Social Distancing to Reduce Transmission of Influenza-Like-Illness on College Campuses

Brian Richardson

Department of Biostatistics,
University of North Carolina at Chapel Hill

December 4, 2025

Scan for slides

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Chapel Hill
Durham
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UNC CFAR
Center for AIDS Research

My Connection to WFU

My Connection to WFU

WINSTON-SALEM JOURNAL

My Connection to WFU

WINSTON-SALEM JOURNAL

Why Biostatistics?

Why Biostatistics?

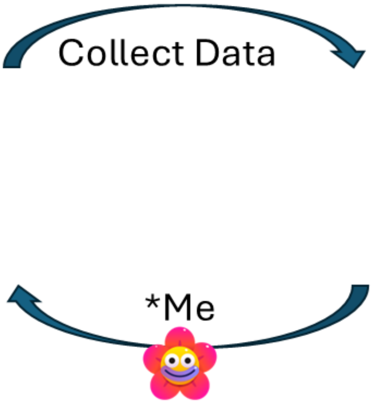
Humans

Collect Data

Data

X	Y	Z
0	100	H
0	50	L
1	100	H
1	120	H

Why Biostatistics?



Data

X	Y	Z
0	100	H
0	50	L
1	100	H
1	120	H

Why Biostatistics?

Humans
(complicated)

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1	**>100**	H

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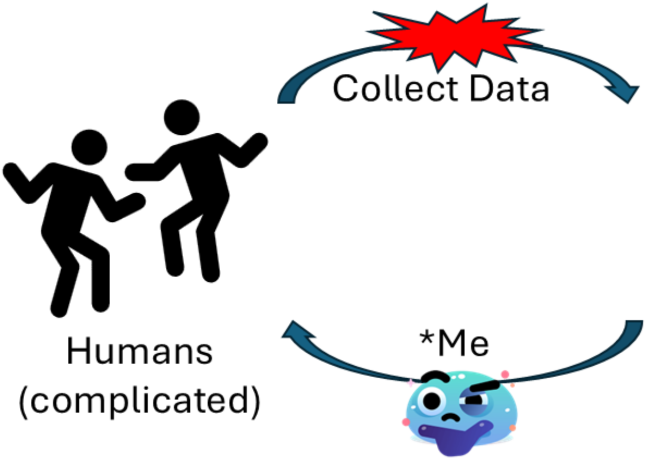

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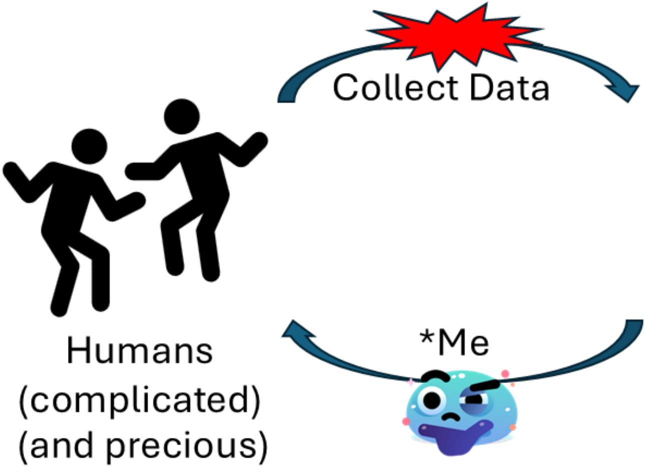

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My Research Questions

1. How can we estimate the viral load of people living with HIV?

Biometrics. 2024 Jan 29;80(1):ujad018. doi: 10.1093/biomtc/ujad018.

Quantifying the HIV reservoir with dilution assays and deep viral sequencing

Sarah C Lotspeich [1] [2], Brian D Richardson [2], Pedro L Baldoni [3] [4], Kimberly P Enders [2], Michael G Hudgens [2]

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Theory and Methods

SPARCC: Semi-Parametric Robust Estimation in a Right-Censored Covariate Model

Seong-ho Lee, Brian D. Richardson, Yanyuan Ma, Karen S. Marder & **Tanya P. Garcia**

Received 18 Sep 2024, Accepted 11 Sep 2025, Accepted author version posted online: 26 Sep 2025

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Addressing confounding and continuous exposure measurement error using corrected score functions

Brian D Richardson [1], Bryan S Blette [2], Peter B Gilbert [3], Michael G Hudgens [1]

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4. Does encouragement to social distance when sick with the flu reduce transmission?

Social Distancing

Does encouragement to social distance when sick with the flu reduce transmission?

eX-FLU Trial

- **eX-FLU**: trial to evaluate a social distancing intervention on a college campus during flu season (Aiello et al., 2016; Zivich et al., 2020)

Design and methods of a social network isolation study for reducing respiratory infection transmission: The eX-FLU cluster randomized trial

Allison E. Aiello[a,*], Amanda M. Simanek[b,1], Marisa C. Eisenberg[c], Alison R. Walsh[c], Brian Davis[c], Erik Volz[d,1], Caroline Cheng[c], Jeanette J. Rainey[e], Amra Uzicanin[e], Hongjiang Gao[e], Nathaniel Osgood[f], Dylan Knowles[f], Kevin Stanley[f], Kara Tarter[c], Arnold S. Monto[c]

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- **Intervention**: encouragement to isolate in dorm for three days upon developing symptoms of **influenza-like illness** (ILI)
- **Central question**: does the encouragement-to-isolate intervention reduce transmission of ILI?

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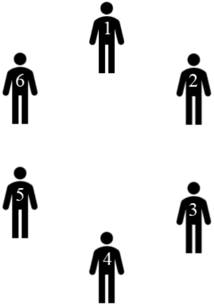
Transmission of Influenza-Like-Illness



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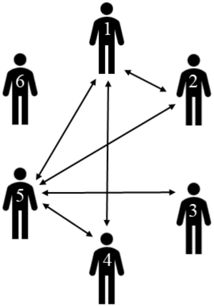

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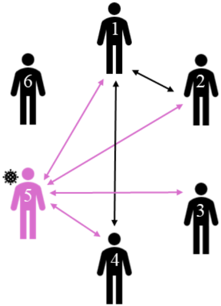

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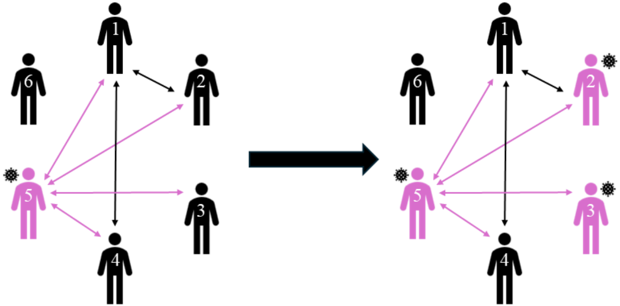
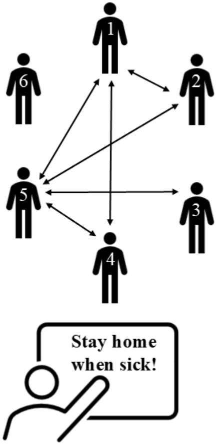


Example I: Intervention Affects Network and Transmission



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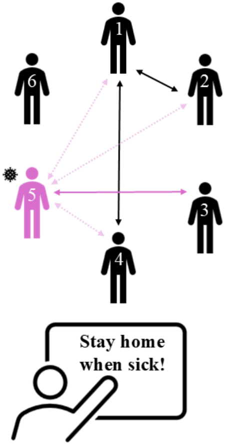

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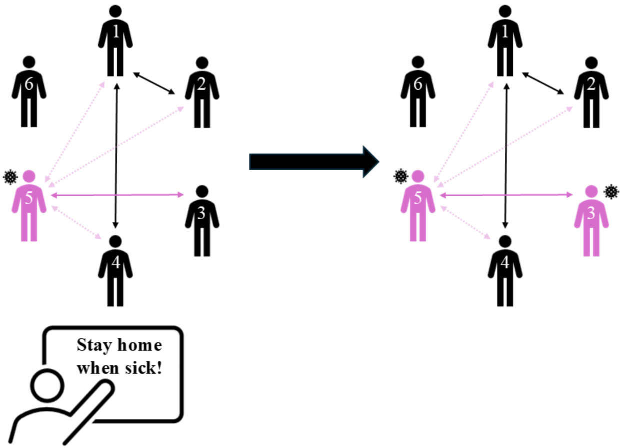
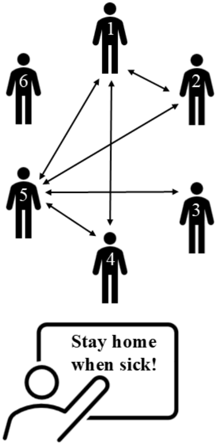


Example II: Intervention Affects Network, Not Transmission



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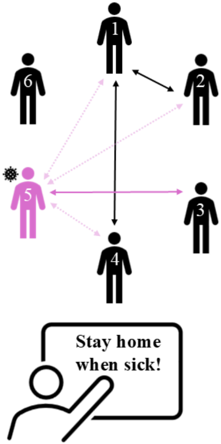

