

Physical Distancing to Prevent Influenza-Like-Illness on College Campuses: the eX-FLU Trial

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Coauthors



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UNC Biostatistics



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Columbia Epidemiology

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

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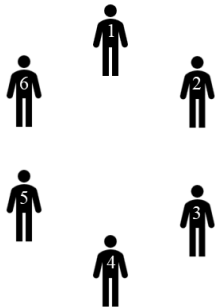
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- **Central question**: does the encouragement-to-isolate intervention prevent ILI infection?

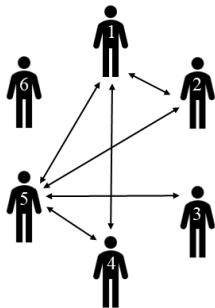
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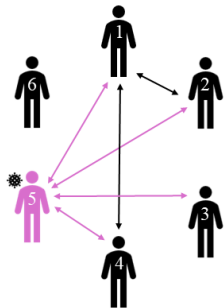
Transmission of Influenza-Like-Illness



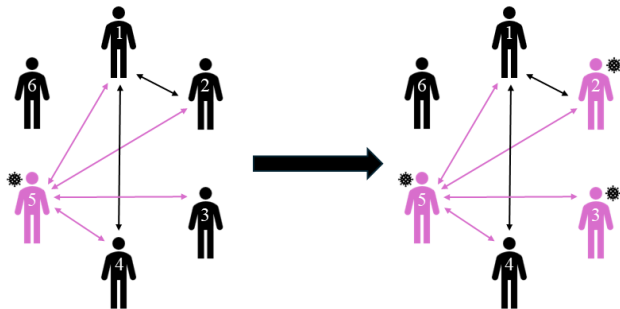
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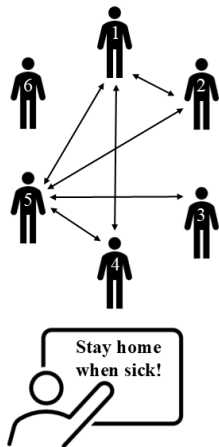
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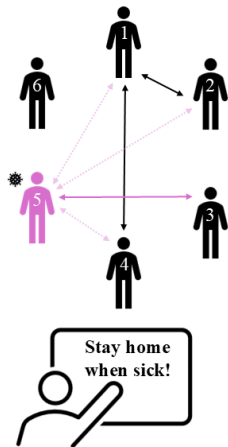
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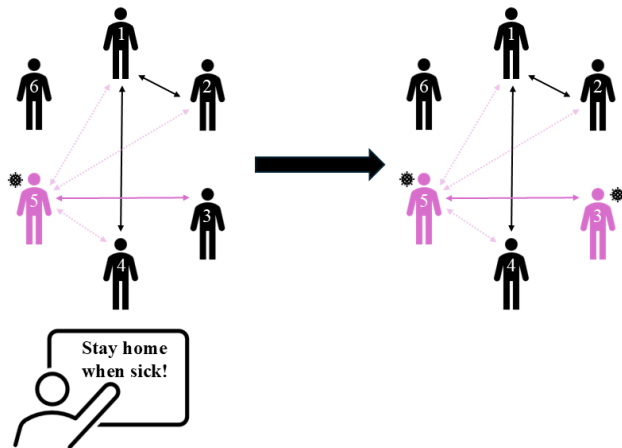
Example I: Intervention Affects Network and Infections



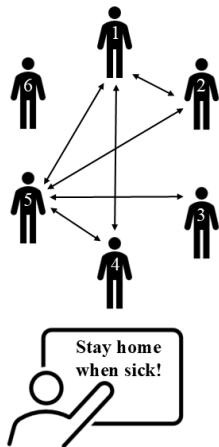
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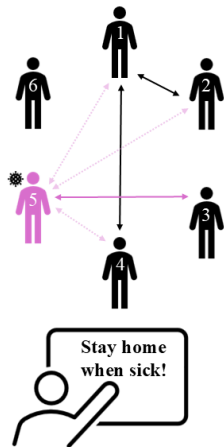
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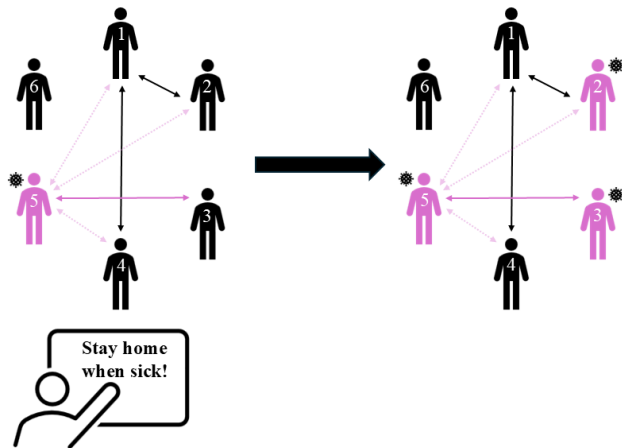
Example II: Intervention Affects Network, Not Infections



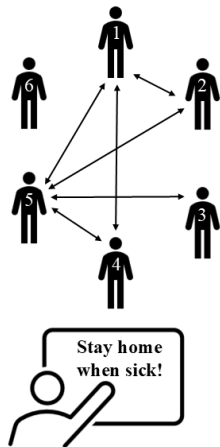
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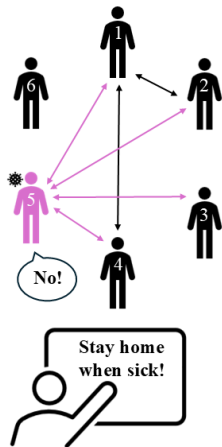
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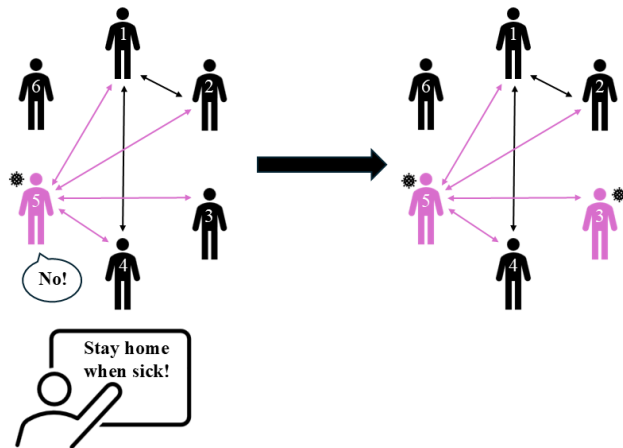
Example III: Intervention Affects Infections, Not Network



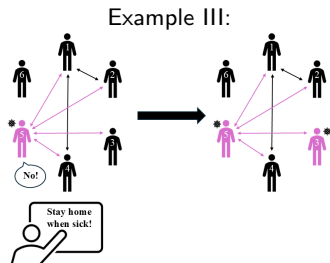
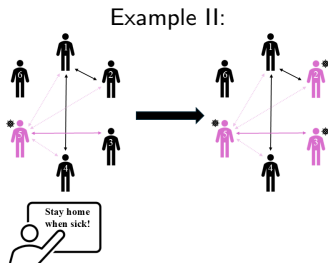
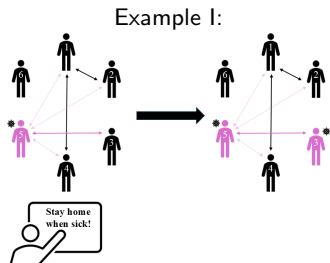
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Central Question: Does the Intervention Prevent ILI Infection?



