APPLIED MECHANISM DESIGN FOR SOCIAL GOOD

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Lecture #18 – 04/01/2021
Lecture #19 – 04/06/2021

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

COMPUTER SCIENCE
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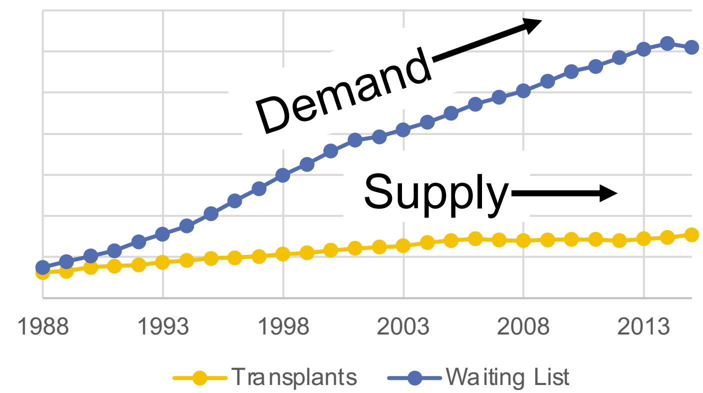
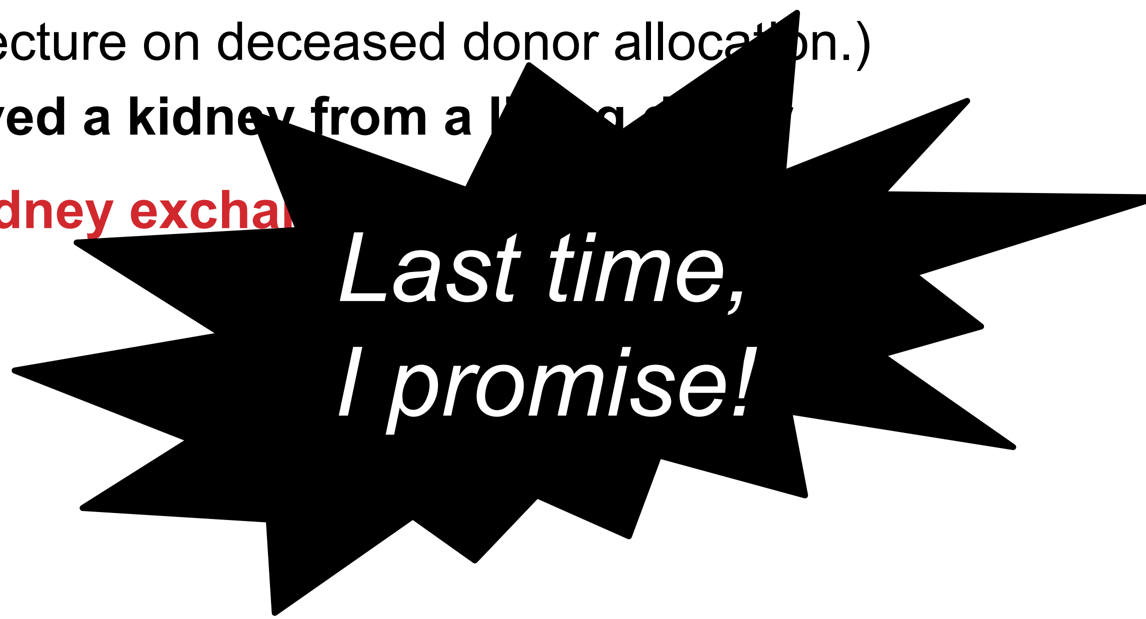
THIS CLASS:
ORGAN EXCHANGE