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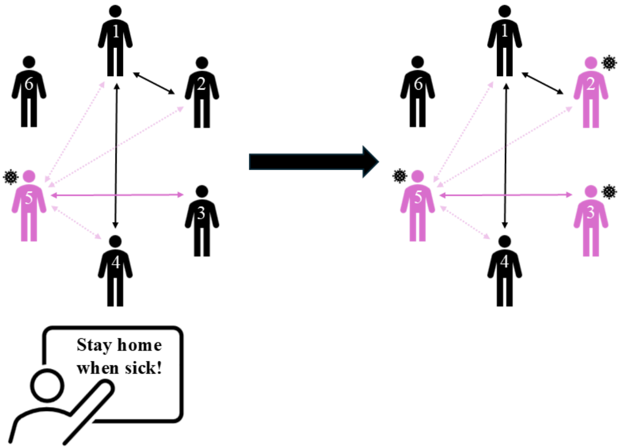
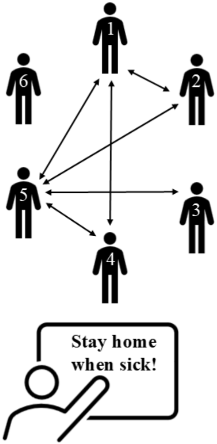


Example III: Intervention Affects Transmission, Not Network



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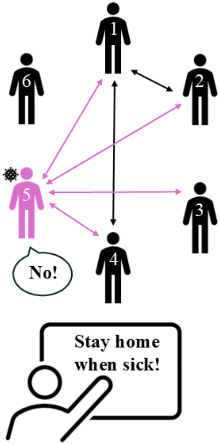

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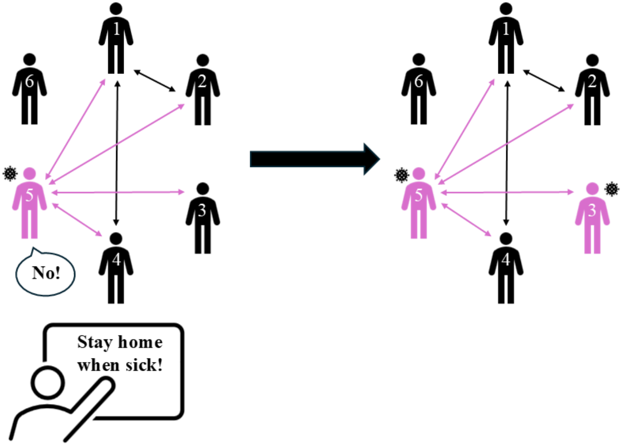
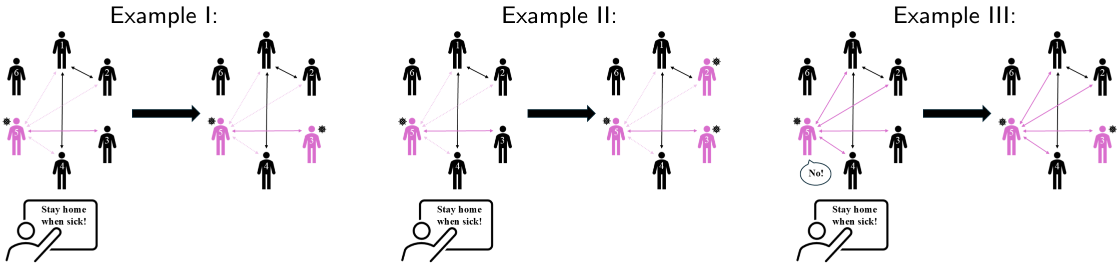


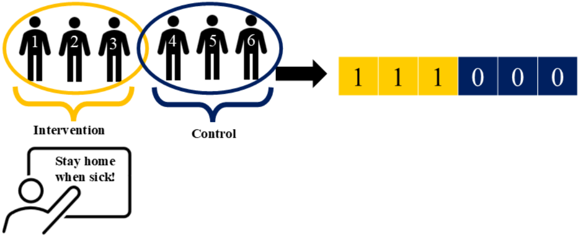
Central Question: Does the Intervention Affect Transmission of ILI?



In Examples I and III, the answer is yes

eX-FLU Observed Data

- Baseline randomization assignments $\mathbf{Z} = (Z_1, \ldots, Z_n) \in \mathcal{Z}$, for $Z_i = \mathbb{1}(\text{student } i \text{ gets intervention})$



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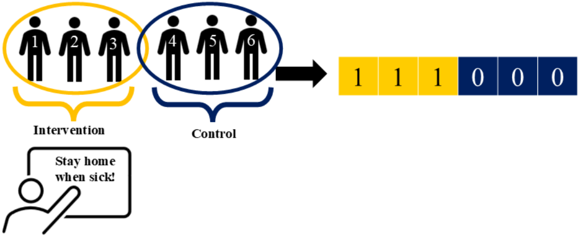
- Baseline randomization assignments $\mathbf{Z} = (Z_1, \ldots, Z_n) \in \mathcal{Z}$, for $Z_i = \mathbb{1}(\text{student } i \text{ gets intervention})$
  - randomization distribution $r(\mathbf{z})$



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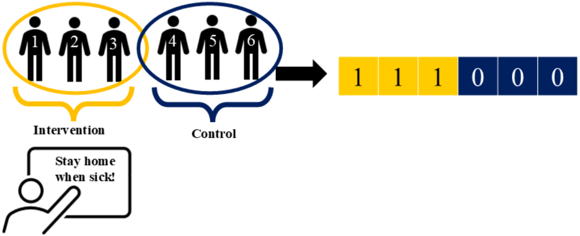
- At weeks $k = 1, \ldots, \tau$, we observe:



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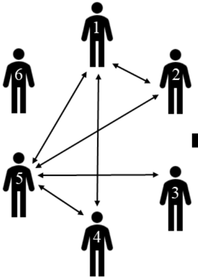
  - networks $\mathbf{A}^k = [A_{ij}^k]$, for $A_{ij}^k = \mathbb{1}(\text{students } i, j \text{ in contact at week } k)$



	1	2	3	4	5	6
1	0	1	0	1	1	0
2	1	0	0	0	1	0
3	0	0	0	0	1	0
4	1	0	0	0	1	0
5	1	1	1	1	0	0
6	0	0	0	0	0	0

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- At weeks $k = 1, \ldots, \tau$, we observe:
  - networks $\mathbf{A}^k = [A^k_{ij}]$, for $A^k_{ij} = \mathbb{1}(\text{students } i, j \text{ in contact at week } k)$
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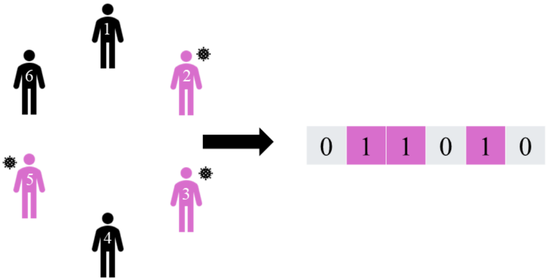

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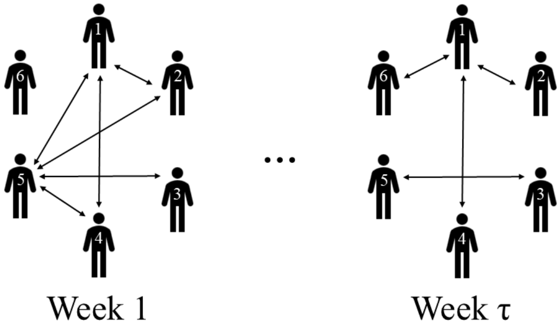
- network history: $\overline{\mathbf{A}} = \{\mathbf{A}^k\}_{k=1}^{\tau}$



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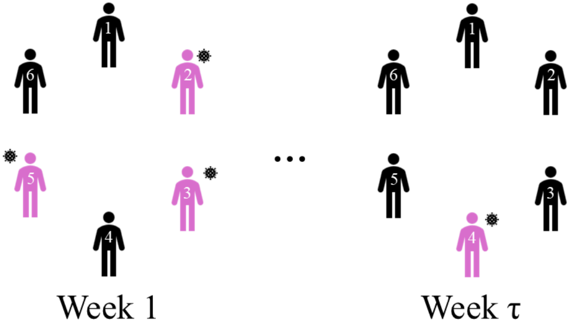

