

Data science for networked data

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Big Data Meetup
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Joint work with:

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Wen Yan (Southeast University), and Muni Pydi (UW-Madison)

Key problems in network modeling

- ① Given data from a network, how do we estimate the network?
- ② How do we model dynamic processes over a network?
- ③ How do we perform efficient search over a network?

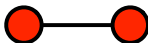
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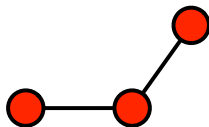
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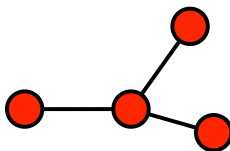
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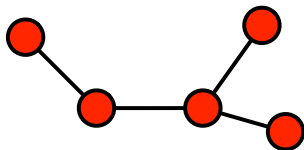
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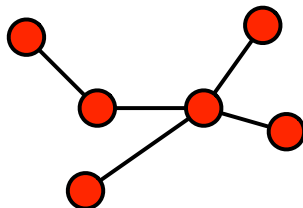
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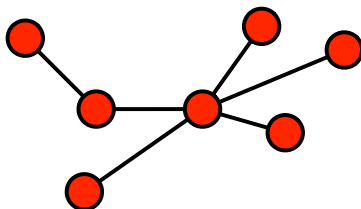
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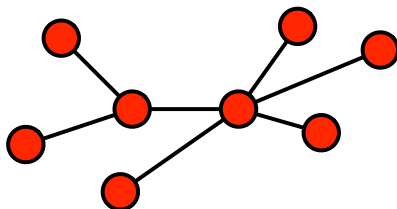
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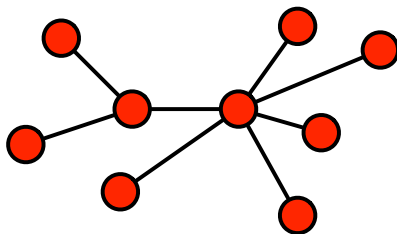
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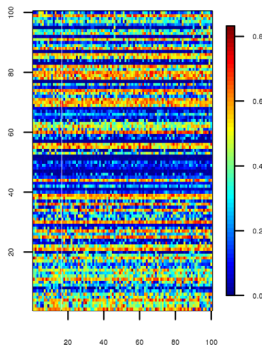


Prelude: Network estimation

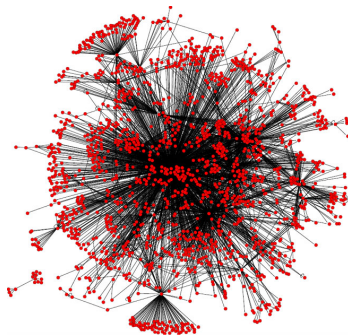
- Method for constructing connectivity network from matrix of data

Graphical models

- Method for constructing connectivity network from matrix of data



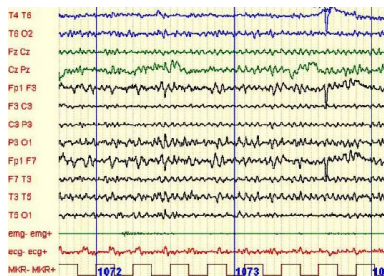
gene expression (mRNA) data



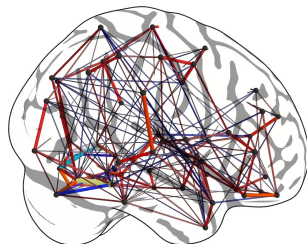
E. coli network

Graphical models

- Method for constructing connectivity network from matrix of data



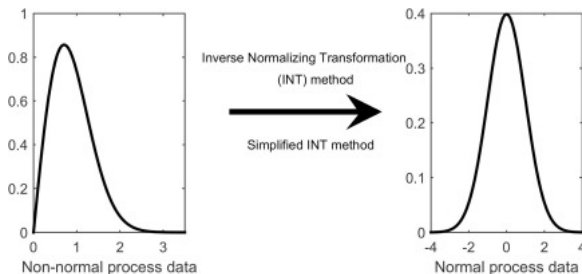
fMRI/EEG readings



“functional connectivity” network

Graphical models

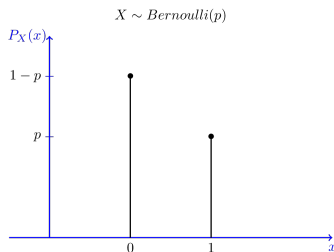
- Mathematical analysis derived for Gaussian data



- In practice, transform data to Gaussian before applying algorithm

Graphical models

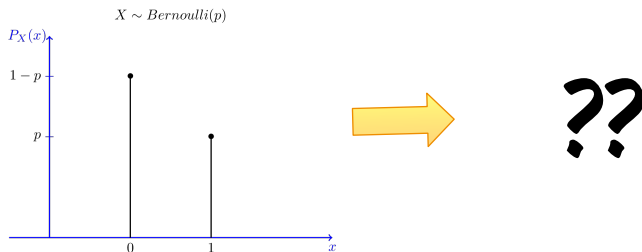
- But not all data are transformable!