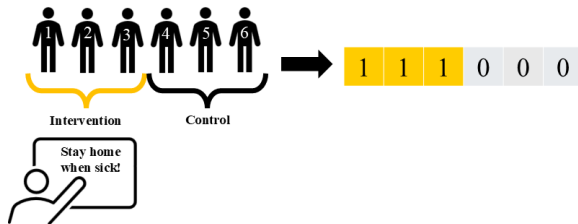
In Examples I and III, the answer is yes

eX-FLU Observed Data

- Baseline randomization assignments

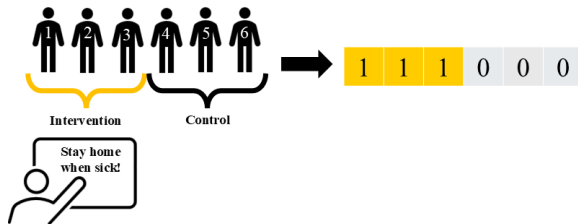
$\mathbf{Z} = (Z_1, \dots, Z_n) \in \mathcal{Z}$, for

$Z_i = \mathbb{1}(\text{student } i \text{ gets intervention})$



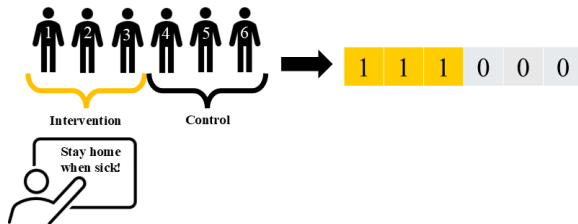
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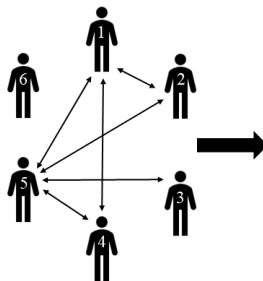
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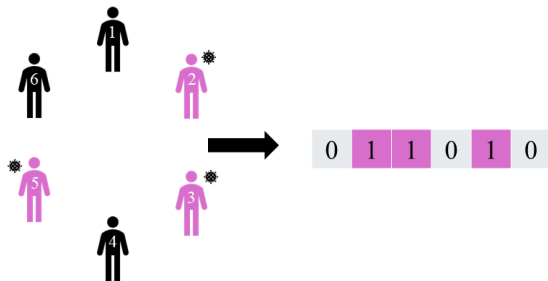
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	1	2	3	4	5	6
1	0	1	0	1	1	0
2	1	0	0	0	1	0
3	0	0	0	0	1	0
4	1	0	0	0	1	0
5	1	1	1	1	0	0
6	0	0	0	0	0	0

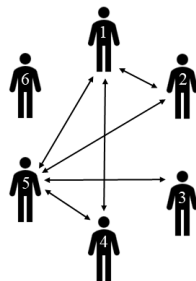
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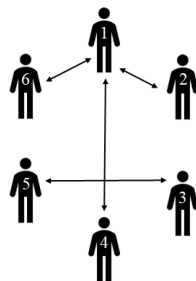
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- Network history: $\bar{\mathbf{A}} = \{\mathbf{A}^k\}_{k=1}^{\tau}$



Week 1

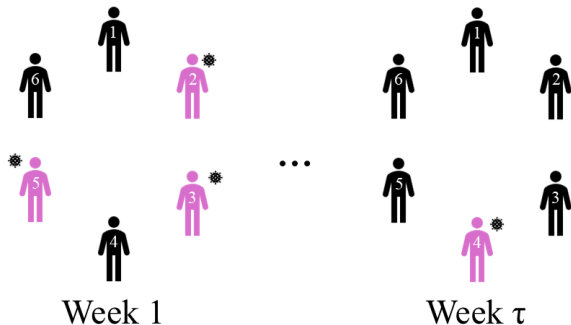
...



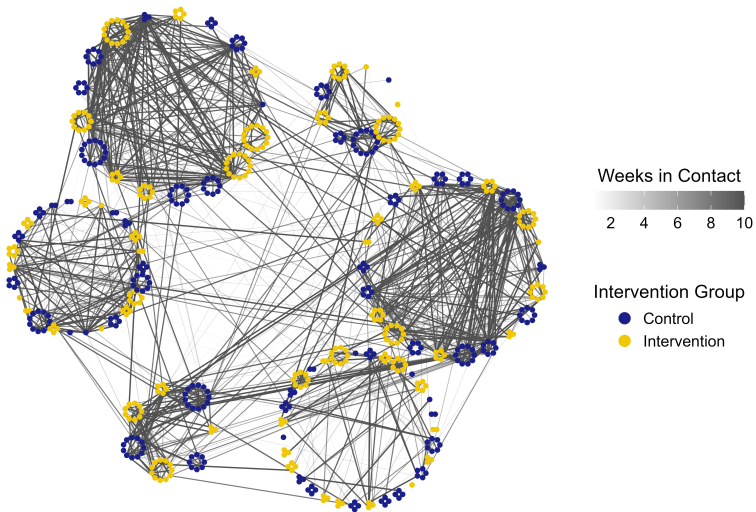
Week τ

eX-FLU Observed Data

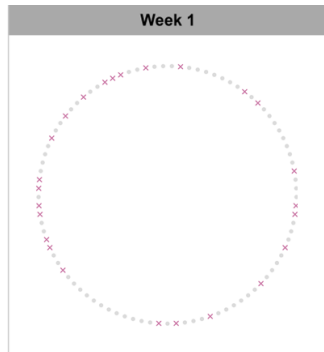
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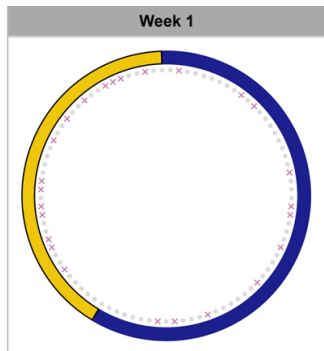


Nodes

- uninfected student
- ✕ infected student

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

eX-FLU Observed Data



Nodes

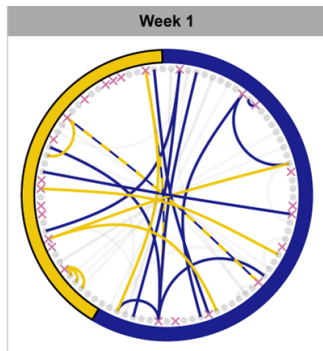
● uninfected student

× infected student

intervention group

control group

eX-FLU Observed Data



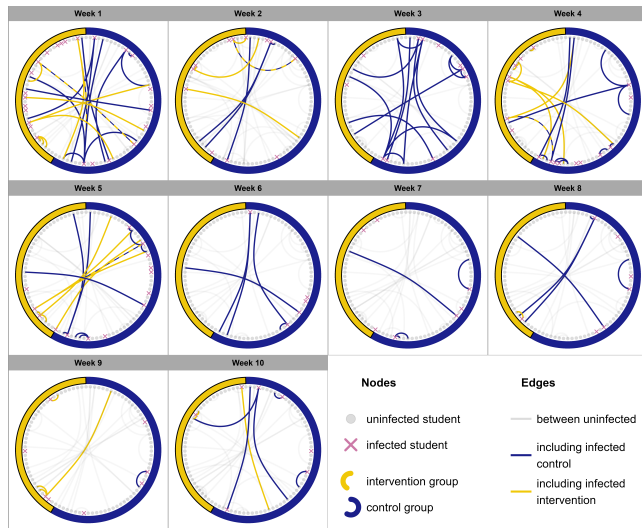
Nodes

- uninfected student
- × infected student
- intervention group
- control group

Edges

- between uninfected
- including infected control
- including infected intervention

eX-FLU Observed Data



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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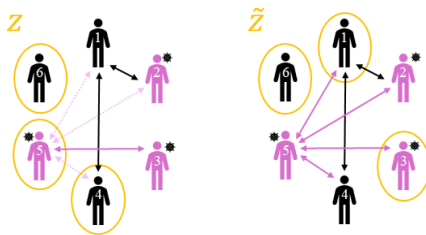
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- Both of these depend on the entire vector $\mathbf{z}$
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([Hudgens and Halloran, 2008](#))
- Assume **causal consistency**:

