

SUPPLEMENT TO “DUAL-DONOR ORGAN EXCHANGE”:
APPENDICES B, C, D, E
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APPENDIX B: DYNAMIC SIMULATIONS

IN THE DYNAMIC SIMULATIONS, PATIENTS AND THEIR DONORS ARRIVE over time and remain in the population until they are matched through exchange. We run statically optimal exchange algorithms once in each period.²⁵ In each simulation, we generate $S = 500$ such populations and report the averages and sample standard errors of the simulation statistics.

B.1. Dynamic Simulations for Lung Exchange

In the dynamic lung-exchange simulations, we consider 200 triples arriving over 20 periods at a uniform rate of 10 triples per period. This time horizon roughly corresponds to more than 1 year of Japanese patient arrival, when exchanges are run once about every 3 weeks. We only consider the 2-way and 2&3-way exchange regimes.

Based on the 2&3-way exchange simulation results reported in Table V, we can increase the number of living-donor transplants by 190%, thus nearly tripling them. This increase corresponds to 24% of all triples in the population. Even the logistically simpler 2-way exchange technology has a potential to increase the number of living-donor transplants by 125%.

B.2. Dynamic Simulations for Dual-Graft Liver Exchange

For dual-graft liver exchange, we consider 500 triples arriving over 20 periods at a uniform rate of 25 triples per period. In each period, we follow the same four-step transplantation scenario we used for the static simulations. The unmatched triples remain in the patient population waiting for the next period.²⁶

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²⁵Moreover, among the optimal matchings, we choose a random one rather than using a priority rule to choose whom to match now and whom to leave to future runs. The number of patients who can be matched dynamically can be further improved using dynamic optimization. For example, see Ünver (2010) for such an approach for kidney exchanges.

²⁶Roughly, a dynamic simulation corresponds to 3.5 months in real time and the exchange is run once every 5–6 days. This is a very crude mapping that relies on our specific patient and paired donor generation

TABLE V
DYNAMIC LUNG-EXCHANGE SIMULATIONS

Population Size	Direct Donation	Exchange Tech.	
		2-way	2& 3-way
200 (in 20 periods)	24.846 (4.5795)	31.2 (6.6568)	47.976 (8.7166)

The dynamic simulation results are reported in Table VI. Under 2&3-way exchanges, the number of transplants via 2-donor exchange is only 15% short of those from 2-donor direct transplants, but 25% more than those from 1-donor exchanges. Hence dual-graft liver exchange is a viable modality under 2&3-way exchanges. With only 2-way exchanges, the number of transplants via 2-donor exchange is 39% less than those from 2-donor direct transplantation, but still 7% more than those from 1-donor exchange. In summary, dual-graft liver exchange increases the number of living-donor liver transplants by nearly 30% when 2&3-way exchanges are possible, and by more than 22% when only 2-way exchanges are possible.

APPENDIX C: SIMULTANEOUS LIVER-KIDNEY TRANSPLANTATION

For end-stage liver disease patients who also suffer from kidney failure, simultaneous liver-kidney transplantation (SLK) is a common procedure. In 2015, 626 patients received SLK transplants from deceased donors in the United States. Transplanting a deceased-donor kidney to a (primarily liver) patient who lacks the highest priority on the kidney waitlist is a controversial topic, and this practice is actively debated in the U.S. (Nadim et al. (2012)). SLK transplants from living donors are not common in the U.S. due to the low rate of living-donor liver donation. In contrast, living donation for both livers and kidneys is the norm in most Asian countries, such as South Korea, and countries with predominantly Muslim populations, such as Turkey. SLK transplantation from living donors is reported in the literature for these two countries, as well as for Azerbaijan and India (see Lee et al. (2011), Astarcioğlu et al. (2003), Ahmadov et al. (2014), Aneja and Upwar (2011), respectively).

TABLE VI
DYNAMIC DUAL-GRAFT LIVER-EXCHANGE SIMULATIONS

Population Size	1-Donor Direct		1-Donor Exchange	2-Donor Direct	2-Donor Exchange
500 (in 20 periods)	119.83 (10.016)	2-way	58.284 (9.6765)	102.24 (10.05)	62.296 (9.1608)
		2&3-way	68.034 (11.494)	100.47 (10.063)	85.632 (12.058)

assumptions. It is obtained as follows: Under the current patient and donor generation scenario, a bit more than half of the patients will have at least one single-graft left- or right-lobe compatible donor or dual-graft compatible two donors (with more than 30% remnant donor liver). There are around 850 direct transplants a year in Korea from live donors, meaning that 1700 patients and their paired donors arrive a year. Then 500 patients arrive in roughly 3.5 months.

For SLK exchange, the analytical model we presented in Section 4 will be an approximation, since, in addition to the blood-type compatibility requirement of solid organs, kidney transplantation requires tissue-type compatibility and (single-graft) liver transplantation requires size compatibility.

C.1. Simulations for Simultaneous Liver-Kidney Exchange

As our last application, we consider simulations for simultaneous liver-kidney (SLK) exchange. We use the underlying parameters reported in Table III in the main text and Table VII here based on (mostly) Korean characteristics. In addition to an isolated SLK exchange, we also consider a possible integration of the SLK exchange with kidney-alone (KA) and liver-alone (LA) exchanges.

Following the South Korean statistics reported in these tables, we assume that the number of liver patients (LA and SLK) is $\frac{9}{11}$ th of the number of kidney patients. We failed to find data on the percentage of South Korean liver patients who are in need of a SLK transplantation.²⁷ Based on data from the U.S., we consider two treatments where 7.5% and 15% of all liver patients are SLK candidates, respectively. We interpret these numbers as lower and upper bounds for SLK diagnosis prevalence.²⁸

TABLE VII
SUMMARY STATISTICS FOR
SIMULTANEOUS-LIVER-KIDNEY-EXCHANGE SIMULATIONS
FROM THE SOUTH KOREAN KIDNEY PATIENTS/DONORS^a

Live Kidney Donation Recipients in 2010–2014 (55% Among Liver and Kidney)	
Female	2555 (53.38%)
Male	2231 (46.62%)
Total	4786 (100.0%)
Live Kidney Donors in 2010–2014	
Female	1922 (41.16%)
Male	2864 (59.84%)
Total	4786 (100.0%)
Patient PRA Distribution	
Range: 0–10%	70.19%
Range: 11–80%	20.00%
Range: 81–100%	9.81%

^aThe patient PRA distribution is obtained from American UNOS data as we could not find detailed Korean PRA distributions. The transplant data were obtained from the Korean Network for Organ Sharing (KONOS) 2014 Annual Report, retrieved from <https://www.konos.go.kr/konosis/index.jsp> on 04/10/2016.