??

Graphical models

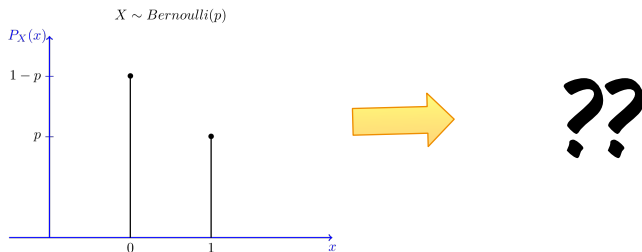
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- We have developed new methods for estimating graphical models for discrete (count) data

Graphical models

- But not all data are transformable!



- We have developed new methods for estimating graphical models for discrete (count) data
- **However, life is more than network estimation...**

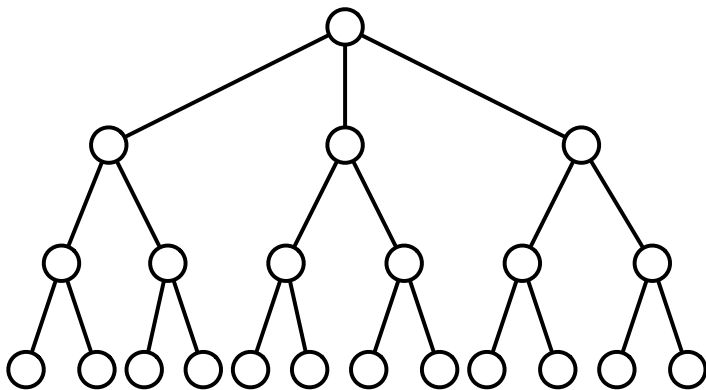
- 1 Statistical inference
 - Confidence sets for source estimation
 - Graph hypothesis testing
- 2 Resource allocation
 - Influence maximization
 - Budget allocation
 - Network immunization
- 3 Local algorithms

Statistical inference

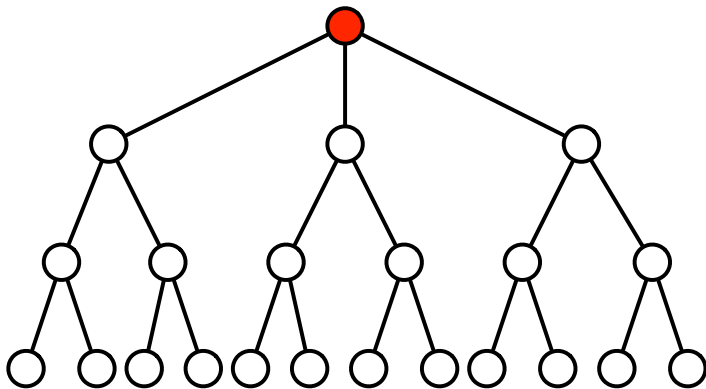


Justin Khim
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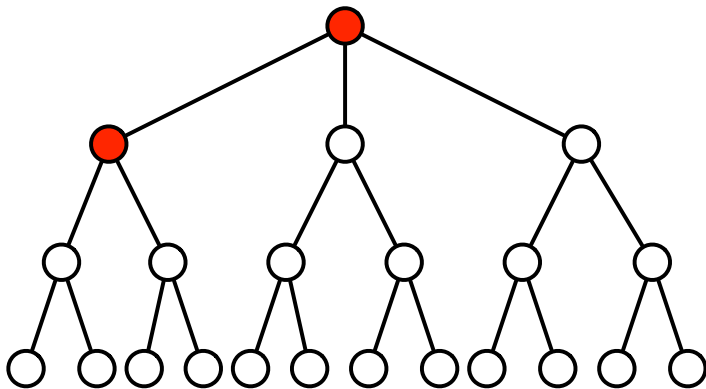
Source estimation



