Matching mechanisms for kidney transplantations

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1 Two Simple Approaches

Question 1

```
Algorithm 1: Direct Donation
   Input: A number n of patient and, for all patients i \in \mathbb{N}, their set of
            compatible donors K_i \subseteq [1, n].
   Output: A set of pairs donor-patient pairs c and a waiting list w.
 1 initialization
       c = \emptyset;
       w = [];
 4 begin
       for i = 1 to n do
 5
           if i \in K_i then
            c = c \cup \{(i, i)\};
 7
           else
 8
               w.add(i)
       return c, w
10
```

The implementation in python is pretty straightforward. The python function takes as parameter an integer n and an integer set array of size n. The use of python set allows to test the if condition in constant times. The only difference with pseudo-code is the use of a list rather than a set for the variable c. This choice was made to avoid the unnecessary heaviness of the set data structure, but does not change the complexity.

Question 2

Our matching algorithm must prioritize the patients with the highest priority. It must also ensure that all patients will leave with a donor that suited them better than their paired donor and the waiting list, otherwise some patients may not participate in the exchange program.

Our greedy algorithm therefore consists of browsing the patients in descending order of priority and matching them to their preferred donor whose paired patient does not prefer the waiting list or his donor to the donor of the priority patient.

Algorithm 2: Greedy Matching

Input: A number n of patient, a strict priority list of the patients U and, for all patients $i \in \mathbb{N}$, their set of compatible donors $K_i \subseteq \llbracket 1, n \rrbracket$ and their strict preference relation P_i over $K_i \cup \{k_i, w\}$. The priority list is an integer list that starts with the index of the highest priority patient and goes to the index of the lowest priority patient.

```
Output: A matching M.
```

```
1 initialization
      M = \emptyset;
 2
      is matched = Boolean[1..n];
 3
      sorted K = IntegerList[1..n];
 4
      for i = 1 to n do
 5
 6
         is matched[i] = False;
         sorted K[i] = sort(K_i, P_i);
                                                            // \mathcal{O}(n\log(n))
 8 begin
      /* Iterate over all patient by decreasing priority
                                                                         */
      for not U.is empty() do
 9
          u = U.pop();
10
          if not is matched[u] then
11
             while not sorted K[u].is empty() do
12
                 v = sorted K[u].pop();
13
                 if not is matched[v] then
14
                     /* If t_v prefer k_u over k_v and w
                                                                         */
                    if t_v P_v t_u and t_v P_v w then
15
                        M = M \cup \{((k_u, t_u), (k_v, t_v))\};
16
                        is matched[u] = True;
17
                        is matched[v] = True;
18
19
      return M
```

We start by initializing an $is_matched$ array to keep track of which pair has already been matched and an integer list array $sorted_K$ that contains, for each patient of index i, the indexes of the preferred donors in descending order of preference. The sort function returns a list of the elements of K_i sorted in descending order according to the preference relation P_i .

2 Efficient stategy-proof exchange mechanism

Question 3

Let (k_1, t_1) be a pair of donor-patient and assume there is no cycle. Consider the chain starting from (k_1, t_1) . Since there is a finite number n of donor-patient pairs and there is no cycle, the chain cannot be infinite. Finally, since the only way for a chain to stop is that w belong to the chain, (k_1, t_1) is indeed a tail of a w-chain.

Thus either there exists a cycle, or each pair is the tail of some w-chain.

Question 4

Question 5

Let's run the Cycles and Chains Matching Algorithm with rule A on this example. The initial state of the graph, before the first round, is shown in figure 1.

The initial graph contains a cycle $C_1 = (k_3, t_3, k_2, t_2, k_{11}, t_{11})$. The first round of the algorithm therefore consists in detecting this cycle, allocating the kidneys to the patients and then eliminating the cycle.

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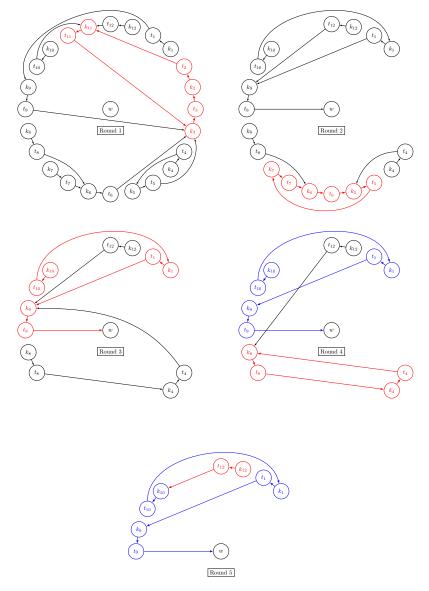


Figure 1: Test