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

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eX-FLU Trial

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

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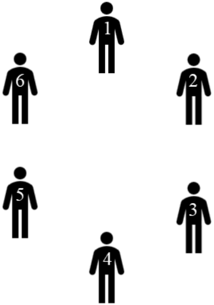
Transmission of Influenza-Like-Illness



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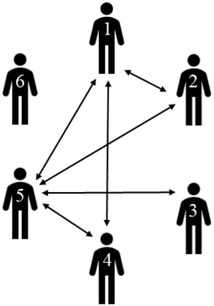

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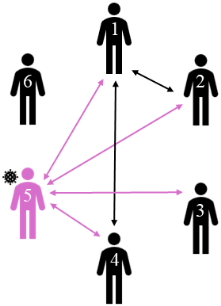

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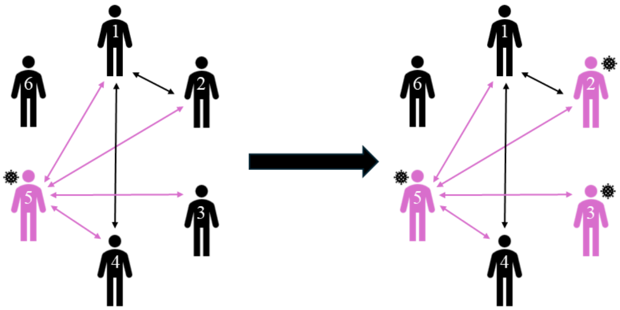
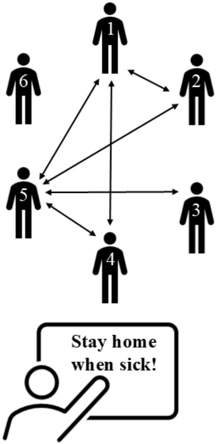


Example I: Intervention Affects Network and Infections



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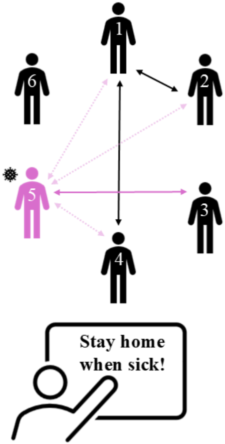

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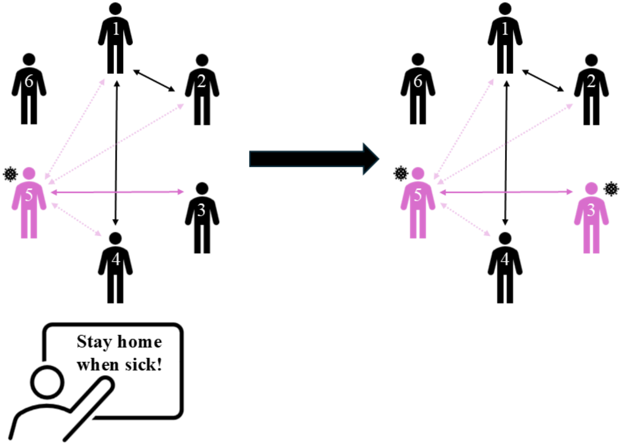

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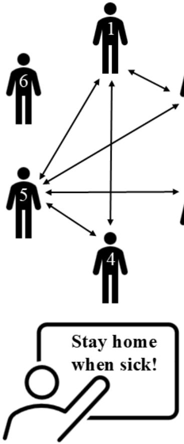

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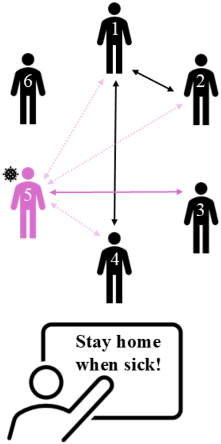

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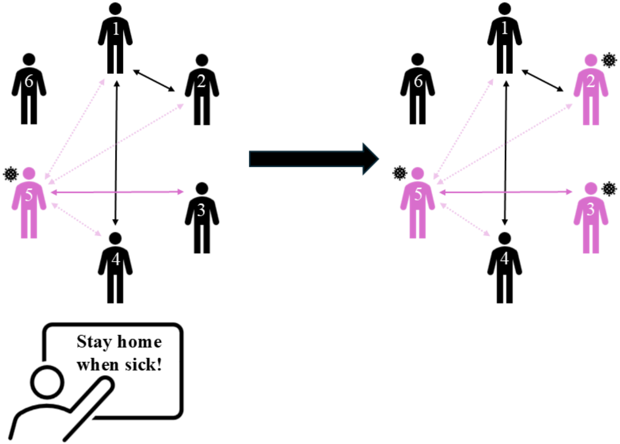

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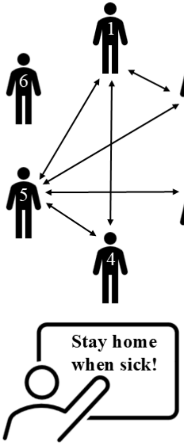

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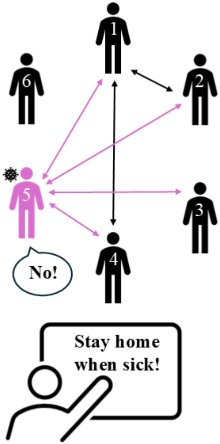

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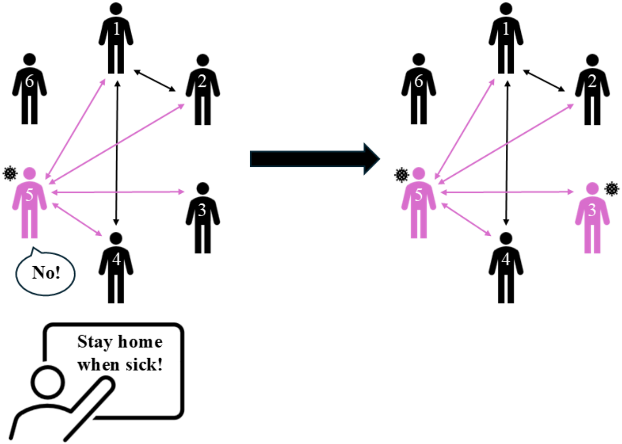
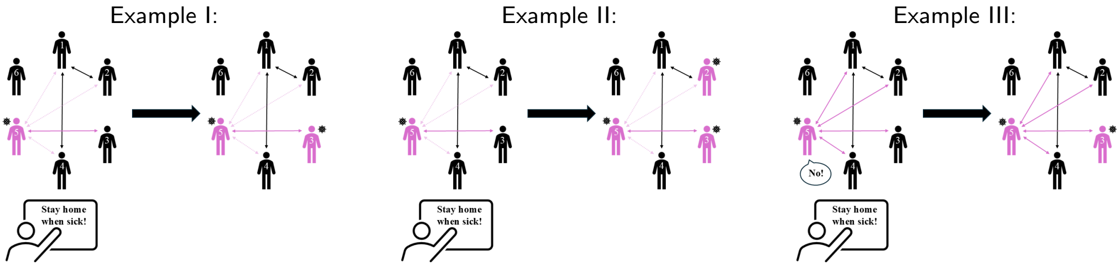