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

eX-FLU Null Hypotheses

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

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



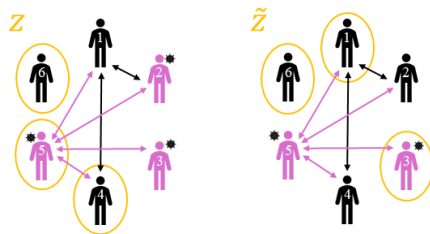
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$$H_0^A : \bar{\mathbf{A}}(\mathbf{z}) = \bar{\mathbf{A}}(\tilde{\mathbf{z}}) \text{ for all } \mathbf{z}, \tilde{\mathbf{z}} \in \mathcal{Z}$$

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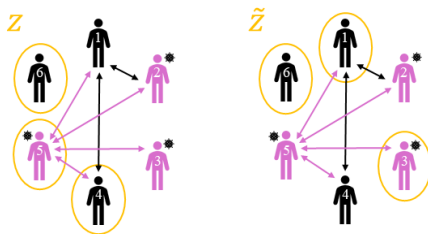
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$$H_0^\sharp = H_0^Y \cap H_0^A : \bar{Y}(z) = \bar{Y}(\tilde{z}) \text{ and } \bar{A}(z) = \bar{A}(\tilde{z}) \text{ for all } z, \tilde{z} \in \mathcal{Z}$$

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

Testing $H_0^\#$

“How unlikely are the observed data under $H_0^\#$?”

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Randomization	Networks	Infections	Test Statistic
$\mathbf{z}_1$			
$\mathbf{z}_2$			
$\dots$			
$\mathbf{z}_{ \mathcal{Z} }$			

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Randomization	Networks	Infections	Test Statistic
$\mathbf{z}_1$	$\bar{\mathbf{A}}(\mathbf{z}_1) = ?$	$\bar{\mathbf{Y}}(\mathbf{z}_1) = ?$	$T(\mathbf{z}_1, ?, ?)$
$\mathbf{z}_2$	$\bar{\mathbf{A}}(\mathbf{z}_2) = ?$	$\bar{\mathbf{Y}}(\mathbf{z}_1) = ?$	$T(\mathbf{z}_1, ?, ?)$
$\dots$	$\dots$	$\dots$	$\dots$
$\mathbf{z}_{ \mathcal{Z} }$	$\bar{\mathbf{A}}(\mathbf{z}_{ \mathcal{Z} }) = ?$	$\bar{\mathbf{Y}}(\mathbf{z}_{ \mathcal{Z} }) = ?$	$T(\mathbf{z}_{ \mathcal{Z} }, ?, ?)$

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$\mathbf{z}_2$	$\bar{\mathbf{A}}(\mathbf{z}_2) = \bar{\mathbf{A}}$	$\bar{\mathbf{Y}}(\mathbf{z}_2) = \bar{\mathbf{Y}}$	$T(\mathbf{z}_2, \bar{\mathbf{A}}, \bar{\mathbf{Y}})$
...	...	...	...
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Randomization	Networks	Infections	Test Statistic
$\mathbf{z}_1$	$\bar{\mathbf{A}}(\mathbf{z}_1) = \bar{\mathbf{A}}$	$\bar{\mathbf{Y}}(\mathbf{z}_1) = \bar{\mathbf{Y}}$	$T(\mathbf{z}_1, \bar{\mathbf{A}}, \bar{\mathbf{Y}})$
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...	...	...	...
$\mathbf{z}_{ \mathcal{Z} }$	$\bar{\mathbf{A}}(\mathbf{z}_{ \mathcal{Z} }) = \bar{\mathbf{A}}$	$\bar{\mathbf{Y}}(\mathbf{z}_{ \mathcal{Z} }) = \bar{\mathbf{Y}}$	$T(\mathbf{z}_{ \mathcal{Z} }, \bar{\mathbf{A}}, \bar{\mathbf{Y}})$

Testing $H_0^\sharp$

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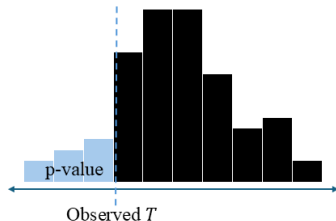
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$$F_T(t|H_0^\sharp) = \Pr(T \leq t|H_0^\sharp) = \sum_{\mathbf{z} \in \mathcal{Z}} r(\mathbf{z}) \mathbb{1}\{T(\mathbf{z}, \bar{\mathbf{A}}, \bar{\mathbf{Y}}) \leq t\}$$

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



Testing $H_0^\sharp$

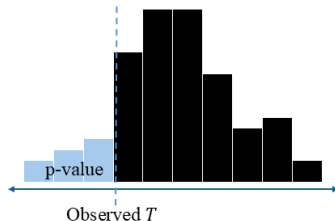
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is the **cumulative distribution function** (CDF) of T

- 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:

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

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

Testing $H_0^\sharp$

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

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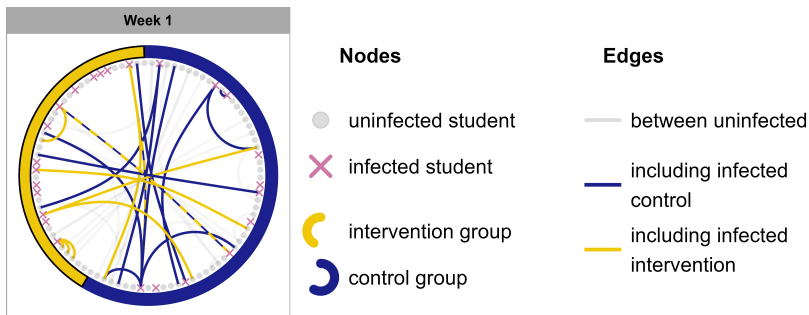
- The **power** of this test:

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

depends on the choice of test statistic

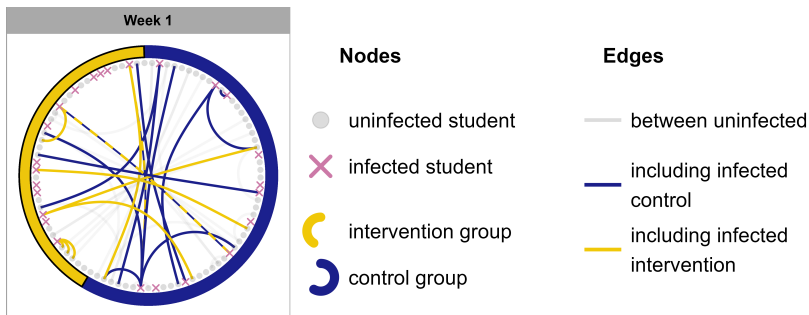
Choice of Test Statistic

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



Choice of Test Statistic

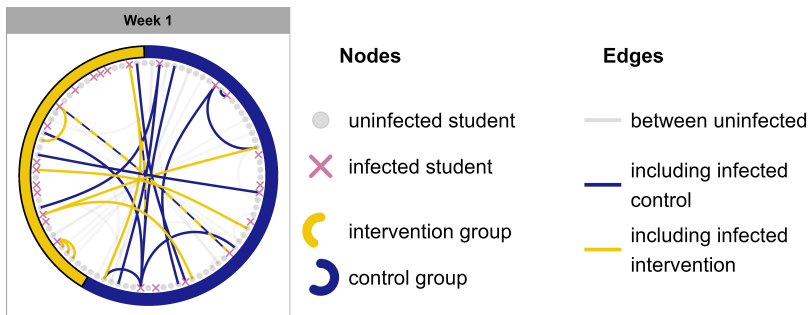
- 93 (out of 579) students with at least one infection
- Bold edges represent possible transmission events



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

"How unlikely are the observed data under H_0^Y ?"

