Causal Inference in the Presence of Networks
Randomization and Observation

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Graph Exploitation Symposium,
A casual stroll through causal inference

- Neyman, 1923, Rubin, 1974, etc.
- $n$ units are potentially assigned to treatments $(Z_1, \ldots, Z_n)$.
- The potential outcome of unit $i$ is given by $Y_i(Z_1, \ldots, Z_n)$.
- Standard assumption: $(Y_i(0), Y_i(1))$ are the PO of unit $i$.
- Frequently interested in the average treatment effect (ATE):

$$ATE = \frac{1}{n} \sum_{i=1}^{n} Y_i(1) - Y_i(0)$$
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- Networks make the above hard! Need:
  - Randomization schemes to control interference and homophily.
  - Matching methods for observational studies with networks.
  - Applications: disease prevalence, social development, online advertising, business transactions.
Causal inference with networks

- How does the classical causal inference setting extend to these?

Some problems:
- Homophily.
- Interference.
- Entangled treatments.

The potential outcome of unit $i$ under assignment vector $(Z_1, \ldots, Z_n)$ is given by $Y_i(Z_1, \ldots, Z_n)$.

Estimands of interest:
- Total network: "maximal effect"
- Direct effect: value of isolation
- Indirect effect: value of interactions with at least someone
- Total node: herd immunity.
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Need “total network effect”
Some context: (im)migration

- Want to know how regime change affects population.
- Politicians during election years care about direct effects.

Source: http://openscience.alpine-geckos.at/courses/social-network-analyses/empirical-network-analysis/
Some context: disease spread

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- Want to study efficacy of isolation as treatment for influenza-like illness.
- Interested in spread, duration of illness, etc.

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Experimental design with networks

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▶ Early work by Sobel 2006, Hudgens and Halloran 2008, Tchetgen Tchetgen and VanderWeele 2012 (and others) consider two stage randomization of groups into treatment regimes and then randomization with groups.
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- We are interested in the direct effect!
- Simplifying assumption: interference/homophily is restricted to the neighborhood of a node.
Model and estimators
joint work with Natesh Pillai and Ravi Jagadeesan at Harvard

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- $d(v) = |\mathcal{N}(v)|$ is the degree of $v$.
- For each vertex $v \in V(G)$ we have
  - $t_v$: direct treatment effect
  - $f_v : 2^{\mathcal{N}(v)} \to \mathbb{R}$ is a function such that $f_v(\emptyset) = 0$.
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- Consider the general linear model as motivation
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  y_v = x_v + 1_T(v)t_v + f_v(T \cap N(v))
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We study $|T| = n$ and the naive estimator
\[ \hat{t} = \frac{1}{n} \sum_{v \in T} y_v - \sum_{v \in V(G) \setminus T} y_v \]
Experimental design with networks

Perfect assignment:

- Assign nodes to treatment to balance interference between treated and untreated nodes.

*Bad quasi-coloring:*

- Nodes 2,3: treated, 2 untreated neighbors.
- Nodes 1,4: untreated, 2 treated neighbors.
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![Graph Diagram]

Nodes 1, 2: treated, 1 treated neighbor, 1 untreated.
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Perfect quasi-colorings
Do they exist?

Short answer: yes.
Slightly longer answer: sometimes.

\[ V(G) = \{1, \ldots, 6\} \]

\[ B: \{1, 2, 3\} \] then \[ d_B(2) = 2 \] and \[ \not\exists w: d_B(w) = 2. \]

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Do we need perfection?
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- The bias is bounded above by

\[
\frac{1}{n} \sum_{\{w_i, w'_i\} \subseteq E(G) \cap P} \left( \frac{K_{w_i}}{d(w_i)} + \frac{K_{w'_i}}{d(w'_i)} \right)
\]
What about variance?

- Simplification and complication...

> Consider $f(v(S)) = f(|S|, |N(v)\setminus S|)$ – this is symmetric interference.

