{p}_B].$$

Note that this is the number of triples with B patients that take part in two and three way exchanges in Step 3 of the sub-algorithm (In Step 3.1, $\bar{p}_B \equiv n(B-B-A) - \underline{l}_B$ many $B-B-A$ triples take part in two-way exchanges; and in Steps 3.2 and 3.3, $\frac{1}{2}[(\gamma_A - 1) - \bar{p}_B]$ many $B - A - A$ triples take part in two and three way exchanges.)

Case 2.2.3. "$n(A - A - B) - \bar{l}_A - [n(B - B - A) - \underline{l}_B]$ *is positive and even*":

Note that $\gamma_A = \bar{\gamma}_A$ and $\gamma_B = \underline{\gamma}_B$ imply that $l_A = \bar{l}_A$, $m_A = \underline{m}_A$, $l_B = \underline{l}_B$, and $m_B = \bar{m}_B$. So $n(A - A - B) - l_A - [n(B - B - A) - l_B]$ is positive and even and Equation (5) holds. Since no other triple is set aside in Step 2, an even number of $A - A - B$ types remain unmatched at the end of Step 3.1. By Equation (5), all triples with A donors that are not set aside in Step 1 take part in two and three-way exchanges in Step 3 of the sub-algorithm.

We next show that it is impossible to match more triples with B patients while respecting constraint $(*)$, which will prove optimality. Since in this case, $\bar{\gamma}_A - \bar{p}_B$ is even and $\gamma_A = \bar{\gamma}_A$, the upper bound in Equation (4) is integer valued:

$$\bar{p}_B + \frac{1}{2}[\gamma_A - \bar{p}_B].$$

Note that this is the number of triples with B patients that take part in two and three way exchanges in Step 3 of the sub-algorithm (In Step 3.1, $\bar{p}_B \equiv n(B - B - A) - \underline{l}_B$ many $B - B - A$ triples take part in two-way exchanges; and in Steps 3.2 and 3.3, $\frac{1}{2}(\gamma_A - \bar{p}_B)$ many $B - A - A$ triples take part in two and three way exchanges.)

Case 2.2.4. "$n(A - A - B) - \bar{l}_A - [n(B - B - A) - \underline{l}_B] \leq 0$":

Note that $\gamma_A = \bar{\gamma}_A$ and $\gamma_B = \underline{\gamma}_B$ imply that $l_A = \bar{l}_A$, $m_A = \underline{m}_A$, $l_B = \underline{l}_B$, and $m_B = \bar{m}_B$. Also Equation (5) holds. Since no other triple is set aside in Step 2 and $n(B - B - A) - l_B \geq n(A - A - B) - l_A$, all $A - A - B$ triples are matched in Step 3.1. By Equation (5), there are sufficient remaining $B - B - A$ and $B - A - A$ triples to ensure that all $A - B - B$ triples take part in two and three-way exchanges in Steps 3.2 and 3.3. So all triples with A donors that are not set aside in Step 1 take part in two and three-way exchanges in Step 3 of the sub-algorithm.

We next show that it is impossible to match more triples with B patients while respecting constraint $(*)$ by considering three cases, which will prove optimality.

Suppose first that $\bar{\gamma}_A - \bar{p}_B \leq 0$. Since matching each triple with a B patient requires at least one B donor of an A patient; and the maximum number of B donors of A patients is $\bar{\gamma}_A$, we can not match more triples with a B patient than $\bar{\gamma}_B$. Since in this case $n(B-B-A)-\underline{l}_B \equiv \bar{p}_B \geq \bar{\gamma}_A = \gamma_A$, the sub-algorithm matches $\bar{\gamma}_A$ many $B - B - A$ triples in Steps 3.1 and 3.2 which achieves this upper bound.

Suppose next that $\bar{\gamma}_A - \bar{p}_B$ is positive and even. Then, the upper bound in Equation (4) is integer valued, and since $\gamma_A = \bar{\gamma}_A$, it can be written as:

$$\bar{p}_B + \frac{1}{2}(\gamma_A - \bar{p}_B).$$

Note that this is the number of triples with B patients that take part in two and three way exchanges in Step 3 of the sub-algorithm (In Steps 3.1 and 3.2, $\bar{p}_B \equiv n(B-B-A) - \underline{l}_B$ many $B-B-A$ triples take part in two- and three-way exchanges; and in Step 3.3, $\frac{1}{2}(\gamma_A - \bar{p}_B)$ many $B-A-A$ triples take part in two-way exchanges.)

Suppose last that $\bar{\gamma}_A - \bar{p}_B$ is positive and odd. Then, since $\gamma_A = \bar{\gamma}_A$, rounding down the upper bound in Equation (4) to the nearest integer gives:

$$\bar{p}_B - 1 + \frac{1}{2}[\gamma_A - (\bar{p}_B - 1)].$$

Note that this is the number of triples with B patients that take part in two and three way exchanges in Step 3 of the sub-algorithm (In Steps 3.1 and 3.2, $\bar{p}_B - 1 \equiv n(B-B-A) - \underline{l}_B - 1$ many $B-B-A$ triples take part in two- and three-way exchanges; and in Step 3.3, $\frac{1}{2}[\gamma_A - (\bar{p}_B - 1)]$ many $B-A-A$ triples take part in two-way exchanges.)