²⁷The gender of an SLK patient is determined using a Bernoulli distribution with a female probability as a weighted average of liver and kidney patients' probabilities reported in Tables III and VII with the ratio of weights 9 to 11.

²⁸In the United States, according to the SLK transplant numbers given in Formica et al. (2016), 7.5% of all liver transplants involved SLK transplants between 2011 and 2015. On the other hand, Eason et al. (2008)

We generate the patients and their attached donors as follows: We assume that each KA patient is paired with a single kidney donor, each LA patient is paired with a single liver donor, and each SLK patient is paired with one liver and one kidney donor. A kidney donor is deemed compatible with a kidney patient (KA or SLK) if he is blood-type and tissue-type compatible with the patient.²⁹ Following the methodology in Section 3.2, a liver donor is deemed compatible with a liver patient (LA or SLK) if he is blood-type compatible and his liver’s left lobe volume is at least 40% of the patient’s liver volume. An SLK patient participates in exchange if any one of her two donors is incompatible, and a KA or LA patient participates in exchange if her only donor is incompatible.

We consider two scenarios, referred to as “isolated” and “integrated,” respectively, for our SLK simulations. For both scenarios, a kidney donor can be exchanged only with another kidney donor, and a liver donor can be exchanged only with another liver donor.

In the “isolated” scenario, we simulate the three exchange programs separately for each patient group, LA, KA, and SLK, using the 2-way exchange technology. Note that a 2-way exchange for the SLK group involves four donors, while a 2-way exchange for other groups involves two donors.

In the “integrated” scenario, we simulate a single exchange program to assess the potential welfare gains from a unification of individual exchange programs. For our simulations, we use the smallest meaningful exchange sizes that would fully integrate KA and LA with SLK. As such, we allow for any feasible 2-way exchange in our integrated scenario along with 3-way exchanges between one LA, one KA, and one SLK patient.³⁰

We consider population sizes of $n = 250, 500,$ and 1000 for our simulations, reported in Table VIII. For a population of $n = 1000$ and assuming 15% of liver patients are in need of SLK transplantation, the integrated exchange increases the number of SLK transplants over those from direct donation by 290%, almost quadrupling the number of SLK transplants. More than 20% of all SLK patients receive liver and kidney transplants through exchange in this case. For the same parameters, this percentage reduces to 5.7% under the isolated scenario. Equivalently, the number of SLK transplants from an isolated SLK exchange is equal to 81% of the SLK transplants from direct transplantation. As such, integration of SLK with KA and LA increases transplants from exchange by about 260% for the SLK population.³¹

When 7.5% of all liver patients are in need of SLK transplantation, integration becomes even more essential for the SLK patients. For a population of $n = 1000$, exchange increases the number of SLK transplants by 55% under the isolated scenario. In contrast, exchange increases the number of SLK transplants by more than 300% under the integrated scenario. Hence, integration increases the number of transplants from exchange by almost 450%, matching 21% of all SLK patients.

reported that only 73% of all SLK candidates received SLK transplants in 2006 and 2007 in the U.S. Moreover, Slack, Yeoman, and Wendon (2010) reported that 47% of liver transplant patients develop either acute kidney injury (20%) or chronic kidney disease (27%), and patients from both of these categories could be suitable for SLK transplants.

²⁹For checking tissue-type compatibility, we generate a statistic known as panel reactive antibody (PRA) for each patient. PRA determines with what percentage of the general population the patient would have tissue-type incompatibility. The PRA distribution used in our simulations is reported in Table VII. Therefore, given the PRA value of a patient, we randomly determine whether a donor is tissue-type compatible with the patient.

³⁰We are not the first ones to propose a combined liver-and-kidney exchange. Dickerson and Sandholm (2014) showed that higher efficiency can be obtained by combining kidney exchange and liver exchange if patients are allowed to exchange a kidney donor for a liver donor. Such an exchange, however, is quite unlikely given the very different risks associated with living-donor kidney donation and living-donor liver donation.

³¹The contribution of integration is modest for other groups with an increase of 4% for KA transplants from exchange, and an increase of 4.5% for LA transplants from exchange.

TABLE VIII
SIMULTANEOUS LIVER-KIDNEY EXCHANGE SIMULATIONS FOR $n = 250, 500, 1000$ PATIENTS

SLK Patient Fraction in Liver Pool	Population Sizes			Direct Donation			Exchange Regime					
							Isolated			Integrated		
	KA	SLK	LA	KA	SLK	LA	KA	SLK	LA	KA	SLK	LA
7.5%	133	9	108	61.114 (5.944)	0.58 (0.70753)	17.128 (3.756)	30.776 (6.7362)	0.128 (0.49)	8.332 (3.91)	31.25 (6.7675)	1.126 (1.008)	8.622 (3.8999)
		$n = 250$										
	267	18	215	121.3 (8.3792)	1.29 (1.1119)	33.786 (5.3514)	70.168 (10.475)	0.452 (0.91945)	21.356 (6.0982)	71.508 (10.48)	3.11 (1.6283)	22.012 (6.0243)
	$n = 500$											
	535	35	430	244.09 (11.783)	2.426 (1.5222)	67.982 (7.8642)	151.34 (14.841)	1.352 (1.5128)	53.26 (9.5101)	154.48 (14.919)	7.468 (2.4366)	54.264 (9.5771)
	$n = 1000$											
15%	129	18	103	59.288 (5.9075)	1.168 (1.0421)	16.364 (3.5996)	29.64 (6.6313)	0.464 (0.9688)	7.812 (3.7886)	30.55 (6.7675)	2.186 (1.4211)	8.434 (3.7552)
		$n = 250$										
	259	36	205	117.64 (8.3432)	2.566 (1.5933)	32.254 (5.2173)	67.916 (10.416)	1.352 (1.6546)	20.052 (5.9837)	70.266 (10.441)	5.782 (2.2442)	21.466 (5.9319)
	$n = 500$											
	518	72	410	236.23 (11.605)	5.076 (2.2646)	64.874 (7.5745)	146.18 (14.758)	4.108 (2.6883)	50.084 (9.3406)	152.17 (14.986)	14.74 (3.5175)	52.376 (9.3117)
	$n = 1000$											

C.2. Dynamic Simulations for Simultaneous Liver-Kidney Exchange

For simultaneous liver-kidney exchange dynamic simulations, we consider a population of $n = 2000$ patients arriving over 20 periods under the identical regimes of our static simulations.³² Table IX reports the results of these simulations.

