# APPLIED MECHANISM DESIGN FOR SOCIAL GOOD

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Lecture #17 - 04/07/2020

CMSC828M Tuesdays & Thursdays 2:00pm – 3:15pm



### THIS CLASS: ORGAN EXCHANGE

# **KIDNEY TRANSPLANTATION**

- US waitlist: over 100,000
  - Over 35,000 added per year
- ~4500 people died while waiting
- ~12000 people received a kidney from the deceased donor waitlist



- (See last class' lecture on deceased donor allocation.)
- ~6000 people received a kidney from a
  - Some through kidney exchanges and the second s

Last time,

I promise!

### **KIDNEY EXCHANGE**



(2- and 3-cycles, all surgeries performed simultaneously)

### **NON-DIRECTED DONORS & CHAINS**

[Rees et al. 2009]



Not executed simultaneously, so no length cap required based on logistic concerns ...

... but in practice edges fail, so often some finite cap is used!

### **THE CLEARING PROBLEM**



# The clearing problem is to find the "best" disjoint set of cycles of length at most *L*, and chains (maybe with a cap *K*)

• Very hard combinatorial optimization problem that we will focus on in the succeeding two lectures.

## **MANAGING INCENTIVES**

#### **Clearinghouse** cares about global welfare:

• How many patients received kidneys (over time)?

#### **Transplant centers** care about their individual welfare:

• How many of my own patients received kidneys?

#### **Patient-donor pairs care about their individual welfare:**

- Did I receive a kidney?
- (Most work considers just clearinghouse and centers)

# INDIVIDUAL RATIONALITY (IR)

Will I be better off participating in the mechanism than I would be otherwise?

#### Long-term IR:

• In the long run, a center will receive at least the same number of matches by participating

#### Short-term IR:

• At each time period, a center receives at least the same number of matches by participating

# STRATEGY PROOFNESS

Do I have any reason to lie to the mechanism?

In any state of the world ...

 { time period, past performance, competitors' strategies, current private type, etc }

... a center is not worse off reporting its full private set of pairs and altruists than reporting any other subset

 $\rightarrow$  No reason to strategize



Does the mechanism result in the absolute best possible solution?

#### **Efficiency:**

 Produces a maximum (i.e., max global social welfare) matching given all pairs, regardless of revelation

#### **IR-Efficiency**:

Produces a maximum matching constrained by short-term individual rationality

# PRIVATE VS GLOBAL MATCHING





# FIRST: ONLY CYCLES (NO CHAINS)

# THE BASIC KIDNEY EXCHANGE GAME [Ashlagi & Roth 2014, and earlier]

Set of *n* transplant centers  $T_n = \{t_1 \dots t_n\}$ , each with a set of incompatible pairs  $V_h$ 

Union of these individual sets is *V*, which induces the underlying compatibility graph

Want: all centers to participate, submit full set of pairs

An allocation *M* is *k*-maximal if there is no allocation *M*' that matches all the vertices in *M* and also more

• Note: *k*-efficient  $\rightarrow$  *k*-maximal, but not vice versa

[Ashlagi & Roth 2014, and earlier]

- Vertices  $a_1$ ,  $a_2$  belong to center  $a_1$ ,  $b_1$ ,  $b_2$  belong to center  $b_1$
- . Center a could match 2 internally
- . By participating, matches only 1 of its own
- . Entire exchange matches 3 (otherwise only 2)



#### **IT CAN GET MUCH WORSE** [Ashlagi & Roth 2014, and earlier]

**Theorem:** For k>2, there exists *G* s.t. no IR *k*-maximal mechanism matches more than 1/(*k*-1)-fraction of those matched by *k*-efficient allocation

- Bound is tight
- All but one of a's vertices is part of another length k exchange (from different agents)
- k-maximal and IR if a matches his k vertices (but then nobody else matches, so k total)
- k-efficient to match (k-1)\*k



### **RESTRICTION #1** [Ashlagi & Roth 2014, and earlier]

**Theorem:** For all *k* and all compatibility graphs, there exists an IR *k*-maximal allocation

Proof sketch: construct *k*-efficient allocation for each specific hospital's pool  $V_h$ 

Repeatedly search for larger cardinality matching in an entire pool that keeps all already-matched vertices matched (using augmenting matching algorithm from Edmonds)

Once exhausted, done

### **RESTRICTION #2** [Ashlagi & Roth 2014, and earlier]

# **Theorem:** For *k*=2, there exists an IR 2-efficient allocation in every compatibility graph

#### Idea: Every 2-maximal allocation is also 2-efficient

This is a PTIME problem with, e.g., a standard  $O(|V|^3)$  bipartite augmenting paths matching algorithm

By Restriction #1, 2-maximal IR always exists  $\rightarrow$  this 2efficient IR always exists

### **RESTRICTION #3** [Ashlagi et al. 2015]

# **Theorem:** No IR mechanism is both maximal and strategyproof (even for *k*=2)

Suppose mechanism is IR and maximal ...