Case 3. "$\bar{\gamma}_B < \underline{\gamma}_A$": Symmetric to Case 2, interchanging the roles of A and B. ■

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Appendix C Proof of Theorem 3 and Other Results for Unrestricted Exchanges

Before delving into the analysis, we introduce some new terminology. For a given exchange pool $\mathcal{E}$, we refer to an exchange pool $\mathcal{K} \leq \mathcal{E}$ as a **sub-pool of** $\mathcal{E}$. We fix a lung exchange pool $\mathcal{E}$ throughout the section. Given a sub-pool $\mathcal{K}$ let $D_X[\mathcal{K}]$ be the *number of X blood-type donors in* $\mathcal{K}$ and $P_X[\mathcal{K}]$ as the *number of X blood-type patients in* $\mathcal{K}$. We also use $n(X-Y-Z)[\mathcal{K}]$ to denote the number of $X-Y-Z$ type triples in $\mathcal{K}$ (while we omit the arguments of these expressions if $\mathcal{K}=\mathcal{E}$). For a sub-pool $\mathcal{K}$, by a slight abuse of notation, let $|\mathcal{K}|$ be the total number of triples in $\mathcal{K}$. Given a matching μ, we will sometimes denote *the sub-pool of triples matched through it* also as μ, with a slight abuse of notation.

We denote by $\mathbb{E}_X$ for $X \in \{A, B\}$, the triple types with X blood-type patients that are **essential** for exchange:

$$\mathbb{E}_A := \left\{A-A-B \ , \ A-O-B \ , \ A-B-B\right\}, \text{ and}$$
$$\mathbb{E}_B := \left\{B-B-A \ , \ B-O-A \ , \ B-A-A\right\}.$$

That is, for any exchange at least one triple with a type in $\mathbb{E}_A$ and one triple with a type in $\mathbb{E}_B$ is needed by Lemma 2. Let $\mathbb{I} \subseteq \mathcal{B}^3$ be all triple types that are exchange eligible (i.e., not compatible). Let $\mathcal{E}_{\mathbb{E}_A \cup \mathbb{E}_B} \leq \mathcal{E}$ be the sub-pool with only essential type triples.

The first lemma will be the most crucial intermediate result and it will reduce the problem and enable us to focus only on essential type triples in constructing an optimal matching. This is a counterpart of Lemma 3 for unrestricted exchange sizes:

Lemma 5 *Suppose that $\mathcal{E}$ satisfies the long-run assumption and μ is an optimal matching (without any exchange size constraints) in the essential type sub-pool $\mathcal{E}_{\mathbb{E}_A \cup \mathbb{E}_B}$. Suppose further that μ matches the maximum possible number of $A-O-B$ and $B-O-A$ type triples that can be matched in any matching in $\mathcal{E}_{\mathbb{E}_A \cup \mathbb{E}_B}$.*

1. *Then μ can be modified to obtain a matching ν such that $n(A-O-B)[\mu]+n(B-O-A)[\mu]$-many $O-O-A$ and $O-O-B$ type triples can be matched in addition to all triples matched by μ.*
2. *Moreover, ν is an optimal matching of $\mathcal{E}$ without any exchange size constraints.*

Proof of Lemma 5: The first part of the Lemma is easy to prove: Take any $B-O-A$ or $A-O-B$ type triple i matched in μ. If i's O donor is donating to an A patient then take a triple

j of type $O-O-A$ and otherwise take a triple j of type $O-O-B$. Modify μ as follows: Let i's and j's O donors donate to j's patient and j's non-O donor donate to the patient i's O donor was previously donating in μ. Otherwise, do not change any other donations in μ. We repeat the procedure for all $B-O-A$ and $A-O-B$ triples matched in μ. Let ν be the matching obtained as a result of this procedure. It matches $n(A-O-B)[\mu]+n(B-O-A)[\mu]$-many $O-O-A$ and $O-O-B$ triples.

For the second part of the lemma, we prove a claim first:

Claim: For any matching η, we can construct another matching using only the *essential type* triples matched by η.

Proof: By Lemma 2, besides the essential type triples, the triples of the types $O-A-B$, $O-A-A$, $O-B-B$, $O-O-A$, and $O-O-B$ can participate in exchange. Take a patient of a triple matched in η of one of these types. Observe that as she is of blood-type O, she receives grafts from either two or one O blood-type donors of some other patient say donor d_1 (and possibly d_2), and in return she exports one or two donors to other patient in η, say patient p_1 (and possibly p_2). We can simply take it out of η and form a new matching η' by d_1 donating to p_1 (and possibly d_2 donating to p_2) and rest of the transplants remain in tact as in η. We repeat this procedure for all triples of types $O-A-B$, $O-A-A$, $O-B-B$, $O-O-A$, and $O-O-B$ in the remaining matchings, iteratively. The final matching is feasible and consists of only essential type triples of η. QED

Suppose that η' is an arbitrary matching in $\mathcal{E}$. By Lemma 2 the types of triples that can be part of a feasible exchange except the essential types are $O-O-A$, $O-O-B$, $O-A-A$, $O-B-B$, $O-A-B$. In η', we replace each $O-A-A$ or $O-A-B$ triple with an $O-O-A$ triple and each $O-B-B$ triple with an $O-O-B$ triple in this matching. Let ν' be this matching. Observe that $|\nu'|=|\eta'|$.

