

Matching Mechanism for Kidney Transplantations

Yutong Meng^a, Hongyu Zhou^b

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1 Direct Donation Algorithm and Greedy Algorithm

1.1 Q1

Algorithm 1.1: Direct Donation Algorithm

Input: Donor-Patient pair $\{k_i, t_i\}$, compatible kidney set $\{K_i\}$, a waiting list W
Output: An assignment of the patients to either a kidney or the waiting list

```
1 W is empty, M is empty.; // W is a priority list, M is a redimensional table to
   store matching pairs
2 for  $t_i$  in patient set do
3     if  $k_i$  in  $K_i$  then
4         | Assign  $k_i$  to  $t_i$ 
5     end
6     else
7         | Add  $t_i$  to W
8     end
9 end
```

1.2 Q2

Greedy algorithm

Input: A priority list P of patients, preference P_i for each patient t_i , compatible kidney set $\{K_i\}$

Output:An assignment of the patients to either a kidney or the waiting list /* patient is a class containing 4 domains:patient t and corresponding donor k ,compatible set K ,preference list Pr */

```

10 M is empty;          // M is a redimensional table to store matching pairs
11 [1]
12 for patient  $t$  in  $P$  do
13   if  $t.k$  in  $t.K$  then
14     | Add ( $t.t, t.k$ ) to M; Remove  $t$  from  $P$ ;
15   end
16 end
17 while  $P$  is not empty do
18   Remove the patient with the highest priority from  $P$ , denoted by  $t$  while  $t.Pr$  is
      not empty do
19     Remove the option with the highest preference from  $t.Pr$ , denoted by  $op$ 
20     if  $op=t$  or  $op=w$  then
21       | Add  $t.t$  to the waiting list  $W$ 
22     end
23     else if  $op$  in  $P$  and  $t.k$  in the compatible set  $op.K$  then
24       | Add ( $t.t, op.k$ ) and ( $op.t, t.k$ ) to M
25     end
26   end
27 end

```

2 Efficient strategy-proof exchange mechanism

2.1 Q3

Lemma 2.1. *Consider a graph, in which vertices are kidneys, patients and the waiting list w . Every patient points to either a kidney or to w . Every kidney points to its paired patient. Then either there exists a cycle, or each pair is the tail of some w -chain.*

Proof. For each kidney-patient pair (k, t) , let c be the longest directed path starting from k (if it is not unique, we just randomly pick one). Let v be the end vertex of the path, then v is either w or another patient t' . If v is w , we conclude that the path is a w -chain and (k, t) is the tail. Otherwise, v is t' . Noting that w has no outedges, w

is not in the path. Since the path is the longest, t' cannot point to w . Suppose that t' points to a kidney k'' , then k'' is in the path. No kidney can be assigned to more than one person, hence $k''=k$, which creates a circle where there is (k,t) . \square

2.2 Q4

Algorithm 2.1: Cycle and Chain Matching Algorithm Rule A

Input: Adjacent list D whose vertices are patients $V = \{t_i\}$ and a waiting list w without arcs

Output: An assignment of the patients to either a kidney or the waiting list

/ patient is a class containing 3 domains: patient t , corresponding donor k and corresponding preference list Pr , and an assignment op */*

```

1  W is empty;                                // W is a waiting priority list
2   $V' = V$ ;                                    // patient to be assigned
3  while  $V'$  is not empty do
4      for  $t$  in  $V'$  do
5          |  $t.op$  = the most preferred option in  $t.Pr$ 
6      end
7      if there exists a cycle denoted by  $c$  then
8          | Remove the vertices in the cycle from  $V'$ ; Remove the vertices in the cycle from
          | the preference lists of the vertices in  $V'$ ;
9      end
10     else
11         | Find the longest  $w$ -chain starting from  $V'$  in a sense of priority; Remove the
          | vertices in the  $w$ -chain from  $V'$ ; Remove the vertices (except for the tail) in the
          |  $w$ -chain from the preference lists of the vertices in  $V'$ ;
12     end
13 end

```

Algorithm 2.2: Cycle and Chain Matching Algorithm Rule B

Input: Adjacent list D whose vertices are patients $V = \{t_i\}$ and a waiting list w without arcs

Output: An assignment of the patients to either a kidney or the waiting list

/ patient is a class containing 3 domains: patient t , corresponding donor k and corresponding preference list Pr , and an assignment op */*

```

14 [1]
15 W is empty;                                // W is a waiting priority list
16  $V' = V$ ;                                    // patient to be assigned