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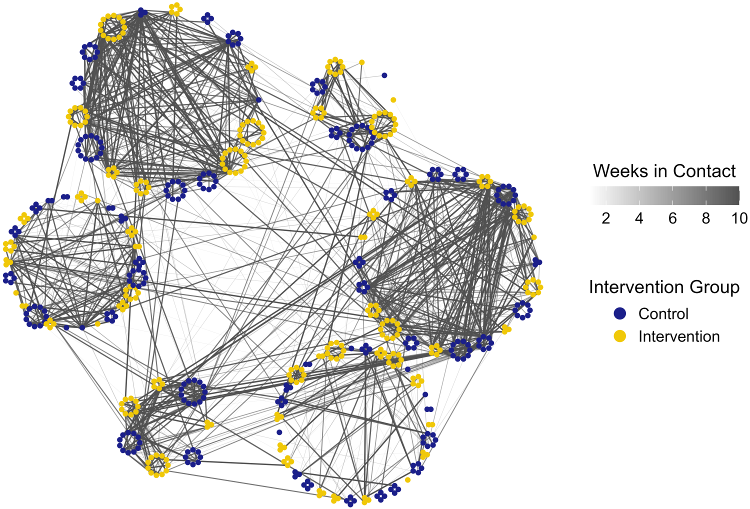

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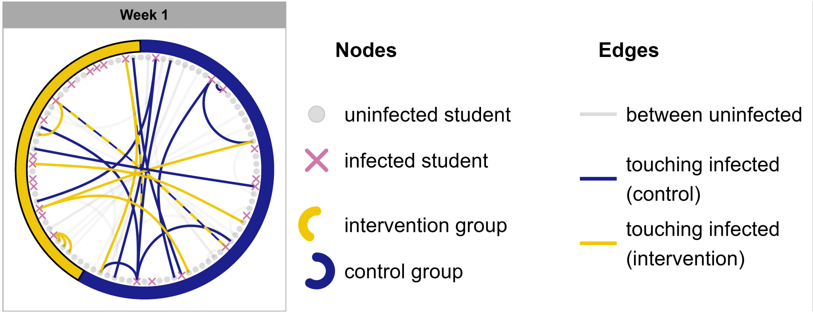

(93 out of 579 students with at least one infection)

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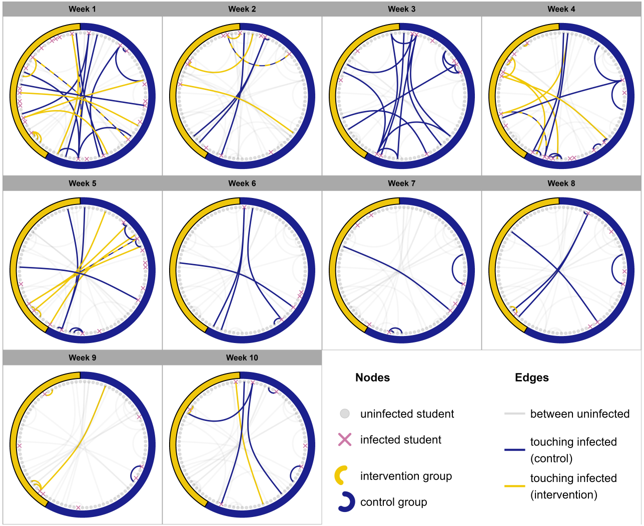

eX-FLU Potential Outcomes

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Potential outcomes are defined for the networks and ILI infections:

$$\overline{\mathbf{A}}(\mathbf{z}), \quad \overline{\mathbf{Y}}(\mathbf{z}) \quad \text{for } \mathbf{z} \in \mathcal{Z}$$

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  - potential outcomes for one student depend on intervention assignment of other students (**interference**) (Hudgens and Halloran, 2008)

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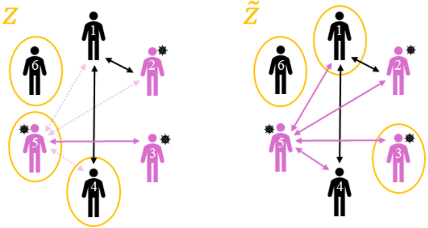
- Both of these depend on the entire vector $\mathbf{z}$
  - potential outcomes for one student depend on intervention assignment of other students (**interference**) (Hudgens and Halloran, 2008)
- Assume **causal consistency**:

$$\overline{\mathbf{A}} = \overline{\mathbf{A}}(\mathbf{Z}) \text{ and } \overline{\mathbf{Y}} = \overline{\mathbf{Y}}(\mathbf{Z})$$

eX-FLU Null Hypotheses

$$H_0^Y : \overline{\mathbf{Y}}(\mathbf{z}) = \overline{\mathbf{Y}}(\tilde{\mathbf{z}}) \text{ for all } \mathbf{z}, \tilde{\mathbf{z}} \in \mathcal{Z}$$

("the intervention has no effect on the infections")



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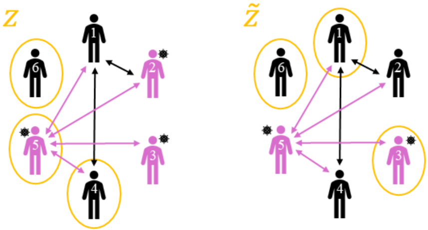
("the intervention has no effect the networks")



eX-FLU Null Hypotheses

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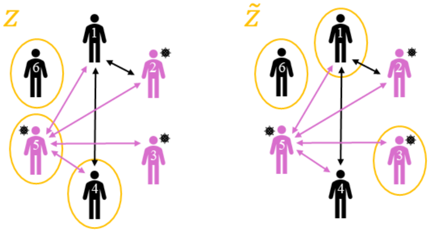
$$H_0^\sharp = H_0^Y \cap H_0^A : \overline{\mathbf{Y}}(\mathbf{z}) = \overline{\mathbf{Y}}(\widetilde{\mathbf{z}}) \text{ and } \overline{\mathbf{A}}(\mathbf{z}) = \overline{\mathbf{A}}(\widetilde{\mathbf{z}}) \text{ for all } \mathbf{z}, \widetilde{\mathbf{z}} \in \mathcal{Z}$$

("the intervention has no effect on the infections or on the networks")



eX-FLU Null Hypotheses

$$H_0^Y : \overline{\mathbf{Y}}(\mathbf{z}) = \overline{\mathbf{Y}}(\widetilde{\mathbf{z}}) \text{ for all } \mathbf{z}, \widetilde{\mathbf{z}} \in \mathcal{Z}$$

(“the intervention has no effect on the infections”)

$$H_0^A : \overline{\mathbf{A}}(\mathbf{z}) = \overline{\mathbf{A}}(\widetilde{\mathbf{z}}) \text{ for all } \mathbf{z}, \widetilde{\mathbf{z}} \in \mathcal{Z}$$

(“the intervention has no effect the networks”)

$$H_0^\sharp = H_0^Y \cap H_0^A : \overline{\mathbf{Y}}(\mathbf{z}) = \overline{\mathbf{Y}}(\widetilde{\mathbf{z}}) \text{ and } \overline{\mathbf{A}}(\mathbf{z}) = \overline{\mathbf{A}}(\widetilde{\mathbf{z}}) \text{ for all } \mathbf{z}, \widetilde{\mathbf{z}} \in \mathcal{Z}$$

(“the intervention has no effect on the infections or on the networks”)

Previous analyses of the eX-FLU trial (Alexandria et al., 2023) tested $H_0^\sharp$, but no analyses have tested H_0^Y

Testing $H_0^\sharp$

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...	...	...	...
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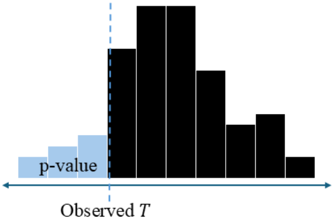
is the **cumulative distribution function** (CDF) of T



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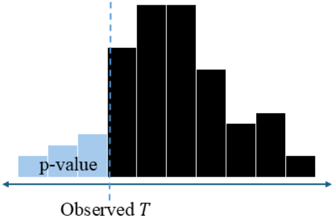
  is the **cumulative distribution function** (CDF) of T
- Reject $H_0^\sharp$ if $\rho^\sharp \leq 0.05$



Testing $H_0^\sharp$

- This test of $H_0^\sharp$ controls the **type I error rate** exactly:

$$\Pr\left(\rho^\sharp \leq \alpha | H_0^\sharp\right) \leq \alpha$$

for any $\alpha \in [0, 1]$, for any sample size, and for any choice of test statistic