When 15% of all liver patients are in need of SLK transplants, most outcomes essentially double with respect to the $n = 1000$ static simulations: For LA and SLK, the changes are slightly more than 100%, while for KA, the changes are slightly less than 100%. The increases for SLK patients are more substantial when 7.5% of all liver patients are in need of SLK transplants: An integrated exchange can facilitate transplants for 25% of all SLK patients, an overall increase of 360% with respect to SLK transplants from direct donation.

APPENDIX D: THE SUBALGORITHM FOR ALGORITHM 2

In this section, we present a subalgorithm that solves the constrained optimization problem in Step 1 of the matching algorithm for 2- & 3-way exchanges. We define

$$\begin{aligned}\kappa_A &:= \min\{n(A - A - B) + n(A - B - B), n(B - O - A)\}, \\ \kappa_B &:= \min\{n(B - B - A) + n(B - A - A), n(A - O - B)\}.\end{aligned}$$

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

Carry out the 2- and 3-way exchanges in Figure 7 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 11 summarizes the 2- and 3-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 11. 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

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

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

$$\gamma_A = n(A - A - B) - l_A + 2[n(A - B - B) - m_A]. \quad (2)$$

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 number 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

$$\begin{aligned}\underline{\gamma}_A &= n(A - A - B) - \underline{l}_A + 2[n(A - B - B) - \bar{m}_A], \quad \text{and} \\ \bar{\gamma}_A &= n(A - A - B) - \bar{l}_A + 2[n(A - B - B) - \underline{m}_A].\end{aligned}$$

³²This arrival rate roughly corresponds to 6 months of liver and kidney patients in South Korea with an exchange carried out every 9 days.

TABLE IX
 DYNAMIC SIMULTANEOUS LIVER-KIDNEY EXCHANGE SIMULATIONS FOR $n = 2000$ PATIENTS

SLK Patient Fraction in Liver Pool	Population Sizes			Direct Donation			Exchange Regime					
							Isolated			Integrated		
	KA	SLK	LA	KA	SLK	LA	KA	SLK	LA	KA	SLK	LA
7.5%	1070	70	860	487.84	4.946	134.93	306.62	5.588	110.35	312.92	18.246	113.17
	(in 20 periods)			(15.948)	(2.1071)	(10.424)	(18.95)	(4.0752)	(12.785)	(19.141)	(4.4835)	(12.941)
15%	1036	144	820	472.38	10.072	128.75	284.24	10.688	105.29	291.01	28.478	106.85
	(in 20 periods)			(15.618)	(3.0314)	(10.151)	(18.79)	(4.2759)	(12.462)	(18.637)	(4.6644)	(12.12)

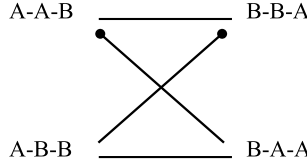


FIGURE 11.—The exchanges in Step 1 of the 2- & 3-way matching algorithm.

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 number 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 subalgorithm, 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 $[\underline{\gamma}_B, \bar{\gamma}_B]$.

SUBALGORITHM 1—Subalgorithm of the Sequential Matching Algorithm for 2- and 3-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 subalgorithm 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 subalgorithm aside, we sequentially maximize three subsets of exchanges among the remaining triples in Figure 11.

Step 3.1: Carry out the maximum number of 2-way exchanges between the $A - A - B$ and $B - B - A$ types.

Step 3.2: Carry out the maximum number of 3-way exchanges consisting of two $A - A - B$ and one $B - A - A$ triples, 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 2-way exchanges between the remaining $A - B - B$ and $B - A - A$ types.

Figure 12 graphically illustrates the 2- and 3-way exchanges that are carried out at Steps 3.1–3.3 of the subalgorithm.

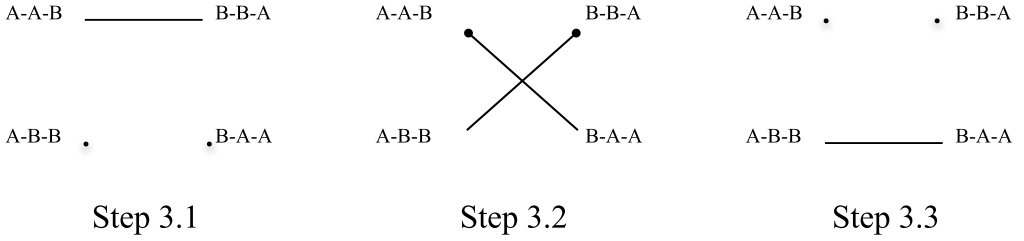


FIGURE 12.—Steps 3.1–3.3 of the subalgorithm.

PROPOSITION 1: The subalgorithm described above solves the constrained optimization problem in Step 1 of the matching algorithm for 2- & 3-way exchanges.

PROOF: Constraint (*) is satisfied by construction, since in Step 1 of the subalgorithm, 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 subalgorithm sets $\gamma_A = \gamma_B$, that is,

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

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 subalgorithm, 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 2- and 3-way exchanges by the end of Step 3 of the subalgorithm. This implies optimality.

Case 2. “ $\bar{\gamma}_A < \underline{\gamma}_B$, that is,

$$\begin{aligned} n(A - A - B) - \bar{l}_A + 2[n(A - B - B) - \bar{m}_A] \\ < n(B - B - A) - \underline{l}_B + 2[n(B - A - A) - \bar{m}_B] \end{aligned} \tag{3}$$

We next establish an upper bound on the number of triples with B patients that can participate in 2- and 3-way exchanges. Suppose that p_B many $B - B - A$ triples and r_B many $B - A - A$ triples can take part in 2- and 3-way exchanges while respecting condition (*). Since matching each $B - B - A$ triple requires one B donor of an A patient, 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 cannot match any more triples with B patients than the bound

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

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),

$$\begin{aligned} n(A - A - B) - l_A + 2[n(A - B - B) - m_A] \\ < n(B - B - A) - l_B + 2[n(B - A - A) - m_B]. \end{aligned} \quad (5)$$

So all the $A - B - B$ types available at the end of Step 3.1 take part in 3-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 2- and 3-way exchanges in Step 3 of the subalgorithm.

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 who take part in 2- and 3-way exchanges in Step 3 of the subalgorithm. (In Step 3.1, $\bar{p}_B \equiv n(B - B - A) - \underline{l}_B$ many $B - B - A$ triples take part in 2-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 2- and 3-way exchanges.)

Case 2.2. We further break Case 2.2 into four 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 2- and 3-way exchanges in Step 3 of the subalgorithm.

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 who take part in 2- and 3-way exchanges in Step 3 of the subalgorithm. (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 2-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 2- and 3-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 choices of γ_A and γ_B in Step 1

of the subalgorithm 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 3-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 2- and 3-way exchanges in Step 3 of the subalgorithm.