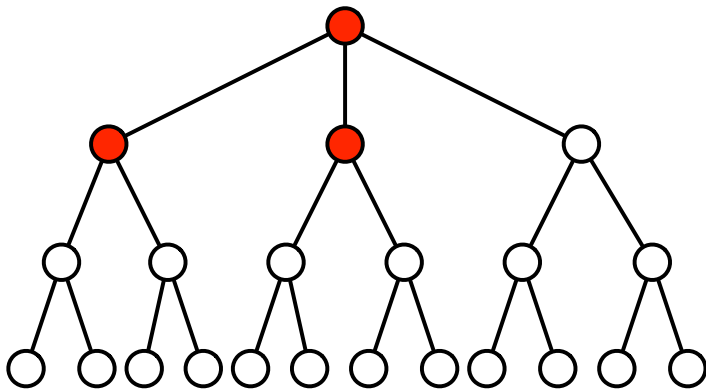
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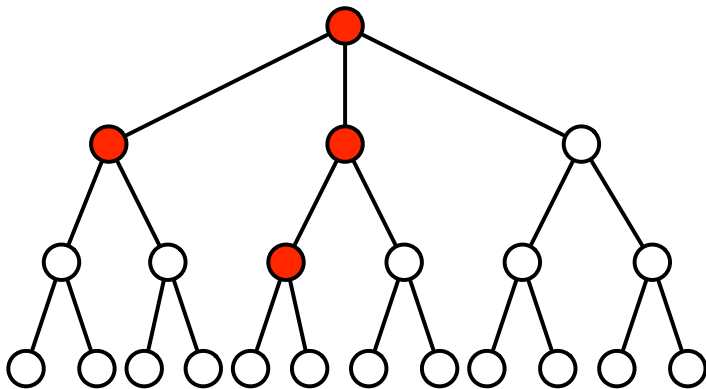
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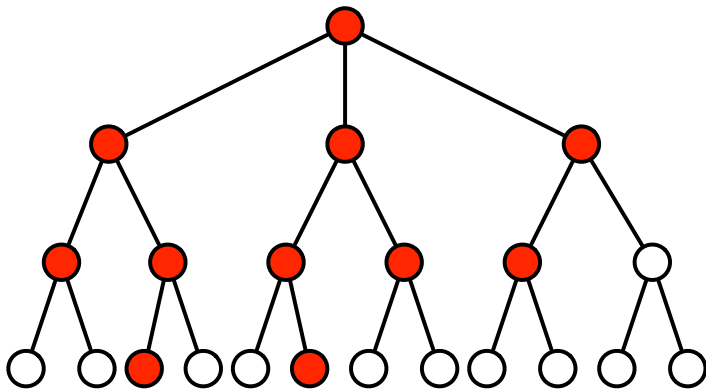
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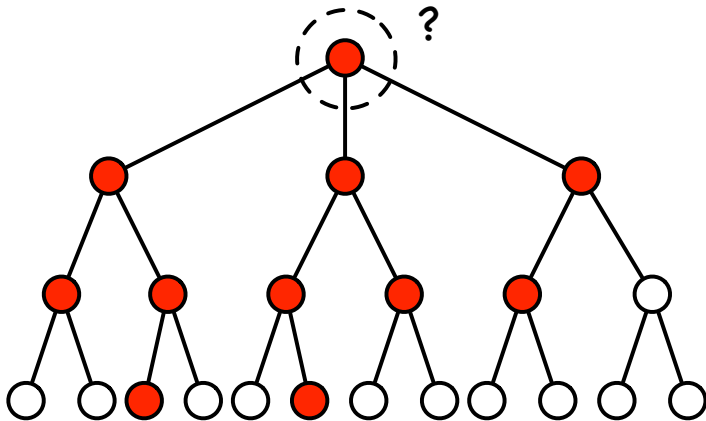
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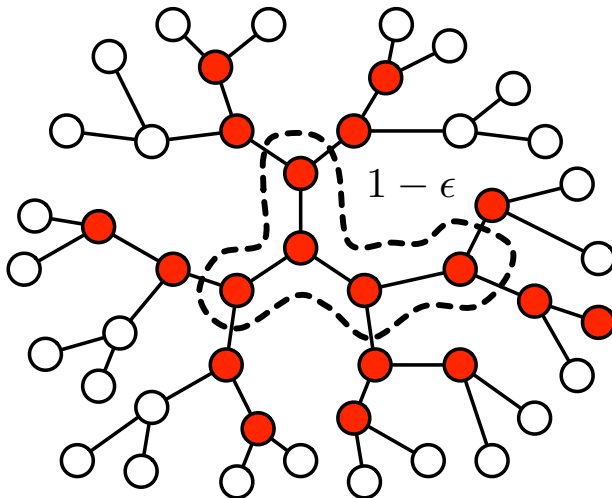


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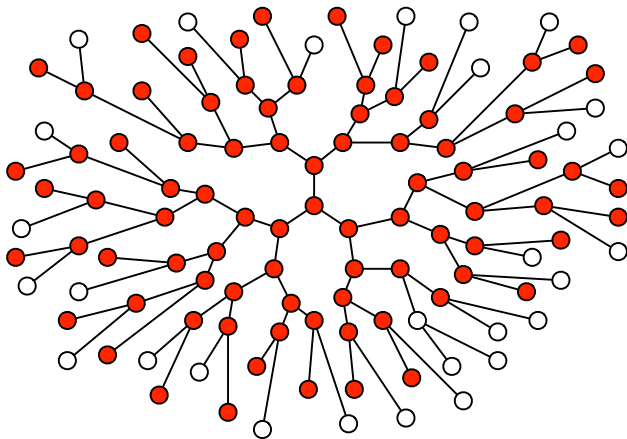
Confidence sets

- **Instead:** Find a *confidence set* that includes root node with probability at least $1 - \epsilon$