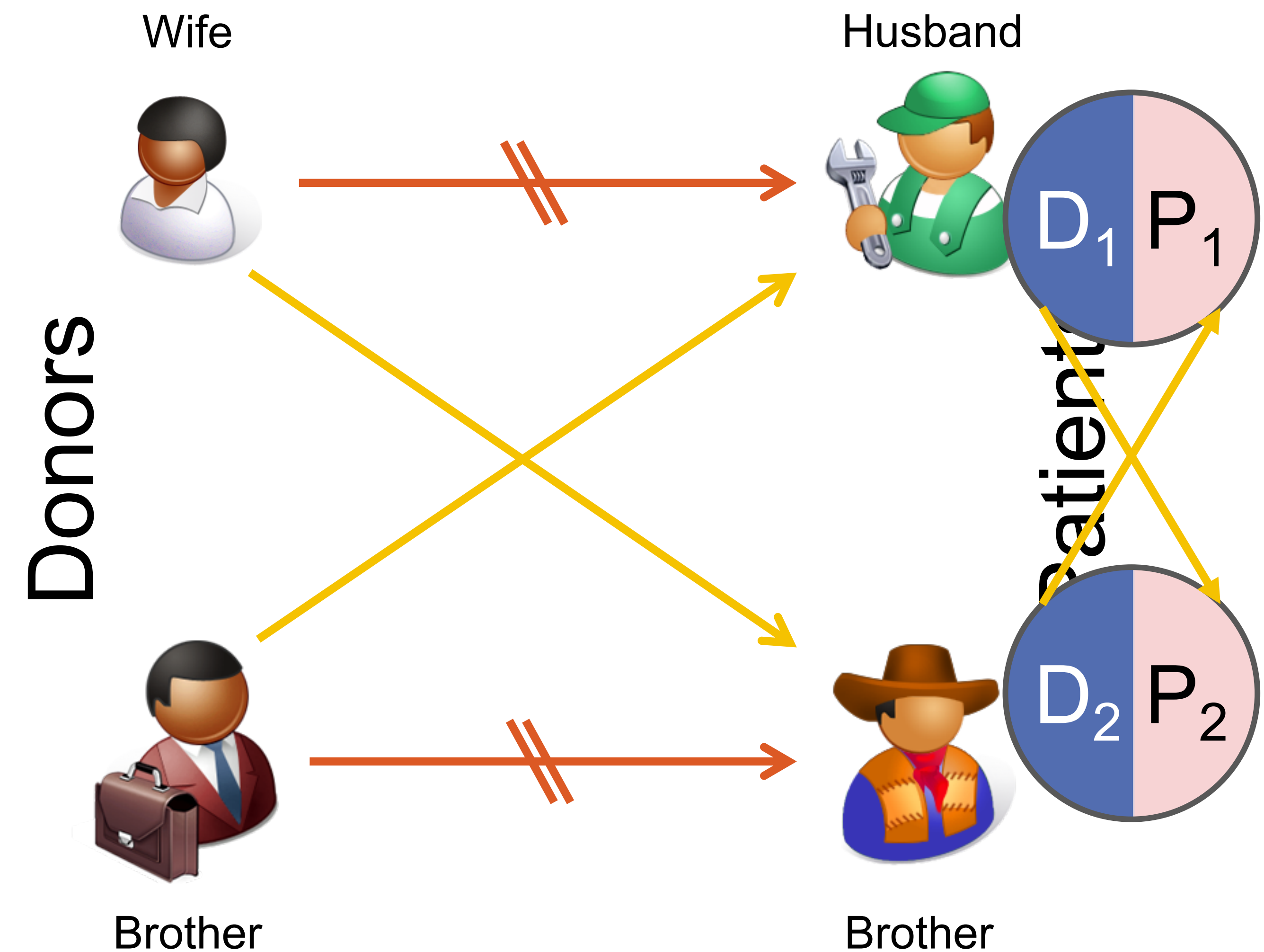
KIDNEY TRANSPLANTATION

- **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 alloca on.)
- **~6000 people received a kidney from a l**
  - Some through **kidney excha**