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 3-way exchanges with $B - A - A$ triples. Each such 3-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 who take part in 2- and 3-way exchanges in Step 3 of the subalgorithm. (In Step 3.1, $\bar{p}_B \equiv n(B - B - A) - \underline{l}_B$ many $B - B - A$ triples take part in 2-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 2- and 3-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 2- and 3-way exchanges in Step 3 of the subalgorithm.

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 who take part in 2- and 3-way exchanges in Step 3 of the subalgorithm. (In Step 3.1, $\bar{p}_B \equiv n(B - B - A) - \underline{l}_B$ many $B - B - A$ triples take part in 2-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 2- and 3-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 2- and 3-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 2- and 3-way exchanges in Step 3 of the subalgorithm.

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 $\bar{\gamma}_A - \bar{\rho}_B \leq 0$. 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 cannot match more triples with a B patient than $\bar{\gamma}_B$. Since in this case $n(B - B - A) - \underline{l}_B \equiv \bar{\rho}_B \geq \bar{\gamma}_A = \gamma_A$, the subalgorithm matches $\bar{\gamma}_A$ many $B - B - A$ triples in Steps 3.1 and 3.2, which achieves this upper bound.

Suppose next that $\bar{\gamma}_A - \bar{\rho}_B$ 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

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

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

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

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

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

Case 3. “ $\bar{\gamma}_B < \gamma_A$ ”: Symmetric to Case 2, interchanging the roles of A and B . *Q.E.D.*

APPENDIX E: 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 *subpool of \mathcal{E}* . We fix a dual-donor exchange pool \mathcal{E} throughout the section. Given a subpool \mathcal{K} , let $D_X[\mathcal{K}]$ be the *number of X blood-type donors in \mathcal{K}* and $P_X[\mathcal{K}]$ be the *number of X blood-type patients in \mathcal{K}* . We also use $n(X - Y - Z)[\mathcal{K}]$ to denote the number of $X - Y - Z$ triples in \mathcal{K} (while we omit the arguments of these expressions if $\mathcal{K} = \mathcal{E}$). For a subpool \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 subpool of triples matched through it* also as μ , with a slight abuse of notation.

We denote with \mathbb{E} the essential types:

$$\mathbb{E} := \{A - A - B, A - O - B, A - B - B, B - B - A, B - O - A, B - A - A\}.$$

Recall that by Lemma 2, each exchange should have at least two pairs of two different types in \mathbb{E} , one with an A patient and one with a B patient. Let $\mathcal{E}_{\mathbb{E}} \leq \mathcal{E}$ be the subpool with only essential-type triples.

Also recall that by Lemma 5, the only types that can be a part of an optimal matching in this setting besides the essential types are $O-O-A$ and $O-O-B$, which are sufficiently many by the long-run assumption. The following lemma will characterize the role of such triples and reduce the problem to focus only on essential types in constructing an optimal matching. This is a counterpart of Lemma 6 for unrestricted exchange sizes:

LEMMA 8: *Suppose that \mathcal{E} satisfies the long-run assumption and μ is an optimal matching in the absence of any exchange-size constraints in the essential type subpool $\mathcal{E}_{\mathbb{E}}$. Suppose further that μ matches the maximum possible number of $A-O-B$ and $B-O-A$ triples that can be matched in any matching in $\mathcal{E}_{\mathbb{E}}$.*

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 $O-O-B$ triples can be matched in addition to all triples matched by μ .*

2. *Moreover, ν is an optimal matching of \mathcal{E} in the absence of any exchange-size constraints.*

PROOF: The first part of the lemma is easy to prove: Take any $B-O-A$ or $A-O-B$ triple i matched in μ . Observe that as μ is a matching within essential types, the O donor of i is necessarily donating to an A or a B patient 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 $O-O-B$. Such triples (which are unmatched in μ) exist by the long-run assumption. 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 to 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 first prove a claim:

CLAIM: *For any optimal matching ν' of \mathcal{E} , we can construct another matching μ' involving only the essential-type triples matched by ν' .*

PROOF OF THE CLAIM: By Lemma 5, besides the essential-type triples, $O-O-A$ and $O-O-B$ types can participate in ν' . Take a patient of a triple matched in ν' of type $O-O-X$ for any $X \in \{A, B\}$. Without loss of generality, assume that her O donor directly donates to her in ν' . Another triple's O donor d_1 donates to her in ν' as well. In return, her X donor donates to a (different) patient p_1 in ν' . We can simply take this $O-O-X$ triple out, and form a new matching by d_1 directly donating to p_1 and rest of the donations remain intact as in ν' . We repeat this procedure for all triples of types $O-A-B$, $O-A-A$, $O-B-B$, $O-O-A$, and $O-O-B$ iteratively. The final matching, which we refer to as μ' , is feasible and consists of only essential-type triples of ν' . Q.E.D.

Let μ and ν be defined as in the hypothesis of the lemma. Suppose that ν' is an arbitrary optimal matching in \mathcal{E} . We will show that $|\nu| = |\nu'|$.

By Lemma 5, the types of triples that can be part of a feasible exchange besides the essential types are $O-O-A$ and $O-O-B$ under the long-run assumption.

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 $\mathcal{E}_{\mathbb{E}}$. We also have

$$\begin{aligned} n(A - O - B)[\mu] + n(B - O - A)[\mu] \\ \geq n(A - O - B)[\mu'] + n(B - O - A)[\mu'] \end{aligned} \quad (7)$$

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

The $O - O - A$ and $O - O - B$ triples matched in ν' require at least $n(O - O - B)[\nu'] + n(O - O - A)[\nu']$ -many other triples with O donors in ν' . Since these triples can only be of types $A - O - B$ and $B - O - A$, we have

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

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 $|\nu| = |\mu| + n(O - O - A)[\nu] + n(O - O - B)[\nu] \geq |\mu'| + n(O - O - A)[\nu'] + n(O - O - B)[\nu'] = |\nu'|$. Since ν' is optimal in \mathcal{E} , ν is optimal in \mathcal{E} with $|\nu| = |\nu'|$, completing the proof. *Q.E.D.*

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

then, using Lemma 8, we can construct an optimal matching using μ , and it matches $|\mu| + n(A - O - B)[\mu] + n(B - O - A)[\mu]$ triples. This will also give us the optimal number of triples that can be matched in the absence of exchange-size constraints.