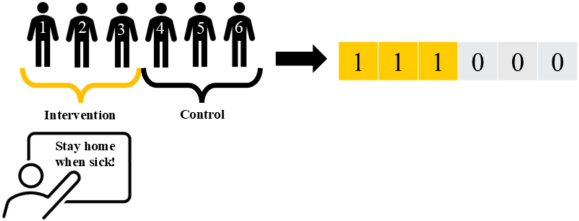
Central Question: Does the Intervention Prevent ILI Infection?



In Examples I and III, the answer is yes

eX-FLU Observed Data

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



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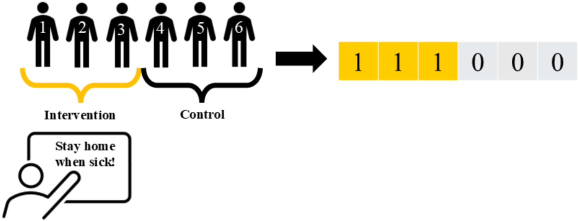

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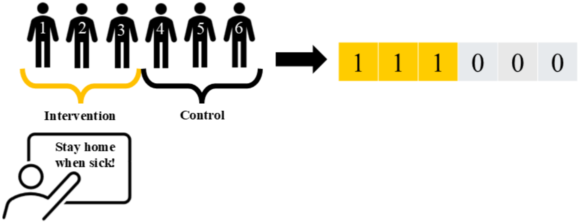

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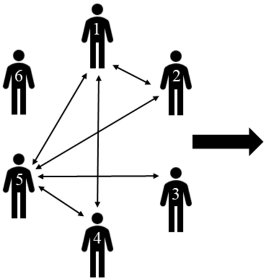

	1	2	3	4	5	6
1	0	1	0	1	1	0
2	1	0	0	0	1	0
3	0	0	0	0	1	0
4	1	0	0	0	1	0
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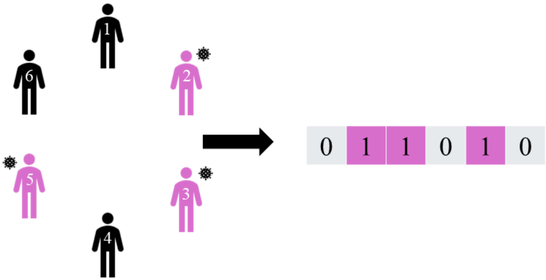

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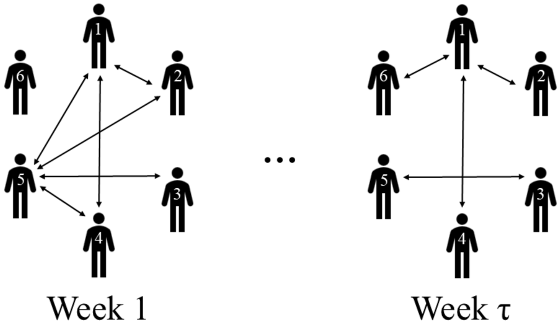
- Network history: $\overline{\mathbf{A}} = \{\mathbf{A}^k\}_{k=1}^{\tau}$



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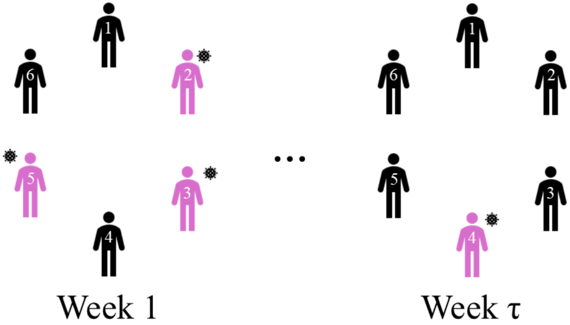

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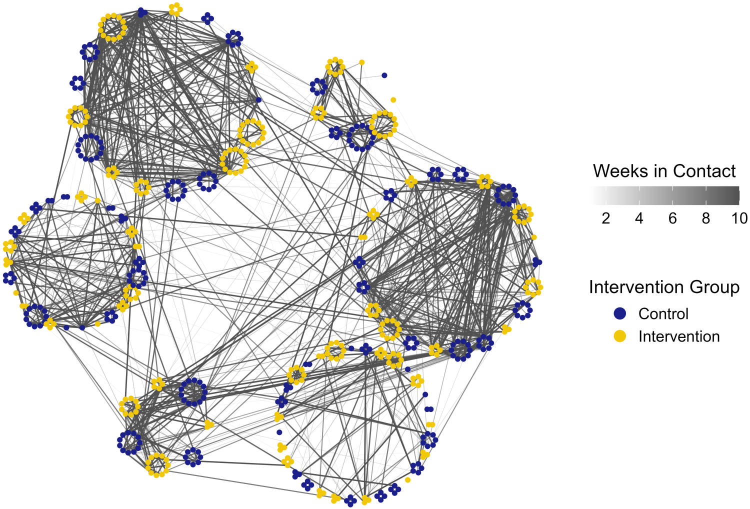

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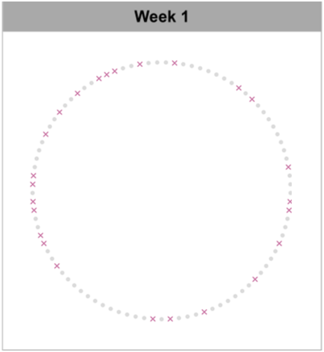