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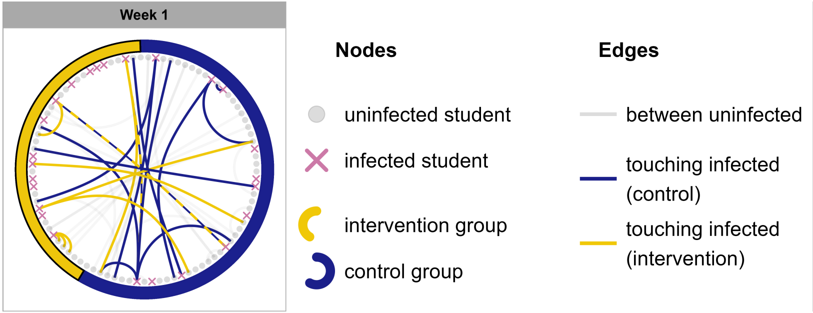
- The **power** of this test:

$$\Pr\left(\rho^\sharp \leq \alpha | H_1^\sharp\right)$$

depends on the choice of test statistic

Choice of Test Statistic

- 93 (out of 579) students with at least one infection



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- 93 (out of 579) students with at least one infection
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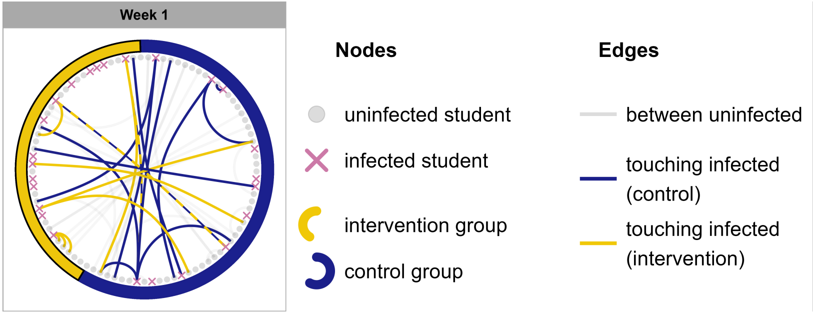
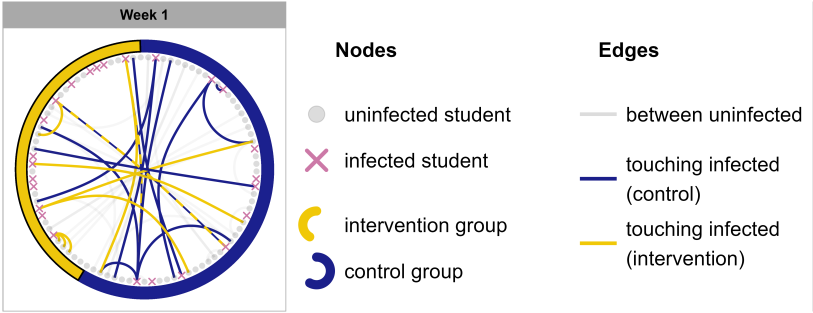


Choice of Test Statistic

- 93 (out of 579) students with at least one infection
- Bold edges represent possible transmission events
  - Proportion of possible transmission events attributable to students in the intervention group:

$$T = \frac{\text{number of yellow edges}}{\text{total number of edges}} = \frac{\sum_{k=2}^{\tau}\sum_{i=1}^{n}\sum_{j\neq i} Z_i Y_i^{k-1} A_{ij}^{k-1}}{\sum_{k=2}^{\tau}\sum_{i=1}^{n}\sum_{j\neq i} Y_i^{k-1} A_{ij}^{k-1}} = 0.359$$



Testing H_0^Y

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  - If/when the double sum $\sum_{\mathbf{z}\in\mathcal{Z}} \sum_{\overline{\mathbf{a}}\in\mathcal{A}}$ cannot be computed exactly, approximate it using a Monte-Carlo method

Testing H_0^Y

Testing Procedure:

1. Estimate the unknown parameter θ in the PMF $q(\bar{\mathbf{a}}, \mathbf{z}; \theta)$ of $\overline{\mathbf{A}}(\mathbf{z})$

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   for $b = 1$ to B **do:**

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   1. generate randomization vector $\mathbf{z}_b$
   2. generate networks $\bar{\mathbf{a}}_b$ from $q(\bar{\mathbf{a}}, \mathbf{z}_b; \widehat{\theta})$
   3. compute the test statistic $T_b = T(\mathbf{z}_b, \bar{\mathbf{a}}_b, \mathbf{Y})$

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3. compute the plug-in p-value testing H_0^Y:

$$\widehat{\rho}_B^Y = B^{-1} \sum_{b=1}^{B} \mathbb{1}(T_b \leq T)$$

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Proposition: This procedure will **asymptotically** control the type I error rate

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Goal: use simulated data to investigate the performance of our testing procedure

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- Three testing procedures:
  1. $\rho_B^{\sharp}$: testing $H_0^{\sharp}$
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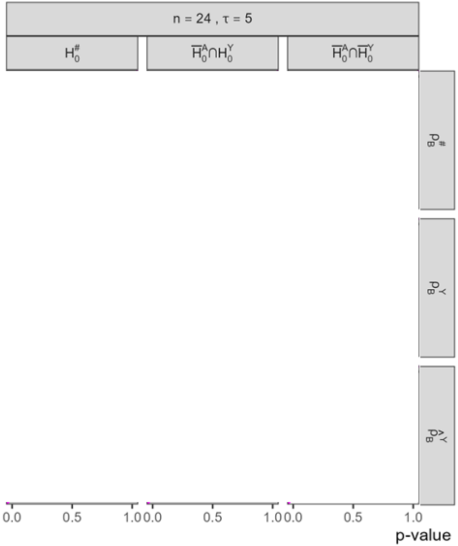
  3. $\widehat{\rho}_B^Y$: testing H_0^Y using estimated q

Simulation Results: Empirical CDF of P-Values



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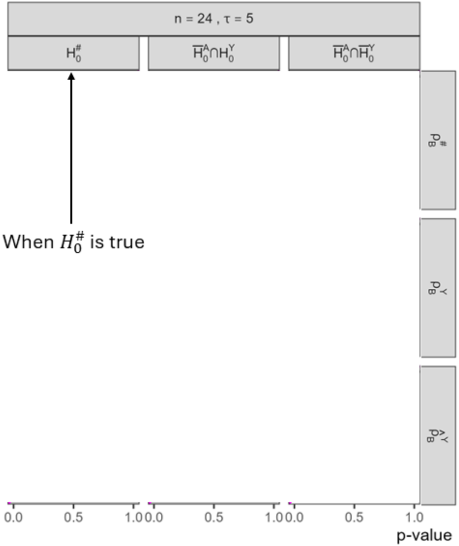

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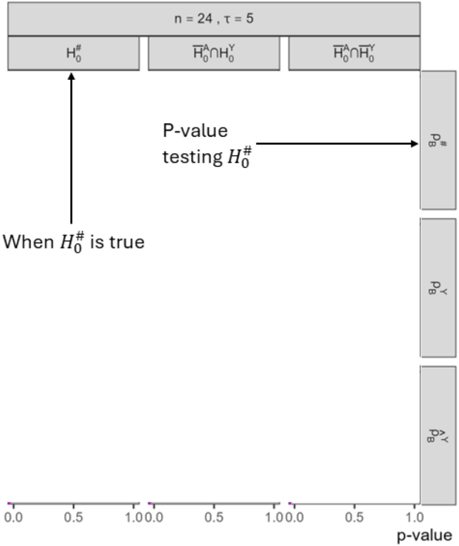

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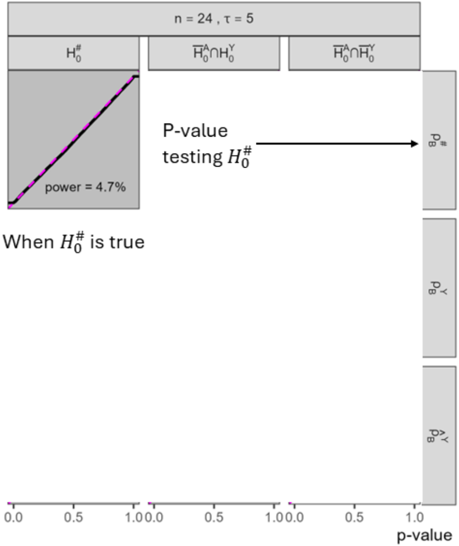

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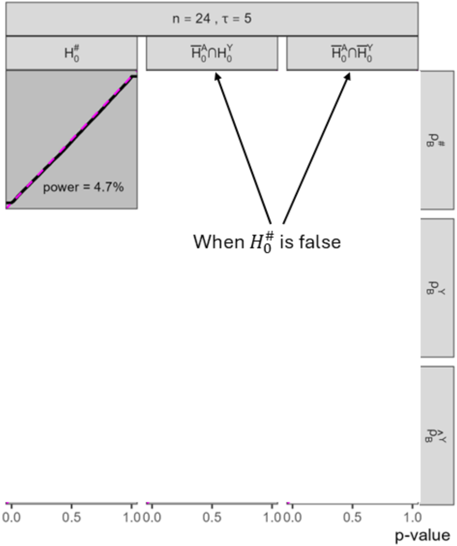

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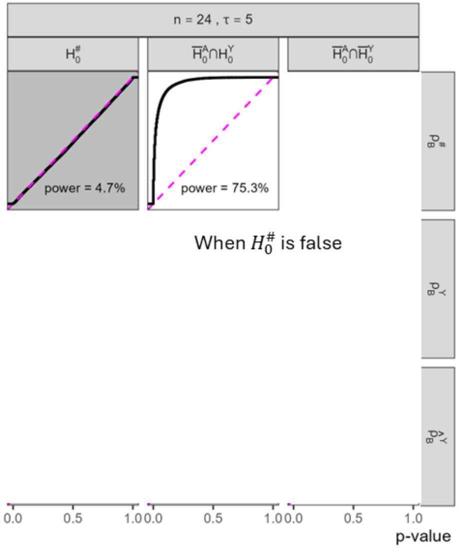