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

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

$$\bar{s}_A := 2n(A - O - B) + n(A - A - B) + 2n(A - B - B). \quad (9)$$

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

In calculating \bar{s}_A , we *treat* $A - O - B$ triples like $A - B - B$'s. Therefore, each of them requires two donors from outside instead of one. Symmetrically, we define \underline{s}_B and \bar{s}_B . Observe that

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

We define a subalgorithm using these numbers:

SUBALGORITHM 2—Group and Match Subalgorithm 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 $\underline{s}_A, \bar{s}_A, \underline{s}_B, \bar{s}_B$, defined in Equations (8) and (9).

Case 1. “ $[\underline{s}_A, \bar{s}_A] \cap [\underline{s}_B, \bar{s}_B] \neq \emptyset$ ”:

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 $\bar{s}_A - \alpha_A = \bar{s}_B - \alpha_B$:

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

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

Case 2. “ $\bar{s}_B < \underline{s}_A$ ”:

1. *Group* all $A - O - B$ triples (i.e., $(\bar{s}_A - \underline{s}_A)$ -many) with $A - A - B$ types (i.e., $\alpha_A = \bar{s}_A - \underline{s}_A$).

2. *Group* all $B - O - A$ triples (i.e., $(\bar{s}_B - \underline{s}_B)$ -many) with $B - A - A$ types (i.e., $\alpha_B = \bar{s}_B - \underline{s}_B$).

Case 3. “ $\bar{s}_A < \underline{s}_B$ ”:

Symmetric situation with Case 2 replacing A blood type with B . We refer to all $X - O - Z$ 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 $X - Y^* - Z$ triples or group. Let $n(X - Y^* - Z)$ be the number of triples in the $X - Y^* - Z$ group and $n(X - O - Z | X - Y^* - Z)$ be the number of $X - O - Z$ triples in the $X - Y^* - Z$ group. Define:

$$\Delta := n(A - A^* - B) - n(B - B^* - A). \quad (10)$$

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

Step 1: Carry out the maximum number of 2-way exchanges between the $A - A^* - B$ and $B - B^* - A$ triples with the following exceptions:

(I) In Case 2 if $\Delta < 0$ and is odd:

(A) If $n(B - O - A) > 0$: add one $B - O - A$ triple to $B - B^* - A$ group from $B - A^* - A$ group and continue with Step 1.

(B) If $n(B - O - A) = 0$ and an exchange can be conducted in Step 1: do not conduct the last $A - A^* - B$ & $B - B^* - A$ 2-way exchange in Step 1 (and thus, exactly one $A - A^* - B$ triple and an even number of $B - B^* - A$ triples remain unmatched in Step 1), and if the remaining $A - A^* - B$ triple is of type $A - O - B$, then move it to the $A - B^* - B$ group.

(II) In Case 3 if $\Delta > 0$ and is odd:

(A) If $n(A - O - B) > 0$: add one $A - O - B$ triple to $A - A^* - B$ group from $A - B^* - B$ group and continue with Step 1.

(B) If $n(A - O - B) = 0$ and an exchange can be conducted in Step 1: do not conduct the last $A - A^* - B$ & $B - B^* - A$ 2-way exchange in Step 1 (and thus, exactly one $B - B^* - A$ triple and an even number of $A - A^* - B$ triples remain unmatched in Step 1), and if the remaining $B - B^* - A$ triple is of type $B - O - A$, then move it to the $B - A^* - A$ group.

Step 2: Carry out the maximum number of 3-way exchanges consisting of two $A - A^* - B$ triples and one $B - A^* - A$ triple, and those consisting of two $B - B^* - A$ triples and one $A - B^* - B$ among the remaining ones.

Step 3: If there are any $A - O - B$ and $B - O - A$ triples left in $A - A^* - B$ and $B - B^* - A$ groups, respectively, then move them to $A - B^* - B$ and $B - A^* - A$ groups, respectively. Carry out the maximum number of 2-way exchanges between the remaining $A - B^* - B$ and $B - A^* - A$ triples.

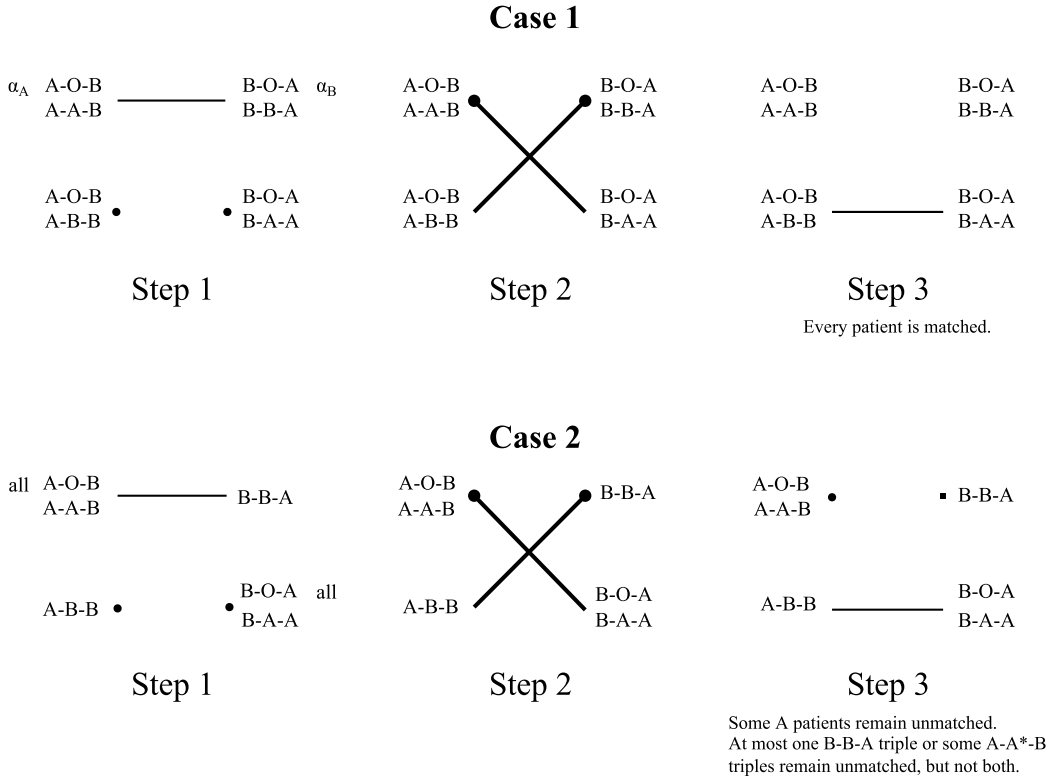


FIGURE 13.—Cases 1 and 2 of *Group and Match Subalgorithm* (Subalgorithm 2). Each solid line represents 2-way exchanges, and each solid line with a dot at the end represents 3-way exchanges in each of which two triples participate from the group that is pointed by the circular end. Only one of the two 3-way exchanges will be conducted in Step 2 in each subfigure. Exceptions are not depicted in Case 2.