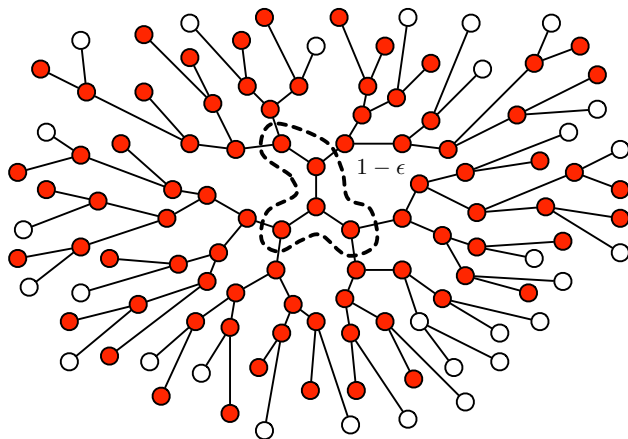


Confidence sets

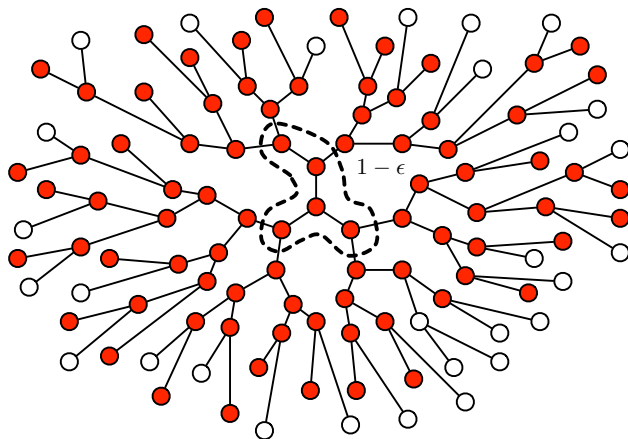
- **Question:** How does size of confidence set grow with number of infected nodes n ?



- **It doesn't!**



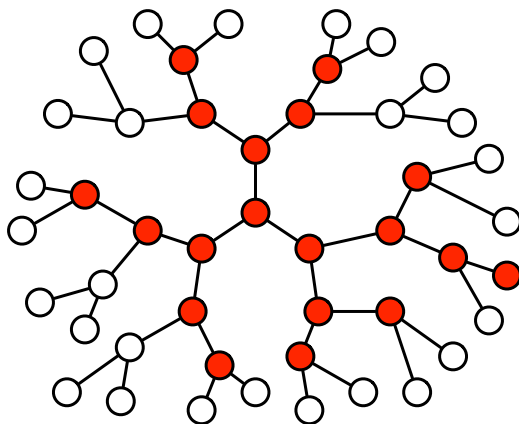
- **It doesn't!**



- **Rough interpretation:** No "information loss" about source as disease spreads

Inference algorithm

- Select nodes that are most “central” to network of infected individuals

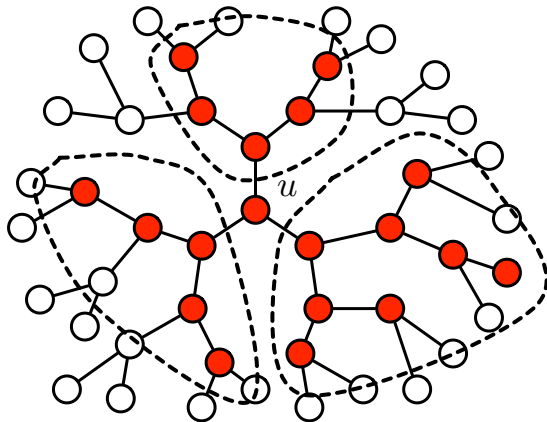


Inference algorithm

- For each node, compute “min-max subtree size”

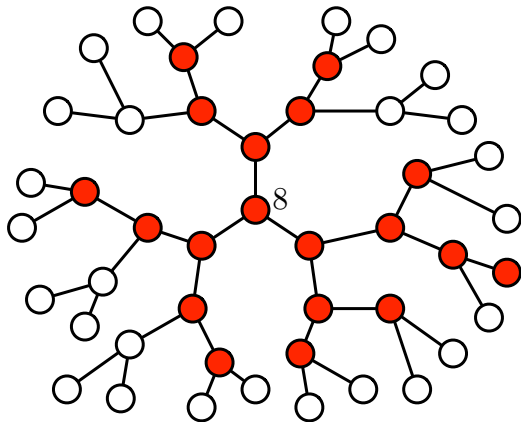
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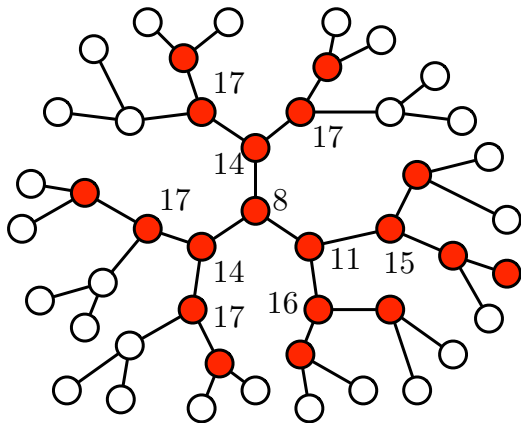
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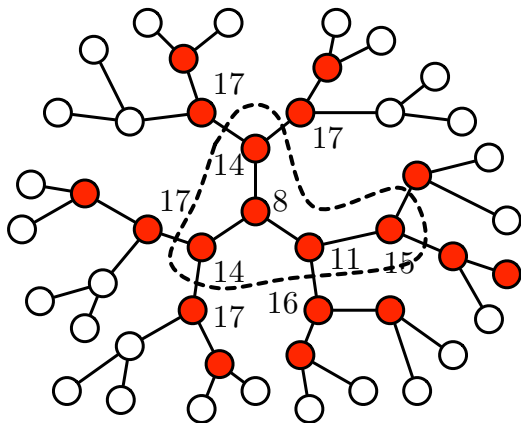
Inference algorithm