```

```

17 while  $V'$  is not empty do
18   for  $t$  in  $V'$  do
19     |  $t.op$  = the most preferred option in  $t.Pr$ 
20   end
21   if there exists a cycle denoted by  $c$  then
22     Remove the vertices in the cycle from  $V'$  Remove the vertices in the cycle from the
     preference lists of the vertices in  $V'$  else
23     |  $p$  = the  $w$ -chain starting from the vertex in  $V'$  with the highest priority Remove the
     vertices in  $p$  from  $V'$  Remove the vertices(except for the tail) in  $p$  from the
     preference lists of the vertices in  $V'$ 
24   end
25 end
26 end

```

3 Examples

3.1 Q5

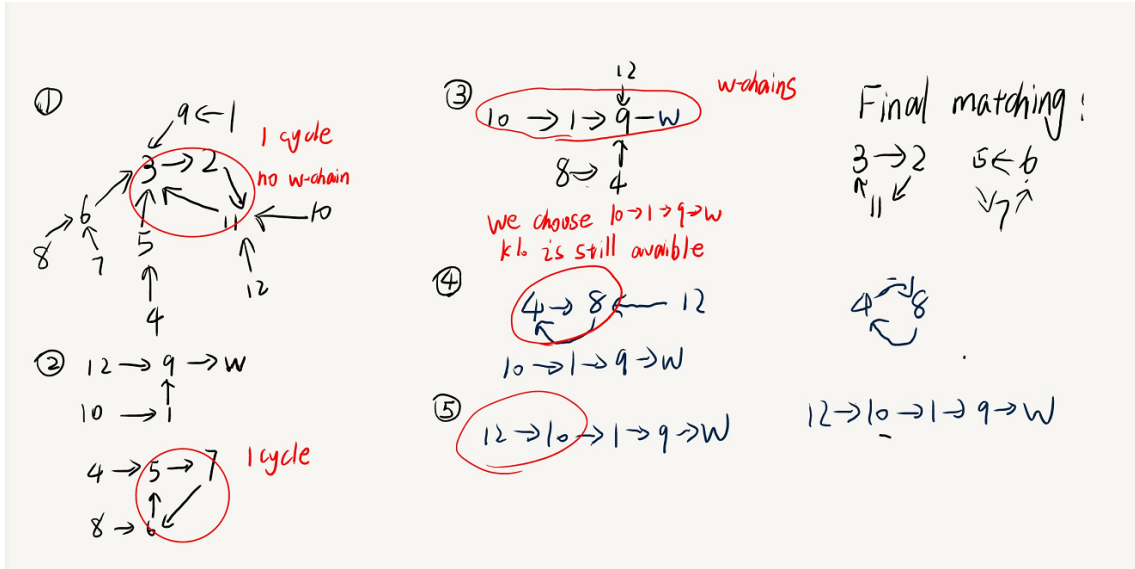


Figure 1: Illustration and final matching for Rule A

3.2 Q6

Theorem 1. Consider a chain selection rule that keeps in the procedure any selected w -chain at a non-terminal round. With such a rule, the exchange mechanism is efficient.

Proof. We note M the result obtained by applying the selection rules. We assume there exists another allocation M' more efficient than M . We use T to represent the ensemble of patients in M' who strictly prefer M' than M and t the patient in T with highest priority. If we look back to the procedures, t is either allocated to the remaining most preferable kidney, or allocated to waiting list. And by the hypothesis of t , we know that all the patients before t (higher priority) are allocated the same kidney in M or M' . So the kidney allocated to t in M' can not be more preferable than in M . This is absurde to the definition of t . so T is empty. Therefore the selection rule is efficient. \square

3.3 Q7

Rule A is not strategy-proof.