> Let $\rightarrow d(v) = (|T \cap N(v)|, |N(v)\setminus T|)$ be the bidegree of $v$.

> The bound on the variance is given as a function of the partition:

$$P = \{\{w_1, w'_1\}, \ldots, \{w_n, w'_n\}\}.$$  

> Constant $K_1, K_2$ that describe the cost of unbalanced treatment.

$$CP = \frac{d_{\text{max}}}{\sum_{\{w, w'\} \in P} |d(w) - d(w')|}.$$ 

> Average of $1/\sqrt{d(v)}$.

> The bound is:

$$K_1 n CP + 2 K_2 n \sum_{v \in V(G)} 1/\sqrt{d(v)}.$$ 

> We can use this information to build a better partition! (by controlling the $CP$ term)
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$$\frac{K_1}{n} C_p + \frac{2K_2}{n} \sum_{v \in V(G)} \frac{1}{\sqrt{d(v)}}$$
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- The bound is:
  $$\frac{K_1}{n} C_P + \frac{2K_2}{n} \sum_{v \in V(G)} \frac{1}{\sqrt{d(v)}}$$
- We can use this information to build a better partition!
What about variance?

- Simplification and complication...
- Consider $f_v(S) = f(|S|, |\mathcal{N}(v) \setminus S|)$ – this is symmetric interference.
- Let $\vec{d}(v) = (|T \cap \mathcal{N}(v)|, |\mathcal{N}(v) \setminus T|)$ be the bidegree of $v$.
- The bound on the variance is given as a function of
  - The partition: $P = \{\{w_1, w'_1\}, \ldots, \{w_n, w'_n\}\}$
  - Constant $K_1, K_2$ that describe the cost of unbalanced treatment.
    - $C_P = \frac{1}{d_{\text{max}}} \sum_{\{w, w'\} \in P} |d(w) - d(w')|$ 
    - Average of $1/\sqrt{d(v)}$.
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- We can use this information to build a better partition!
- (by controlling the $C_P$ term)
Better partitions

- Order the vertices as $V(G) = \{w_1^*, w_1', \ldots, w_n^*, w_n'\}$ such that
  \[ d(w_1^*) \geq d(w_1') \geq \cdots \geq d(w_n^*) \geq d(w_n') \]

- Define the partition as
  \[ P^* = \{\{w_1^*, w_1'\}, \ldots, \{w_n^*, w_n'\}\} \]

- By definition: $C_p \leq 1$.

- The bias and $L^2$ norm are bounded by
  \[ \frac{2K_2}{d_{\text{min}}} \quad \text{and} \quad \frac{K_1}{n} + \frac{2K_2}{\sqrt{d_{\text{min}}}} \]

- In a dense graph we have $n \to \infty$ implies $d_{\text{min}} \to \infty$.

- So MSE goes to zero!
What about sparse graphs?
We need a little more math to get bounds that still go to zero

What about fancier interference?
Everything holds for $f_v = f_{\text{type}(v)}$ (mutatis mutandis)
Small simulation

Linear interference, Erdos-Renyi graph

ER graphs have lots of nodes with the same degree...
Small simulation

Linear interference, Erdos-Renyi graph

ER graphs have lots of nodes with the same degree...
Small simulation

Linear interference, Preferential-Attachment graph

as.factor(m)

- 2
- 4
- 6

variable

- ATE_us_MSE
- ATE_bern_MSE

Lots of degree heterogeneity...
Small simulation

Linear interference, Preferential-Attachment graph

Lots of degree heterogeneity...
Small simulation

Generic interference, Preferential-Attachment graph
Small simulation

Generic interference, Preferential-Attachment graph

Lots of degree heterogeneity... and possibly huge interference
Natural extension to homophily

- Nodes are often similar in behavior because of underlying traits.
Natural extension to homophily