- For each node, compute “min-max subtree size”



Inference algorithm

- Select $K(\epsilon)$ nodes with smallest values



Theorem

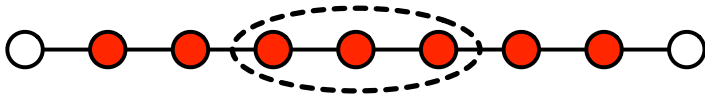
Suppose $d \geq 3$. Then the min-max subtree estimator with $K_\psi(\epsilon) = \frac{C(d)}{\epsilon}$ yields a $1 - \epsilon$ confidence set for the root.

Theory for confidence sets

Theorem

Suppose $d \geq 3$. Then the min-max subtree estimator with $K_\psi(\epsilon) = \frac{C(d)}{\epsilon}$ yields a $1 - \epsilon$ confidence set for the root.

- **Note:** Cannot construct finite confidence set for $d = 2$; need set of size $K = \Theta(\sqrt{n})$



Extensions and open directions

- Similar result holds for broader class of “regular” trees
- **Robustness:** Confidence set eventually settles down after finitely many steps

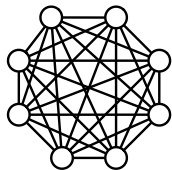
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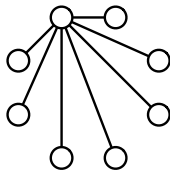
Open directions:

- What if underlying graph is not a tree?
- What if network is asymmetric?
- What if nodes can heal?

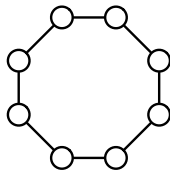
Graph testing



VS.

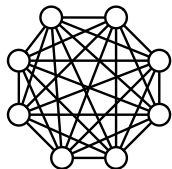


VS.

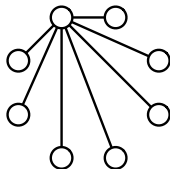


- **Question:** Can we use epidemic data to infer network structure?

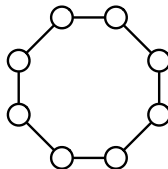
Graph testing



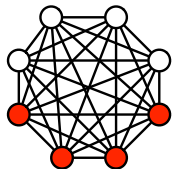
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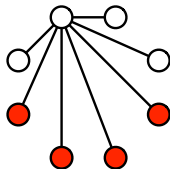
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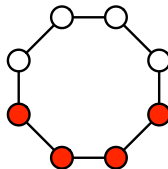
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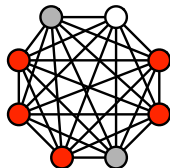
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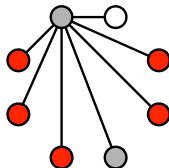
Graph testing

- **Observations:** Infection status of n nodes in graph

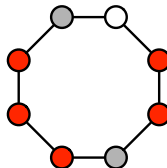
- k infected nodes (1)
- c censored (nonreporting) nodes (\star)
- $n - k - c$ uninfected nodes (0)



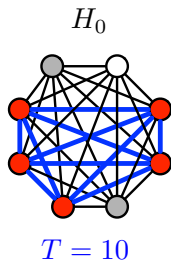
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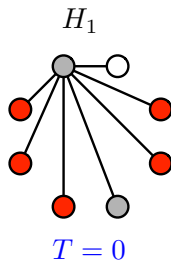
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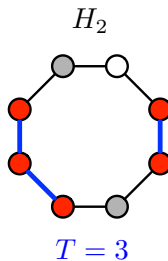
Graph testing



vs.



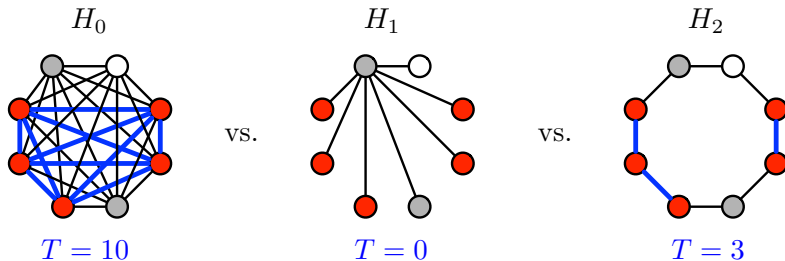
vs.