Testing H_0^Y

“How unlikely are the observed data under H_0^Y ?”

- Choose a test statistic $T = T(\mathbf{Z}, \overline{\mathbf{A}}, \overline{\mathbf{Y}})$

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Randomization	Networks	Infections	Test Statistic
$\mathbf{z}_1$			
$\mathbf{z}_2$			
$\dots$			
$\mathbf{z}_{ \mathcal{Z} }$			

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$\mathbf{z}_2$	$\bar{\mathbf{A}}(\mathbf{z}_2) = ?$	$\bar{\mathbf{Y}}(\mathbf{z}_1) = ?$	$T(\mathbf{z}_1, ?, ?)$
...	...	...	...
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 - ▶ Define $q(\bar{\mathbf{a}}, \mathbf{z}) = \Pr\{\bar{\mathbf{A}}(\mathbf{z}) = \bar{\mathbf{a}}\}$, the **probability mass function** (PMF) of $\bar{\mathbf{A}}(\mathbf{z})$

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- ▶ If/when the double sum $\sum_{\mathbf{z} \in \mathcal{Z}} \sum_{\bar{\mathbf{a}} \in \mathcal{A}}$ 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 $\bar{\mathbf{A}}(\mathbf{z})$

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

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 - ① generate randomization vector $\mathbf{z}_b$ from $r(\mathbf{z})$

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

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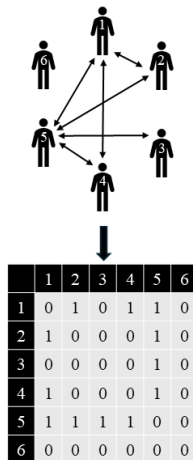
Proposition: This procedure will **asymptotically** control the type I error rate

Exponential Family Random Graph Models (ERGMs)

Goal: model a network (**A**) given covariates (**X**)

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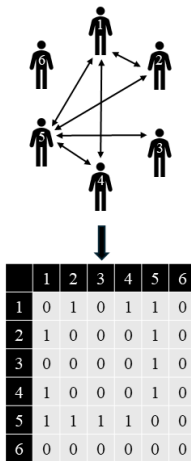


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Goal: model a network ($\mathbf{A}$) given covariates ($\mathbf{X}$)

An **ERGM** assumes:

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



Exponential Family Random Graph Models (ERGMs)

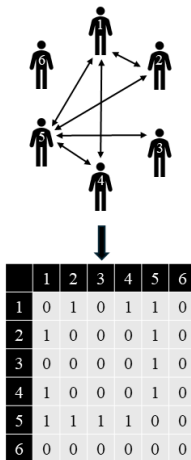
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- normalizing constant:

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



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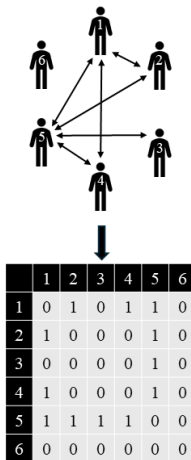
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Exponential Family Random Graph Models (ERGMs)

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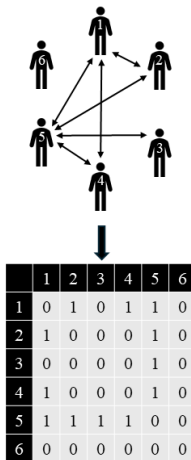
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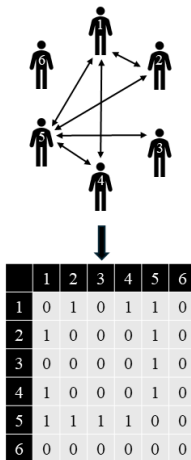
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Goal: model a network ($\mathbf{A}$) given covariates ($\mathbf{X}$)

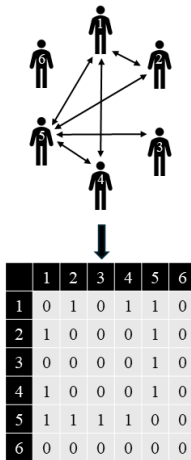
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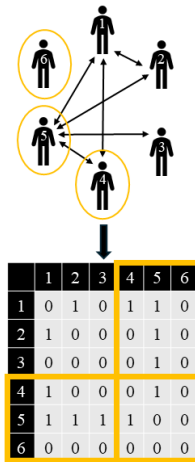
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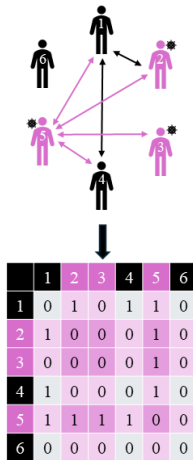
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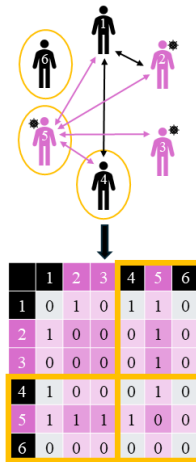
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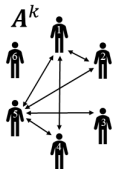
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- ▶ $g_{ZY}(\mathbf{a}, \mathbf{x}) = \sum_{i,j} a_{ij}(z_i y_i + z_j y_j)$



Separable Temporal Exponential Family Random Graph Models

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

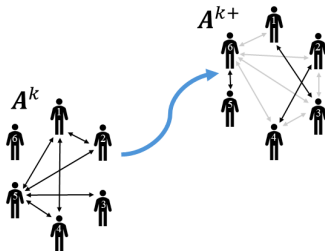


Separable Temporal Exponential Family Random Graph Models

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

$$\Pr_{\theta^+}(\mathbf{A}^{k+1} = \mathbf{a}^{k+1} | \mathbf{A}^k = \mathbf{a}^k, \mathbf{X}^{k+1} = \mathbf{x}^{k+1}) = \frac{\exp(\theta^+ \mathbf{g}^+(\mathbf{a}^{k+1}, \mathbf{a}^k, \mathbf{x}^{k+1}))}{\kappa_{\mathbf{g}^+}(\theta^+, \mathcal{A}^+(\mathbf{a}^k), \mathbf{a}^k, \mathbf{x}^{k+1})},$$

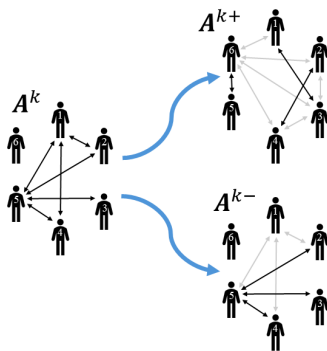


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$$\Pr_{\theta^-}(\mathbf{A}^{k-} = \mathbf{a}^{k-} | \mathbf{A}^k = \mathbf{a}^k, \mathbf{X}^{k+1} = \mathbf{x}^{k+1}) = \frac{\exp(\theta^- \mathbf{g}^-(\mathbf{a}^{k-}, \mathbf{a}^k, \mathbf{x}^{k+1}))}{\kappa_{\mathbf{g}^-}(\theta^-, \mathcal{A}^-(\mathbf{a}^k), \mathbf{a}^k, \mathbf{x}^{k+1})},$$