Figure 13 summarizes how the Group and Match Subalgorithm works, along with its consequences (to be proven in Propositions 2 and 3 below). This subalgorithm is embedded in the optimal matching algorithm as follows:

ALGORITHM 3—Sequential Matching Algorithm in the Absence of Exchange-Size Constraints:

Step 1: Use Subalgorithm 2, *Group and Match*, to match triples of types \mathbb{E} .

Step 2: In any exchange determined in this matching, for each $A - O - B$ or $B - O - A$ triple in the exchange, insert an $O - O - A$ or an $O - O - B$ triple using Lemma 8.

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 9—Upper Bound Lemma: *Consider the subpool $\mathcal{E}_{\mathbb{E}}$. Then \bar{m} , defined below, is an upper bound to the number of triples that can be matched in a matching consisting only of triples in $\mathcal{E}_{\mathbb{E}}$:*

$$\bar{m} := \bar{m}_A + \bar{m}_B \quad \text{where}$$

$$\begin{aligned} \bar{m}_A &:= \min \left\{ P_A[\mathcal{E}_{\mathbb{E}}], \left\lfloor \frac{D_A[\mathcal{E}_{\mathbb{E}}] + D_O[\mathcal{E}_{\mathbb{E}}]}{2} \right\rfloor, \bar{s}_B \right\} \quad \text{and} \\ \bar{m}_B &:= \min \left\{ P_B[\mathcal{E}_{\mathbb{E}}], \left\lfloor \frac{D_B[\mathcal{E}_{\mathbb{E}}] + D_O[\mathcal{E}_{\mathbb{E}}]}{2} \right\rfloor, \bar{s}_A \right\}. \end{aligned} \quad (11)$$

PROOF: The first term in \bar{m}_A , $P_A[\mathcal{E}_{\mathbb{E}}]$, is the number of A blood-type patients and the second term, $\lfloor \frac{D_A[\mathcal{E}_{\mathbb{E}}] + D_O[\mathcal{E}_{\mathbb{E}}]}{2} \rfloor$, is the maximum number of A blood-type patients who can receive two lobes from donors who are compatible with A blood-type patients, that is, O and A blood-type donors in $\mathcal{E}_{\mathbb{E}}$. Hence, each of them is an upper bound for the number of triples with A blood-type patients in $\mathcal{E}_{\mathbb{E}}$ who can receive a transplant. Next consider the third term: $\bar{s}_B = n(B - B - A) + 2n(B - O - A) + 2n(B - A - A)$ is the maximum number of A or O blood-type donors whom the B blood-type patients can provide for the triples with A blood-type patients in $\mathcal{E}_{\mathbb{E}}$. Each triple with an A blood-type patient in $\mathcal{E}_{\mathbb{E}}$ requires at least one A or O blood-type donor coming from another triple to be matched feasibly, as it can provide at most one compatible donor for itself. Hence, \bar{s}_B is also an upper bound to the number of A blood-type patients who can be matched within $\mathcal{E}_{\mathbb{E}}$, establishing the formula for \bar{m}_A .

The argument is the same in \bar{m}_B for B blood-type patients. There are no triples with AB or O blood-type patients in $\mathcal{E}_{\mathbb{E}}$. This concludes the proof and establishes \bar{m} as an upper bound to the essential types that can be matched. *Q.E.D.*

We will prove that the upper bound found above is *almost* tight, and the Group and Match subalgorithm matches always at least one fewer patient than \bar{m} upper bound, and often matches exactly \bar{m} patients. Moreover, we show that when Group and Match matches $\bar{m} - 1$ triples, no more triples can be matched among the essential types. This shows that Group and Match is an optimal matching algorithm for the essential types. It also uses entirely 2- and 3-way exchanges.

PROPOSITION 2: In the absence of any exchange-size constraints, an optimal matching within $\mathcal{E}_{\mathbb{E}}$ exactly matches \bar{m} or $\bar{m} - 1$ patients, and moreover, Subalgorithm 2, Group and Match, finds such a matching in this subpool using only 2- and 3-way exchanges.

PROOF: First observe that by construction, Group and Match conducts only 2- and 3-way exchanges. For notational and expositional simplicity, suppose $\mathcal{E} = \mathcal{E}_{\mathbb{E}}$, that is, $\mathcal{E}_{\mathbb{E}}$ is the whole pool. Thus, we drop the argument $\mathcal{E}_{\mathbb{E}}$ from D_X and P_X throughout.

Case 1. “ $[\underline{s}_A, \bar{s}_A] \cap [\underline{s}_B, \bar{s}_B] \neq \emptyset$ ”: We will prove that all triples are matched by the subalgorithm, and that is \bar{m} -many. Without loss of generality assume that

$$\Delta = n(A - A^* - B) - n(B - B^* - A) \geq 0.$$

Thus, all $B - B^* - A$ triples are matched in 2-way exchanges with $A - A^* - B$ triples in Step 1 of the Match stage of the subalgorithm.

We first show that Δ is even. This will be used in the proofs for other cases to rule out certain scenarios:

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

showing Δ is even.

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

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

Thus, all $B - A^* - A$ triples are just sufficient to match all remaining $A - A^* - B$ triples in Step 2 and all $A - B^* - B$ triples in Step 3. Hence, all triples, that is, $P_A + P_B$ of them, are matched through the subalgorithm. Thus, $\bar{m} \leq P_A + P_B \leq \bar{m}$, where the second inequality follows from Lemma 9. Thus, we have $\bar{m} = P_A + P_B$.

Case 2. “ $\underline{s}_A > \bar{s}_B$ ”: First, we show that $\bar{m}_B = P_B$. We have

$$\begin{aligned}
P_B &= n(B - B - A) + n(B - O - A) + n(B - A - A) \leq \underline{s}_B \leq \bar{s}_B < \underline{s}_A \leq \bar{s}_A, \quad \text{and} \\
P_B &\leq n(B - B - A) + n(B - O - A) + n(B - A - A) + \left\lfloor \frac{\bar{s}_A - \underline{s}_B}{2} \right\rfloor \\
&= n(A - O - B) + n(A - B - B) \\
&\quad + \left\lfloor \frac{n(B - B - A) + n(B - O - A) + n(A - A - B)}{2} \right\rfloor \\
&= \left\lfloor \frac{D_B + D_O}{2} \right\rfloor.
\end{aligned}$$

Since $\bar{m}_B = \min\{P_B, \lfloor \frac{D_B + D_O}{2} \rfloor, \bar{s}_A\}$, we obtain $\bar{m}_B = P_B$.