- Compute test statistic

$$T = \# \text{ edges between infected nodes}$$

Graph testing



- Compute test statistic

$$T = \# \text{ edges between infected nodes}$$

- Need to construct proper rejection rule based on T , derive validity of hypothesis test

- Parameters λ, η
 - For each node v , generate $T_v \sim \text{Exp}(\lambda)$
 - For each edge (u, v) , generate $T_{uv} \sim \text{Exp}(\eta)$
- Infection time of any vertex v is $t_v = \min_{u \in N(v)} \{T_u + T_{uv}\} \wedge T_v$

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- Observation vector corresponds to infection states at a certain time
- Subset of censored nodes chosen uniformly at random

Permutation test

- **Goal:** For $\alpha \in (0, 1)$, construct rejection rule such that

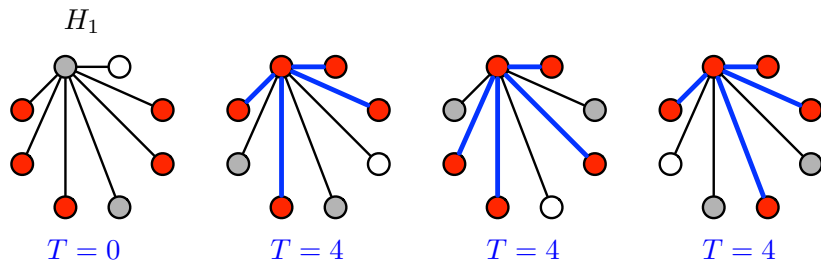
$$P(\text{reject} \mid H_0 \text{ is true}) \leq \alpha$$

Permutation test

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- Use *permutation test* that computes T for $\binom{n}{k, c, n-k-c}$ reassignments of infected/nonreporting/uninfected nodes

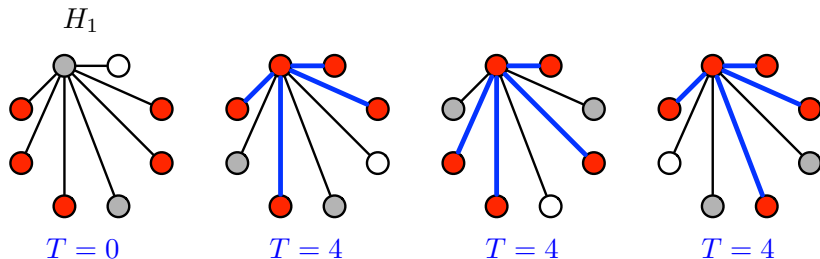


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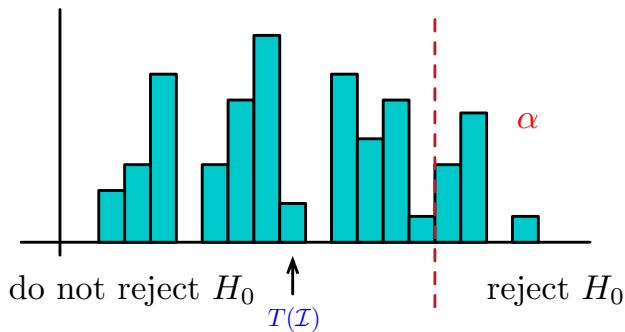
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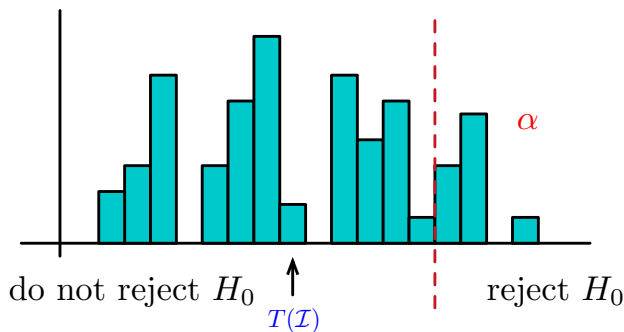


- Based on (randomly chosen) permutations, compute p -value/rejection region and reject H_0 if $(p\text{-value of } T) \leq \alpha$

Permutation test



Permutation test



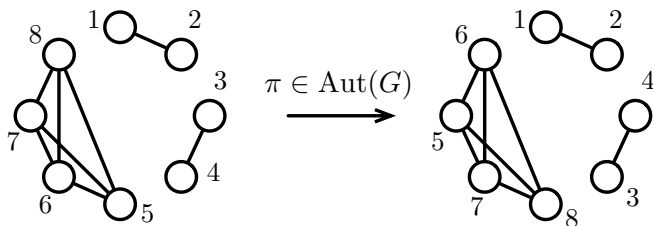
- In practice, sufficient to compute empirical distribution from large number of random permutations

Theory for permutation test

- Success depends on *symmetries* of underlying networks rather than parameters λ, η
- Consider $\Pi_0 = \text{Aut}(G_0)$ and $\Pi_1 = \text{Aut}(G_1)$, subsets of S_n

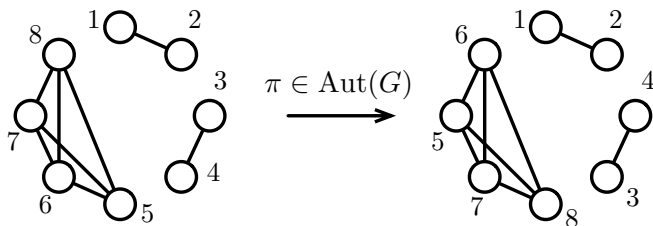
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Theorem

Let π be drawn uniformly from S_n . If $\Pi_1 \Pi_0 = S_n$, the permutation test controls Type I error at level α .