We form a matching μ' by removing the non-essential type triples from ν' by the Claim. We have

$$|\mu| \geq |\mu'| \tag{6}$$

by optimality of μ in $\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$. We also have

$$n(A-O-B)[\nu]+n(B-O-A)[\nu] \geq n(A-O-B)[\nu']+n(B-O-A)[\nu'] \tag{7}$$

by the fact that μ maximizes the number of $A-O-B$ and $B-O-A$ triples matched in $\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$.

The $O-O-A$ and $O-O-B$ triples in ν' require at least $n(O-O-B)[\nu']+n(O-O-A)[\nu']$-many other triples with O donors in ν'. Hence, we have

$$\begin{aligned} n(O-O-A)[\nu]+n(O-O-B)[\nu] &= n(A-O-B)[\nu]+n(B-O-A)[\nu] \\ &\geq n(A-O-B)[\nu']+n(B-O-A)[\nu'] \\ &\geq n(O-O-A)[\nu']+n(O-O-B)[\nu'], \end{aligned}$$

where the equality follows from the construction of ν, the first inequality follows from Equation 7, and the last inequality follows from the feasibility of ν'. This and Equation 6 imply $|\nu| \geq |\nu'| = |\eta'|$. ■

If we can show that it is possible to construct a matching μ, which simultaneously matches

1. the maximum number of $A-O-B$ and $B-O-A$ type triple in any possible matching, and
2. the maximum number of essential type triples,

then using Lemma 5, we can construct an optimal matching using μ and it matches $|\mu|+n(A-O-B)[\mu]+n(B-O-A)[\mu]$ triples receiving transplants. This will also give us the optimal number of triples that can be matched through lung exchange using unrestricted sizes of exchanges.

Hence, our goal is two reach the above two goals simultaneously. Next, we define two non-negative numbers for triples in $\mathcal{E}_{\mathbb{E}_A \cup \mathbb{E}_B}$. These tell us the minimum ($\underline{s}_A$) and maximum ($\overline{s}_A$) numbers of donors compatible with B blood-type patients that can be **supplied** by patients with A blood-type patients:

$$\underline{s}_A := n(A-O-B)+n(A-A-B)+2n(A-B-B) \tag{8}$$

$$\overline{s}_A := 2n(A-O-B)+n(A-A-B)+2n(A-B-B) \tag{9}$$

Here, $\underline{s}_A$ assumes that all $A-O-B$ type triples are *treated* like $A-A-B$ types and hence, the O blood-type donor can be utilized internally. Hence, each $A-O-B$ type triple requires one donor from outside, so does each $A-A-B$ triple. On the other hand, each $A-B-B$ type triple needs 2 donors from outside.

In calculation of $\overline{s}_A$, we *treat* $A-O-B$ type triples like $A-B-B$'s. Therefore, each of them requires 2 donors from outside instead of 1. Symmetrically, we define $\underline{s}_B$ and $\overline{s}_B$. Observe that

$$\overline{s}_A - \underline{s}_A = n(A-O-B) \quad \text{and} \quad \overline{s}_B - \underline{s}_B = n(B-O-A).$$

We define a sub-algorithm using these numbers through the intuition given above:

Sub-algorithm 2 (Group and Match Sub-algorithm for Triple Types $A-O-B$, $A-B-B$, $A-A-B$, $B-O-A$, $B-A-A$, $B-B-A$)

Group: Two cases are possible for $\underline{s}_A, \overline{s}_A, \underline{s}_B, \overline{s}_B$ defined in Equations 8 and 9.

Case 1. "$[\underline{s}_A, \overline{s}_A] \cap [\underline{s}_B, \overline{s}_B] \neq \emptyset$":

Fix α_A, α_B such that $0 \leq \alpha_A \leq n(A-O-B)$, $0 \leq \alpha_B \leq n(B-O-A)$, and $\overline{s}_A - \alpha_A = \overline{s}_B - \alpha_B$:

1. **Group** α_A-many $A-O-B$ type triples with $A-A-B$ types and the rest with $A-B-B$ types.
2. **Group** α_B-many $B-O-A$ type triples with $B-B-A$ types and the rest with $B-A-A$ types.

Case 2. "$\overline{s}_B < \underline{s}_A$":

1. **Group** all $A-O-B$ type triples (that is, $(\overline{s}_A - \underline{s}_A)$-many) with $A-A-B$ types (i.e., $\alpha_A = \overline{s}_A - \underline{s}_A$).
2. **Group** all $B-O-A$ type triples (that is $(\overline{s}_B - \underline{s}_B)$-many) with $B-A-A$ types (i.e., $\alpha_B = \overline{s}_B - \underline{s}_B$).