In the Group stage, all $A - O - B$ triples are grouped with $A - A - B$'s and all $B - O - A$ triples are grouped with $B - A - A$'s. There are two subcases, $\Delta \geq 0$ and $\Delta < 0$:

Case 2.1. “ $\Delta \geq 0$ ”: We have $\Delta = n(A - A^* - B) - n(B - B^* - A) = n(A - A - B) + n(A - O - B) - n(B - B - A)$. First, since $\Delta \geq 0$, Exception (I) is not needed. Second, invoking Exception (II) requires $\underline{s}_B > \bar{s}_A$, contradicting we are in Case 2. Thus, no exceptions are invoked in Step 1. Then

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

A blood-type patients are matched in the subalgorithm.

We claim that $a = \bar{m}_A$: Recall that $a \leq \bar{m}_A$ by the upper bound by Lemma 9. Also recall that

$$\begin{aligned} \bar{m}_A &= \min \left\{ P_A, \left\lfloor \frac{D_A + D_O}{2} \right\rfloor, \bar{s}_B \right\} \quad \text{and} \\ P_A &= n(A - A - B) + n(A - O - B) + n(A - B - B), \\ \left\lfloor \frac{D_A + D_O}{2} \right\rfloor &= n(B - A - A) + n(B - O - A) \\ &\quad + \left\lfloor \frac{n(A - A - B) + n(A - O - B) + n(B - B - A)}{2} \right\rfloor, \\ \bar{s}_B &= n(B - B - A) + 2n(B - O - A) + 2n(B - A - A). \end{aligned}$$

Consider the following two subcases:

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

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

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

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

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

Next, consider B blood-type patients. Observe that all B patients are matched in the subalgorithm. As $\bar{m}_B = P_B$, we have $\bar{m} = \bar{m}_A + \bar{m}_B$ (the maximum possible number by Lemma 9) patients matched.

Case 2.2. “ $\Delta < 0$ ”: Below, we will prove that \bar{m} patients can be matched except when Δ is odd and yet Exception (I) cannot be invoked. In this case, we will show that (a) only \bar{m}_A A patients and $\bar{m}_B - 1$ B patients can be matched at most, and (b) our subalgorithm matches exactly that many agents. (Recall that Exception (II) is never invoked in Case 2.) Then by Lemma 9, the result will follow. We analyze Case 2.2 in three subcases:

(a) “ $\Delta < 0$ is odd and Exception (I)(A) is invoked in Match stage”:

Since $\underline{s}_A > \bar{s}_B$, we have $n(A - B^* - B) - n(B - A^* - A) - \lfloor \frac{-\Delta}{2} \rfloor > 0$. Moreover, $n(B - O - A) \lfloor B - A^* - A \rfloor > 0$.

Thus,

$$\begin{aligned} b &:= \underbrace{n(A - A - B) + n(A - O - B)}_{\text{in Step 1}} + \underbrace{(-\Delta + 1)}_{\text{in Step 2}} + \underbrace{n(B - A - A) + n(B - O - A) - 1}_{\text{in Step 3}} \\ &= n(B - A - B) + n(B - A - A) + n(B - O - A) \\ &= P_B = \bar{m}_B \end{aligned}$$

B patients are matched. On the other hand, the number of A patients matched is

$$\begin{aligned}
 a &:= \underbrace{n(A-A-B) + n(A-O-B)}_{\text{in Step 1}} + \underbrace{\frac{-\Delta+1}{2}}_{\text{in Step 2}} + \underbrace{n(B-A-A) + n(B-O-A) - 1}_{\text{in Step 3}} \\
 &= n(B-A-A) + n(B-O-A) + n(A-A-B) + n(A-O-B) + \left\lfloor \frac{-\Delta}{2} \right\rfloor \\
 &= n(B-A-A) + n(B-O-A) \\
 &\quad + \left\lfloor \frac{n(A-A-B) + n(A-O-B) + n(B-B-A)}{2} \right\rfloor \\
 &= \left\lfloor \frac{D_A + D_O}{2} \right\rfloor.
 \end{aligned} \tag{12}$$

Recall that $a \leq \overline{m}_A \leq \lfloor \frac{D_A + D_O}{2} \rfloor$, where the first inequality follows from Lemma 9. Thus, $a = \overline{m}_A$.

(b) “ $\Delta < 0$ is odd and Exception (I)(B) is invoked in Match stage”:

Since $\underline{s}_A > \overline{s}_B$, $n(A-B^*-B) - n(B-A^*-A) - \lfloor \frac{-\Delta}{2} \rfloor > 0$. Moreover, $n(B-O-A|B-A^*-A) = 0$, and at least one exchange can be conducted in Step 1.

Now, the last $A-A^*-B$ & $B-B^*-A$ 2-way exchange in Step 1 is not conducted: Hence, exactly one $A-A^*-B$ triple and an even number of $B-B^*-A$ triples remain unmatched in Step 1. In Step 2, all remaining $B-B^*-A$ triples are matched with $A-B^*-B$ triples. Moreover, in Step 3, all $B-A^*-A$ triples are matched. Thus, $\overline{m}_B = P_B$ B patients are matched. On the other hand,

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

A patients are matched (where the equality follows from Equation (12)). Thus, $a = \overline{m}_A$.

(c) “ $\Delta < 0$ is odd and yet none of the exceptions are invoked, or $\Delta < 0$ is even”:

As $\underline{s}_A > \overline{s}_B$, in Steps 1 and 2 of the Match stage, if Δ is odd, only one of the $B-B-A$ triples is unmatched, and otherwise, all $B-B-A$ triples are matched. In Step 3, all $B-A-A$ and $B-O-A$ triples are matched with $A-B-B$ triples in 2-way exchanges. Hence, all B blood-type patients, but at most one, are matched. Next we prove the following claim:

CLAIM: *In Case 2.2(c), the subalgorithm matches the maximum possible number of B patients that can be matched, that is, $\overline{m}_B - \mathbf{1}\{\Delta \text{ is odd}\}$.*³³

PROOF OF THE CLAIM: If P_B -many B patients are matched, then we are done. Suppose the subalgorithm matches $P_B - 1$ -many B blood-type patients. In this case, $\overline{m}_B = P_B$.

³³Function $\mathbf{1}\{S\}$ gets value 1 when statement S is true and 0 otherwise.