Nodes

uninfected student

infected student

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

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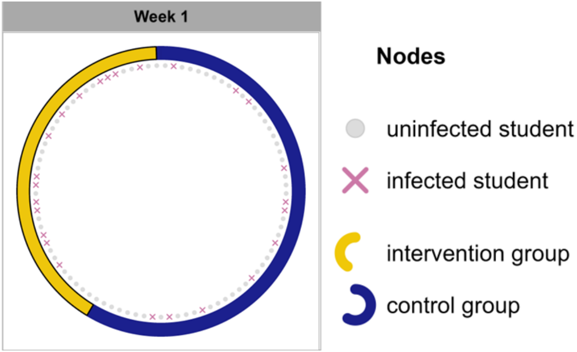

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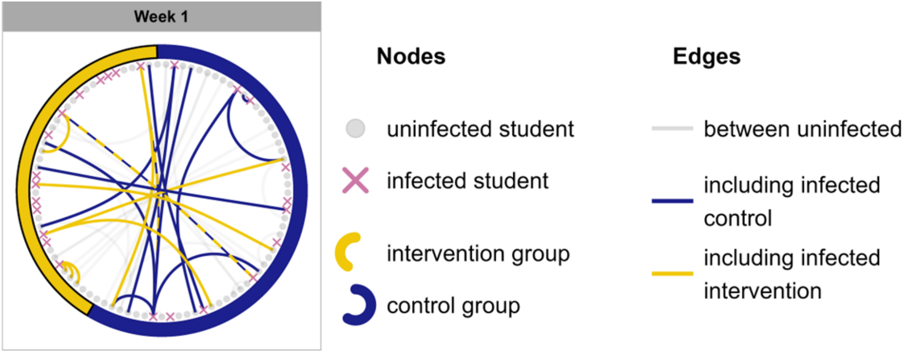

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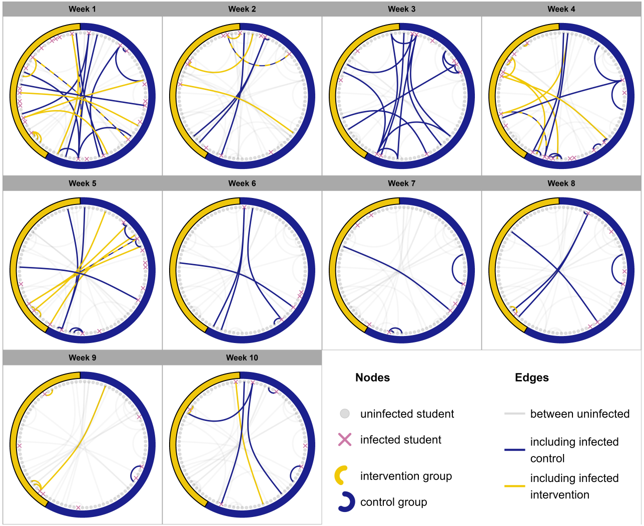

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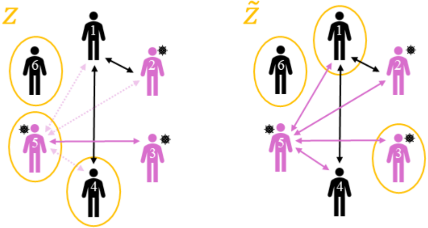
- Assume **causal consistency**:

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

eX-FLU Null Hypotheses

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

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



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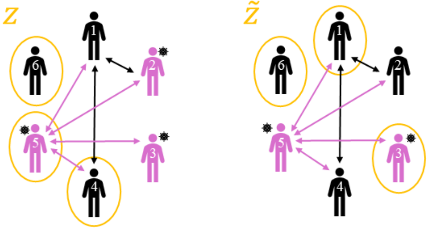

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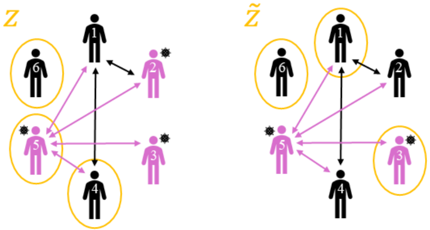

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Previous analyses of the eX-FLU trial (Alexandria et al., 2023) tested $H_0^\sharp$, but no analyses have tested H_0^Y

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

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$\mathbf{z}_2$	$\overline{\mathbf{A}}(\mathbf{z}_2) =?$	$\overline{\mathbf{Y}}(\mathbf{z}_1) =?$	$T(\mathbf{z}_1, ?, ?)$
$\dots$	$\dots$	$\dots$	$\dots$
$\mathbf{z}_{\lvert\mathcal{Z}\rvert}$	$\overline{\mathbf{A}}(\mathbf{z}_{\lvert\mathcal{Z}\rvert}) =?$	$\overline{\mathbf{Y}}(\mathbf{z}_{\lvert\mathcal{Z}\rvert}) =?$	$T(\mathbf{z}_{\lvert\mathcal{Z}\rvert}, ?, ?)$

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$\mathbf{z}_2$	$\overline{\mathbf{A}}(\mathbf{z}_2) = \overline{\mathbf{A}}$	$\overline{\mathbf{Y}}(\mathbf{z}_2) = \overline{\mathbf{Y}}$	$T(\mathbf{z}_2, \overline{\mathbf{A}}, \overline{\mathbf{Y}})$
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$\mathbf{z}_{\lvert\mathcal{Z}\rvert}$	$\overline{\mathbf{A}}(\mathbf{z}_{\lvert\mathcal{Z}\rvert}) = \overline{\mathbf{A}}$	$\overline{\mathbf{Y}}(\mathbf{z}_{\lvert\mathcal{Z}\rvert}) = \overline{\mathbf{Y}}$	$T(\mathbf{z}_{\lvert\mathcal{Z}\rvert}, \overline{\mathbf{A}}, \overline{\mathbf{Y}})$

Testing $H_0^\sharp$

"How unlikely are the observed data under $H_0^\sharp$?" We can answer this using a **randomization test** (Fisher, 1936; Alexandria et al., 2023; Zhang and Zhao, 2023; Ritzwoller et al., 2024)

- Choose a test statistic $T = T(\mathbf{Z}, \overline{\mathbf{A}}, \overline{\mathbf{Y}})$
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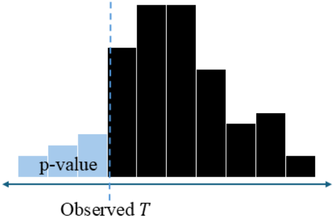
  is the **cumulative distribution function** (CDF) of T