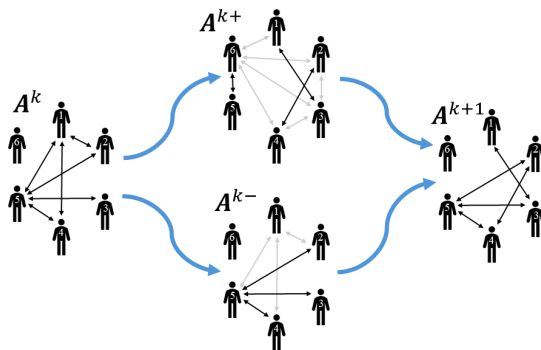


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$$\mathbf{A}^{k+1} = \underbrace{\mathbf{A}^k}_{\text{previous network}} \cup \underbrace{(\mathbf{A}^{k+} - \mathbf{A}^k)}_{\text{new edges formed}} - \underbrace{(\mathbf{A}^k - \mathbf{A}^{k-})}_{\text{old edges not persisting}}$$

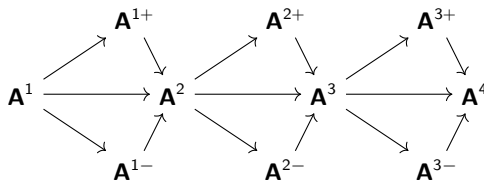


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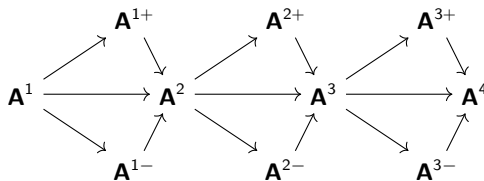
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- 1 $\mathbf{A}^{k+} \perp\!\!\!\perp \mathbf{A}^{k-} | \mathbf{A}^k$, i.e., the formation and persistence processes are conditionally independent given the network at time k
- 2 the parameter space for $\theta = (\theta^+, \theta^-)$ is the product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