Extensions and open directions

- Characterization of condition $\Pi_1 \Pi_0 = S_n$ for various graph families
- Bounds on Type II error for specific graphs
- Conditioning on identity of censored nodes

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Open directions:

- How to identify which graphs to use as null/alternative hypotheses?
- Inhomogeneous λ and η ?
- Confidence sets for underlying network?

Resource allocation



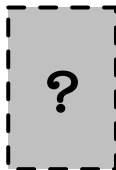
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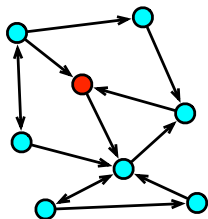
Ashley Hou
(UW-Madison)



Wen Yan
(Southeast University)

Influence maximization (with Justin Khim and Varun Jog)

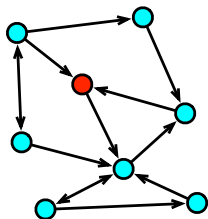
- **New goal:** Seed a network to “infect” as many nodes as possible
- Useful for information dissemination, marketing, etc.



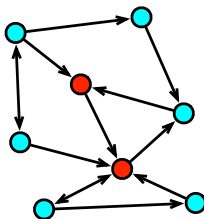
$t = 0$

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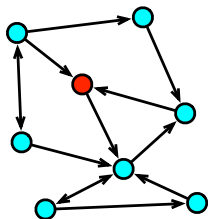
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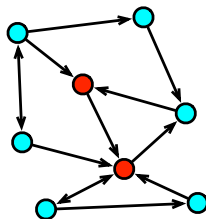
$t = 1$

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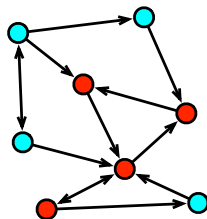
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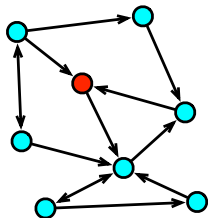
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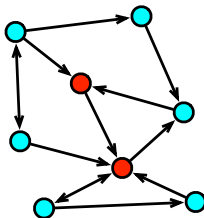
$t = 2$

Influence maximization (with Justin Khim and Varun Jog)

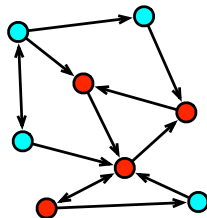
- **New goal:** Seed a network to “infect” as many nodes as possible
- Useful for information dissemination, marketing, etc.



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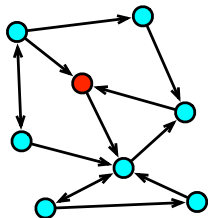
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Questions

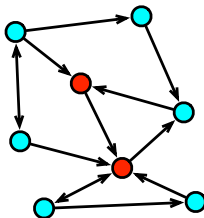
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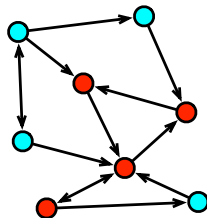
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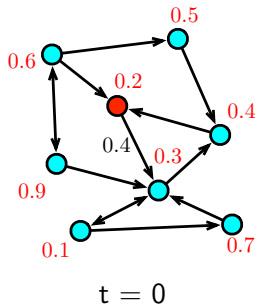
- 1 If k nodes may be infected initially, which nodes should be selected to maximize infection spread?
- 2 How to determine maximal set efficiently?

Model: Linear threshold model (broadly, triggering models)

- Edges have weights (b_{ij}) , satisfying $\sum_j b_{ji} \leq 1$
- Nodes choose thresholds $\theta_i \in [0, 1]$ i.i.d., uniformly at random

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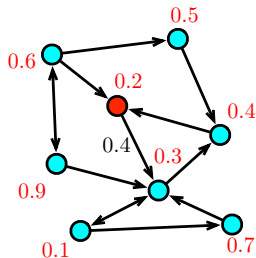