# MORE NEGATIVE MECHANISM DESIGN RESULTS [Ashlagi et al. 2015]

Just showed IR + strategyproof  $\rightarrow$  not maximal

No IR + strategyproof mechanism can guarantee more than <sup>1</sup>/<sub>2</sub>-fraction of efficient allocation

 Idea: same counterexample, note either the # matched for hospital a < 3, or # matched for hospital b < 2. Proof by cases follows

# No IR + strategyproof randomized mechanism can guarantee 7/8-fraction of efficiency

 Idea: same counterexample, bounds on the expected size of matchings for hospitals a, b

### **HOPELESS** ...?



# DYNAMIC, CREDIT-BASED MECHANISM [Hajaj et al. AAAI-2015]

#### **Repeated game**

#### Centers are risk neutral, self interested

#### Transplant centers have (private) sets of pairs:

- Maximum capacity of 2k<sub>i</sub>
- General arrival distribution, mean rate is  $k_i$
- Exist for one time period

Centers reveal subset of their pairs at each time period, can match others internally

### CREDITS

Clearinghouse maintains a credit balance  $c_i$  for each transplant center over time

High level idea:

- **REDUCE** c<sub>i</sub>: center *i* reveals fewer than expected
- **INCREASE** *c<sub>i</sub>*: center *i* reveals more than expected
- **REDUCE** *c<sub>i</sub>*: mechanism tiebreaks in center *i*'s favor
- INCREASE c<sub>i</sub>: mechanism tiebreaks against center I

Also remove centers who misbehave "too much."

Credits now  $\rightarrow$  matches in the future

# THE DYNAMIC MECHANISM

#### 1. Initial credit update

- Centers reveal pairs
- Mechanism updates credits according to k<sub>i</sub>
- 2. Compute maximum global matching
  - Gives the utility  $U_g$  of *a* max matching
- 3. Selection of a final matching
  - Constrained to those matchings of utility  $U_g$
  - Take c<sub>i</sub> into account to (dis)favor utility given by matching to a specific center i
  - Update  $c_i$  based on this round's (dis)favoring
- 4. Removal phase if center is negative for "too long"

## THEORETICAL GUARANTEES

Theorem: No mechanism that supports cycles and chains can be both long-term IR and efficient

Theorem: Under reasonable assumptions, the prior mechanism is both long-term IR and efficient

# LOTS OF OPEN PROBLEMS HERE

#### Dynamic mechanisms are more realistic, but ...

- Vertices disappear after one time period
- All hospitals the same size
- No weights on edges
- No uncertainty on edges or vertices
- Upper bound on number of vertices per hospital
- Distribution might change over time



### WHAT DO EFFICIENT MATCHINGS EVEN LOOK LIKE ...?

Next class: given a specific graph, what is the "optimal matching"

This class: given a **family of graphs**, what do "optimal matchings" tend to look like?

Use a stylized random graph model, like [Saidman et al. 2006]:

- Patient and donor are drawn with blood types randomly selected from PDF of blood types (roughly mimics US makeup), randomized "high" or "low" CPRA
- Edge exists between pairs if candidate and donor are ABOcompatible and tissue type compatible (random roll weighted by CPRA)

# **RANDOM GRAPH PRIMER**

Canonical Erdős-Rényi random graph G(m,p) has m vertices and an (undirected) edge between two vertices with probability p

Let Q be the property of "there exists a perfect matching" in this graph

The convergence rate to 1 (i.e., "there is almost certainly a near perfect matching in this graph) is exponential in *p* 

- $Pr(G(m,m,p) \text{ satisfies } Q) = 1 o(2^{-mp})$
- At least as strong with non-bipartite random graphs

Early random graph results in kidney exchange are for "in the large" random graphs that (allegedly) mimic the real compatibility graphs

• All models are wrong, but some are useful?

### A STYLIZED ERDŐS-RÉNYI-STYLE MODEL OF KIDNEY EXCHANGE

In these random (ABO- & PRA-) graphs:

- # of O-{A, B, AB} pairs > {A, B, AB}-O pairs
- # of {A, B}-AB pairs > AB-{A, B} pairs
- Constant difference between # A-B and # B-A

Idea #1: O-candidates are hard to self-match

Idea #2: {A, B}-candidates are hard to self-match

Idea #3: "symmetry" between A-B and B-A (equally hard to self-match, give or take)

### EFFICIENT MATCHING IN DENSE GRAPHS WITH ONLY CYCLES

Under some other assumptions about PRA ...

Almost every large random (ABO- & PRA-) graph has an efficient allocation that requires exchanges of size at most 3 with the following:

- X-X pairs are matched in 2- or 3-way exchanges with other X-X pairs (so-called "self-demand")
- B-A pairs are 2-matched with A-B pairs
- The leftovers of {A-B or B-A} are 3-matched with "good" {O-A, O-B} pairs and {O-B, O-A pairs}
- 3-matches with {AB-O, O-A, A-AB}
- All the remaining 2-matched as {O-X, X-O}

### VISUALLY ...



### NEXT CLASS: OPTIMAL BATCH CLEARING OF ORGAN EXCHANGES