

# NEAR-OPTIMAL SPECTRAL DISEASE MITIGATION IN HEALTHCARE FACILITIES

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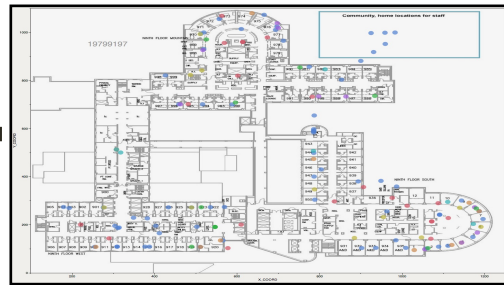
Nov, 2022

# CONTACT NETWORKS IN HOSPITALS

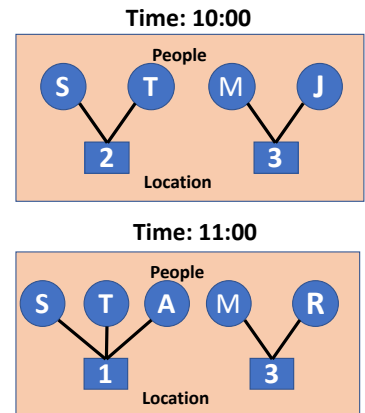
- Temporally dynamic bipartite people-location networks

Person	Location	Time
Sam	Room2	10:00
Tom	Room2	10:00
Matt	Room3	10:00
Julie	Room3	10:00
Matt	Room3	11:00
Ria	Room3	11:00
Sam	Room1	11:00
Tom	Room1	11:00
Alice	Room1	11:00

Schedule logs



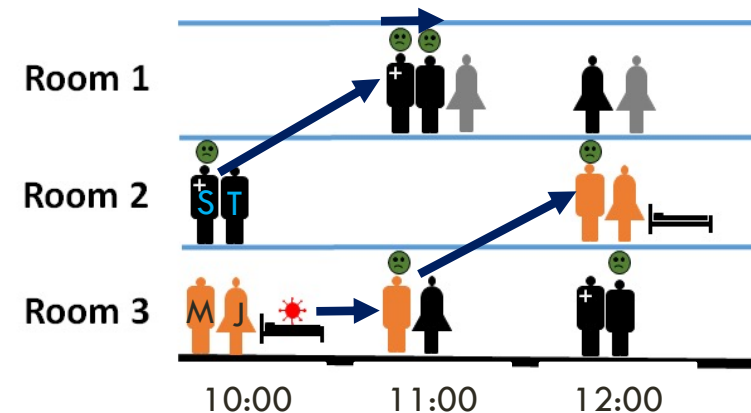
Spatial layout



High resolution  
dynamic bipartite networks

# PATHOGEN SPREAD IN HOSPITALS

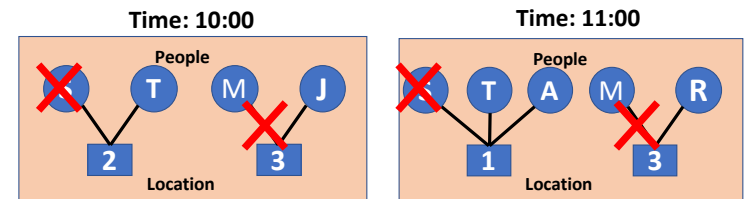
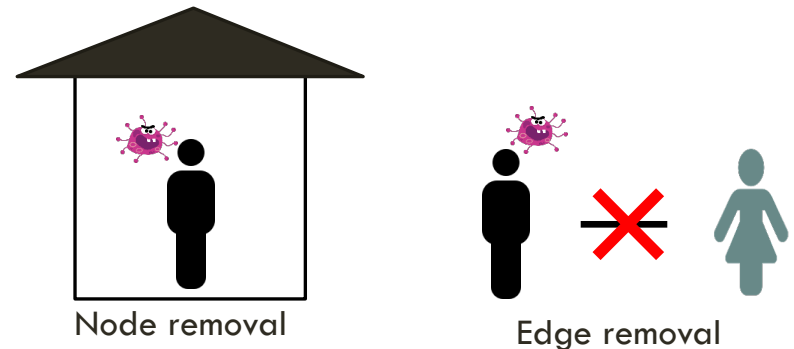
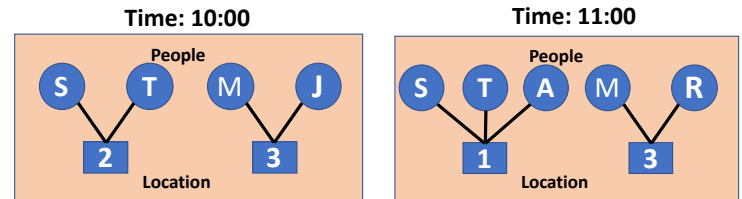
- ❑ Hospital Acquired Infections (HAI) spread in hospitals to/from healthcare workers and patients
- ❑ Examples: C. Diff, MRSA etc
- ❑ A major financial and health burden
- ❑ Bacterial load accumulates on surfaces
- ❑ Infects individuals



How to combat HAI spread?

# INFORMAL PROBLEM STATEMENT

- **Given:** a sequence of mobility graphs
- **Determine:** top-k nodes/edges to remove
  - Node removal: quarantine
  - Edge removal: contact prevention
- **Such that:** the resulting graph is less vulnerable to outbreak



# FORMULATION CHALLENGES

- ❑ Formulation challenge 1: How to define vulnerability?
  - How to characterize the disease spread?
  - How to quantify ‘vulnerability’?
  
- ❑ Formulation challenge 2: How to formalize node/edge removals?
  - Node edges repeat over time
  - How to handle that?