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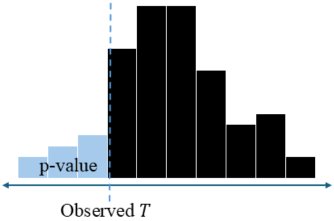
  is the **cumulative distribution function** (CDF) of T
- Reject $H_0^\sharp$ if $\rho^\sharp \le 0.05$



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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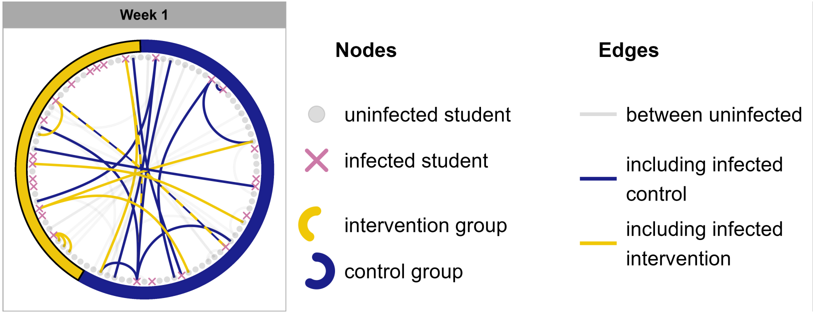
- The **power** of this test:

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

  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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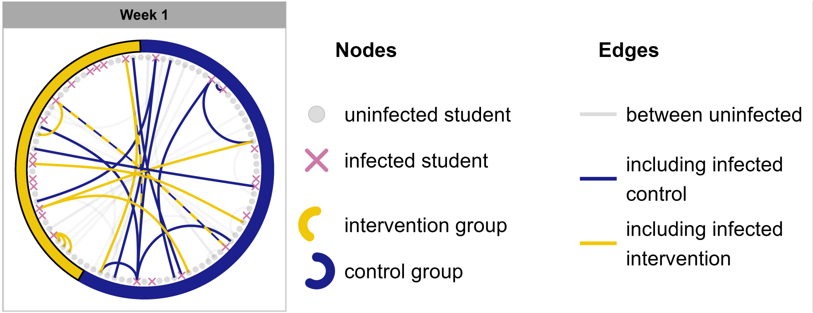
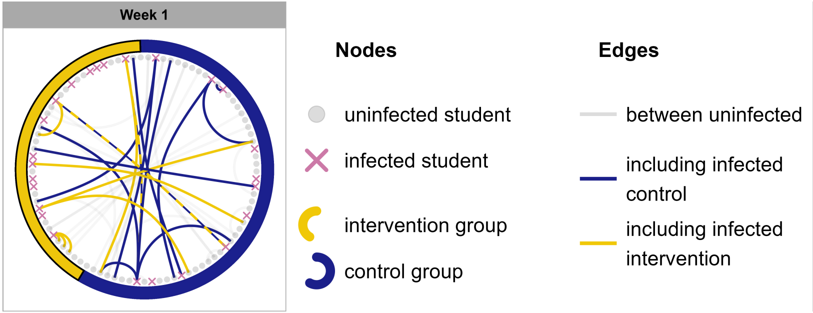


Choice of Test Statistic

- 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:

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



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

Exponential Family Random Graph Models (ERGMs)

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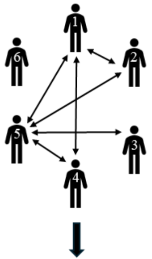

	1	2	3	4	5	6
1	0	1	0	1	1	0
2	1	0	0	0	1	0
3	0	0	0	0	1	0
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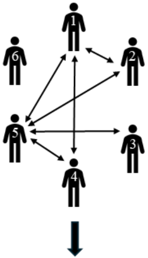
An **ERGM** assumes:

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



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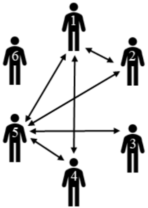
- normalizing constant: $\kappa_{\mathbf{g}}(\theta, \mathcal{A}, \mathbf{x}) = \sum_{\mathbf{a} \in \mathcal{A}} \exp\{\theta \mathbf{g}(\mathbf{a}, \mathbf{x})\}$



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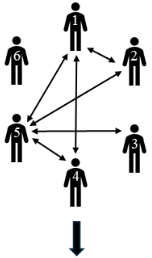

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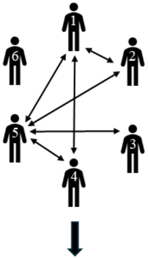

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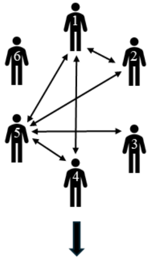

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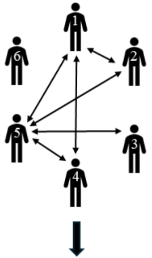

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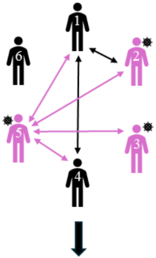

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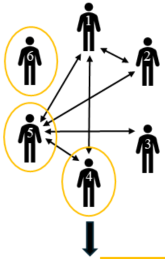

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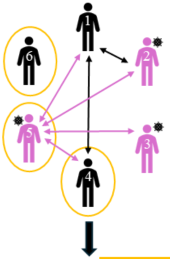

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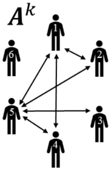

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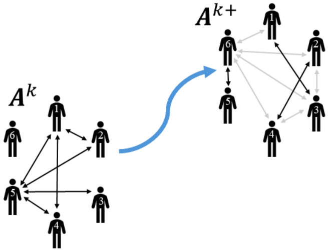

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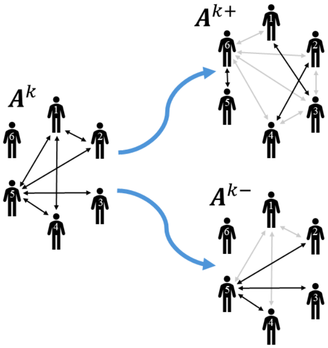