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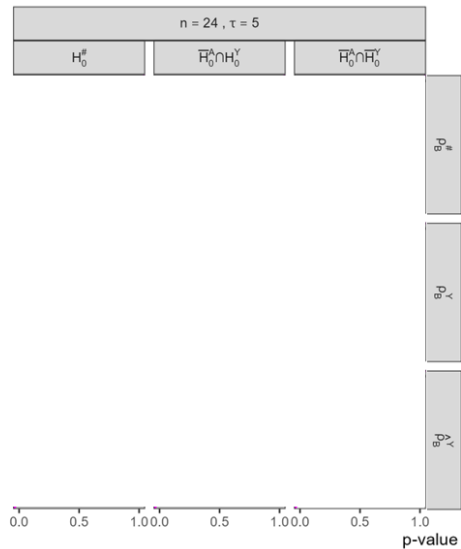
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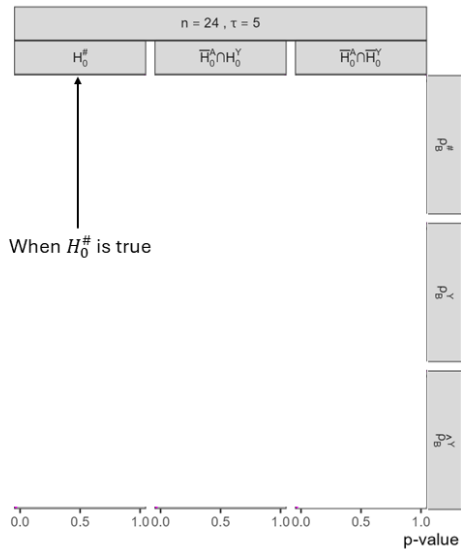
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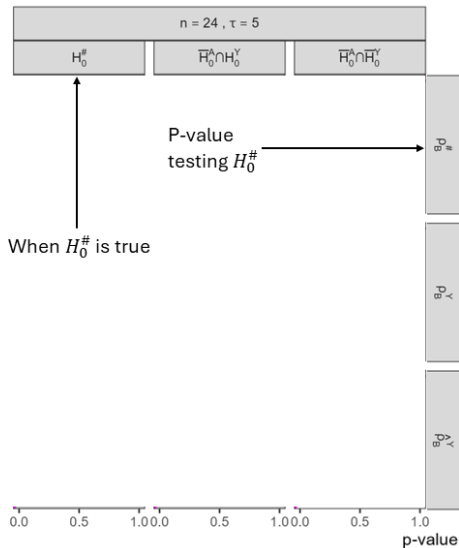
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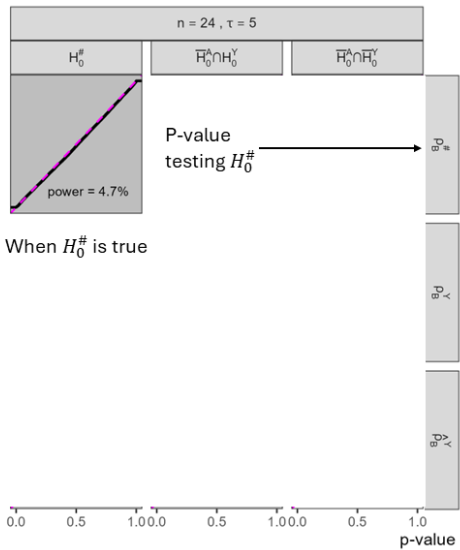
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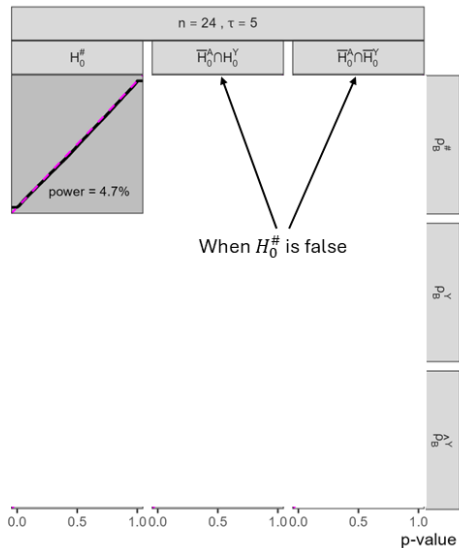
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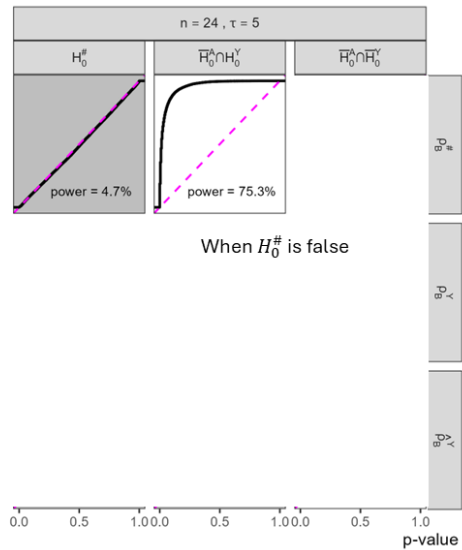
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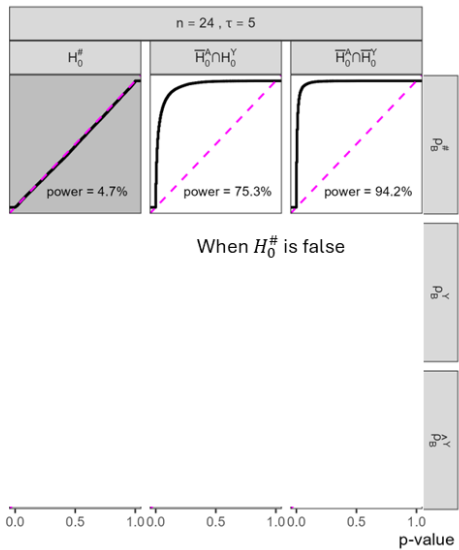
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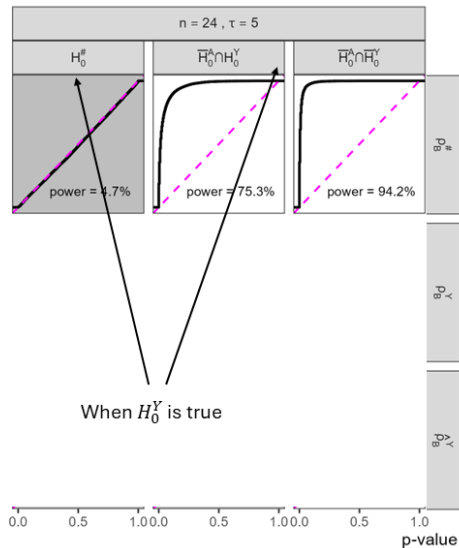
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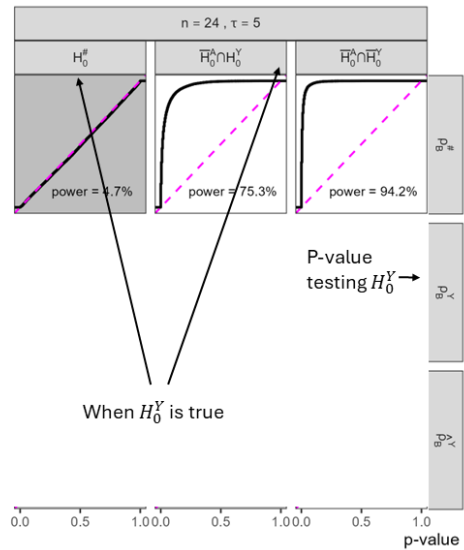
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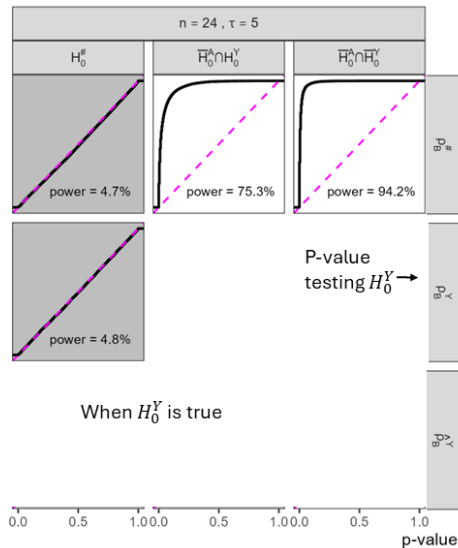
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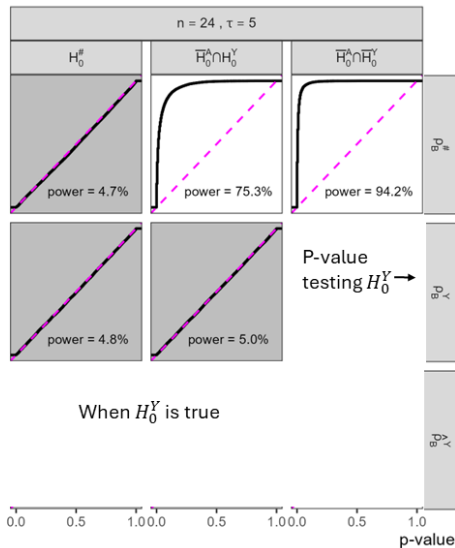
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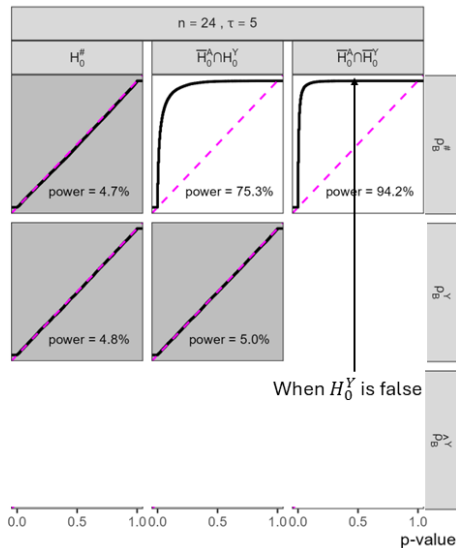
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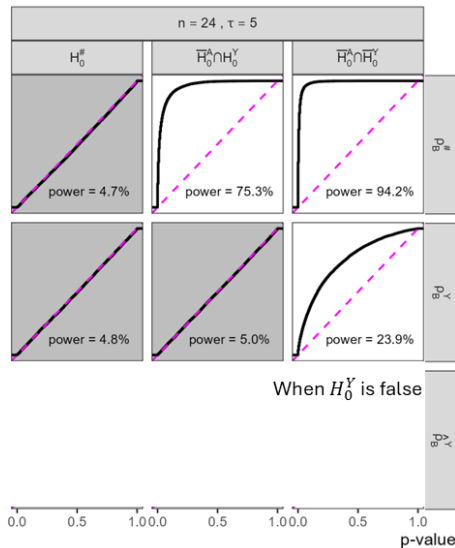
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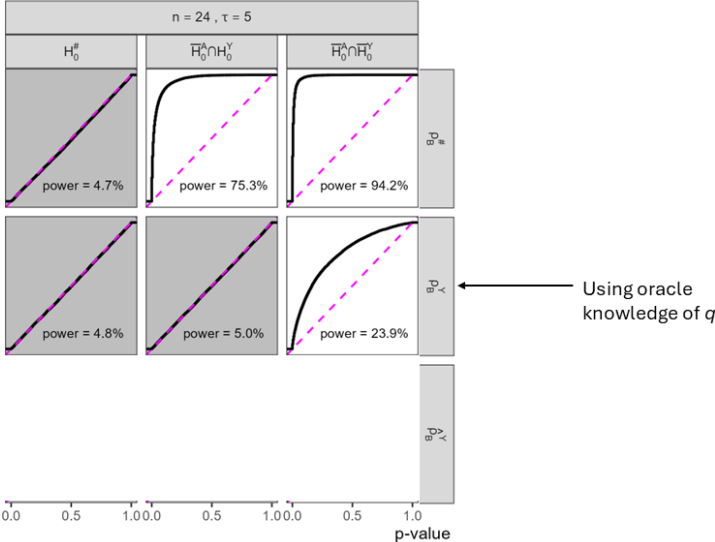
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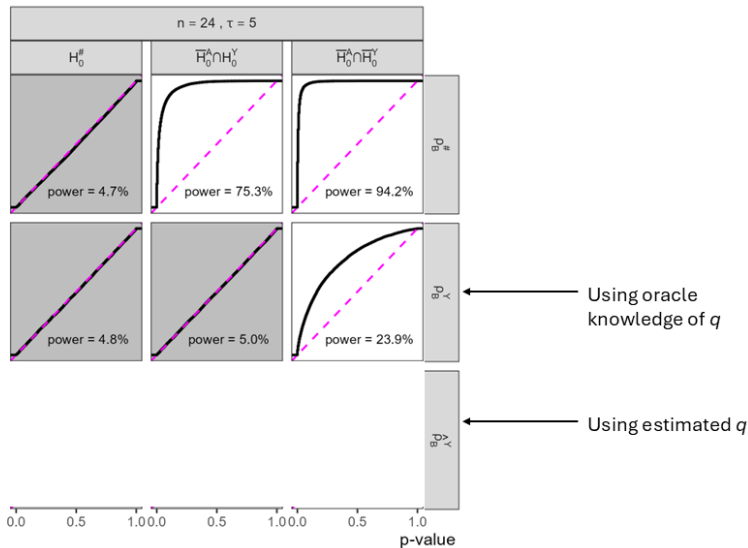
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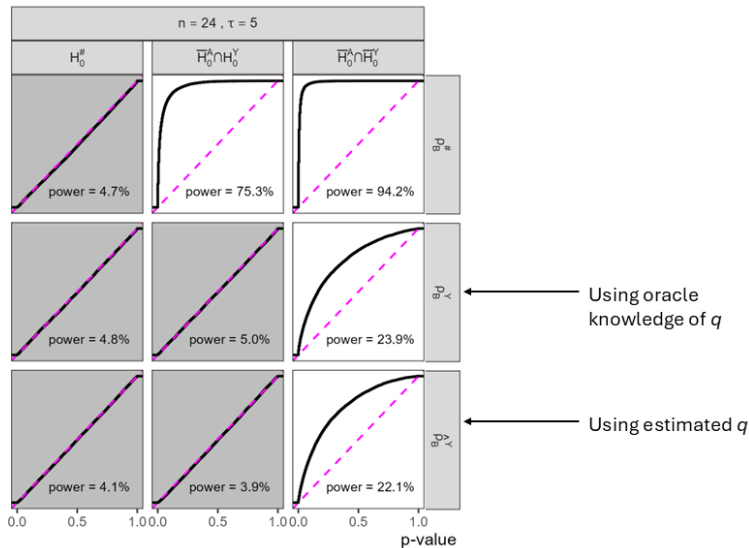
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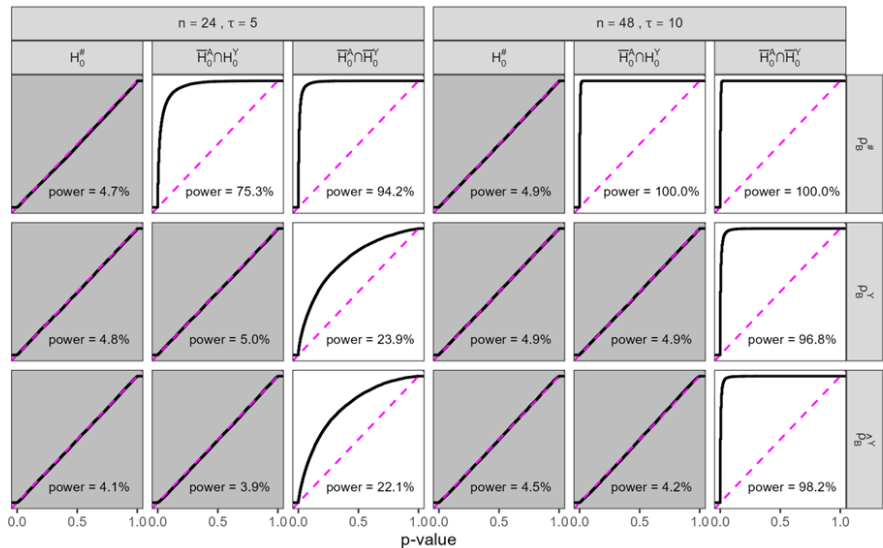
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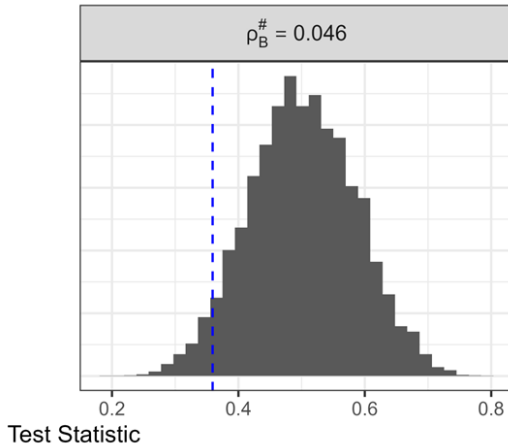
eX-FLU: Hypothesis Test Results