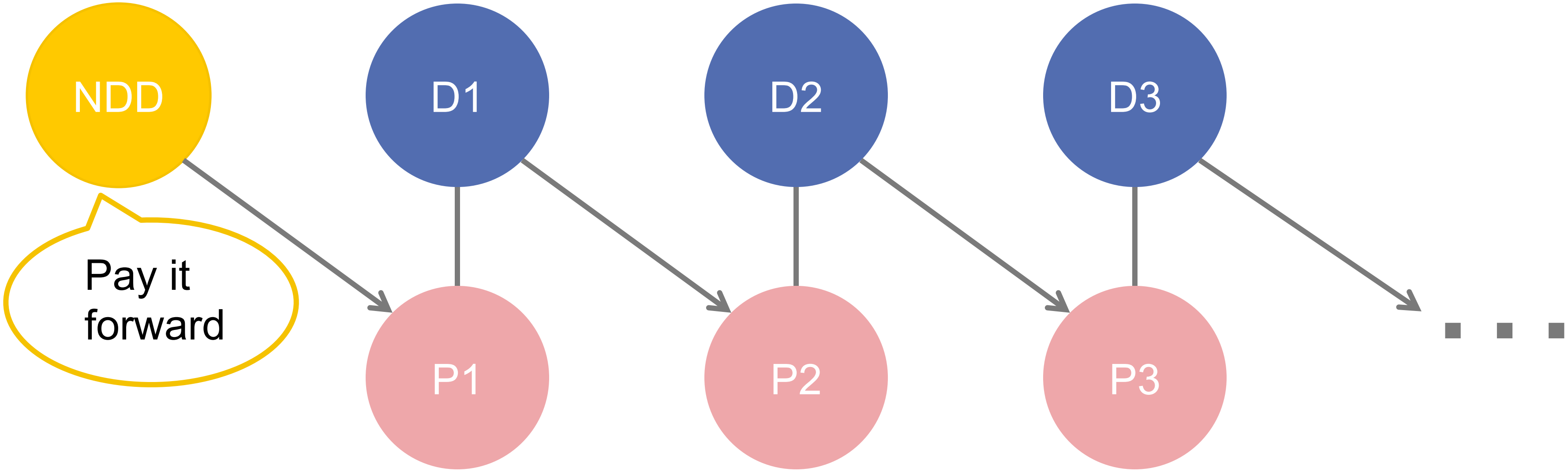
KIDNEY EXCHANGE



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

NON-DIRECTED DONORS & CHAINS

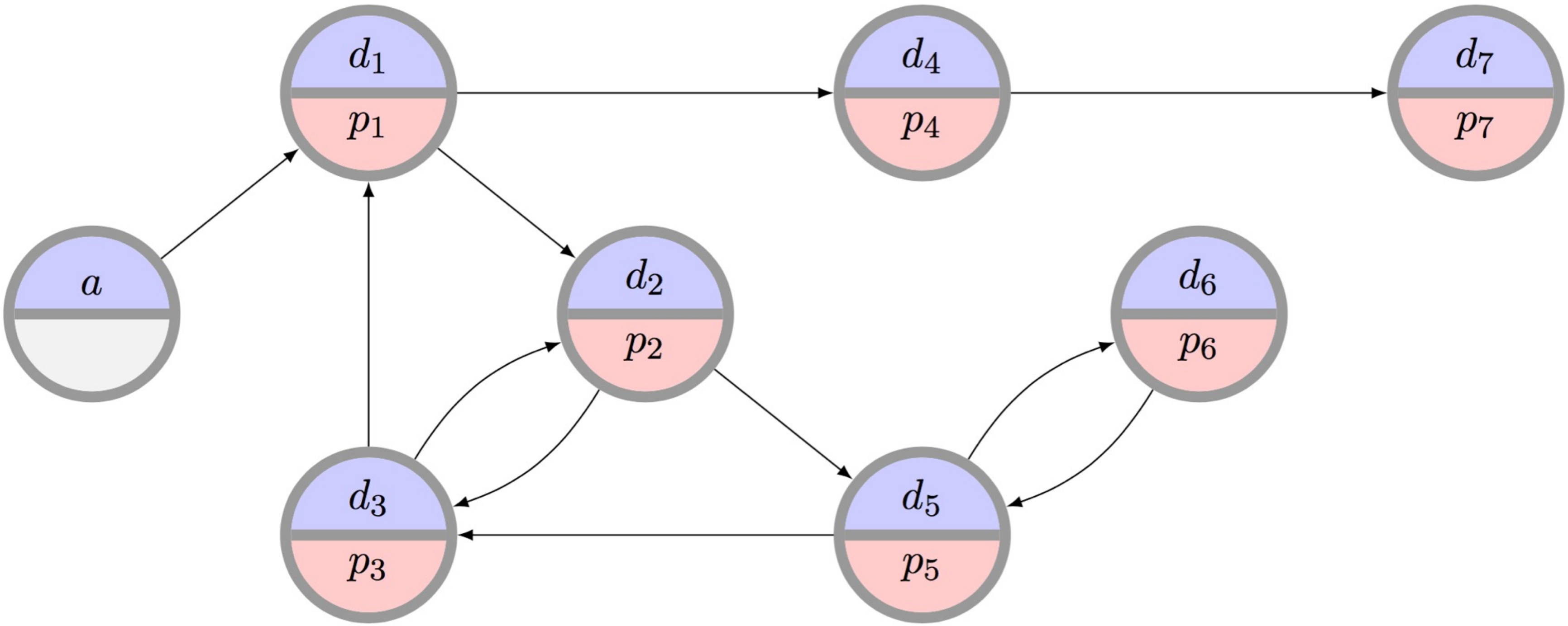
[Rees et al. 2009]



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

→ No reason to strategize

EFFICIENCY

Does the mechanism result in the absolute best possible solution?