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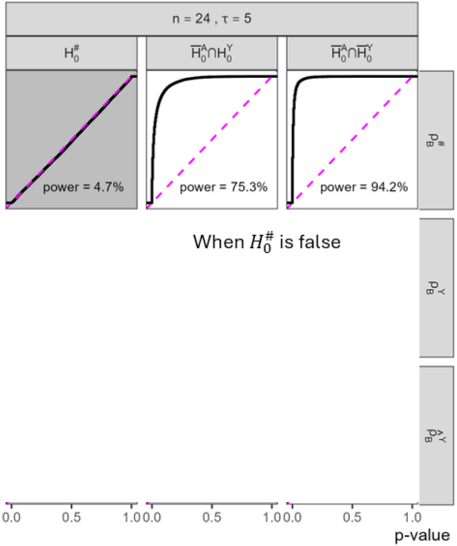

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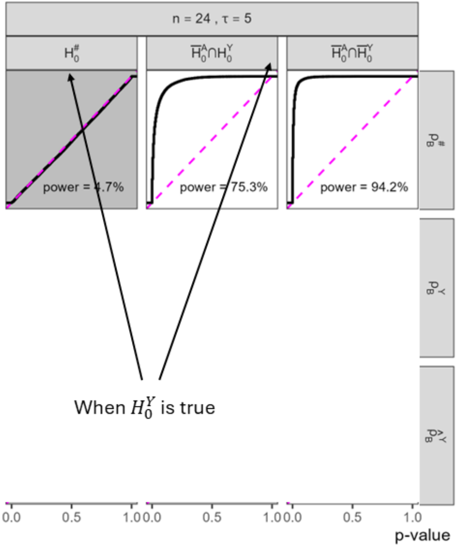

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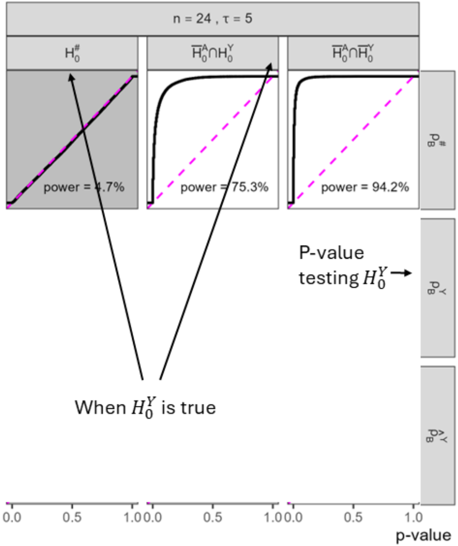

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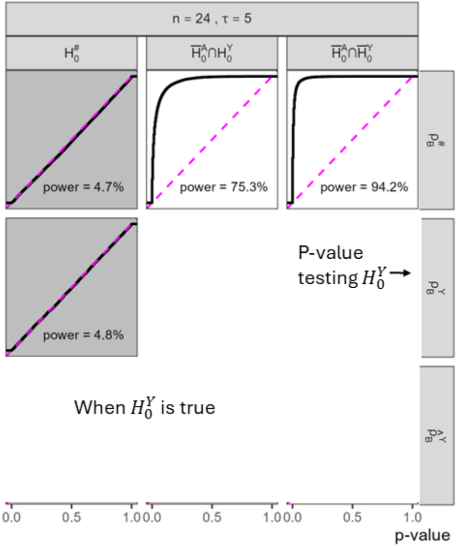

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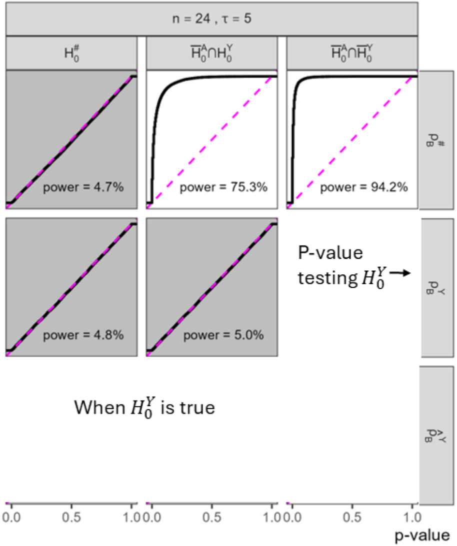

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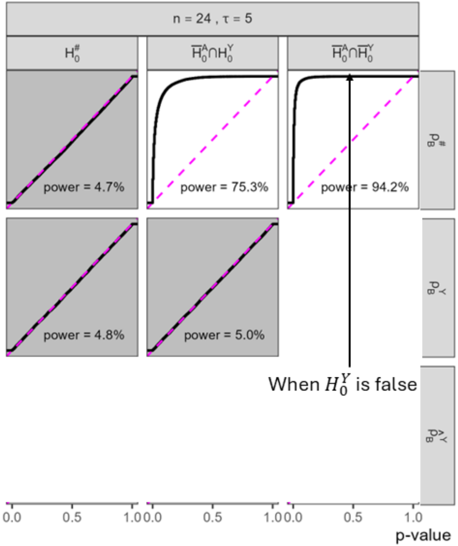

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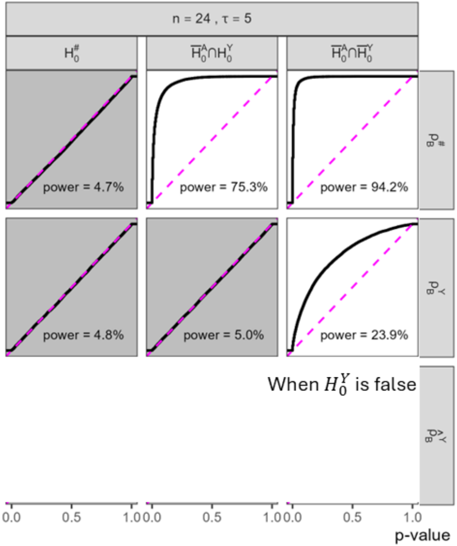

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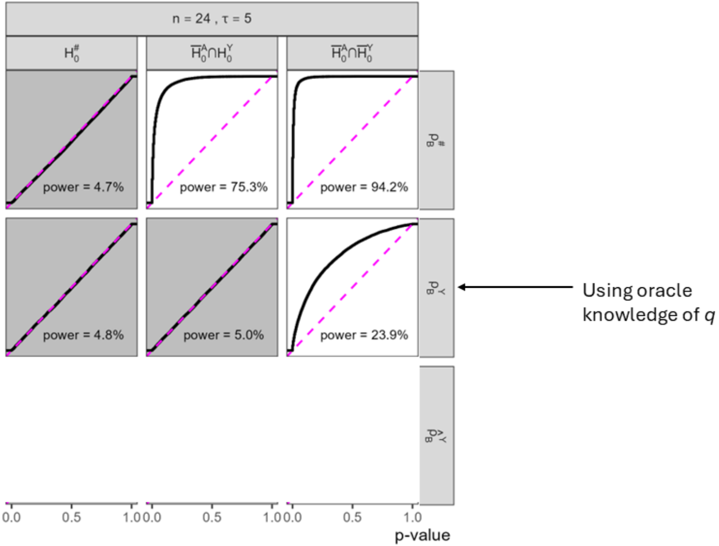

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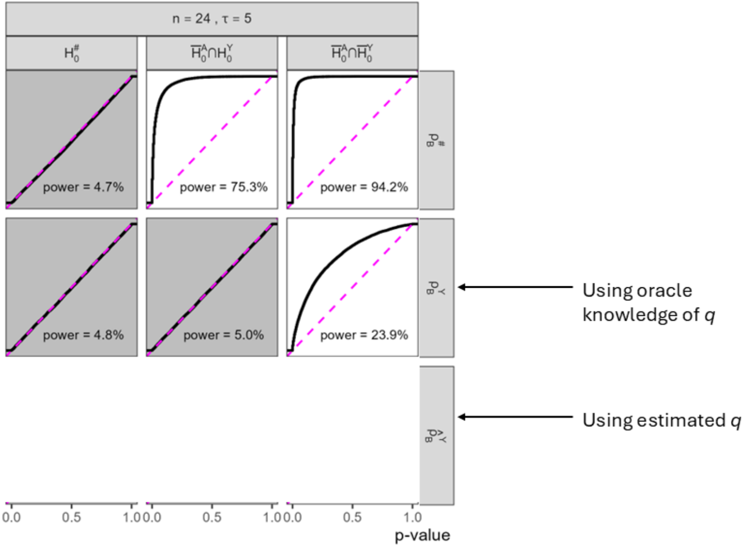