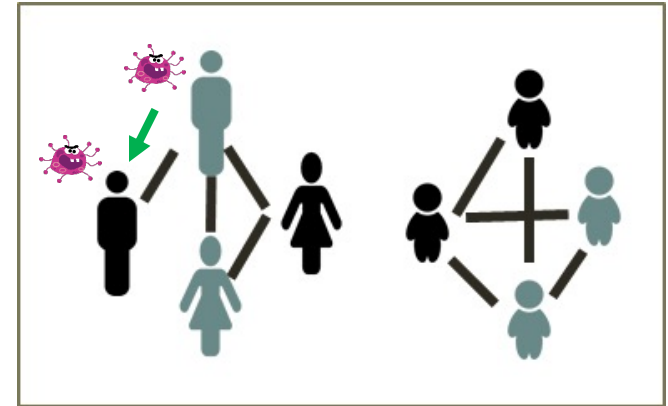
# FC1: DISEASE SPREAD MODEL

## □ SI MODEL

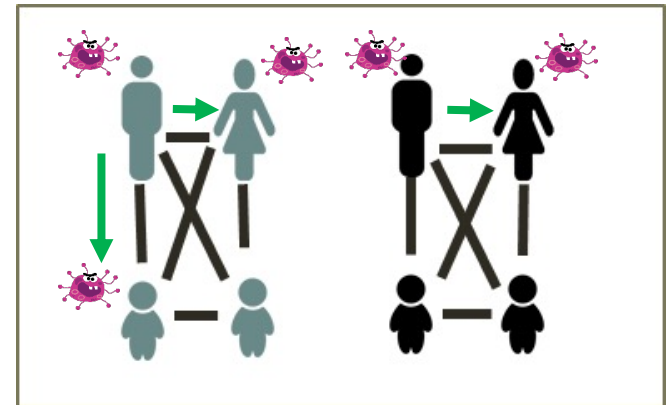
- “**Infected**” nodes infect “**Susceptible**” neighbors
- With **probability** given by **edge-weight**
- Once a node is infected, it **remains** infected
- Nodes get **multiple chances** to infect

## □ IC MODEL

- Nodes get **single chance** to infect
- Nodes get **cured** in the next time-step
- **Never** become infected again