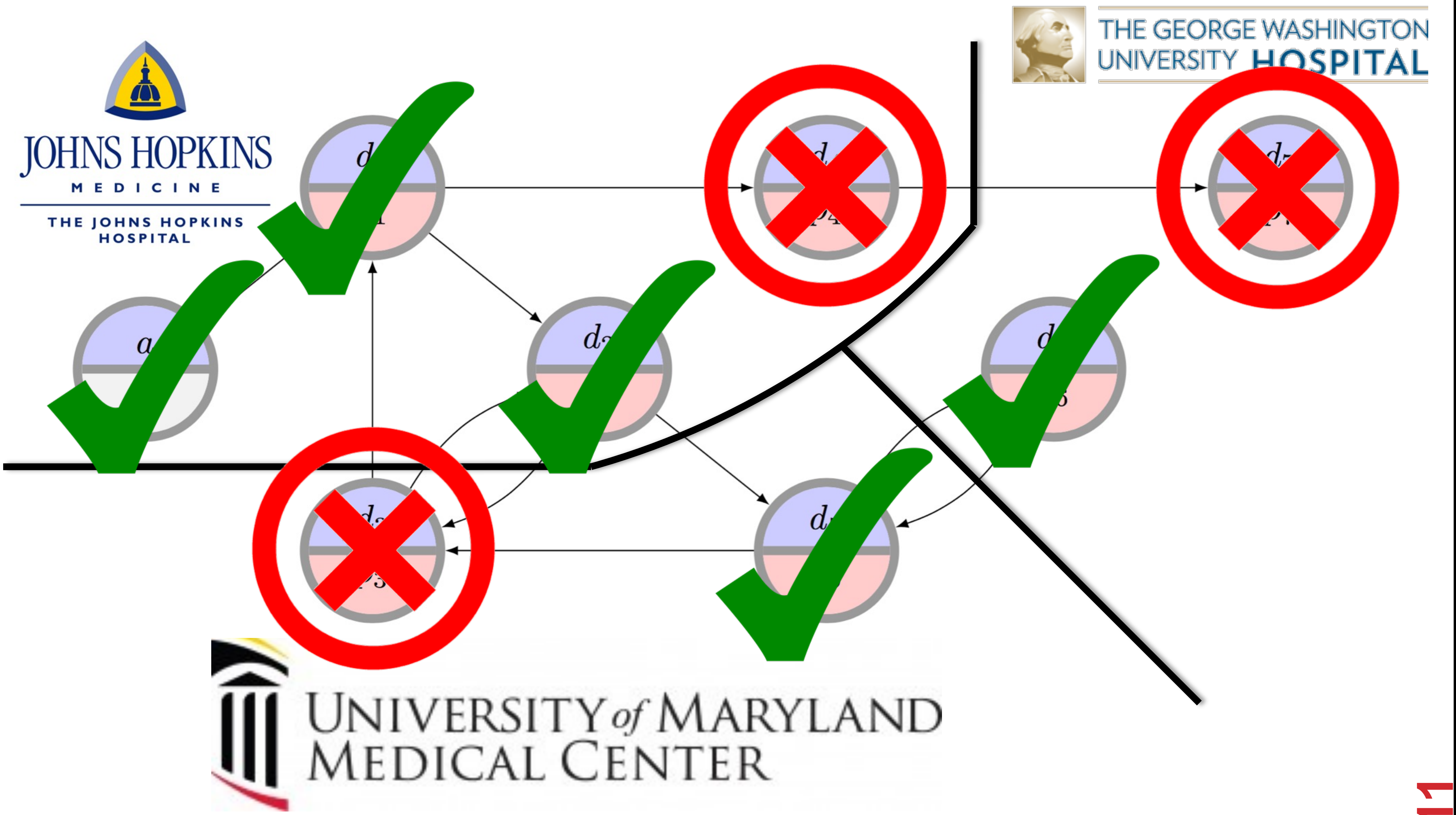
Efficiency:

- 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



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FIRST: ONLY CYCLES (NO CHAINS)

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

Set of *n* transplant centers $T_n = \{t_1 \ldots t_n\}$, 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