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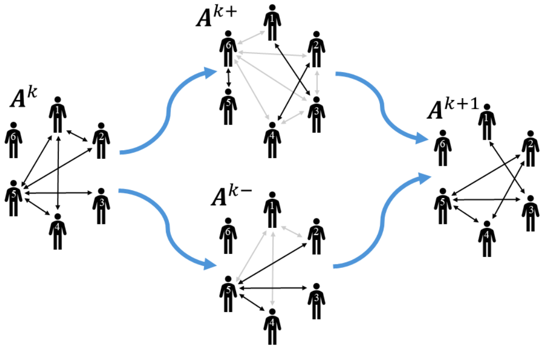
$$\mathbf{A}^{k+1} = \underbrace{\mathbf{A}^{k}}_{\text{previous network}} \cup \underbrace{(\mathbf{A}^{k+} - \mathbf{A}^{k})}_{\text{new edges formed}} - \underbrace{(\mathbf{A}^{k} - \mathbf{A}^{k-})}_{\text{old edges not persisting}}$$



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- Three testing procedures:
  1. $\rho_B^\sharp$: testing $H_0^\sharp$
  2. ρ_B^Y: testing H_0^Y using known q
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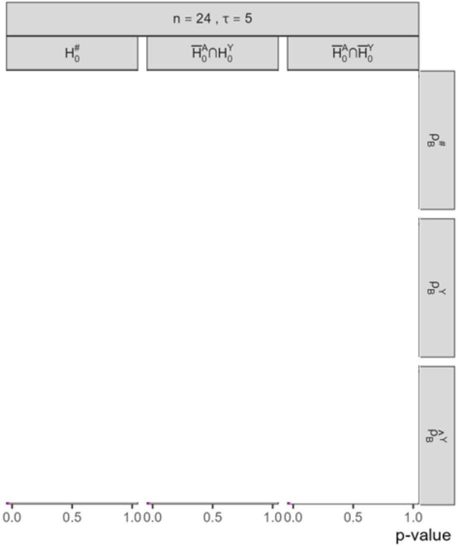
Simulation Results: Empirical CDF of P-Values



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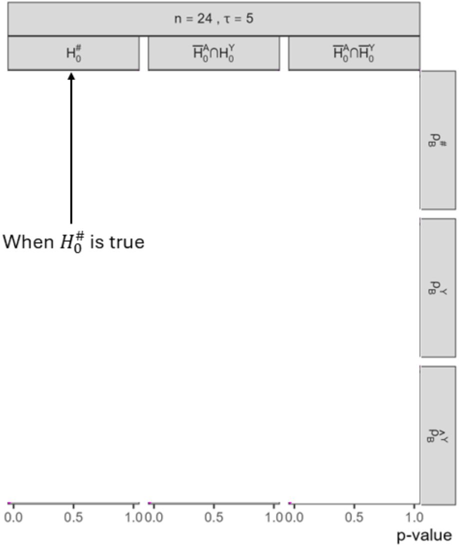

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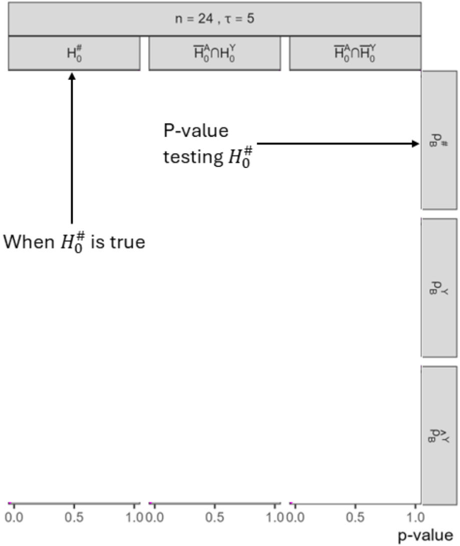

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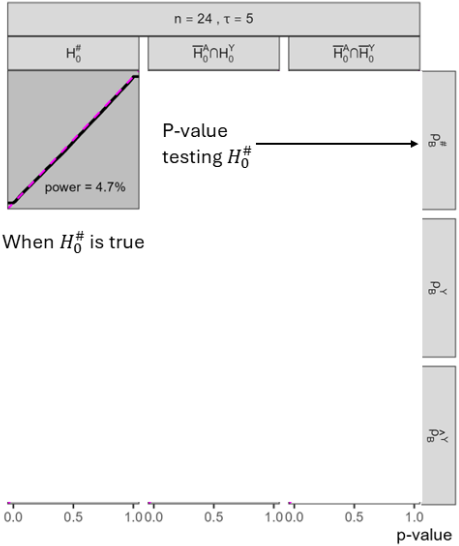

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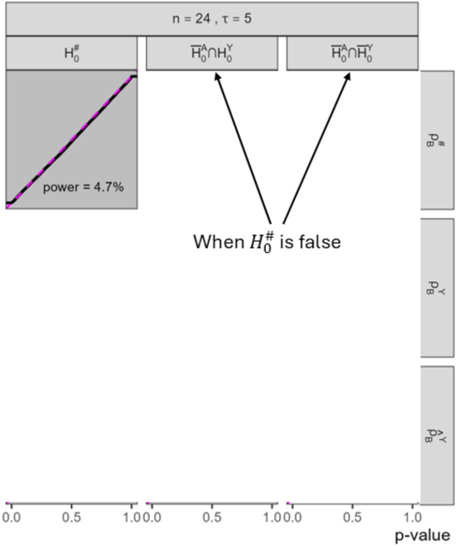

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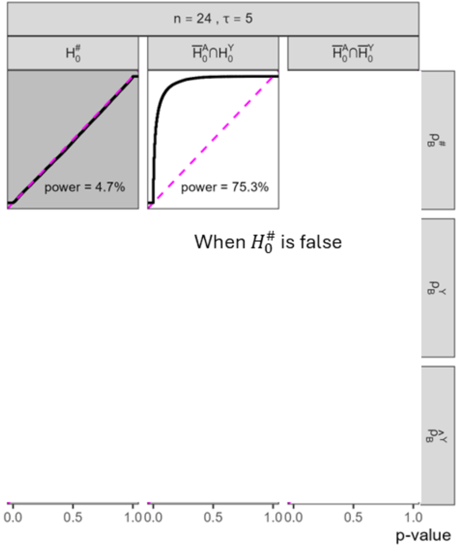