Case 3. "$\overline{s}_A < \underline{s}_B$": Symmetric situation with Case 2 replacing A blood type with B.

We refer to all $X-O-Z$ type triples *grouped* with $X-Y-Z$ triples and all $X-Y-Z$ triples for all for $X, Y, Z \in \{A, B\}$ such that $X \neq Z$ as $X-Y-Z$**-like group**.

Match: Starting with the triples with O donors in each group determined:

Step 1: Carry out the maximum number of two-way exchanges between the $A-A-B$-like group and $B-B-A$-like group triples.

Step 2: Carry out the maximum number of three-way exchanges consisting of two $A-A-B$-like group triples and one $B-A-A$-like group triple, and those consisting of two $B-B-A$-like group triples and one $A-B-B$-like group triple among the remaining triples with the following exception:

- ∗ If all $B-B-A$-like group triples are matched, and an odd number of $A-O-B$ type triples and no $A-A-B$ type triples remain in the $A-A-B$-like group after Step 1: **Re-group** one of the $A-O-B$ type triples in the $A-B-B$-like group and handle it in Step 3 with the other $A-O-B$ types in the $A-B-B$-like group.
- ∗ If all $A-A-B$-like group triples are matched, and an odd number of $B-O-A$ type triples and no $B-B-A$ type triples remain in the $B-B-A$-like group after Step 1: **Re-group** one of the $B-O-A$ type triples in the $B-A-A$-like group type and handle it in Step 3 with the other $B-O-A$ types in the $B-A-A$-like group.

Step 3: Carry out the maximum number of two-way exchanges between the remaining $A-B-B$-like group and $B-A-A$-like group triples.

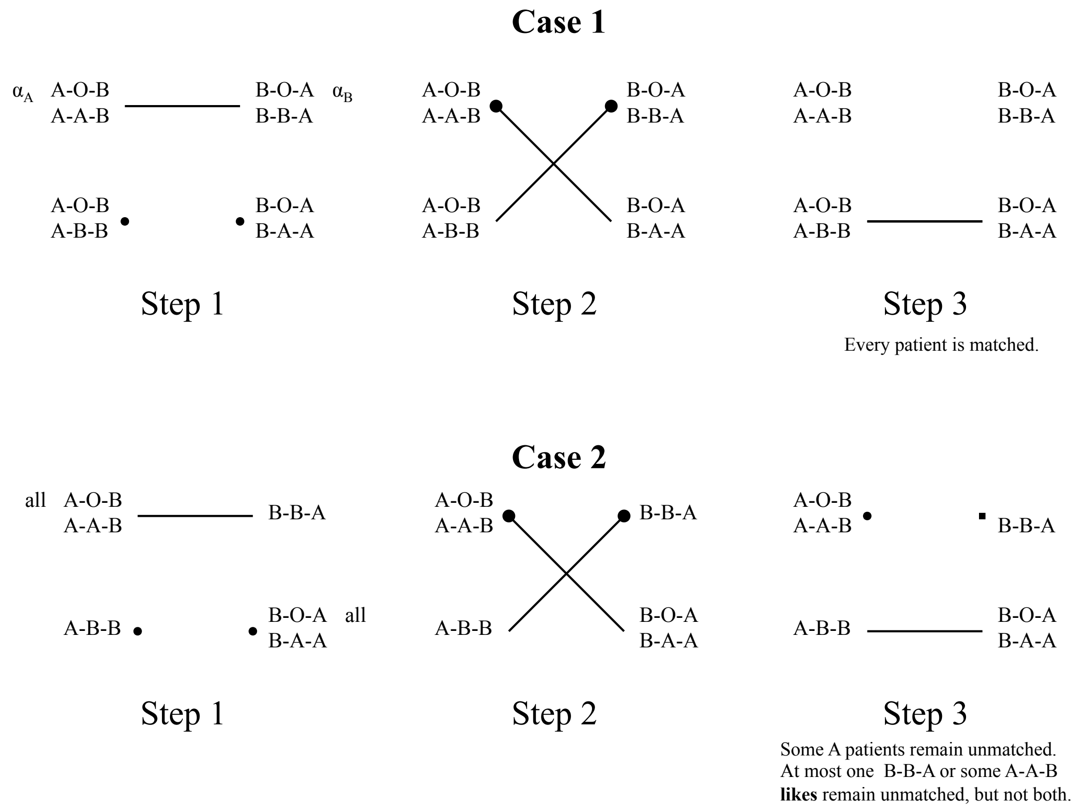

Figure 12: Cases 1 and 2 of **Group and Match Sub-algorithm** (Sub-algorithm 2). Each solid line represents two-way exchanges, and each solid line with a dot at the end represents three-way exchanges in each of which two triples participate from the group that is pointed by the circular end. Only one of the two kind three-way exchanges will be conducted in Step 2 in each subfigure.

Figure 12 summarizes how the Group and Match Sub-algorithm works, along with its consequences (to be proven in Propositions 2 and 3 below). This sub-algorithm is embedded in the optimal matching algorithm as follows:

Algorithm 3 (Sequential Matching Algorithm without Exchange Size Constraints)

Step 1: Use Sub-algorithm 2, **Group and Match**, to match triples of types $\mathbb{E}_A \cup \mathbb{E}_B$.