**Day graph:** Office/School

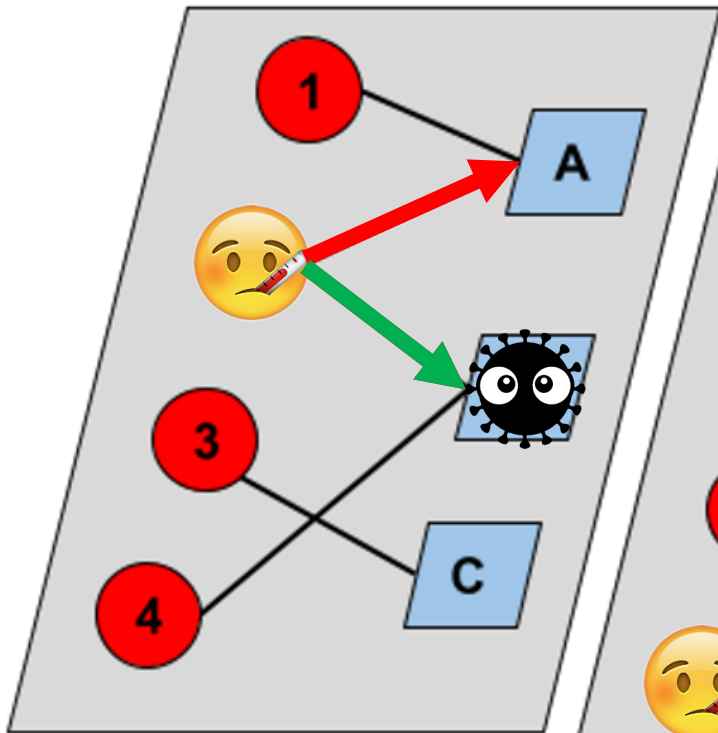


**Night graph:** Family

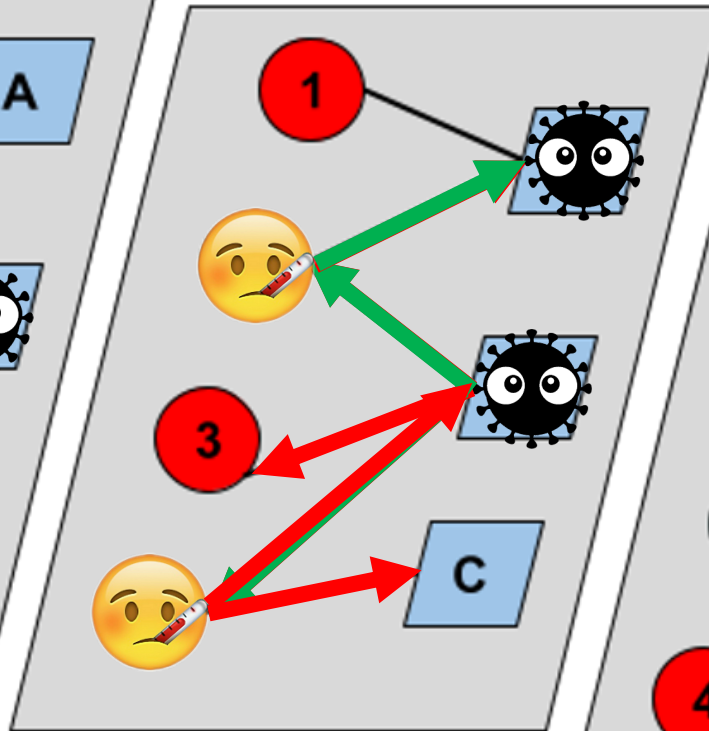
# FC1: DISEASE SPREAD MODEL

- Extended SI model for HAI

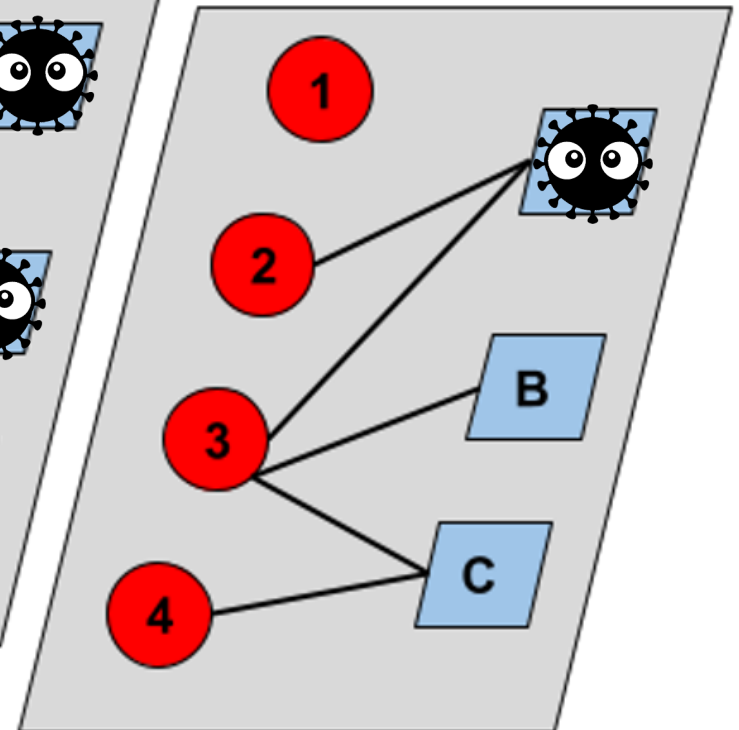
Day 1



Day 2

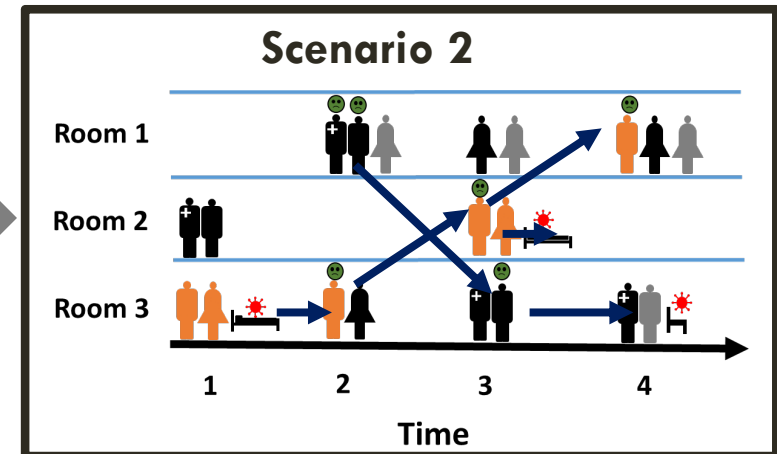
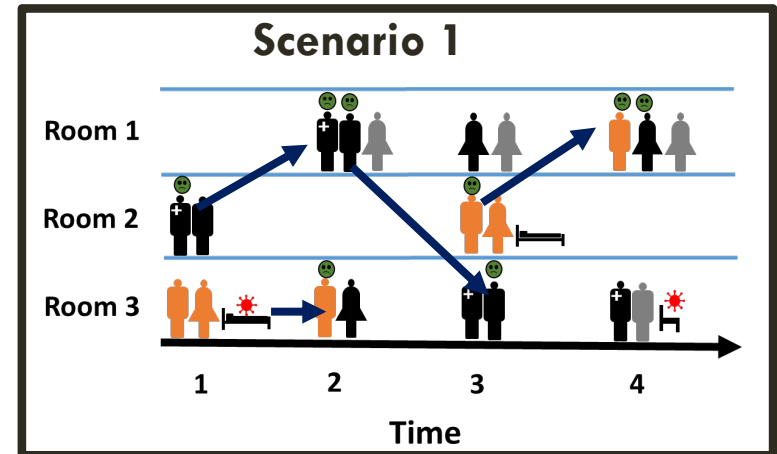
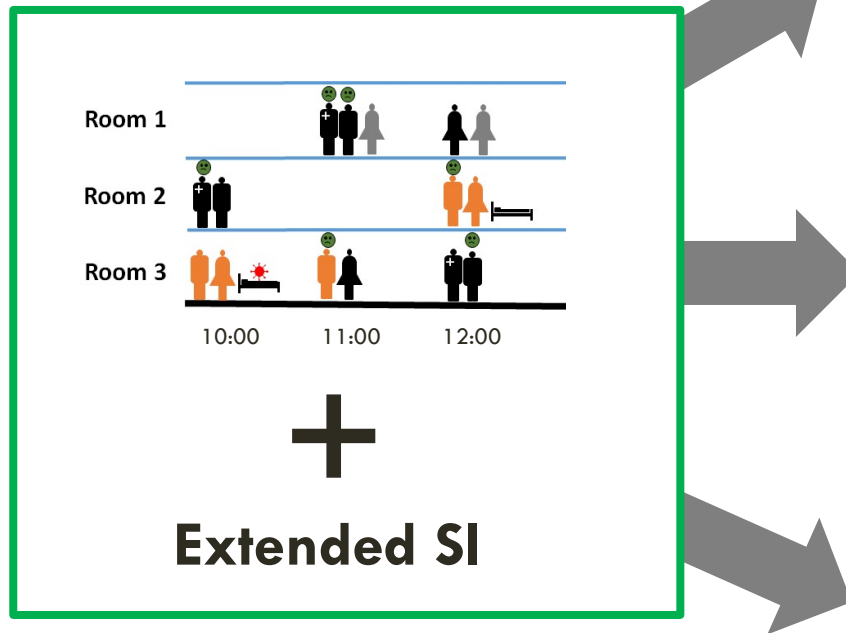


Day 3



# FC1: QUANTIFYING VULNERABILITY

- Use the calibrated SI model and the mobility log to produce possible outbreak scenarios



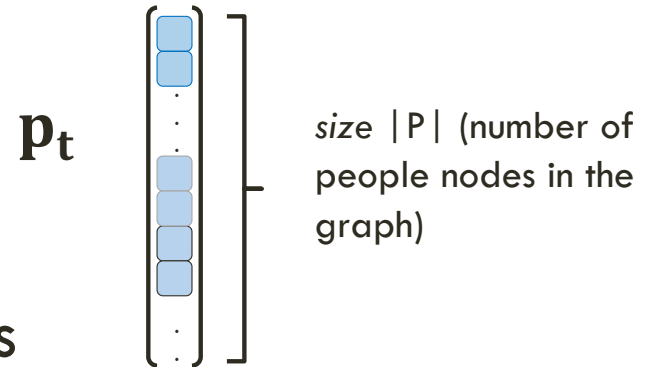
⋮

**Problem: computationally too expensive**



# IDEA: LOOK FOR ASYMPTOTIC BEHAVIORS

- We are given a sequence of graphs  $\mathcal{G} = \{G_1, G_2, \dots, G_T\}$
- Imagine a vector  $\mathbf{p}_t$  which captures probability of infections
- Easy to see that  $\mathbf{p}_t$  depends on  $\mathbf{p}_{t-1}$  and  $G_t$



$$\mathbf{p}_t = f(G_t, \mathbf{p}_{t-1})$$

The equation is visually represented with a vector  $\mathbf{p}_t$  on the left, an equals sign, a function  $f$  in the middle, a square box labeled  $G_t$  as the first argument, a comma, and another vector  $\mathbf{p}_{t-1}$  as the second argument. All vectors are shown as vertical columns of blue boxes with vertical ellipses between them.