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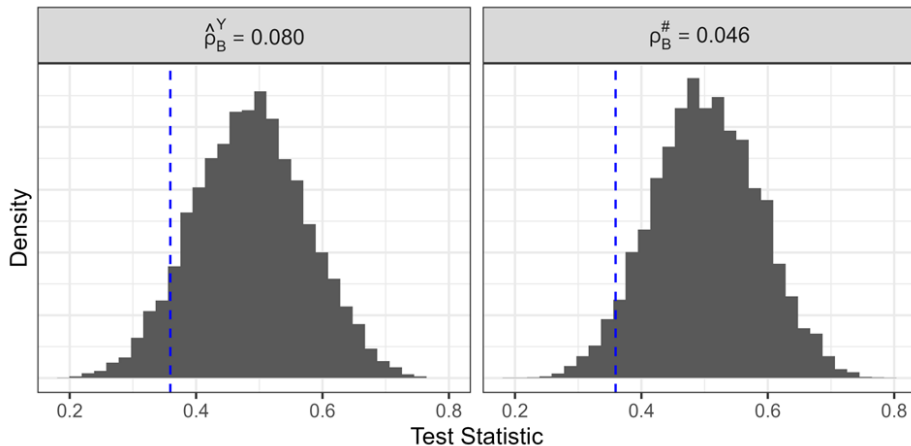
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Density



eX-FLU: Hypothesis Test Results

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- Theoretical and empirical demonstration of type I error control
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Project status:

- Under revision with *PNAS*

Questions?

contact: richabr@wfu.edu

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Supplementary Slides

Choice of Test Statistic

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

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

	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 .

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 $\text{Uniform}(0, 1)$ distribution for any N .
 - ② If the test statistic T_N has a continuous limiting distribution, then $F_N(T_N) \rightarrow^d \text{Uniform}(0, 1)$.
- **Corollary 2.2:**
 - ① Under $H_0^\sharp$, the sharp null p-value $\rho_N^\sharp$ stochastically dominates a $\text{Uniform}(0, 1)$ distribution for any N .
 - ② Under H_0^Y , the oracle p-value ρ_N^Y stochastically dominates a $\text{Uniform}(0, 1)$ distribution for any N .
 - ③ If the test statistic T_N has a continuous limiting distribution, then $\rho_N^\sharp \rightarrow^d \text{Uniform}(0, 1)$ under $H_0^\sharp$ and $\rho_N^Y \rightarrow^d \text{Uniform}(0, 1)$ 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 $\hat{\theta}_N$ 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) $\hat{\theta}_N \rightarrow^P \theta_0$

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

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

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

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

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

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

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 $T_N^* = h_N(T_N), F_N^*(\cdot; \theta) = F_N\{h_N^{-1}(\cdot); \theta\}$.

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 1:1 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 ($k = 1$) face-to-face 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 $k \in \{2, \dots, \tau\}$ with probability $\Pr(Y_i^k = 1 | \mathbf{A}^{k-1}, \mathbf{Y}^{k-1}) = h_i(\mathbf{S}^{k-1})$ depending on the vector $\mathbf{S}^{k-1} = \mathbf{A}^{k-1} \mathbf{Y}^{k-1}$ of counts of infected contacts for each student at week $k - 1$.