Step 2: In any exchange determined in this matching, for each $A-O-B$ or $B-O-A$ type triple in the exchange, insert an $O-O-A$ or an $O-O-B$ type triple using Lemma 5.

Before proving the optimality of Algorithm 3, we find an upper-bound to the number of triples that can be matched in an exchange pool:

Lemma 6 (Upper-bound Lemma) *Consider the sub-pool $\mathcal{E}_{\mathbb{E}_A \cup \mathbb{E}_B}$. Then $\overline{m}$, defined below, is an upper bound to the number of triples that can be matched in a matching only consisting of triples in*

$\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$:

$$\overline{m} := \overline{m}_A + \overline{m}_B \text{ where} \tag{10}$$
$$\overline{m}_A := \min\left\{P_A[\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}], \left\lfloor\frac{D_A[\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}] + D_O[\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}]}{2}\right\rfloor, \overline{s}_B\right\} \text{ and}$$
$$\overline{m}_B := \min\left\{P_B[\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}], \left\lfloor\frac{D_B[\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}] + D_O[\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}]}{2}\right\rfloor, \overline{s}_A\right\}.$$

Proof of Lemma 6: The first term in $\overline{m}_A$, $P_A[\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}]$, is the number of A blood-type patients and the second term, $\left\lfloor\frac{D_A[\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}]+D_O[\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}]}{2}\right\rfloor$, is the maximum number of A blood-type patients that can receive two lobes from donors that are compatible with A blood-type patients, i.e., O and A blood-type donors in $\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$. Hence, each of them is an upper-bound for the number of triples with A blood-type patients in $\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$ that can receive transplant. Next consider the third term, $\overline{s}_B = n(B-B-A) + 2n(B-O-A) + 2n(B-A-A)$ is the maximum number of A blood-type donors that the B blood-type patients can provide for the triples with A blood-type patients in $\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$. Each triple with an A blood-type patient in $\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$ requires at least one A or O blood-type donor coming from another triple to be matched feasibly, as it can at most provide one compatible donor for itself. To the contrary assume that, there exists a perfect matching for some sub-pool $\mathcal{L} \leq \mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$ such that $P_A[\mathcal{L}] > \overline{s}_B$. Hence, each of the triples with A blood-type patients in $\mathcal{L}$ requires itself one or more A or O blood-type donors from other triples, while additionally at most $\overline{s}_B$-many A or O blood-type donors are feasible within $\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$. This is a contradiction to the fact that triples in $\mathcal{L}$ can form a feasible matching. Hence, $\overline{s}_B$ is also an upper bound to the number of A blood-type patients that can be matched within $\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$, establishing the formula for $\overline{m}_A$.

The argument is the same in $\overline{m}_B$ for B blood-type patients. There are no triples with AB or O blood-type patients in $\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$. This concludes the proof and establishes $\overline{m}$ as an upper bound. ■

We will prove that the upper-bound found above is *almost* tight, and Group and Match Sub-algorithm matches always at least one less patient than $\overline{m}$ upper-bound, and sometimes matches exactly $\overline{m}$ patients. Moreover, we show that when group and match finds 1-approximate matching to the upper-bound, no more triples can be matched among the essential type triples; and thus, group and match is an optimal matching algorithm for the essential types.

Proposition 2 *An optimal matching without any exchange size constraints within $\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$ exactly matches $\overline{m}$ or $\overline{m}-1$ patients, and moreover, Sub-algorithm 2, Group and Match, finds such an optimal matching.*

Proof of Proposition 2: For notational simplicity suppose $\mathcal{E} = \mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$, i.e., $\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$ is the whole pool. Let $\widetilde{n}(X-Y-Z)$ refer to the number of $X-Y-Z$-like triples determined after the Group stage of the sub-algorithm for all $\{X, Y\} = \{A, B\}$ and $Z \in \{A, B\}$.

Case 1. "$[\underline{s}_A, \overline{s}_A] \cap [\underline{s}_B, \overline{s}_B] \neq \emptyset$": We will prove that all triples in $\mathcal{E}_{\mathbb{E}_A \cup \mathbb{E}_B}$ are matched by the sub-algorithm, and that is $\overline{m}$-many. Without loss of generality assume that

$$\Delta := \widetilde{n}(A - A - B) - \widetilde{n}(B - B - A) \geq 0.$$

Thus, all $B - B - A$-likes are matched in two-way exchanges with $A - A - B$-likes in Step 1 of the Match stage of the sub-algorithm. We first show that Δ is even, and hence, in Step 2 of the Match stage no $A - O - B$ type from the $A - A - B$-like group is re-grouped into the $A - B - B$-like group:

$$\begin{aligned}\Delta &= \alpha_A + n(A - A - B) - \alpha_B - n(B - B - A)\\ &= \overline{s}_B - \overline{s}_A + n(A - A - B) - n(B - B - A)\\ &= 2\big(n(A - B - B) + n(A - O - B) - n(B - A - A) - n(B - O - A)\big),\end{aligned}$$

showing Δ is even.