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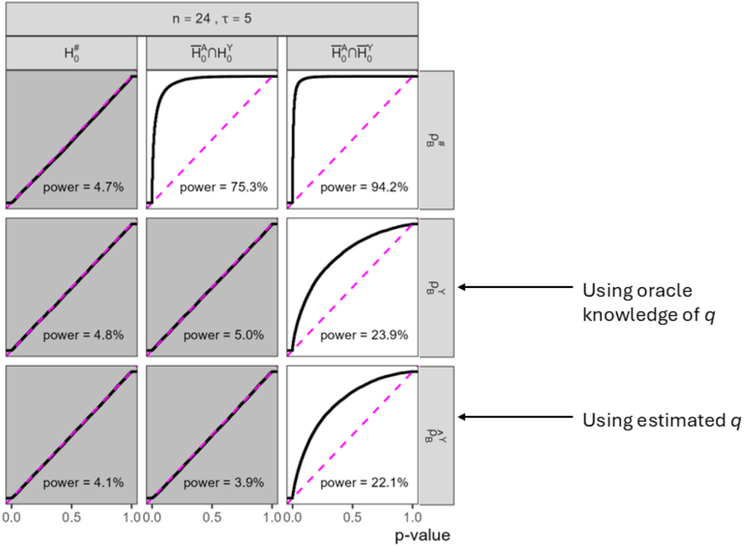

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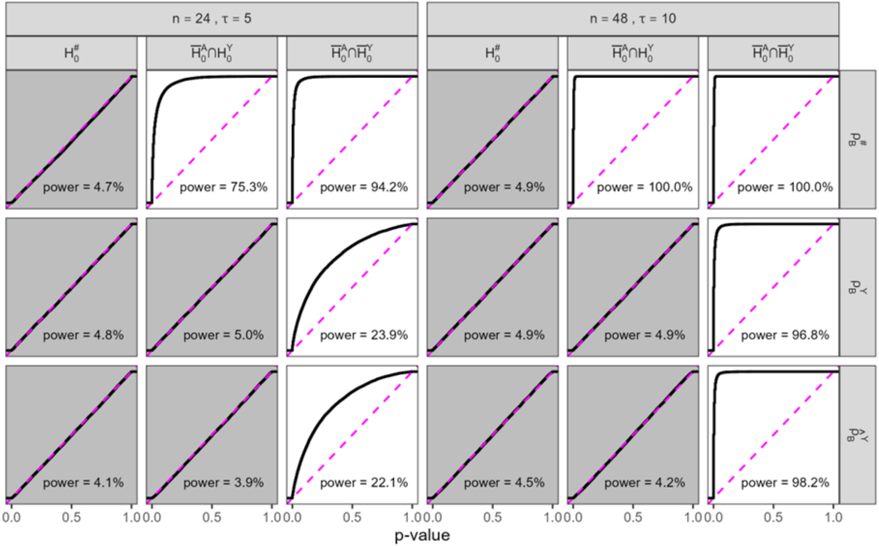

eX-FLU: Hypothesis Test Results

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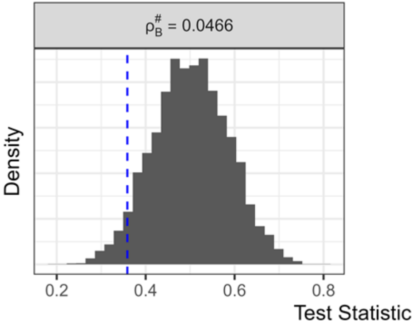

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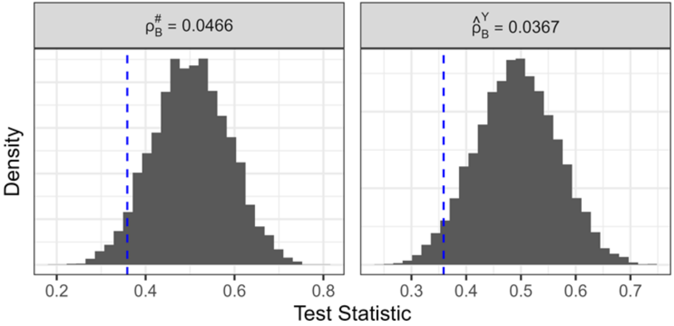

- Encouragement to isolate affects the social network and/or influenze-like illness ($\rho_B^{\sharp} = 0.0466$)
- Encouragement to isolate specifically affects influenze-like illness ($\widehat{\rho}_B^{Y} = 0.0367$)

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   - trade-off between robustness and utility
3. **Design future trials** with independent clusters
   - can allow **identification** of more causal estimands

Thank you!

Questions?

References I

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Choice of Test Statistic

Test statistics: "proportion of possible transmission events attributable to students in the intervention group:"

$$T^{**}(\mathbf{Z}, \overline{\mathbf{A}}, \overline{\mathbf{Y}}) = \frac{\sum_{k=2}^{\tau} \sum_{i=1}^{n} \sum_{j \neq i} Z_i E_{ijk}^{**}}{\sum_{k=2}^{\tau} \sum_{i=1}^{n} \sum_{j \neq i} E_{ijk}^{**}}.$$

	From Infected to Infected	**From Infected**
Contact at $k-1$	$E_{ijk}^{11} = Y_i^{k-1} A_{ij}^{k-1} Y_j^k$	$E_{ijk}^{12} = Y_i^{k-1} A_{ij}^{k-1}$
Contact at k	$E_{ijk}^{21} = Y_i^{k-1} A_{ij}^{k} Y_j^k$	$E_{ijk}^{22} = Y_i^{k-1} A_{ij}^{k}$
Contact at $k-1$ or k	$E_{ijk}^{31} = Y_i^{k-1} (A_{ij}^{k-1} \vee A_{ij}^{k}) Y_j^k$	$E_{ijk}^{32} = Y_i^{k-1} (A_{ij}^{k-1} \vee A_{ij}^{k})$
Contact at $k-1$ and k	$E_{ijk}^{41} = Y_i^{k-1} (A_{ij}^{k-1} * A_{ij}^{k}) Y_j^k$	$E_{ijk}^{42} = Y_i^{k-1} (A_{ij}^{k-1} * A_{ij}^{k})$

Table: Definitions of a possible transmission event E_{ijk} from student i to student j at time k. Y_i^k is an indicator for student i being infected at week k, A_{ij}^k is an indicator for students i and j being in contact at week k, and $a \vee b$ denotes the maximum of a and b.

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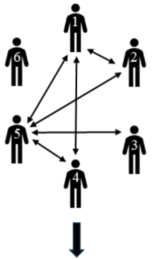

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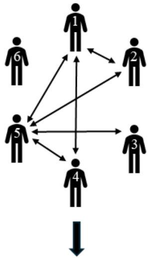

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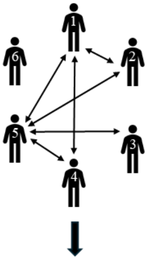

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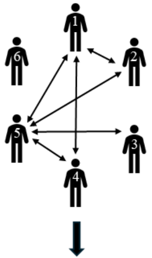

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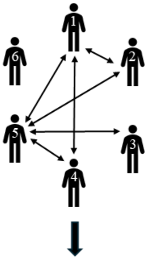

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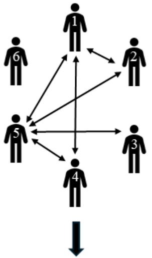

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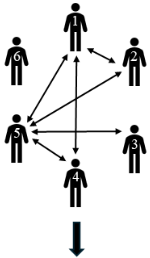

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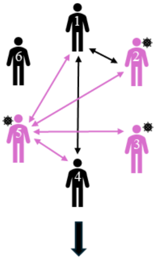

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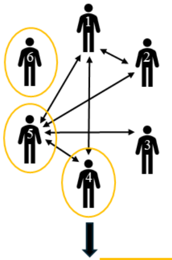
  - number of edges touching treated students
  - number of edges touching infected students



	1	2	3	4	5	6
1	0	1	0	1	1	0
2	1	0	0	0	1	0
3	0	0	0	0	1	0
4	1	0	0	0	1	0
5	1	1	1	1	0	0
6	0	0	0	0	0	0

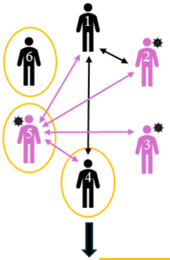
Exponential Family Random Graph Models

Goal: model a network ($\mathbf{A}$) given covariates ($\mathbf{X}$)

An **ERGM** assumes:

$$\Pr_{\theta}(\mathbf{A} = \mathbf{a} | \mathbf{X} = \mathbf{x}) = \frac{\exp\{\theta \cdot \mathbf{g}(\mathbf{a}, \mathbf{x})\}}{\kappa(\theta, \mathcal{A}, \mathbf{x})}$$

- normalizing constant:
  $\kappa(\theta, \mathcal{A}, \mathbf{x}) = \sum_{\mathbf{a} \in \mathcal{A}} \exp\{\theta \cdot \mathbf{g}(\mathbf{a}, \mathbf{x})\}$
- $\mathcal{A}$: space of possible networks
- θ: model coefficients
- $\mathbf{g}(\mathbf{a}, \mathbf{x})$: sufficient statistics
  - number of edges
  - number of edges touching treated students
  - number of edges touching infected students
  - number of edges touching treated $\times$ infected students