Moreover, Δ is odd. If we could use all B blood-type patients in exchange, we can collectively provide at most $\bar{s}_B = n(B - B - A) + 2n(B - A - A) + 2n(B - O - A)$ 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 $\Delta < 0$, i.e., $n(A - A - B) + n(A - O - B) < n(B - B - A)$, this is feasible), and $\bar{r}_A := \lfloor \frac{n(B - B - A) + 2n(B - A - A) + 2n(B - O - A) - n(A - A - B) - n(A - O - B)}{2} \rfloor$ -many $A - B - B$'s, each of which demands two outside donors. Observe that $\bar{r}_A = n(B - A - A) + n(B - O - A) + \lfloor \frac{-\Delta}{2} \rfloor$. 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 subalgorithm is matching the maximum possible number of B blood-type patients. *Q.E.D.*

The number of A blood-type patients matched by the subalgorithm is

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

by Equation (12). Since we have $a \leq \bar{m}_A \leq \lfloor \frac{D_A + D_O}{2} \rfloor$, we get $a = \bar{m}_A$.

Case 3. “ $\underline{s}_B > \bar{s}_A$ ”: It is the symmetric version of Case 2 switching the roles of A and B . *Q.E.D.*

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

PROPOSITION 3: Consider $\mathcal{E}_{\mathbb{E}}$, that is, the subpool with types in \mathbb{E} . Subalgorithm 2, Group and Match, matches the maximum number of $A - O - B$ and $B - O - A$ triples possible in any matching; and these numbers are $\min\{n(A - O - B), \bar{s}_B\}$ and $\min\{n(B - O - A), \bar{s}_A\}$, respectively.

PROOF: First, we show that Group and Match subalgorithm matches $\min\{n(A - O - B), \bar{s}_B\}$ -many $A - O - B$ triples and $\min\{n(B - O - A), \bar{s}_A\}$ -many $B - O - A$ triples. We prove this for $A - O - B$'s (the proof for $B - O - A$'s is symmetric). Define κ as the number of $A - O - B$ triples matched in the algorithm.

Case 1. “ $[\underline{s}_A, \bar{s}_A] \cap [\underline{s}_B, \bar{s}_B] \neq \emptyset$ ”: All triples in $\mathcal{E}_{\mathbb{E}}$ are matched by the subalgorithm (by the proof of Proposition 2). Hence $n(A - O - B)$ -many $A - O - B$ triples are matched. We have that \bar{m}_A -many A blood-type patients are matched by Lemma 9. Since $n(A - O - B) \leq \bar{m}_A \leq \bar{s}_B$, κ -many $A - O - B$ triples are matched. Thus, $\kappa = n(A - O - B) \leq P_A = m_A \leq \bar{s}_B$.

Case 2. “ $\underline{s}_A > \bar{s}_B$ ”: In the subalgorithm, triples with O donors are matched before any other triple in their respective group. Observe that after Steps 1 and 2, either all $A - O - B$'s are matched, or no $A - A - B$'s are matched, as they are always processed before $A - A - B$'s. Similarly, after Step 3, either all $A - O - B$'s are matched, or no $A - B - B$'s are matched (as remaining $A - O - B$ types are moved to the $A - B^* - B$ group after

Step 2). Suppose some $A - O - B$'s are unmatched. Since we have \bar{m}_A A patients matched in this case by the Proof of Proposition 2, all of them are from triples of type $A - O - B$. Since \bar{m}_A is the upper-bound of A patients matched, then maximum possible number of $A - O - B$ triples are matched. Thus, $\kappa = \min\{\bar{m}_A, n(A - O - B)\} = \min\{n(A - O - B), \bar{s}_B, \lfloor \frac{D_A + D_O}{2} \rfloor\}$. Moreover, we have

$$\begin{aligned} \left\lfloor \frac{D_A + D_O}{2} \right\rfloor &= n(B - A - A) + n(B - O - A) \\ &\quad + \left\lfloor \frac{n(A - A - B) + n(A - O - B) + n(B - B - A)}{2} \right\rfloor \\ &= \left\lfloor \frac{n(A - A - B) + \bar{s}_B + n(A - O - B)}{2} \right\rfloor \\ &\geq \min\{n(A - O - B), \bar{s}_B\}. \end{aligned}$$

Thus, $\kappa = \min\{n(A - O - B), \bar{s}_B\}$.

Case 3. " $\bar{s}_B > \bar{s}_A$ ": All $A - O - B$'s are in the $A - B^* - B$ group. If $\Delta \leq 0$ or $\Delta > 0$ is even, then all $A - O - B$ triples are matched following the proof of Proposition 2. If Exception (II)(A) is invoked, then one $A - O - B$ is moved to the $A - A^* - B$ group after Step 1, but is immediately matched in Step 2. Moreover, all remaining $A - O - B$'s are matched in Step 3. If Exception (II)(B) or if $\Delta > 0$ is odd and yet no Exception is invoked, then there are no $A - O - B$ triples. Thus, $\kappa = n(A - O - B) \leq \bar{m}_A \leq \bar{s}_B$.

Hence, $\kappa = \min\{n(A - O - B), \bar{s}_B\}$. By Lemma 9, this is the maximum number of $A - O - B$ type triples that can be matched (i.e., if there were no other A patients, we would have $\bar{m}_A = \kappa$). *Q.E.D.*

THEOREM 4: *Suppose that the dual-donor exchange pool \mathcal{E} satisfies the long-run assumption. In the absence of exchange-size constraints, an optimal matching can be found through Algorithm 3, which uses only 2–6-way exchanges. Moreover, the number of patients matched in an optimal matching is given by*

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

where $\mathcal{I} \in \{0, 1\}$, \bar{s}_X for $X \in \{A, B\}$ is defined as in Equation (9), and \bar{m} is defined in Equation system (11).

PROOF: By Proposition 2, $\bar{m} - \mathcal{I}$ patients from the essential triple types \mathbb{E} are matched through the Group and Match subalgorithm (in the first step of the sequential matching algorithm in absence of exchange-size constraints), and by Proposition 3, this algorithm also matches the maximum possible number of $A - O - B$ and $B - O - A$ triples. Let μ be the outcome of this subalgorithm, which is optimal for triples from \mathbb{E} . By Lemma 8, we can add additionally one triple from types not in \mathbb{E} for each $A - O - B$ and $B - O - A$ triple matched in μ . This is the maximum number of triples we can match from types not in \mathbb{E} in any matching by the same lemma. Since the number of $A - O - B$ and $B - O - A$ triples matched in μ is $\min\{n(A - O - B), \bar{s}_B\} + \min\{n(B - O - A), \bar{s}_A\}$ (by Proposition 3), then the sequential matching algorithm in absence of exchange-size constraints matches a total of $\bar{m} - \mathcal{I} + \min\{n(A - O - B), \bar{s}_B\} + \min\{n(B - O - A), \bar{s}_A\}$ 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. Q.E.D.

Theorem 4 implies Theorem 3.

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