Non-linear dynamical system

# EVOLUTION OF P

$$\mathbf{p}_t = f(G_t, \mathbf{p}_{t-1})$$

□  $f(\cdot)$  can be viewed as a discrete time NLDS

$$\mathbf{p}_t[v] = \mathbf{p}_{t-1}[v](1 - \delta) + \beta_p \beta_l \sum_{l=1}^L \sum_{p=1}^P \mathbf{B}_{t-1}[l, u] \mathbf{B}_{t-1}^T[i, v] \mathbf{p}_{t-1}[u]$$

↑  
**Probability that node  $v$  is infected at time  $t$**

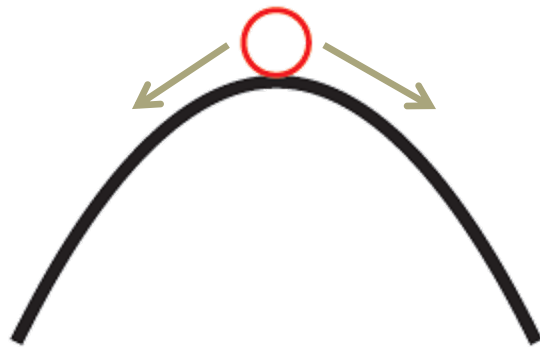
← **Probability that it is infected at time  $t-1$  and does not recover**

↑  
**Probability that  $v$  is infected by a location  $l$  which was infected by node  $u$  at  $t-1$**

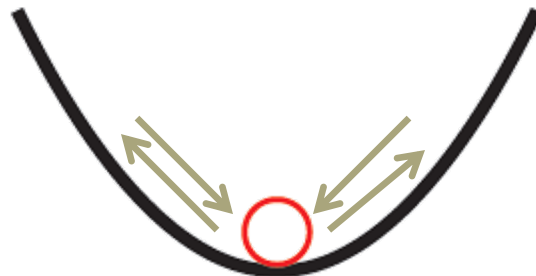
# STABILITY OF A NLDS

THEOREM 3.1. (HIRSCH AND SMALE [1]) *The system given by a NDLS  $\mathbf{p}_t = g(\mathbf{p}_{t-1})$  is asymptotically stable at an equilibrium point  $\mathbf{p}^*$  (in our case the zero vector), if the eigenvalues of the Jacobian  $J = \nabla g(\mathbf{p}_{t-1})$  are less than 1 in absolute value, where,*

$$J_{i,j} = \nabla g(\mathbf{p}_{t-1})_{i,j} = \left. \frac{\partial p_{i,t}}{\partial p_{j,t-1}} \right|_{\mathbf{p}_t = \mathbf{p}^*}$$



(A) Unstable



(B) Stable



(C) Neutral (at threshold)

# EPIDEMIC THRESHOLD OF G

□ Jacobian of  $f()$  at  $\mathbf{p}_t = \mathbf{0}$

$$\mathbf{S} = \prod_{t=1}^{\tau} (1 - \delta_p) \mathbf{I} + \beta_p \beta_l \mathbf{B}_t \mathbf{B}_{(t \bmod \tau) + 1}^{\top}$$

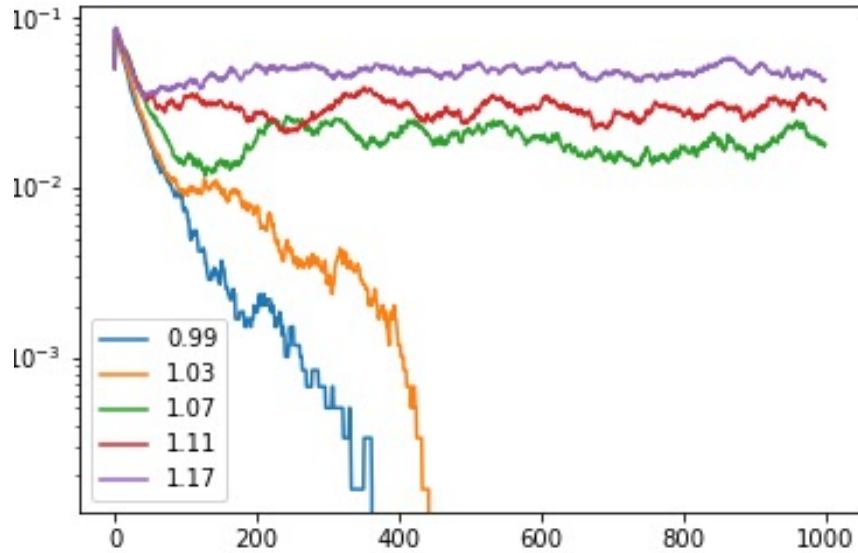
Disease Parameters

Adjacency matrices

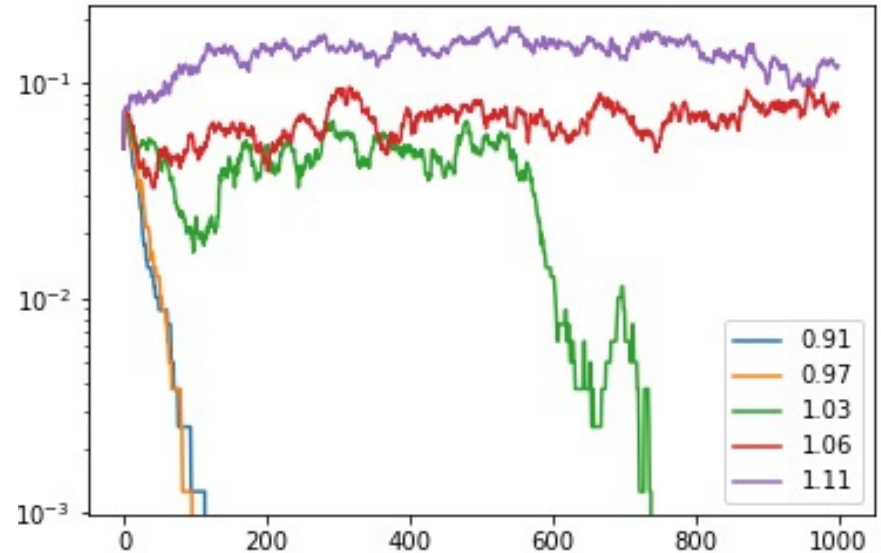
□ Therefore,

**THEOREM 3.1.** *If  $\lambda_{\mathbf{S}} < 1$ , then  $\mathbf{p}_t$  is asymptotically stable at  $\mathbf{0}$ .*

# EPIDEMIC THRESHOLD VALIDATION



UIHC



Commercial HC 1

Infection dies out when  $\lambda_S \ll 1$ , survives for few time-stamps when  $\lambda_S \approx 1$ , and continues on when  $\lambda_S \gg 1$