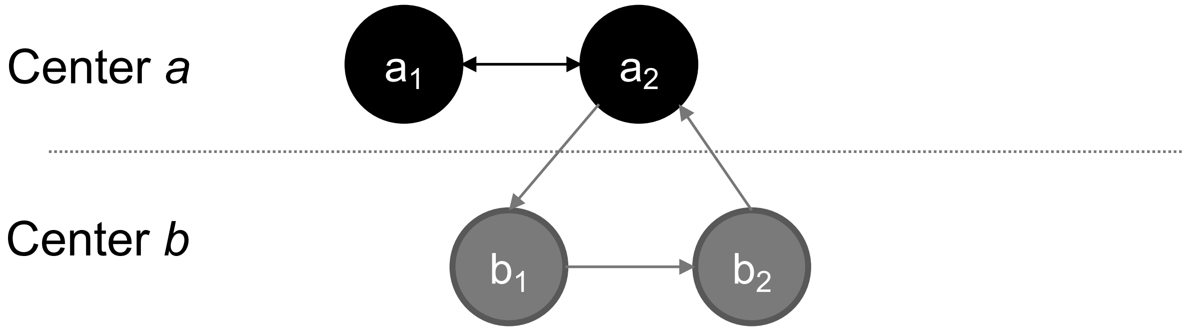
An allocation *M* is *k*-maximal if there is no allocation *M'* that matches all the vertices in *M* and also more

- Note: *k*-efficient → *k*-maximal, but not vice versa

INDIVIDUALLY RATIONAL?

[Ashlagi & Roth 2014, and earlier]

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

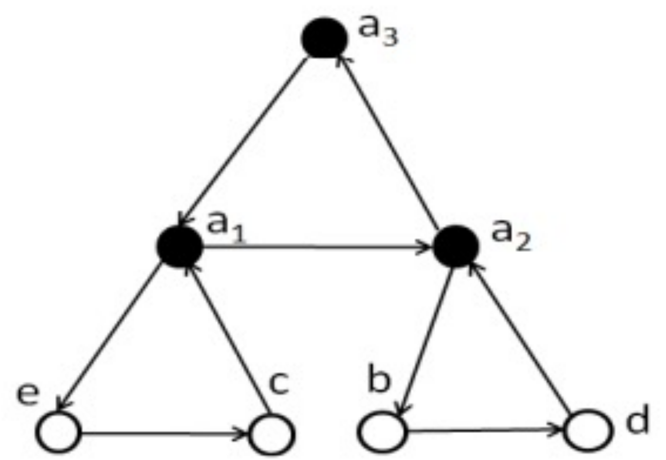


IT CAN GET MUCH WORSE

[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**



Example: k=3

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

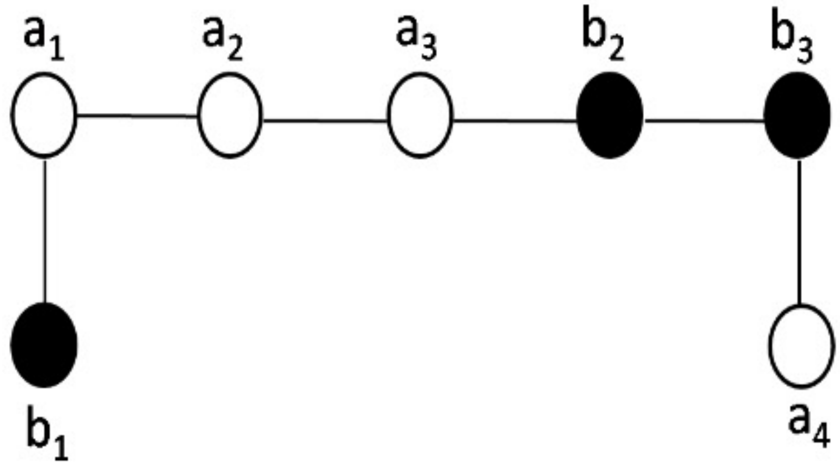
- This is a PTIME problem with, e.g., a standard $O(|V|^3)$ bipartite augmenting paths matching algorithm

By Restriction #1, 2-maximal IR always exists → this 2-efficient 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 → not maximal

No IR + strategyproof mechanism can guarantee more than ½-fraction of efficient allocation

- Idea: same counterexample, note either the # matched for hospital a $\leq$ 3, or # matched for hospital b $\leq$ 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 $2k_i$
- 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_i: center *i* reveals fewer than expected
- **INCREASE** c_i: center *i* reveals more than expected

- **REDUCE** c_i: mechanism tiebreaks in center *i*'s favor
- **INCREASE** c_i: mechanism tiebreaks against center *I*

Also remove centers who misbehave "too much."