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6	0	0	0	0	0	0

ERGM Model Formulation

$$\Pr_{\theta}(\mathbf{A} = \mathbf{a} | \mathbf{X} = \mathbf{x}) = \frac{\exp\{\theta \cdot \mathbf{g}(\mathbf{a}, \mathbf{x})\}}{\kappa(\theta, \mathcal{A}, \mathbf{x})},$$

$$\kappa(\theta, \mathcal{A}, \mathbf{x}) = \sum_{\mathbf{a} \in \mathcal{A}} \exp\{\theta \cdot \mathbf{g}(\mathbf{a}, \mathbf{x})\}$$

For example, in the simulation study and eX-FLU application,

$$\mathbf{g}(\mathbf{a}, \mathbf{x}) = \begin{bmatrix} \text{\# edges} \\ \text{\# edges touching a treated node} \\ \text{\# edges touching an infected node} \\ \text{\# edges touching a treated and infected node} \\ \text{\# edges between roommate pairs} \end{bmatrix} = \begin{bmatrix} \sum_{i,j} a_{ij} \\ \sum_{i,j} a_{ij}(z_i + z_j) \\ \sum_{i,j} a_{ij}(y_i + y_j) \\ \sum_{i,j} a_{ij}(z_i y_i + z_j y_j) \\ \sum_{i,j} a_{ij} \mathbb{1}(i, j \text{ roomates}) \end{bmatrix}$$

ERGM Change Statistic Model Formulation

- **Change statistic**: $\delta_{\mathbf{g}}(\mathbf{a},\mathbf{x})_{ij} = \mathbf{g}(\mathbf{a}_{ij}^{+},\mathbf{x}) - \mathbf{g}(\mathbf{a}_{ij}^{-},\mathbf{x})$ is the change in network statistic that would occur if a_{ij} were changed from 0 to 1
  - where $\mathbf{a}_{ij}^{+}$ and $\mathbf{a}_{ij}^{-}$ represent the network $\mathbf{a}$ with dyad a_{ij} set to 1 or 0, respectively
- Then the equivalent ERGM specification is

$$\text{logit}\{\Pr_{\theta}(A_{ij} = 1 | \mathbf{A}_{ij}^{C} = \mathbf{a}_{ij}^{C}, \mathbf{X} = \mathbf{x})\} = \theta^{k}\delta_{\mathbf{g}}(\mathbf{a},\mathbf{x})_{ij}$$

  - where $\mathbf{A}_{ij}^{C}$ represents all dyads in $\mathbf{A}$ except A_{ij}
- **Interpretation of θ**: the change in conditional log-odds of the network associated with a one-unit increase in the corresponding component of $\mathbf{g}(\mathbf{a},\mathbf{x})$ resulting from switching a particular dyad A_{ij} from 0 to 1 and leaving the rest of the network fixed at $\mathbf{A}_{ij}^{C}$

Dyadic Independence EGRMs

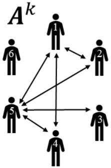
- **Dyadic independence term**: a component g of $\mathbf{g}$ in an ERGM for which the corresponding change statistic $\delta_g(\mathbf{a}, \mathbf{x})_{ij}$ can be calculated for any i, j without knowing $\mathbf{a}$
  - For example, if $g(\mathbf{a}, \mathbf{x}) = \sum_{i,j} a_{ij}(Z_i + Z_j)$ counts the number of edges touching treated nodes, then $\delta_g(\mathbf{a}, \mathbf{x})_{ij} = z_i + z_j$ doesn't depend on $\mathbf{a}$
- **Dyadic independence ERGM**: an ERGM with only dyadic independence terms
  - replace $\delta_g(\mathbf{a}, \mathbf{x})_{ij}$ with $\delta_g(\mathbf{x})_{ij}$ and write the model as

$$\text{logit}\{\Pr\big(A_{ij} = 1 | \mathbf{X} = \mathbf{x}\big)\} = \theta \cdot \delta_g(\mathbf{x})_{ij}$$

- **Interpretation of θ**: the change in log-odds of the network associated with a one-unit increase in the corresponding component of $\mathbf{g}(\mathbf{a}, \mathbf{x})$ resulting from switching a particular dyad A_{ij} from 0 to 1

Separable Temporal Exponential Family Random Graph Models

A **STERGM** assumes that, at each time step $k = 1, \ldots, \tau - 1$:

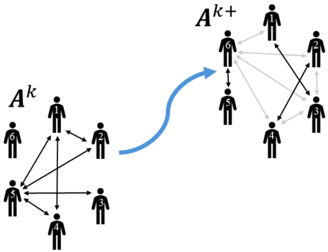


Separable Temporal Exponential Family Random Graph Models

A **STERGM** assumes that, at each time step $k = 1, \ldots, \tau - 1$:

- New edges form according to a **formation** ERGM

$$\Pr_{\theta^+}(\mathbf{A}^{k+} = \mathbf{a}^{k+} | \mathbf{A}^k = \mathbf{a}^k, \mathbf{X} = \mathbf{x}) = \frac{\exp\{\theta^+ \cdot \mathbf{g}^+(\mathbf{a}^{k+}, \mathbf{x})\}}{\kappa\{\theta^+, \mathcal{A}^+(\mathbf{a}^k), \mathbf{x}\}}$$

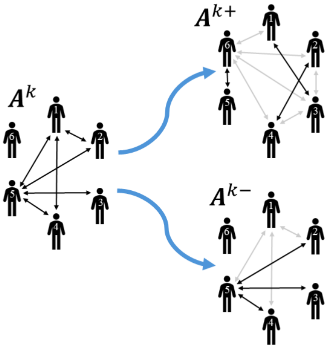


Separable Temporal Exponential Family Random Graph Models

A **STERGM** assumes that, at each time step $k = 1, \ldots, \tau - 1$:

- New edges form according to a **formation** ERGM
- Old edges persist according to a **persistence** ERGM

$$\Pr_{\theta^-}(\mathbf{A}^{k-} = \mathbf{a}^{k-} | \mathbf{A}^k = \mathbf{a}^k, \mathbf{X} = \mathbf{x}) = \frac{\exp\{\theta^- \cdot \mathbf{g}^-(\mathbf{a}^{k-}, \mathbf{x})\}}{\kappa\{\theta^-, \mathcal{A}^-(\mathbf{a}^k), \mathbf{x}\}}.$$

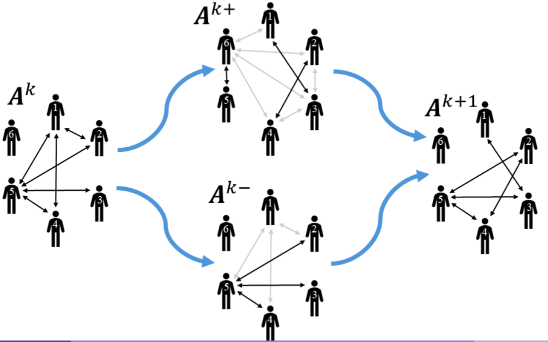


Separable Temporal Exponential Family Random Graph Models

A **STERGM** assumes that, at each time step $k = 1, \ldots, \tau - 1$:

- New edges form according to a **formation** ERGM
- Old edges persist according to a **persistence** ERGM
- The network at time step $k + 1$ is the result of formation and persistence

$$\mathbf{A}^{k+1} = \underbrace{\mathbf{A}^{k}}_{\text{previous network}} \cup \underbrace{(\mathbf{A}^{k+} - \mathbf{A}^{k})}_{\text{new edges formed}} - \underbrace{(\mathbf{A}^{k} - \mathbf{A}^{k-})}_{\text{old edges not persisting}}$$



STERGM Model Formulation

- **Formation model** is an ERGM conditional on only adding edges:

$$\Pr_{\theta^+}(\mathbf{A}^{k+} = \mathbf{a}^{k+} | \mathbf{A}^k = \mathbf{a}^k, \mathbf{X} = \mathbf{x}) = \frac{\exp\{\theta^+ \cdot \mathbf{g}^+(\mathbf{a}^{k+}, \mathbf{x})\}}{\kappa\{\theta^+, \mathcal{A}^+(\mathbf{a}^k), \mathbf{x}\}}$$

  - $\mathcal{A}^+(\mathbf{a})$: space of possible networks that can be formed by adding edges to $\mathbf{a}$

- **Persistence model** is an ERGM conditional on only removing edges:

$$\Pr_{\theta^-}(\mathbf{A}^{k-} = \mathbf{a}^{k-} | \mathbf{A}^k = \mathbf{a}^k, \mathbf{X} = \mathbf{x}) = \frac{\exp\{\theta^- \cdot \mathbf{g}^-(\mathbf{a}^{k-}, \mathbf{x})\}}{\kappa\{\theta^-, \mathcal{A}^-(\mathbf{a}^k), \mathbf{x}\}}$$