# FORMULATION CHALLENGES



Formulation challenge 1: How to define vulnerability?

- **How to characterize the disease spread?**
- **How to quantify ‘vulnerability’?**

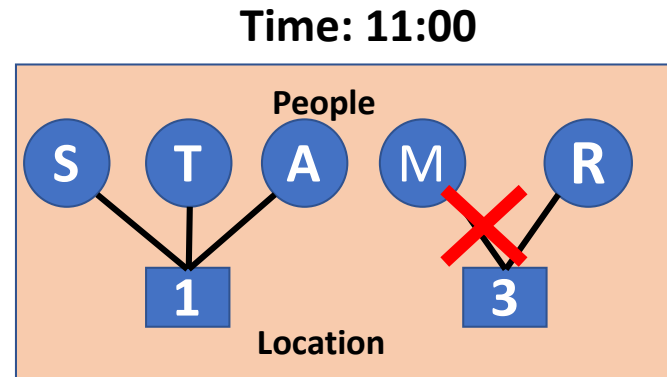
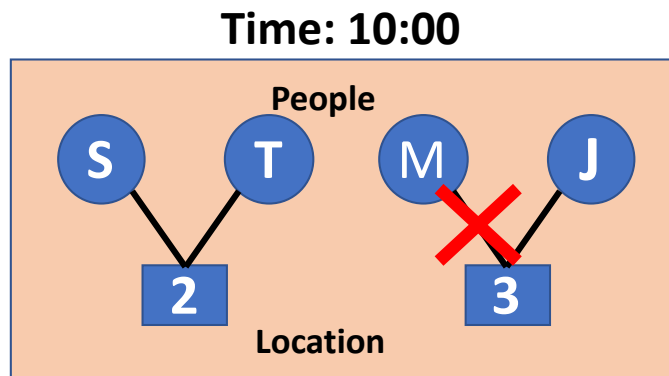


Formulation challenge 2: How to formalize node/edge removals?

- Node edges repeat over time
- How to handle that?

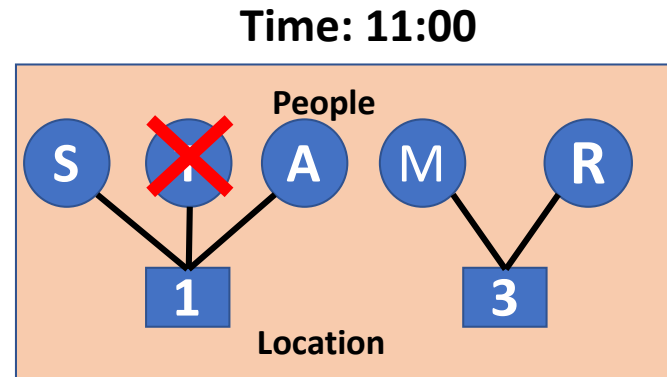
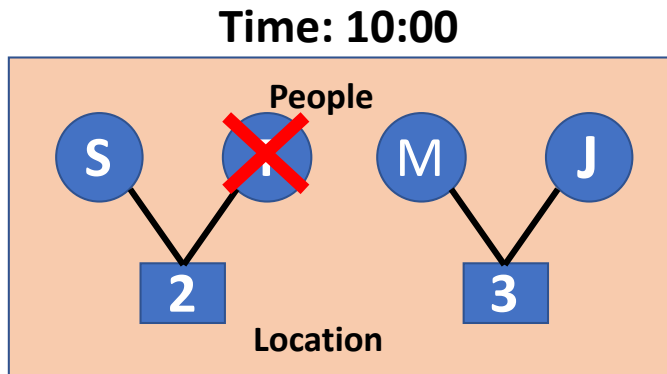
# FC2: EDGE REMOVAL

- When we remove an edge from  $G = g_1, g_2, \dots, g_\tau$ , we remove it from all time-stamps



# FC2: NODE REMOVAL

- When we remove a node from  $G = g_1, g_2 \dots, g_\tau$ , we remove it from all time-stamps



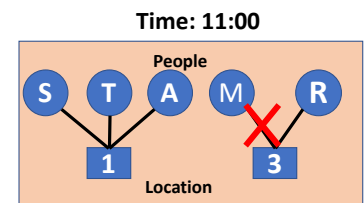
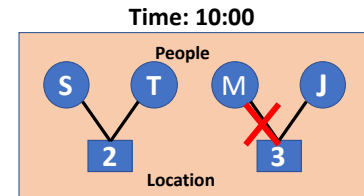
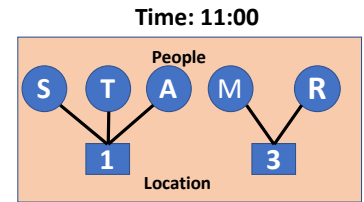
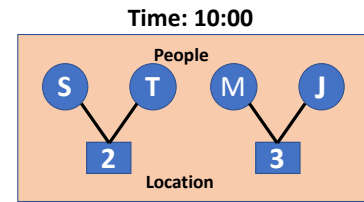


# FORMAL PROBLEM DEFINITION

□ **Given:** A temporal bipartite network  $\mathcal{G} = \{G_1, G_2, \dots, G_T\}$  and  $\alpha_E \in (0, 1]$