Credits now → matches in the future

THE DYNAMIC MECHANISM

1. **Initial credit update**
   - Centers reveal pairs
   - Mechanism updates credits according to k_i
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_i 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
- ...

Project?

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 ABO-compatible 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)

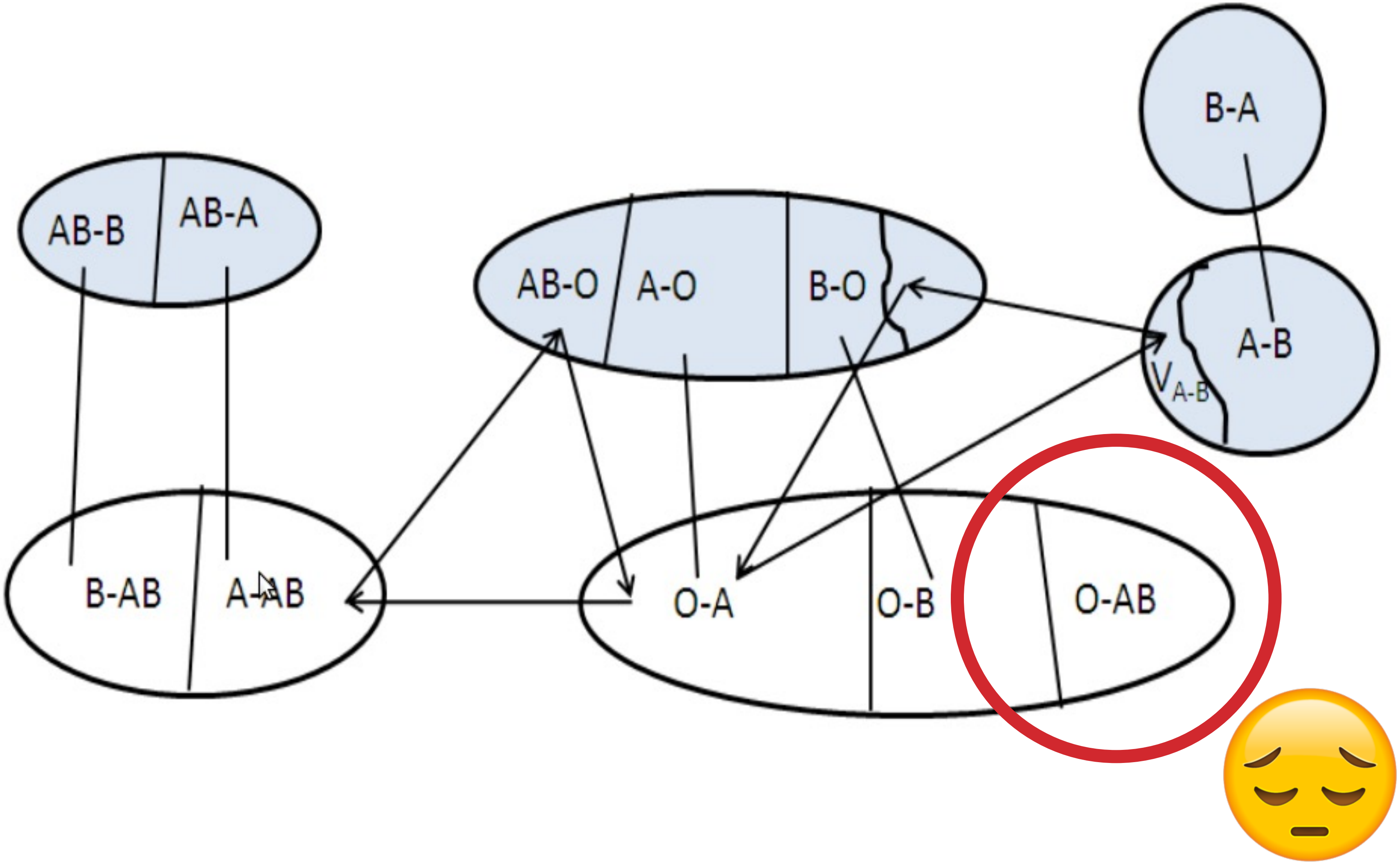
EFFICIENT MATCHING IN DENSE GRAPHS WITH ONLY CYCLES

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