Next, we write down the number of $B - A - A$-like triples needed to match all A blood-type patients remaining in Step 2 and Step 3 of the Match stage:

$$\begin{aligned}&\underbrace{\frac{\Delta}{2}}_{\text{in Step 2}} + \underbrace{n(A - B - B) + n(A - B - O) - \alpha_A}_{\text{in Step 3}}\\ =&\frac{\alpha_A + n(A - A - B) - \alpha_B - n(B - B - A)}{2} + n(A - B - B) + n(A - B - O) - \alpha_A\\ =&\frac{-\alpha_B - \alpha_A + \overline{s}_A - n(B - B - A)}{2} = n(B - A - A) + n(B - O - A) - \alpha_B = \widetilde{n}(B - A - A).\end{aligned}$$

Thus, all $B-A-A$-like triples are just sufficient to match all remaining $A-A-B$-like triples in Step 2 and all $A-B-B$-like triples in Step 3. Hence, all triples, i.e., $|\mathcal{E}_{\mathbb{E}_A \cup \mathbb{E}_B}|$-many of them, are matched through the sub-algorithm. Thus, $\overline{m} \leq P_A[\mathcal{E}_{\mathbb{E}_A \cup \mathbb{E}_B}] + P_B[\mathcal{E}_{\mathbb{E}_A \cup \mathbb{E}_B}] = |\mathcal{E}_{\mathbb{E}_A \cup \mathbb{E}_B}| \leq \overline{m}$ where the first inequality follows from Equation 10, and the last inequality follows from Lemma 5. Thus, we have $\overline{m} = \mathcal{E}_{\mathbb{E}_A \cup \mathbb{E}_B}$.

Case 2. "$\underline{s}_A > \overline{s}_B$": In the Group stage, all $A - O - B$ type triples are grouped with $A - A - B$'s and all $B - O - A$ type triples are grouped with $B - A - A$'s. There are two subcases: $\widetilde{n}(A-A-B)+n(A-O-B) \geq n(B-B-A) = \widetilde{n}(B-B-A)$ and $\widetilde{n}(A-A-B)+n(A-O-B) < n(B - B - A) = \widetilde{n}(B - B - A)$.

Case 2.1. "$\widetilde{n}(A-A-B) = n(A-A-B)+n(A-O-B) \geq n(B-B-A) = \widetilde{n}(B-B-A)$": We will prove that $\overline{m}$ triples are matched by the sub-algorithm, and hence, the sub-algorithm finds an optimal matching.

First observe that all $B-B-A$ type triples are matched in Step 1 of the Match stage. Let $\Delta := n(A-A-B)+n(A-O-B)-n(B-B-A)$. In this subcase, $\Delta \geq 0$. In Step 2, if Δ is odd and there are no $A-A-B$ type triples, the last of the $A-O-B$ type triples left in Step 2 is re-grouped with $A-B-B$-like types in Step 3. Since $\underline{s}_A > \overline{s}_B$, all B blood-type patients are matched. Moreover,

$$a := \underbrace{n(B-B-A)}_{\text{in Step 1}} + \underbrace{2\min\left\{n(B-A-A)+n(B-O-A), \left\lfloor \frac{\Delta}{2} \right\rfloor\right\}}_{\text{in Step 2}}$$
$$+ \underbrace{\max\left\{0, n(B-A-A)+n(B-O-A) - \left\lfloor \frac{\Delta}{2} \right\rfloor\right\}}_{\text{in Step 3}}$$

A blood-type patients are matched.

Observe that $\overline{m}_B = P_B$, as all B blood-type patients can be matched. We claim that $a = \overline{m}_A$. If $a = \overline{m}_A$, then this will prove that Group and Match Sub-algorithm matches upper-bound $\overline{m} = \overline{m}_A + \overline{m}_B$ triples in $\mathcal{E}_{\mathbb{E}_A \cup \mathbb{E}_B}$, concluding this subcase's proof. Now, we have $a \leq \overline{m}_A$, the upper bound by Lemma 6. Recall that,

$$\overline{m}_A = \min\left\{P_A, \left\lfloor \frac{D_A + D_O}{2} \right\rfloor, \overline{s}_B\right\}$$
$$P_A = n(A-A-B)+n(A-O-B)+n(A-B-B)+\left\lfloor \frac{n(A-A-B)+n(A-O-B)+n(B-B-A)}{2} \right\rfloor$$
$$\overline{s}_B = n(B-B-A)+2n(B-O-A)+2n(B-A-A)$$

Consider the following two cases:

If $n(B-A-A)+n(B-O-A) \geq \lfloor \frac{\Delta}{2} \rfloor$, then

$$\begin{aligned}\overline{m}_A &\geq a \\ &= n(B-B-A)+\left\lfloor \frac{n(A-A-B)+n(A-O-B)-n(B-B-A)}{2} \right\rfloor + n(B-A-A)+n(B-O-A) \\ &= \left\lfloor \frac{D_A+D_O}{2} \right\rfloor \ \geq \ \overline{m}_A.\end{aligned}$$

If $n(B-A-A)+n(B-O-A) < \lfloor \frac{\Delta}{2} \rfloor$, then

$$\overline{m}_A \geq a = n(B-B-A)+2n(B-O-A)+2n(B-A-A) = \overline{s}_B \ \geq \ \overline{m}_A.$$

Hence, in either case, we have $a = \overline{m}_A$.