□ **Find:** A smaller graph  $\mathcal{G}^* = \{G_1^*, G_2^*, \dots, G_T^*, \}$

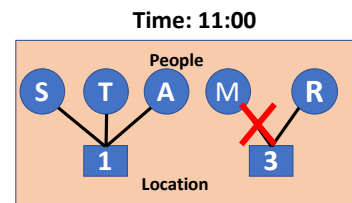
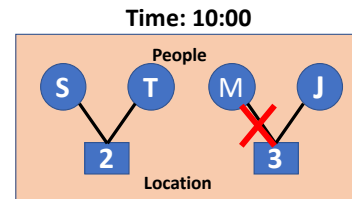
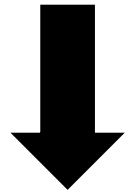
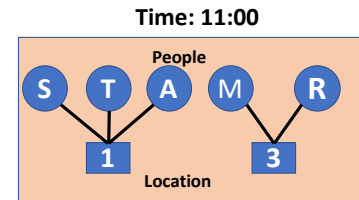
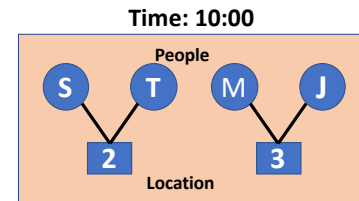
□ **Such that:**  $1 - \alpha_E$  edges are removed at maximum and  $\mathcal{G}^* = \arg \min_{\mathcal{G}'} \lambda_{\mathcal{S}'}$



# HOW TO SOLVE THE PROBLEM

## NAÏVE- Top-k

1. For each edge in the graph
  1. Remove it
  2. Compute  $\Delta$ -scores = the drop in the largest eigenvalue of S
2. Sort the edges in decreasing order of  $\Delta$ -scores
3. Until the graph is small enough do
  1. Delete the best possible edge



# PROBLEM WITH THE NAÏVE APPROACH

- ❑ Expensive to compute  $S$

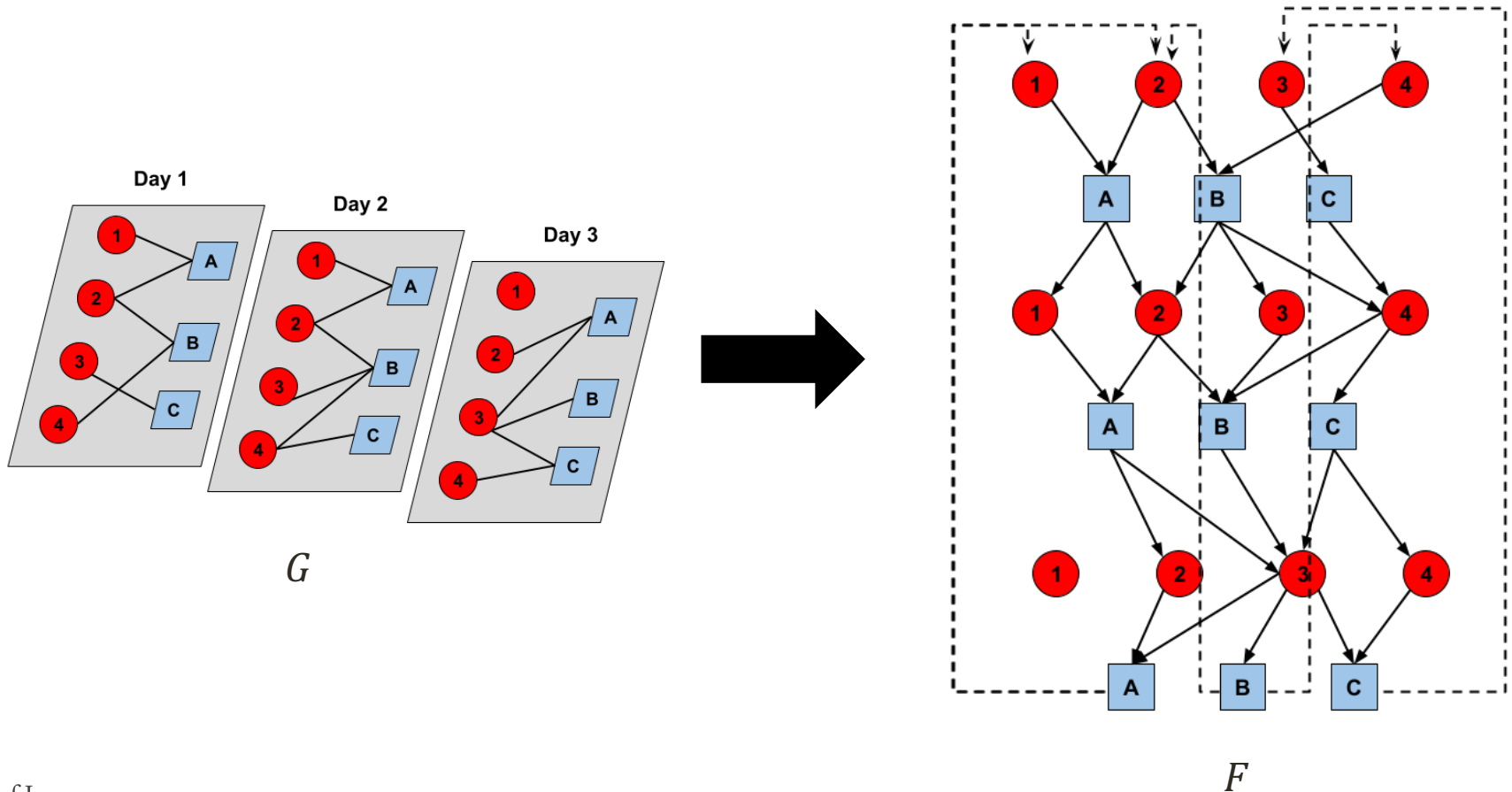
$$S_G = \square \times \square \times \dots$$