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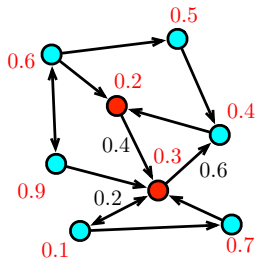
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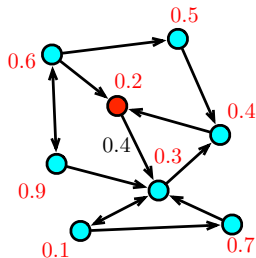
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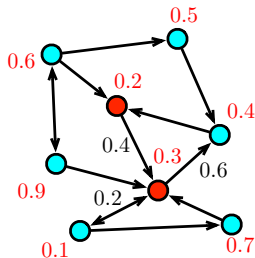
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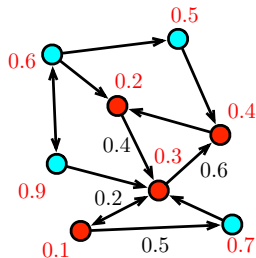
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- However, method involves approximating \mathcal{I} at each iteration of greedy algorithm via simulations

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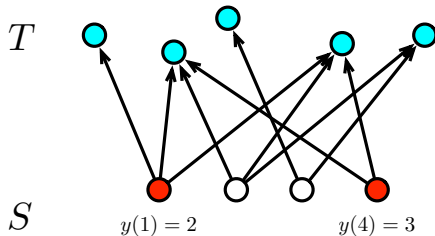
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 $\implies (1 - \frac{1}{e})$ -approximation for sequential greedy algorithm
- Leads to significant speed-ups:

	LB_1	LB_2	UB	Simulation
Erdős-Renyi	1.00	2.36	27.43	710.58
Preferential attachment	1.00	2.56	28.49	759.83
2D-grid	1.00	2.43	47.08	1301.73

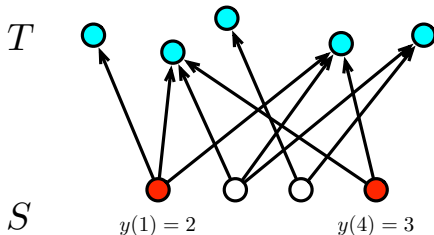
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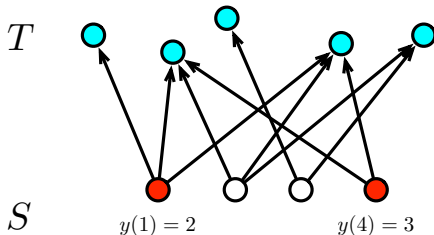


- **Mathematical formulation:** If resources $\{y(s)\}_{s \in S}$ are allocated among source nodes S , probability of influencing customer t is

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so we solve $\max \sum_{t \in T} I_t(y)$ s.t. $\sum_{s \in S} y(s) \leq B$

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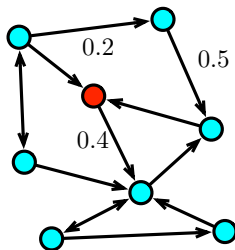
- **Goal:** Develop efficient algorithms for robust budget allocation with provable approximation guarantees
- **Ingredients:** Maximization of min of submodular functions, extensions to integer lattices and budget constraints

Network immunization (with Wen Yan)

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- **Goal:** Given a budget of interventions at nodes/edges of a graph, how to optimally distribute resources to retard an epidemic?
- Interested in *fractional immunization*, which only decreases infectiveness of nodes/edges



- Formulation as influence maximization problem:

$$\min_{\sum \theta_{ij} \leq B} \left\{ \max_{A \subseteq V: |A| \leq k} \mathcal{I}(A; \{b_{ij}\} - \{\theta_{ij}\}) \right\}$$

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- **Challenges:**

- 1 Bilevel optimization problem involving discrete and continuous variables
- 2 No computable closed-form expression for \mathcal{I} or $\nabla \mathcal{I}$

Local algorithms



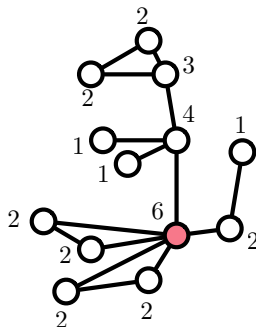
Muni Pydi
(UW-Madison)



Varun Jog
(UW-Madison)

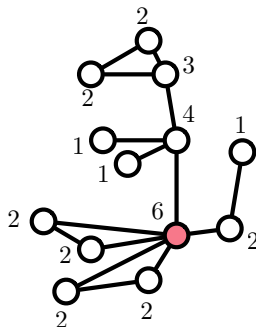
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- Given function f defined on nodes of a graph
- Examples:** Degree, age of node, power/population level, etc.



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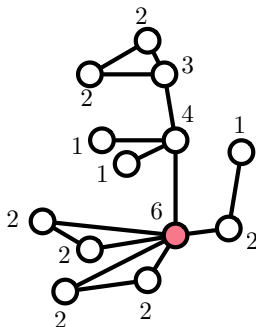
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- Goal:** Maximize f by “walking” along edges and querying values
- Could use “vanilla random walk” with transition probabilities $P_{ij} = \frac{w_{ij}}{d_i}$, but can we leverage smoothness/structure of graph function?

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- **Idea:** Build a density p_f maximized wherever f is maximized, hope that MH algorithm finds maximizers quickly

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 - **Theoretical results:** Rates of convergence in TV distance, hitting time bounds for both algorithms in terms of graph/function characteristics

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