Case 2.2. "$\widetilde{n}(A-A-B) = n(A-A-B)+n(A-O-B) < n(B-B-A) = \widetilde{n}(B-B-A)$": We will prove that $\overline{m}$ or $\overline{m}-1$ triples are matched by the sub-algorithm and that the sub-algorithm finds an optimal matching.

First observe that all $A-A-B$-like triples are matched in Step 1 of the Match stage. Let $\Delta := n(B-B-A) - n(A-A-B) - n(A-O-B) \geq 0$. In Step 2 of the Match stage, if Δ is odd, the last of the $B-B-A$ type triples left in Step 2 is unmatched and the rest are matched with $A-B-B$ type triples in 3-way exchanges as $\underline{s}_A > \overline{s}_B$. In Step 3, all $B-A-A$-like triples are matched with $A-B-B$ type triples in 2-way exchanges as $\underline{s}_A > \overline{s}_B$. Hence, all B blood-type patients, but at most one, are matched. We claim that this is the most number of B blood-type patients that can be matched. If P_B-many B patients are matched then we are done. Suppose the sub-algorithm matches $P_B - 1$-many B blood-type patients. Then Δ is odd. If we could use all B blood-type patients in exchange, we can collectively provide at most $\overline{s}_B = n(B-B-A) + 2n(B-A-A) + 2n(B-O-A)$ donors to A blood-type patients. Therefore, the maximum number of A patients that can be matched (if it were possible) is: All $A-A-B$'s and all $A-O-B$'s each of which demands one A donor from outside (since $n(A-A-B)+n(A-O-B) < n(B-B-A)$ this is feasible), and $\overline{r}_A := \left\lfloor \frac{n(B-B-A)+2n(B-A-A)+2n(B-O-A)-n(A-A-B)-n(A-O-B)}{2} \right\rfloor$-many $A-B-B$'s, each of which demands two outside donors. Observe that $\overline{r}_A = n(B-A-A) + n(B-O-A) + \left\lfloor \frac{\Delta}{2} \right\rfloor$. Since Δ is odd, one of the A blood-type donors provided by one of the B blood-type patients is not used in this upper-bound, even though some A patients remain unmatched. Thus, at least one B patient will not be matched in any matching. Thus, the sub-algorithm is matching the maximum possible number of B blood-type patients.

Moreover, the number of A blood-type triples matched by the sub-algorithm is

$$
\begin{aligned}
a :=& \underbrace{n(A-A-B) + n(A-O-B)}_{\text{in Step 1}} + \underbrace{\left\lfloor \frac{\Delta}{2} \right\rfloor}_{\text{in Step 2}} + \underbrace{n(B-A-A) + n(B-O-A)}_{\text{in Step 3}} \\
=& n(B-A-A) + n(B-O-A) + \left\lfloor \frac{n(B-B-A) + n(A-O-B) + n(A-A-B)}{2} \right\rfloor
\end{aligned}
$$

Thus, all O and A donors, with the possible exception of one, are used to match A patients in the sub-algorithm: $\left\lfloor \frac{D_A+D_O}{2} \right\rfloor = a$. Since we have $a \leq \overline{m}_A \leq \left\lfloor \frac{D_A+D_O}{2} \right\rfloor$ for the upper bound by Lemma 6 for A blood-type patients, we get $a = \overline{m}_A$, finishing the proof of this subcase.

Case 3. "$\underline{s}_B > \overline{s}_A$": It is symmetric version of Case 2 switching the roles of A and B.

■

Note that, in the Group and Match sub-algorithm, whenever we can, we prioritized $A-O-B$ and $B-O-A$ type triples in their group. There is a reason for that. Next, we prove that not only Group and Match finds and optimal matching within $\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$, but also matches the maximum number of $A-O-B$ and $B-O-A$ type triples possible.

Proposition 3 *Consider $\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$, i.e., the sub-pool with types only from $\mathbb{E}_A\cup\mathbb{E}_B$. Sub-algorithm 2, Group and Match, matches the maximum number of $A-O-B$ and $B-O-A$ type triples possible in any matching within $\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$; and these numbers are $\min\{n(A-O-B),\overline{s}_B\}$ and $\min\{n(B-O-A),\overline{s}_A\}$, respectively.*

Proof of Proposition 3: We first show that Group and Match Sub-algorithm matches $\min\{n(A-O-B),\overline{s}_B\}$- and $\min\{n(B-O-A),\overline{s}_A\}$-many $A-O-B$ and $B-O-A$ type triples, respectively. Consider $A-O-B$ type triples. Define $\kappa:=\min\{n(A-O-B),\overline{s}_B\}$.