  - $\mathcal{A}^-(\mathbf{a})$: space of possible networks that can be formed by removing edges to $\mathbf{a}$

- A **STERGM** assumes the network at time $k+1$ is then the result of applying the changes in $\mathbf{A}^{k+}$ and $\mathbf{A}^{k-}$ to $\mathbf{A}^k$:

$$\mathbf{A}^{k+1} = \underbrace{\mathbf{A}^k}_{\text{previous network}} \cup \underbrace{(\mathbf{A}^{k+} - \mathbf{A}^k)}_{\text{new edges formed}} - \underbrace{(\mathbf{A}^k - \mathbf{A}^{k-})}_{\text{old edges not persisting}}$$

Separability of STERGMs

1. $\mathbf{A}^{k+} \perp\!\!\!\perp \mathbf{A}^{k-} | \mathbf{A}^{k}$, i.e., the formation and persistence processes are conditionally independent give the network at time k

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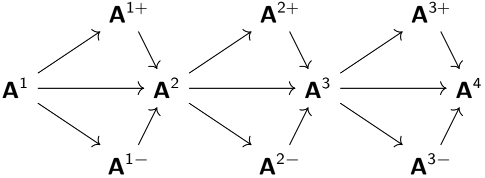
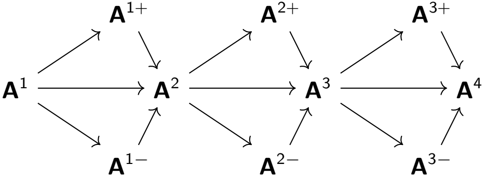


Separability of STERGMs

1. $\mathbf{A}^{k+} \perp\!\!\!\perp \mathbf{A}^{k-} | \mathbf{A}^{k}$, i.e., the formation and persistence processes are conditionally independent give the network at time k
2. the parameter space for $\theta = (\theta^{+}, \theta^{-})$ is the product of the parameter spaces for θ^{+} and θ^{-}



Simulation Setup

- $n \in \{24, 48\}$ students were equally divided into two residence halls, each with six clusters of equal size
- Within each residence hall group, the clusters were randomized using a 50:50 allocation to either the intervention group or the control group
- Five pairs of students were randomly selected to be roommates, meaning they had contact with each other each week
- Baseline ($k = 1$) social contacts were simulated between each pair of students with probability 0.5
- Baseline infection statuses were simulated for each student with probability 0.5
- Social networks were simulated over the remaining $\tau \in \{5, 10\}$ weeks according to a STERGM with both formation and persistence models including edge count, intervention assignment Z, infection status Y, $Z \times Y$ interaction, and an offset to force constant edges between roommates
- Infection statuses were simulated for each student i at each week $k \in \{2, \ldots, \tau\}$ with probability $\Pr\left(Y_i^k = 1 | \overline{\mathbf{A}}^{k-1}, \overline{\mathbf{Y}}^{k-1}\right) = g(\sum_{j=1}^n A_{ij}^{k-1} Y_j^{k-1})$, where $\sum_{j=1}^n A_{ij}^{k-1} Y_j^{k-1}$ is the number of infected contacts at the previous week, and $g : [0, \infty) \to [0, 1]$ is a non-decreasing function

Simulation Setup

Three scenarios:

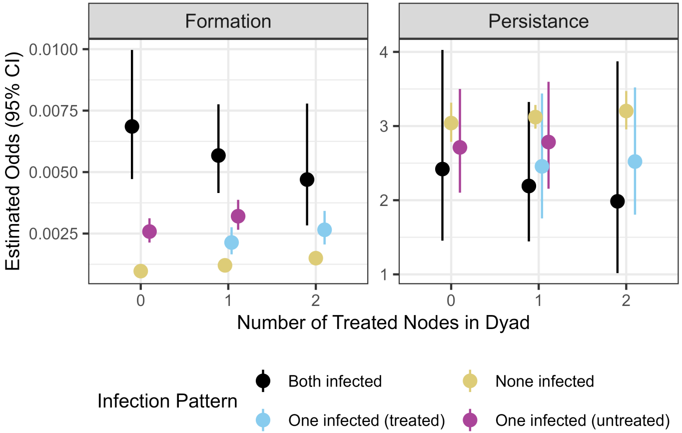
Null Hypothesis	Formation Model Parameters θ^+	Persistence Model Parameters θ^-	Infection Probability Function g
$H_0^\sharp$	$(-0.5, 0, 0, 0)$	$(-0.5, 0, 0, 0)$	$g(s) = 0.5$
$\overline{H}_0^A \cap H_0^Y$	$(-0.2, 0, 0, -1)$	$(-0.2, 0, 0, -1)$	$g(s) = 0.5$
$\overline{H}_0^A \cap \overline{H}_0^Y$	$(-0.2, 0, 0, -1)$	$(-0.2, 0, 0, -1)$	$g(s)$ increasing in s

Table: Data generating process for the simulation study. The null hypothesis refers to the null hypothesis that is true under the data generating process, formation model parameters are $\theta^+ = (\theta^+_{\text{edges}}, \theta^+_Z, \theta^+_Y, \theta^+_{ZY})$, persistence model parameters are $\theta^- = (\theta^-_{\text{edges}}, \theta^-_Z, \theta^-_Y, \theta^-_{ZY})$, and the infection probability function g provides a unit's probability of being infected at week k given their number of infected neighbors at week $k-1$.

Three p-values:

- $\rho_B^\sharp$: testing the sharp null
- ρ_B^Y: testing H_0^Y using known q
- $\widehat{\rho}_B^Y$: testing H_0^Y using estimated q

eX-FLU: STERGM Results



Type I Error Control

- **Proposition 2.1**: Let T_N be a test statistic with CDF F_N under H_0.
    1. Under H_0, $F_N(T_N)$ stochastically dominates a Uniform$(0,1)$ distribution for any N.
    2. If the test statistic T_N has a continuous limiting distribution, then $F_N(T_N) \rightarrow^d$ Uniform$(0,1)$.
- **Corollary 2.2**:
    1. Under $H_0^\sharp$, the sharp null p-value $\rho_N^\sharp$ stochastically dominates a Uniform$(0,1)$ distribution for any N.
    2. Under H_0^Y, the oracle p-value ρ_N^Y stochastically dominates a Uniform$(0,1)$ distribution for any N.
    3. If the test statistic T_N has a continuous limiting distribution, then $\rho_N^\sharp \rightarrow^d$ Uniform$(0,1)$ under $H_0^\sharp$ and $\rho_N^Y \rightarrow^d$ Uniform$(0,1)$ under H_0^Y.

Type I Error Control

- **Proposition 2.3**: Let $q(\mathbf{a}, \mathbf{z}, \theta) \equiv \Pr\{\mathbf{A}(\mathbf{z}) = \mathbf{a}; \theta\}$ denote the PMF of the distribution of stochastic potential networks $\mathbf{A}(\mathbf{z})$ at parameter value θ, let $\widehat{\theta}_N$ denote the estimator of θ, and let $F_N(\cdot; \theta)$ denote the CDF of the test statistic T_N at θ, with limiting CDF $F(\cdot; \theta)$. Let θ_0 denote the true value of θ. Assume the following:

(A1) $\widehat{\theta}_N \to^p \theta_0$

(A2) $F(t; \theta_0)$ is continuous in t on $\mathbb{R}$

(A3) there exists a $\delta_0 > 0$ such that

$$\sup_{\theta \in B_{\delta_0}(\theta_0)} \sup_{t \in \mathbb{R}} |F_N(t; \theta) - F(t; \theta)| \to 0$$

(A4) $F(t; \theta)$ is continuous in θ at θ_0 uniformly in t, i.e.,

$$\lim_{\theta \to \theta_0} \sup_{t \in \mathbb{R}} |F(t; \theta) - F(t; \theta_0)| = 0$$

Then the plug-in p-value $\widehat{\rho}_N^Y$ converges in distribution to Uniform$(0, 1)$.

Type I Error Control

- **Proposition 2.4**: Let $\rho_N = F_N(T_N)$ for test statistic T_N and CDF F_N (not necessarily the true CDF of T_N). Let $T_N^* = h_N(T_N)$ for a sequence of deterministic, strictly increasing functions h_N. Define $F_N^*(t) = F_N\{h_N^{-1}(t)\}$, the (not necessarily true) CDF of the transformed test statistic, and let $\rho_N^* = F_N^*(T_N^*)$. Then $\rho_N^* = \rho_N$.
- **Corollary 2.5**: Let h_N be a sequence of deterministic, strictly increasing functions.
  1. If the hypotheses of Proposition 2.1 are met for a test statistic T_N, then the results also hold for $T_N^* = h_N(T_N)$.
  2. If the hypotheses of Proposition 2.3 are met for $T_N, F_N(\cdot;\theta)$, then the results also hold for $T_N^* = h_N(T_N), F_N^*(\cdot;\theta) = F_N\{h_N^{-1}(\cdot);\theta\}$.