Proof. We have an example with 6 patients and their preference list is

1: $k2 > k1$ 2: $k1 > k2$ 3: $k2 > w$

4: $k2 > k3 > k5 > k4$ 5: $k2 > k3 > k5$

6: $k2 > k5 > k6$ we have: situation 1

If Patient4 lies that his preference list is $k2 > k5 > k4$, we have situation 2

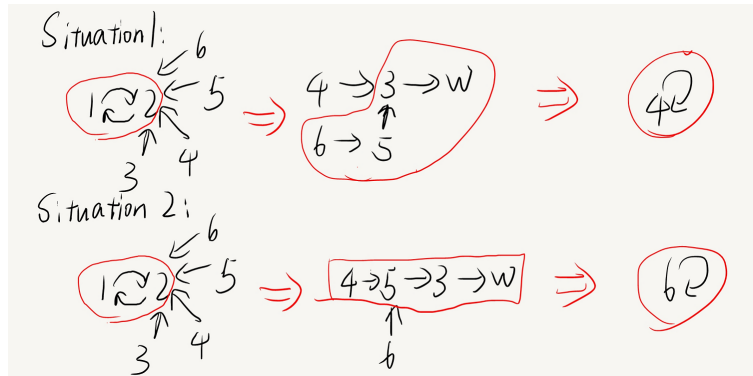


Figure 2: no lie vs lie

So Patient4 will be matched with the kidney5 rather than 4, he benefits from lying. Therefore, Rule A is not strategy-proof. \square

3.4 Q8

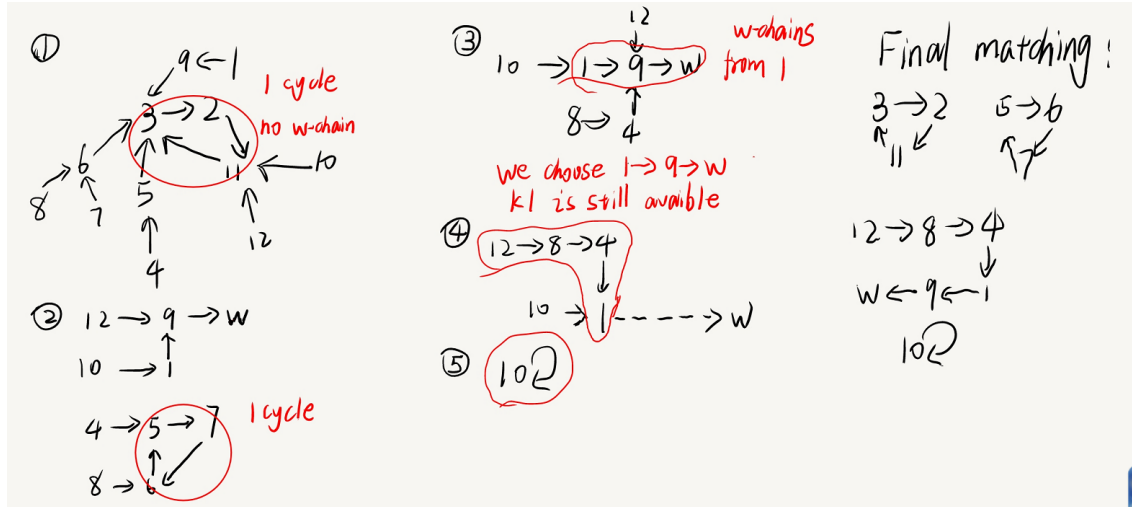


Figure 3: Illustration and final matching for Rule B

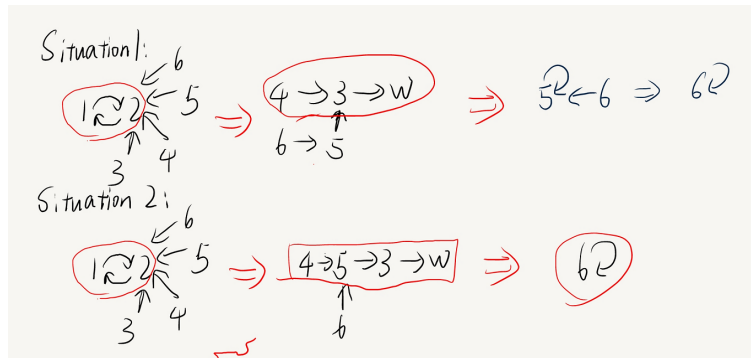


Figure 4: no lie vs lie

With the same example in Q7. This time we can see that patient 4 doesn't benefit from lying. He get 5 instead of 3.

4 Integer Linear programming

4.1 Q9

In this question, we use the BFS algorithm.