- ❑ Expensive to repeatedly compute largest eigenvalue

$$\mathbf{X} \mathbf{u} = \lambda_{\mathbf{X}} \mathbf{u}$$

# HOW TO AVOID COMPUTING $S$ AND $\lambda$

- First create a static graph  $F$  from  $G$



# WHAT IS SO SPECIAL ABOUT F?

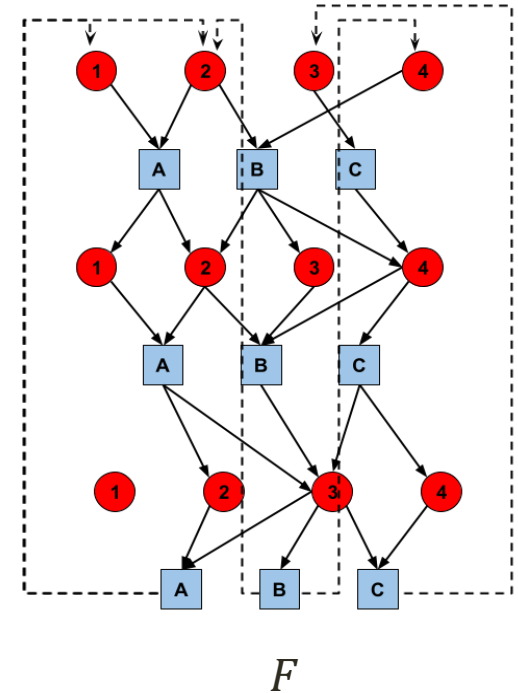
- Turns out the number of closed walks in  $F$  and the sum of eigenvalues of  $S$  are very closely related.

$$\sum_{w \in W(F)} \text{nodes}(w) = \frac{k}{(\beta_p \beta_l)^{k/2}} \sum_i^n (\lambda_i(\mathbf{S}_{IC}))^{k/2\tau}$$

↑  
Sum of unique nodes in each closed walks in  $F$

↑  
Hyper and disease parameters

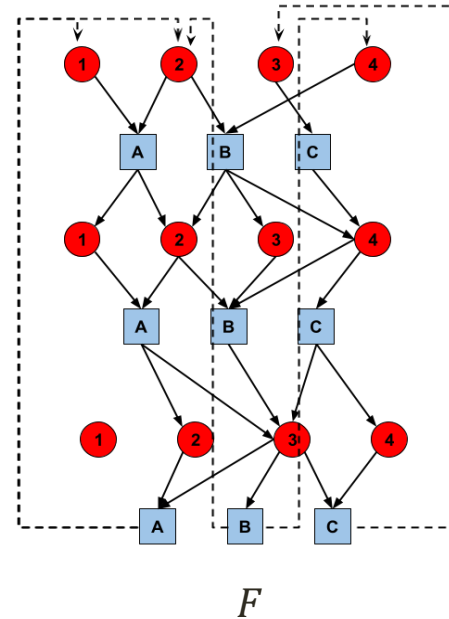
↑  
Sum of eigenvalues



# A NEAR OPTIMAL ALGORITHM

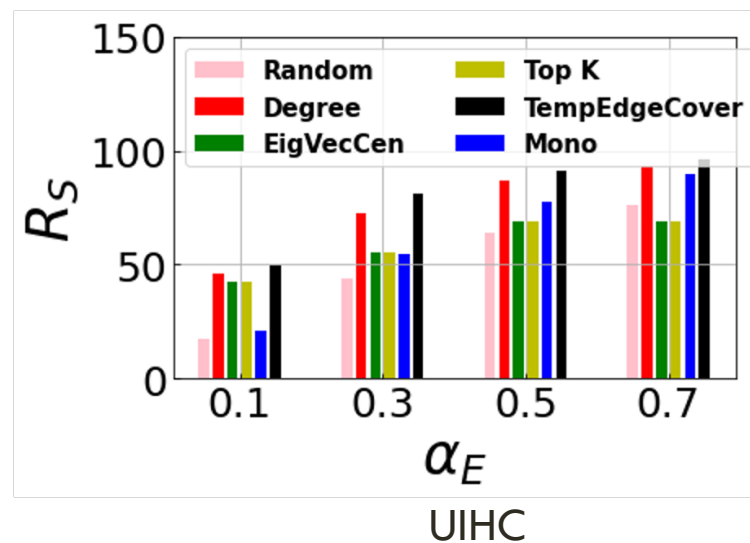
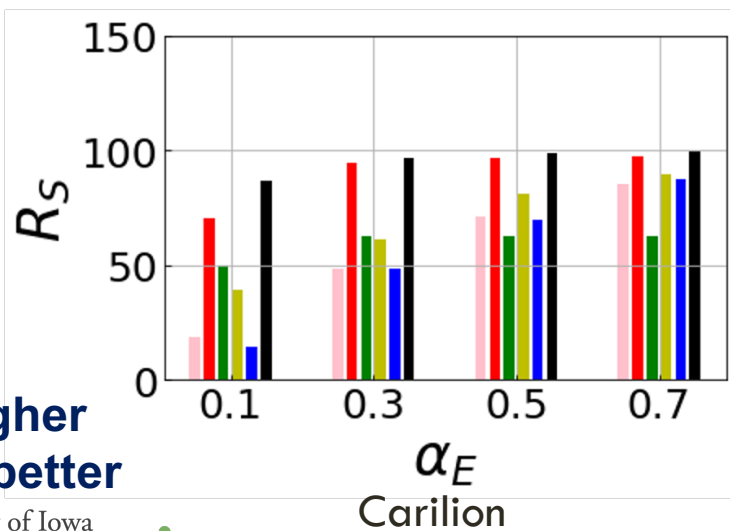
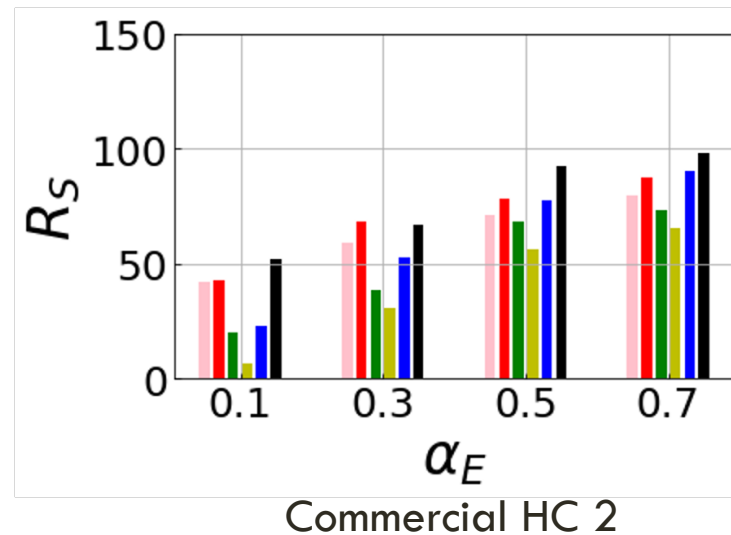
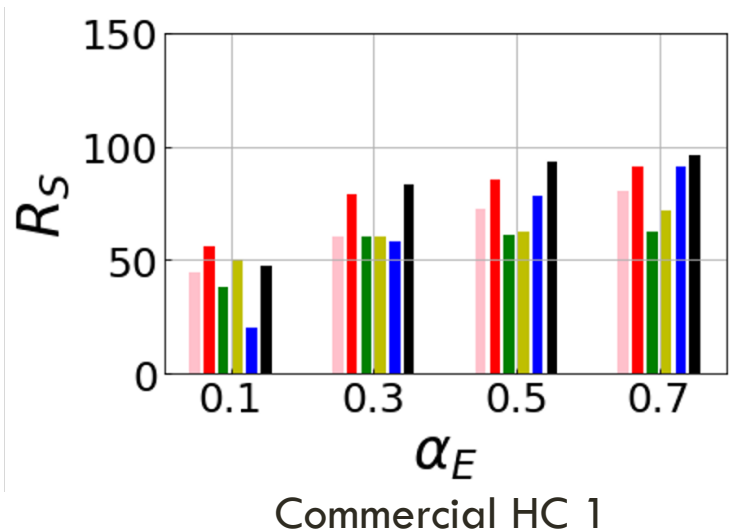
## Temporal Edge Cover