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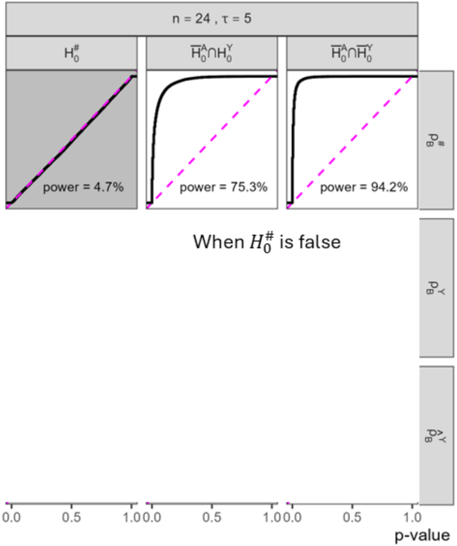

When $H_0^{\#}$ is false

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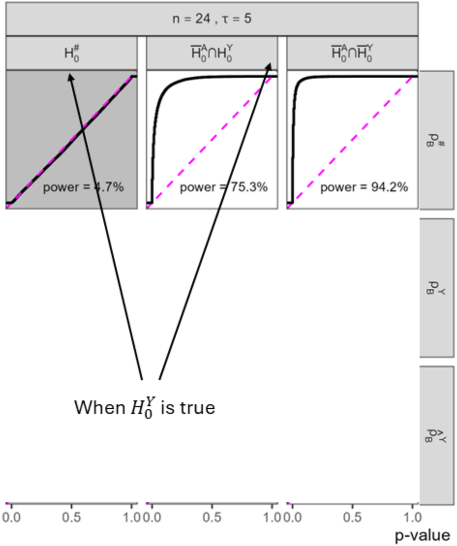

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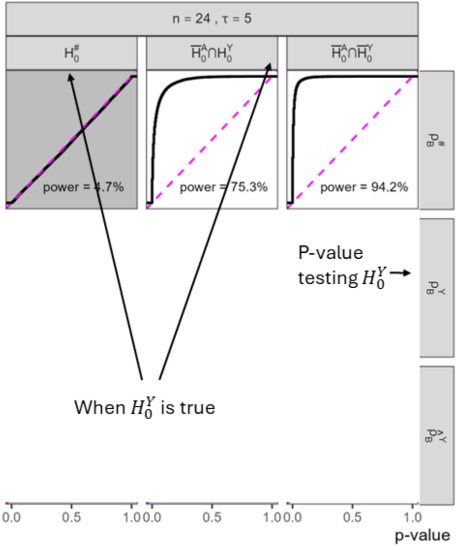

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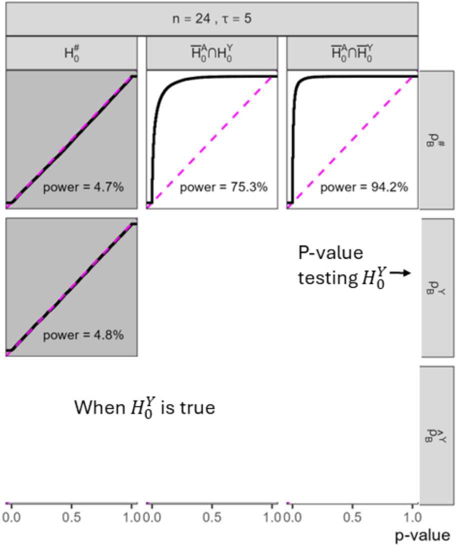

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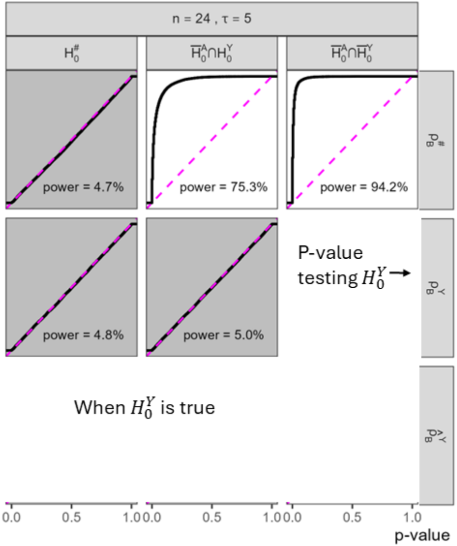

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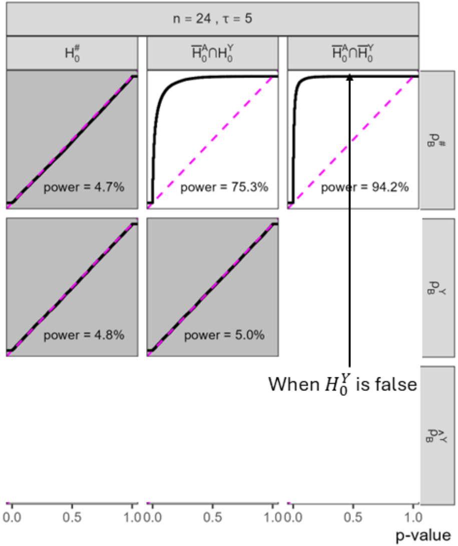

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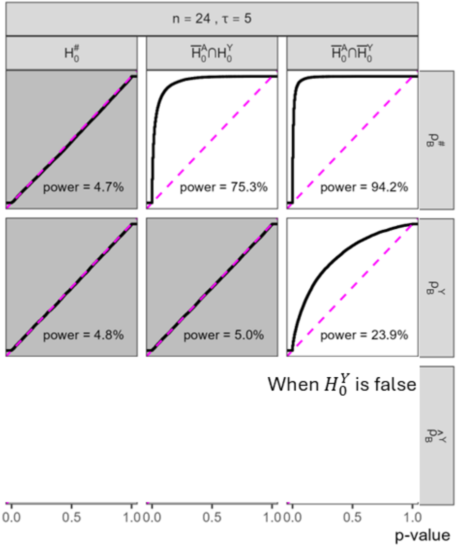

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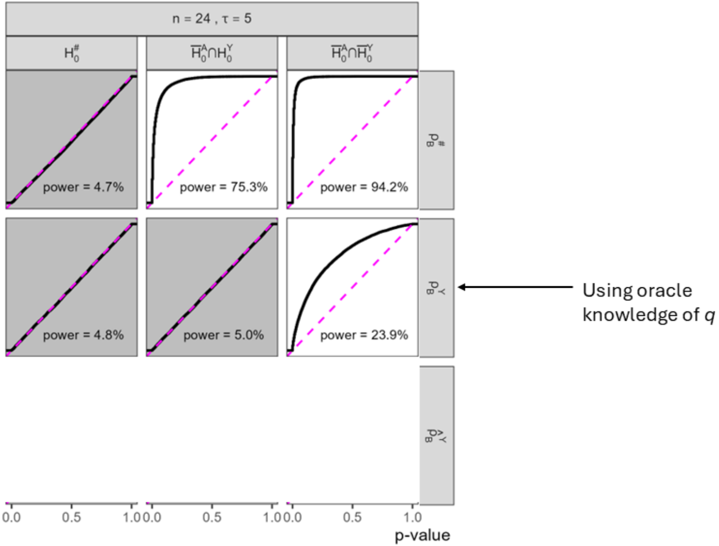