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- We can sometimes typify the nodes.
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- Essentially working with

\[ y_v = x_v + 1_{T(v)}t_v + f_v(T \cap N(v)) \]
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- Given such a collection of types \( \Pi \) and a bound on the variability of individuals inside each type \( \sigma^2 \) we have similar looking bounds on bias and MSE.
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- Given such a collection of types \( \Pi \) and a bound on the variability of individuals inside each type \( \sigma^2 \) we have similar looking bounds on bias and MSE.
- Need information on \( (x_v - \sum_{v \in \pi} x_v)^2 \).
- Interesting conclusion: if we can identify these “types” well then a new cluster-randomized-design is reasonable for estimating the direct effect: treat half of every “type”.
Interference/homophily makes network experiments hard...
Interference/homophily makes network experiments hard... and some randomization schemes are better than others.
Interference/homophily makes network experiments hard... and some randomization schemes are better than others.

Observational studies with network data are hard even without any formal interference or homophily...
Observational studies and entangled treatments
joint work with Panos Toulis at Chicago Booth and Edo Airoldi at Harvard

- Most work concentrates on questions of interference of outcomes.
- Let's take a step back from that — what if the treatments are entangled?
Most work concentrates on questions of interference of outcomes.

Let's take a step back from that — what if the treatments are entangled?

- Treatment: number of new friends in an online game.
- Treatment: popularity measure of a website due to new links.
- Treatment: number of new professional connections.
- Treatment: number of new people in a working group.
Toy example

pre-treatment network

There are two individuals and the pre-treatment period network $G^-$ is disconnected:

1  2

No one is treated, that is $Y_1(0, 0)$ and $Y_2(0, 0)$ are observed.

OR

Both are treated, that is $Y_1(1, 1)$ and $Y_2(1, 1)$ are observed.

The treatment is "number of new friends" which is an edge count — and we can't observe one person with an edge and one without.
Toy example

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There are two individuals and the pre-treatment period network $G^-$ is disconnected:

post-treatment network

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The treatment is “number of new friends” which is an edge count — and we can’t observe one person with an edge and one without.
We will use the potential outcomes framework.

There are $n$ units that are connected in some network $G^-$. 

What's special about this world?

No interference but notation still requires us to write $Y_i(Z_1, ..., Z_n)$ as the potential outcome of individual $i$ under treatment vector $Z = (Z_1, ..., Z_n)$.

Still in an observational framework so need to understand how to perform matching/weighting.

Many estimands of interest: $\tau_m = E(Y_i(m+1)) - E(Y_i(m))$. 

Causal inference with networks
Causal inference with networks

- We will use the potential outcomes framework.
- There are $n$ units that are connected in some network $G^-$. 
- Treatment is a function of a change of the network $G^-$ to a network $G^+$. For example $Z_i = f_i(G^-, G^+) = d_i(G^+) - d_i(G^-)$.
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\tau_m = E(Y_i(m + 1)) - E(Y_i(m)).
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So what goes wrong?

- Classical methods assume that no interference means we can write $Y_i(Z_i)$ and will in turn model the following propensity:

$$e(k, X_i) = P(Z_i = k | X_i, G^-)$$
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$$P(Z_i = k|X, G^-) = \int_{f_i(G^-, G^+)=k} p(G^+|G^-, X)\,d\mu(G^+)$$

This accounts for the uncertainty in the treatment due to the network evolving from $G^-$ to $G^+$. 
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The network $G^-$ is empty and $G^+$ has independent edges, each of which has probability

$$P(g_{ij}^{+} = 1| G^-, X) \propto \exp(X_i X_j + 1).$$
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Numerical example – results

Ignoring information about the network we fit

\[ P(Z_i = k|X_i) \propto \text{Pois}(\lambda_i), \quad \log \lambda_i = \alpha \beta X_i \]
Numerical example – results

Ignoring information about the network we fit

\[ P(Z_i = k | X_i) \propto \text{Pois}(\lambda_i), \quad \log \lambda_i = \alpha \beta X_i \]