Simulation Setup

Three scenarios:

Null	Formation Model	Persistence Model	Infection Probability
Hypothesis	Parameters θ^+	Parameters θ^-	Function h_i
$H_0^\sharp$	$(-0.5, 0, 0, 0)$	$(-0.5, 0, 0, 0)$	$h_i(\mathbf{s}) = 0.5$
$\overline{H_0^A} \cap H_0^Y$	$(-0.2, 0, 0, -1)$	$(-0.2, 0, 0, -1)$	$h_i(\mathbf{s}) = 0.5$
$\overline{H_0^A} \cap \overline{H_0^Y}$	$(-0.2, 0, 0, -1)$	$(-0.2, 0, 0, -1)$	$h_i(\mathbf{s}) = \frac{n}{2} \text{expit}(s_i - \bar{s}) / \sum_{j=1}^n \text{expit}(s_j - \bar{s})$

Table: 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 $\theta^- = (\theta_{\text{edges}}^-, \theta_Z^-, \theta_Y^-, \theta_{ZY}^-)$, the infection probability function $h_i(\mathbf{s})$ gives the probability of student i being infected at week k given the vector $\mathbf{S}^{k-1} = \mathbf{s} = (s_1, \dots, s_n)$ of infected contact counts for each student at week $k-1$, and $\bar{s} = n^{-1} \sum_{i=1}^n s_i$.

Three p-values:

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

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

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

- ▶ 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

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

- **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

eX-FLU: STERGM Specification

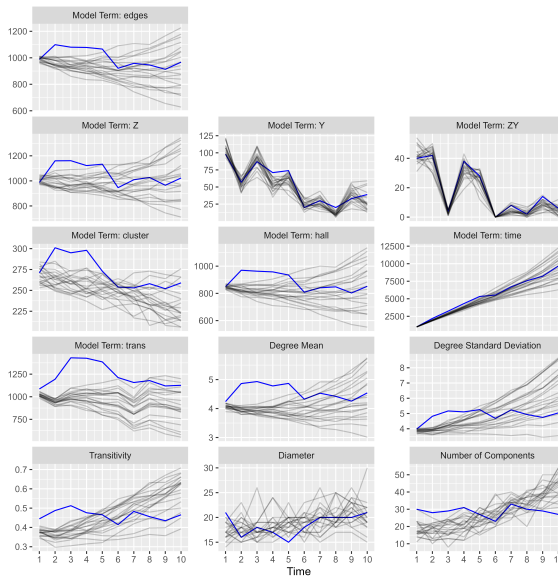
$$\mathbf{g}^+(\mathbf{a}^{k+}, \mathbf{a}^k, \mathbf{x}^{k+1}) =$$

$$\begin{bmatrix} g_{\text{edges}}^+(\mathbf{a}^{k+}, \mathbf{x}^{k+1}) \\ g_Z^+(\mathbf{a}^{k+}, \mathbf{x}^{k+1}) \\ g_Y^+(\mathbf{a}^{k+}, \mathbf{x}^{k+1}) \\ g_{ZY}^+(\mathbf{a}^{k+}, \mathbf{x}^{k+1}) \\ g_{\text{room}}^+(\mathbf{a}^{k+}, \mathbf{x}^{k+1}) \\ g_{\text{cluster}}^+(\mathbf{a}^{k+}, \mathbf{x}^{k+1}) \\ g_{\text{hall}}^+(\mathbf{a}^{k+}, \mathbf{x}^{k+1}) \\ g_{\text{time}}^+(\mathbf{a}^{k+}, \mathbf{x}^{k+1}) \\ g_{\text{trans}}^+(\mathbf{a}^k, \mathbf{x}^{k+1}) \end{bmatrix} = \begin{bmatrix} \sum_{i,j} a_{ij}^{k+} \\ \sum_{i,j} a_{ij}^{k+} (z_i + z_j) \\ \sum_{i,j} a_{ij}^{k+} (y_i^{k+1} + y_j^{k+1}) \\ \sum_{i,j} a_{ij}^{k+} (z_i y_i^{k+1} + z_j y_j^{k+1}) \sum_{i,j} a_{ij}^{k+} \mathbb{1}(i,j \text{ roommates}) \\ \sum_{i,j} a_{ij}^{k+} \mathbb{1}(i,j \text{ cluster-mates}) \\ \sum_{i,j} a_{ij}^{k+} \mathbb{1}(i,j \text{ hall-mates}) \\ \sum_{i,j} a_{ij}^{k+} \\ \sum_{i,j} \log(1 + \sum_l a_{il}^k a_{jl}^k) \end{bmatrix}$$

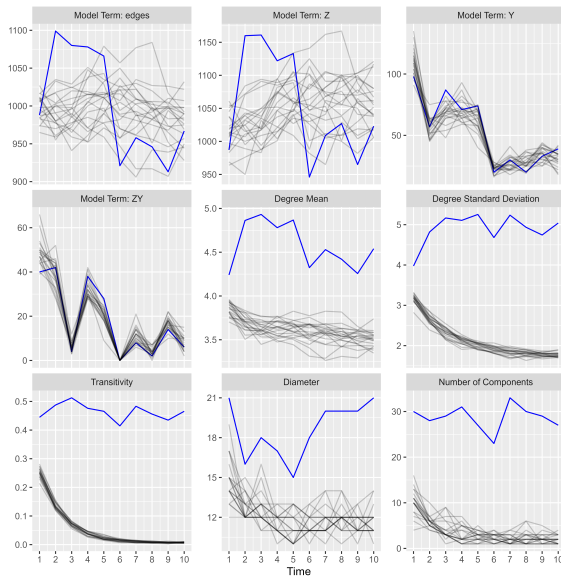
eX-FLU: STERGM Results

Model	Parameter	Estimate (95% Confidence Interval)
Formation	θ_{edges}^+	-7.85 (-8.00, -7.71)
	θ_Z^+	0.09 (0.02, 0.15)
	θ_Y^+	0.71 (0.50, 0.93)
	θ_{ZY}^+	-0.42 (-0.79, -0.05)
	θ_{room}^+	∞ (offset)
	$\theta_{\text{cluster}}^+$	2.02 (1.90, 2.14)
	θ_{hall}^+	1.71 (1.57, 1.84)
	θ_{time}^+	-0.09 (-0.11, -0.07)
	θ_{trans}^+	2.88 (2.82, 2.94)
Persistence	θ_{edges}^-	0.16 (-0.02, 0.33)
	θ_Z^-	0.03 (-0.03, 0.10)
	θ_Y^-	-0.06 (-0.32, 0.21)
	θ_{ZY}^-	-0.11 (-0.55, 0.33)
	θ_{room}^-	∞ (offset)
	$\theta_{\text{cluster}}^-$	0.26 (0.13, 0.39)
	θ_{hall}^-	0.15 (0.00, 0.31)
	θ_{time}^-	0.04 (0.02, 0.06)
	θ_{trans}^-	0.42 (0.35, 0.48)

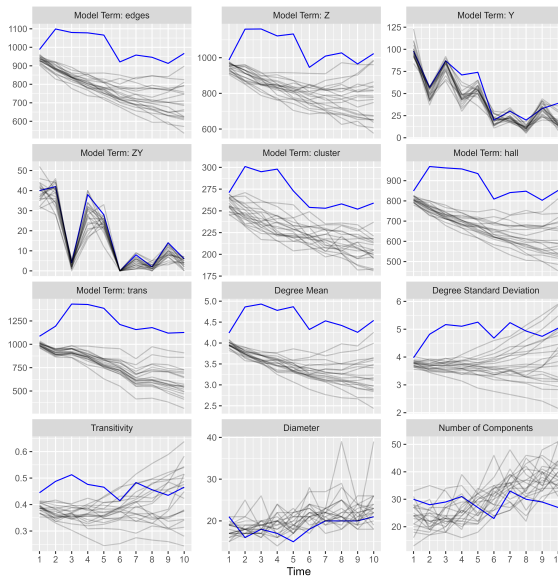
eX-FLU Diagnostics: STERGM



eX-FLU Diagnostics: Alternate STERGM 1



eX-FLU Diagnostics: Alternate STERGM 2



eX-FLU Sensitivity Analysis