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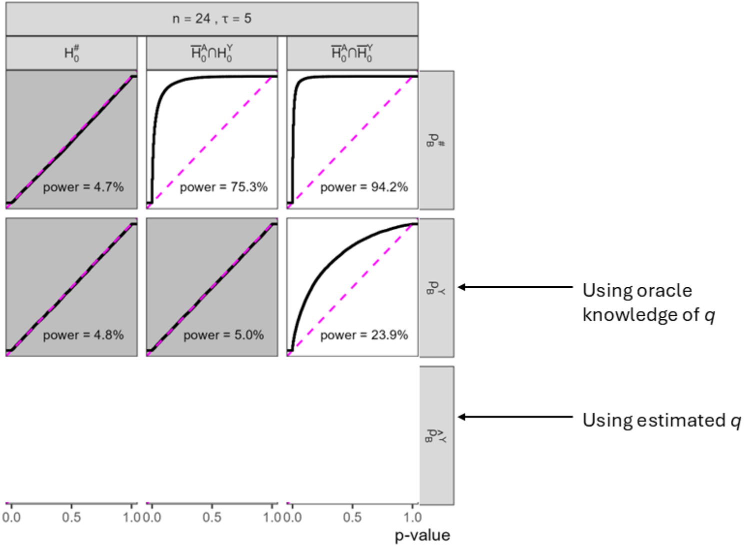

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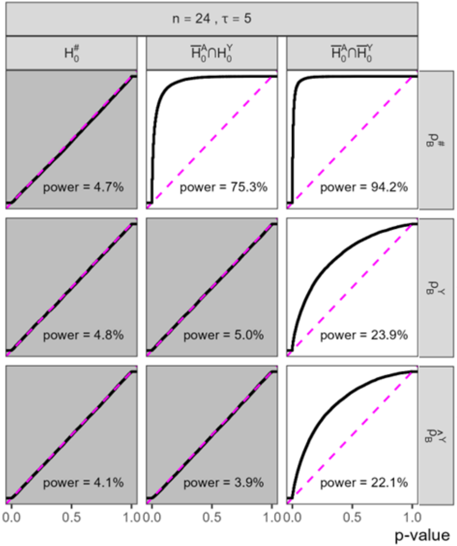

Using oracle knowledge of q

Using estimated q

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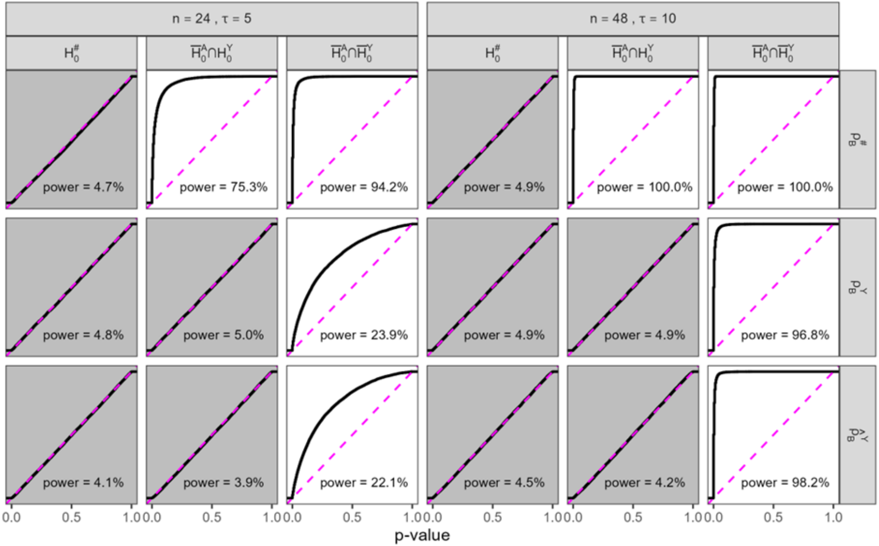

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$$
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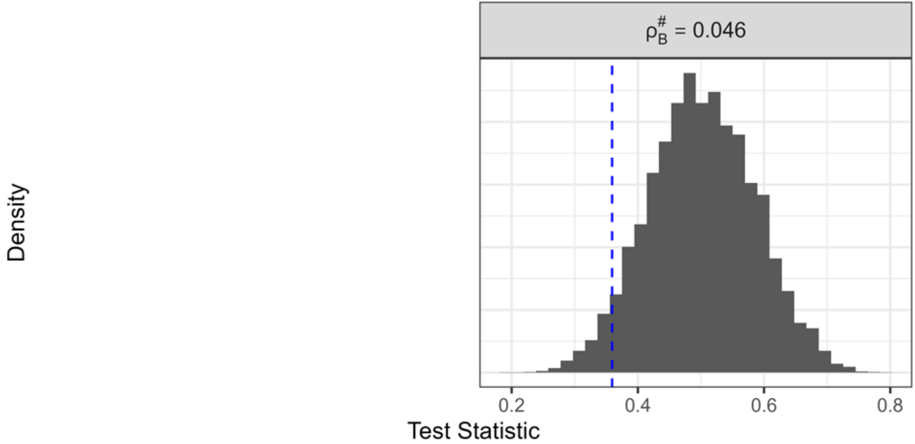

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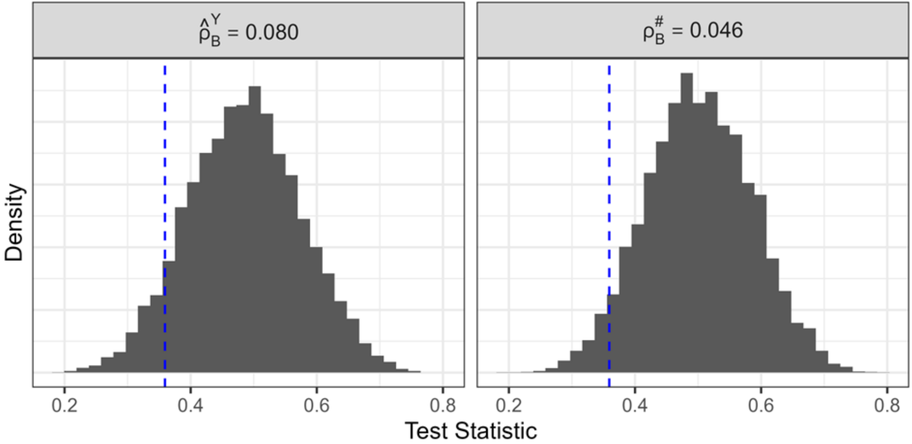

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Project status:

- Under revision with *PNAS*

Questions?