Algorithm 4.1: Find Minimal Infeasible Paths (FMIP)

Input: Seuil K , A directed graph G . **Output:**All the minimal infeasible paths. */* */*

```

27 [1] P=[] //P is a vector contains all the paths of length K
28 Map= is a hashmap containing all the k,P couples.
29 if  $K$  is in Map.keys then
30   | P=Map.find(K)
31 end
32 else if  $K=1$  then
33   | Add all the directed edges to P;
34   | Add 1,P to Map
35 end
36 else if  $K\%2=0$  then
37   | P1=FMIP( $K/2$ );
38   | add  $k/2, P1$  to Map;
39   | P=all the possible combination of paths in P1
40 end
41 else
42   | P1=FMIP( $k/2$ ),P2=FMIP( $K-k/2$ );
43   | add  $k/2, P1$   $k-K/2, P2$  to Map;
44   | P=all the possible combination of paths in P1,P2
45 end
46 Return P;

```

Algorithm 4.2: DFS_{limit}

Input: seuil,patient, A directed graph G **Output:**All the minimal infeasible paths. */* */*

```

47 [1] P=[],P is a vector contains all the paths of length K
48 if seuil==1 then
49   | for all the neighbors  $n$  for patient do
50     | if  $n$  hasn't been visited; Q=DFSlimit(seuil - 1,  $p, g$ );
51     | connect the paths in Q to patient to formulate P
52   end
53   return P;
54 end
55 else if seuil $\geq 2$  then
56   | for all the neighbors  $n$  for patient do
57     | if  $n$  hasn't been visited;
58     | P.add(the path containing only  $n$  );
59   end
60   return P;
61 end

```

```

62 for patient  $p:G.vertices$  do
63    $Q=DFS_{limit}(data.seuil, p, g);$ 
64   for Path  $pa:Q$  do
65      $P.add(pa);$ 
66   end
67end
68Return  $P;$ 

```

4.2 Q10

Objective: $\max \sum_{(i,j \in E)} X_{i,j}$

We have the constraints as follows:

1. $\max \sum_{(i_0, j \in E)} X_{i_0, j} \leq 1$ for all $i_0 \in V$.
2. $\max \sum_{(i, j_0 \in E)} X_{i, j_0} \leq 1$ for all $j_0 \in V$.
3. $\sum_{(i_0, j \in E)} X_{i_0, j} = \sum_{(i, j_0 \in E)} X_{j, i_0}$ for all $i_0 \in V$.
4. $\sum_{e \in p} X_e \leq K - 1$ for all $p \in P[K + 1]$.
5. $X_{i,j} \in 0, 1$.

4.3 Q11

Algorithm4.2: Branch-and Bound Algorithm

Input: lpsole problem, edges Q , depth

Output: Non because the reslut is stored in problem(pass by adress /* E=ensemble of edges in the graph */
/* depth=the depth of problem in the BB tree(the number of extra-constraints we suppose on the edges. */
/* problem= we create a class containing the basic constraints in question 10 mainly using the lp solve class */
/* */

```

69 if the problem has no solution or depth  $\geq Q.size$  then
70   return;
71 end
72 else if obj  $\leq lowerBound$  then
73   return;
74 end
75 else if depth ==  $Q.size() - 1$  then
76   lowerBound=obj;
77   note the solution;
78   solver.solve();
79   return;

```



```

80 end
81 create two new constraints for the depth-th edge.
82 cons1:depth-th edge=0;
83 cons2:depth-th edge=1;
84 problem1=problem.add(cons1);
85 problem2=problem.add(cons2);
86 Branch-and Bound(problem1,edges,depth+1);
87 Branch-and Bound(problem2,edges,depth+1);
88 return;

```

4.4 13

```

<terminated> ExamResults [Java Application] C:\Program Files\Java\jdk-14\bin\javaw.exe
The transplantation rate for direct donation: 0.725
The transplantation rate for 2-way exchange 0.754
The transplantation rate for 2-way exchange without direct donation 0.886
The transplantation rate for rule B:0.7806666666666666
The transplantation rate for rule B without direct donation:0.778
The transplantation rate for rule A:0.781
The transplantation rate for rule A without direct donation:0.7826666666666666

```

Figure 5: results for different algorithms

We can see that the transplantation rate becomes higher and higher from algorithm1 to algorithm2 to algorithm3A and 3B. So with cycle and w-chain we can conduct to better results. Moreover we can see that running the direct donation algorithm as a preprocessing step doesn't help other algorithms because direct donation will also be seen as a cycle for Algo3A and 3B, as quote(Option ki either means that ki is compatible with ti, in which case ki is the most preferred option) . For algo2 without preprocessing, we see that the compatible rate is much higher, that's because those who have a compatible donor sacrifice somewhere in their preference. Finally we can see the gain allowing multiple-way change is about $78\%-75\%=3\%$ as shown in results.