<table>
<thead>
<tr>
<th>unit ((i))</th>
<th>propensity score for (Z_i = \ldots)</th>
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<tr>
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<tr>
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Numerical example – results

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Set of units that have similar propensities to make one connection or two connections: \( S = \{1, 2, 3, 4\} \)
Numerical example – results

Ignoring information about the network we fit

\[ P(Z_i = k | X_i) \propto \text{Pois}(\lambda_i), \quad \log \lambda_i = \alpha \beta X_i \]

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<td>0.15</td>
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<td></td>
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The network $G^-$ is empty and $G^+$ has independent edges, each of which has probability

$$P(g_{ij}^+ = 1|G^-, X) \propto \exp(X_i X_j + 1).$$

<table>
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<tr>
<th>unit</th>
<th>$X_i$</th>
<th>$Z_i$</th>
<th>$Y_i^{obs}$</th>
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<tbody>
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Numerical example – results

Using the information about the network:

<table>
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<tr>
<th>unit ($i$)</th>
<th>0</th>
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Numerical example – results

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<tbody>
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Practical guide

- Integral is usually analytically intractable.
- Fit favorite model for $G^+|G^-, X$.
- Sample $J$ networks from the fitted model.
- Use the samples $\{G^+_{(j)}\}, j = 1, \ldots, J$ to compute estimates $\hat{e}(k, X)$ of the propensity score $e(k, X)$:

$$\hat{e}(k, X) = \frac{1}{J} \sum_{j=1}^{J} \mathbb{I}\{f_i(G^-, G^+_{(j)}) = k\}$$

- Group according to estimated propensity scores.
- Compute estimates within groups and combine information across groups.
All nice in practice, but how does it work in theory?

- Matching on the correct propensity score means the assignment is ignorable.
- In that case the conditional distributions of covariates for treated and control are the same.
- What happens if you condition on the wrong propensity score?
- Let $S_c(X), S_w(X)$ be the correct and wrong propensity score given covariates $X$. For $\mu(s) = E(S_c|S_w = s)$ we have

$$E(X|Z = 1, S_w = s) - E(X|Z = 0, S_w = s) = \frac{\text{cov}(S_c(X), X|S_w = s)}{\mu(s)(1 - \mu(s))}$$
Some thoughts about moving forward

- We have a new design for experiments on networks.
  - Gives estimates of the direct effect.
  - Controls bias and MSE!
- How do we port this to observational studies?

- We develop entangled treatments in observational studies.
  - Theory for balancing of covariates.
  - Random graph connects with network analysis.
- How do we port this to randomization schemes?

- How do we do any of this fast?
- How do we communicate these ideas to practitioners?
Thank you!
Why is this randomization better?

Example

- Let $V(G) = \{v_1, \ldots, v_{2k}, w_1, \ldots, w_{2k}\} = V \cup W$. 

- $G$ is a disjoint union of a complete graph on $2k$ vertices and a $2k$ vertex empty graph.

- Consider symmetric linear interference $f(a, b) = \gamma a$.

- Fixing a treatment group $T$, let $\alpha = |T \cap V|$ then $\xi = \gamma \left( \alpha (\alpha - 1) - (2k - \alpha) \alpha \right)$.

- When we use our partition scheme we have $\alpha = k$ and so $\xi = -\gamma 2^k$ is independent of the size of the graph.

- Now letting $T$ be uniform on all possible partitions it is clear that while $E \xi \to 0$ we have a growing variance!
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Example

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- Let $E(G) = \{(v_i, v_j)\}$
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- Let $E(G) = \{(v_i, v_j)\}$
- $G$ is a disjoint union of a complete graph on $2k$ vertices and a $2k$ vertex empty graph.
- Consider symmetric linear interference $f(a, b) = \gamma a$. 
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- Now letting \( T \) be uniform on all possible partitions it is clear that while \( E\xi \to 0 \) we have a growing variance!