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References I

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Supplementary Slides

Choice of Test Statistic

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

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

	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.

Testing H_0^Y

Testing Procedure:

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

Testing H_0^Y

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2. Approximate $F_T(t|H_0^Y)$ using B Monte-Carlo replicates:
   for $b = 1$ to B **do:**

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   2. generate networks $\overline{\mathbf{a}}_b$ from $q(\overline{\mathbf{a}}, \mathbf{z}_b; \widehat{\theta})$

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   3. compute the test statistic $T_b = T(\mathbf{z}_b, \bar{\mathbf{a}}_b, \mathbf{Y})$

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   2. generate networks $\bar{\mathbf{a}}_b$ from $q(\bar{\mathbf{a}}, \mathbf{z}_b; \widehat{\theta})$
   3. compute the test statistic $T_b = T(\mathbf{z}_b, \bar{\mathbf{a}}_b, \mathbf{Y})$
3. compute the plug-in p-value testing H_0^Y:

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

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

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 $k \in \{2, \ldots, \tau\}$ with probability $\Pr\left(Y_i^k = 1 | \overline{\mathbf{A}}^{k-1}, \overline{\mathbf{Y}}^{k-1}\right) = h_i(\mathbf{S}^{k-1})$ 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 Hypothesis	**Formation Model Parameters** θ^+	**Persistence Model Parameters** θ^-	**Infection Probability 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 $\mathbf{S}^{k-1} = \mathbf{s} = (s_1, \ldots, s_n)$ 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
- $\widehat{\rho}_B^Y$: 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

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

  - 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

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

- **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

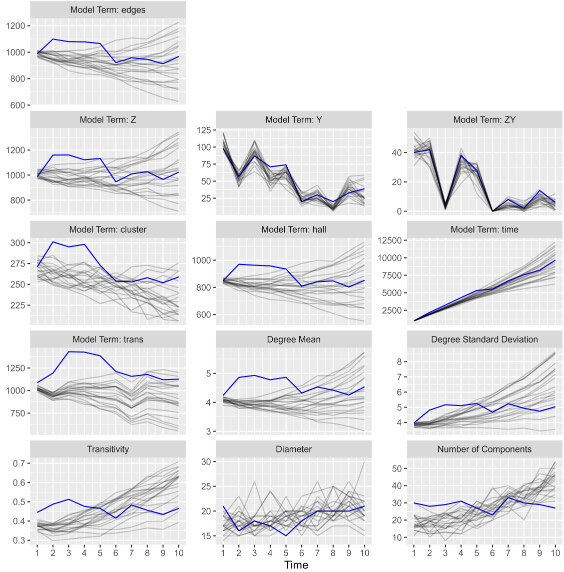
$$\mathbf{g}^{+}(\mathbf{a}^{k+}, \mathbf{a}^{k}, \mathbf{x}^{k+1}) =$$

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

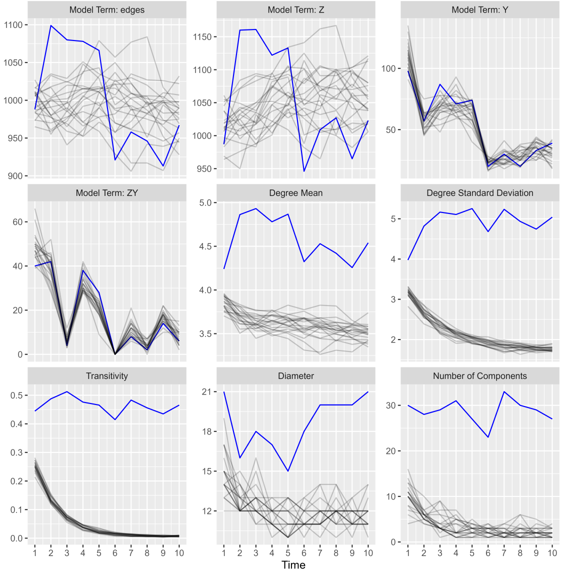
eX-FLU: STERGM Results

Model	Parameter	Estimate (95% Confidence Interval)
Formation	$\theta^{+}_{\text{edges}}$	-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)
	$\theta^{+}_{\text{trans}}$	2.88 (2.82, 2.94)
Persistence	$\theta^{-}_{\text{edges}}$	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)
	$\theta^{-}_{\text{trans}}$	0.42 (0.35, 0.48)

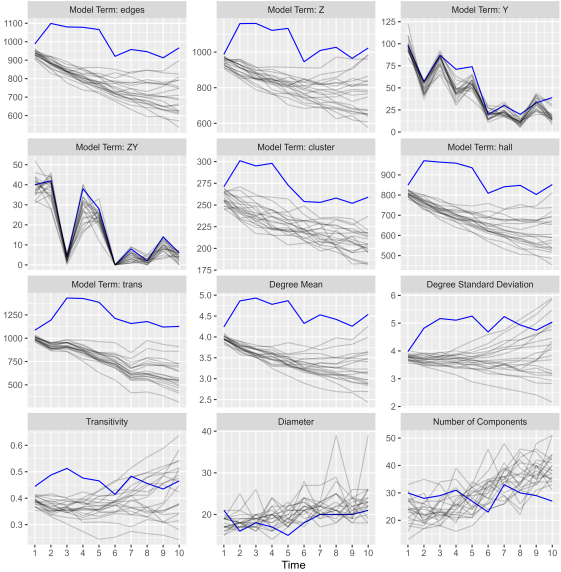
eX-FLU Diagnostics: STERGM



eX-FLU Diagnostics: Alternate STERGM 1



eX-FLU Diagnostics: Alternate STERGM 2



eX-FLU Sensitivity Analysis