Case 1. "$[\underline{s}_A,\overline{s}_A]\cap[\underline{s}_B,\overline{s}_B]\neq\emptyset$": All triples in $\mathcal{E}_{\mathbb{E}_A\cup\mathbb{E}_B}$ are matched by the sub-algorithm (by the proof of Proposition 2). Hence $n(A-O-B)$-many $A-O-B$ type triples are matched. We have $\overline{m}_A$-many A blood-type patients are matched by Lemma 6. Since $n(A-O-B)\leq\overline{m}_A\leq\overline{s}_B$, κ-many $A-O-B$ type triples are matched.

Case 2. "$\underline{s}_A>\overline{s}_B$": All $B-O-A$'s are treated like $B-A-A$'s, while $A-O-B$'s are treated like $A-A-B$'s. By Lemma 6, we match either $\overline{m}_A$- or $\overline{m}_A-1$-many A blood type patients. Since we process $A-O-B$'s first before the real $A-A-B$ type triples within the $A-A-B$-like group in the sub-algorithm, we either finish matching all B blood-type patients before all $A-O-B$'s are matched or all $A-O-B$-type triples are matched but possibly one. However, in the second case, one $A-O-B$ type triple cannot be left unmatched by the following arguments: If one $A-O-B$ type triple is left unmatched in Step 2 of the Match stage, then this one triple is treated like an $A-B-B$ type triple in Step 3. At least one $B-A-A$ type triple remains in Step 3, as all B blood-type patients were not matched before matching $A-O-B$'s. We match these two triples in a two-way exchange. Thus, we match κ-many $A-O-B$ type triples.

Case 3. "$\underline{s}_B>\overline{s}_A$": All $A-O-B$'s are treated like $A-B-B$'s, while $B-O-A$'s are treated like $B-B-A$'s. We match all A blood-type patients by Lemma 6 and $\overline{m}_A=P_A$. Hence $n(A-O-B)\leq P_A\leq\overline{s}_B$. Thus, we match exactly κ-many $A-O-B$ type triples.

In the last part of the proof, we show that the maximum number of $A-O-B$ type triples that can be matched is κ. To prove this result we directly use Lemma 6. Observe that an upper-bound to the number of A blood-type patients among $\mathbb{E}_A=\{A-O-B\ ,\ A-A-B\ ,\ A-B-B\}$ types that can be matched is $\overline{m}_A=\min\left\{P_A,\left\lfloor\frac{D_O+D_A}{2}\right\rfloor,\overline{s}_B\right\}$ by Lemma 6. Then an upper-bound to the number of $A-O-B$ type triples that can be matched is $\overline{m}_{A-O-B}:=\min\left\{n(A-O-B),\left\lfloor\frac{D_O+D_A}{2}\right\rfloor,\overline{s}_B\right\}$. As $\overline{m}_{A-O-B}$ is an upper-bound to the number of $A-O-B$'s that can be matched, $\kappa\leq\overline{m}_{A-O-B}$. However, by definition of κ and construction of $\overline{m}_{A-O-B}$, $\kappa\geq\overline{m}_{A-O-B}$. Thus, $\kappa=\overline{m}_{A-O-B}$. ■

Theorem 4 *Suppose that the lung exchange pool $\mathcal{E}$ satisfies the long-run assumption and all sizes of exchanges are allowed. An optimal exchange can be found through Algorithm 3. Moreover, the number of patients matched in an optimal matching is given by*

$$\overline{m} - \mathcal{I} + \min\{n(A-O-B), \overline{s}_B\} + \min\{n(B-O-A), \overline{s}_A\},$$

where $\mathcal{I} \in \{0,1\}$, $\overline{s}_X$ for $X \in \{A,B\}$ is defined as in Equation 9, and $\overline{m}$ is defined in Equation system 10.

Proof of Theorems 3 and 4: By Proposition 2, $\overline{m} - \mathcal{I}$ patients from the essential triple types $\mathbb{E}_A \cup \mathbb{E}_B$ are matched through the Group and Match Sub-algorithm (in the first step of the sequential matching algorithm without size constraints) and by Proposition 3, this algorithm also matches the maximum number of $A-O-B$ and $B-O-A$ type triples possible. Let μ be the outcome of this sub-algorithm, which is optimal for triples from $\mathbb{E}_A \cup \mathbb{E}_B$. By Lemma 5, we can add additionally one triple from types $\mathbb{I} \setminus \mathbb{E}_A \cup \mathbb{E}_B$ for each $A-O-B$ and $B-O-A$ type triple matched in μ. This is the maximum number of triples we can match from types in $\mathbb{I} \setminus \mathbb{E}_A \cup \mathbb{E}_B$ *in any matching* by the same lemma. Since the number of $A-O-B$ and $B-O-A$ type triples matched in μ is $\min\{n(A-O-B), \overline{s}_B\} + \min\{n(B-O-A), \overline{s}_A\}$ (by Proposition 3) then the sequential matching algorithm without size constraints matches a total of $\overline{m} - \mathcal{I} + \min\{n(A-O-B), \overline{s}_B\} + \min\{n(B-O-A), \overline{s}_A\}$ triples and its outcome is optimal. Matching μ has exchanges no larger than 3-ways. Since at most one additional triple is inserted in each exchange for each triple matched in the second step of the algorithm, then the final outcome has exchanges no larger than 6-ways. ∎