1. Compute  $F$  from  $G$
2. While not enough edges are removed
  1. Compute the number of closed walks each edge participates in
  2. Remove the edge that is in the most number of closed walks



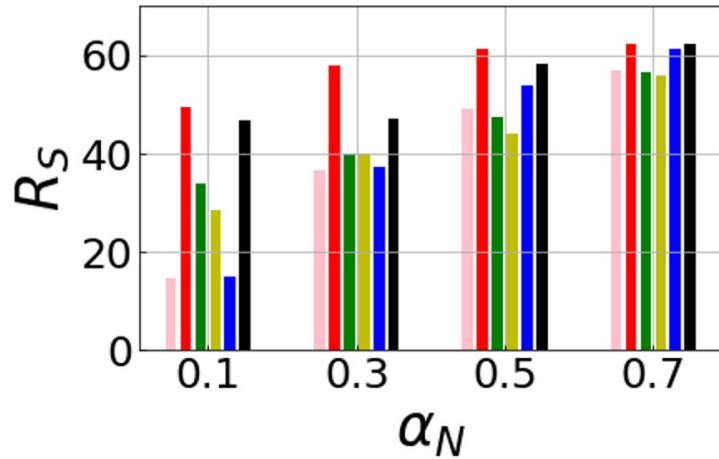
Provably near optimal.

# PERFORMANCE: EDGE DELETION

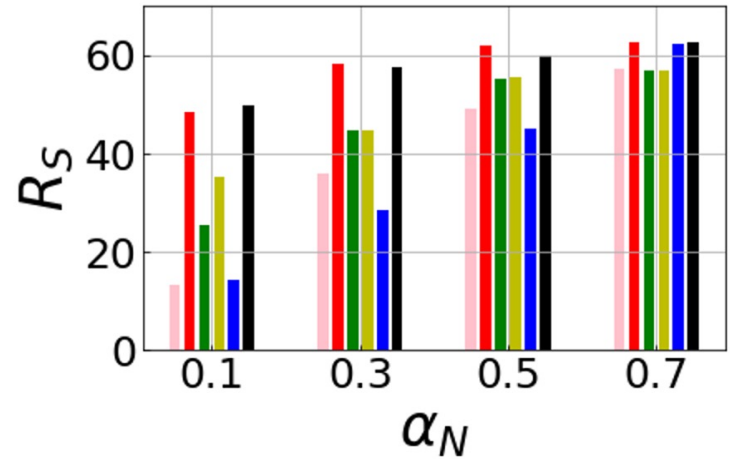


↑ Higher is better

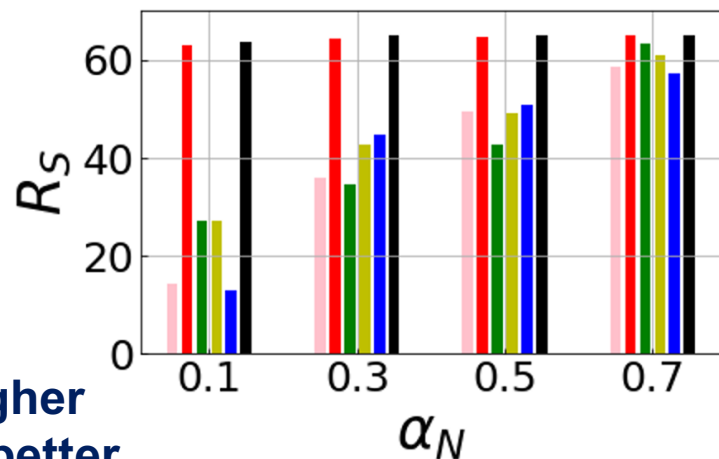
# PERFORMANCE: NODE DELETION



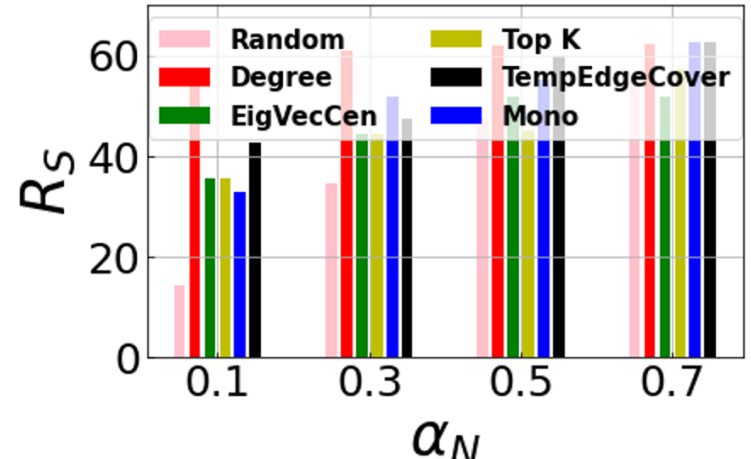
Commercial HC 1



Commercial HC 2



Carilion

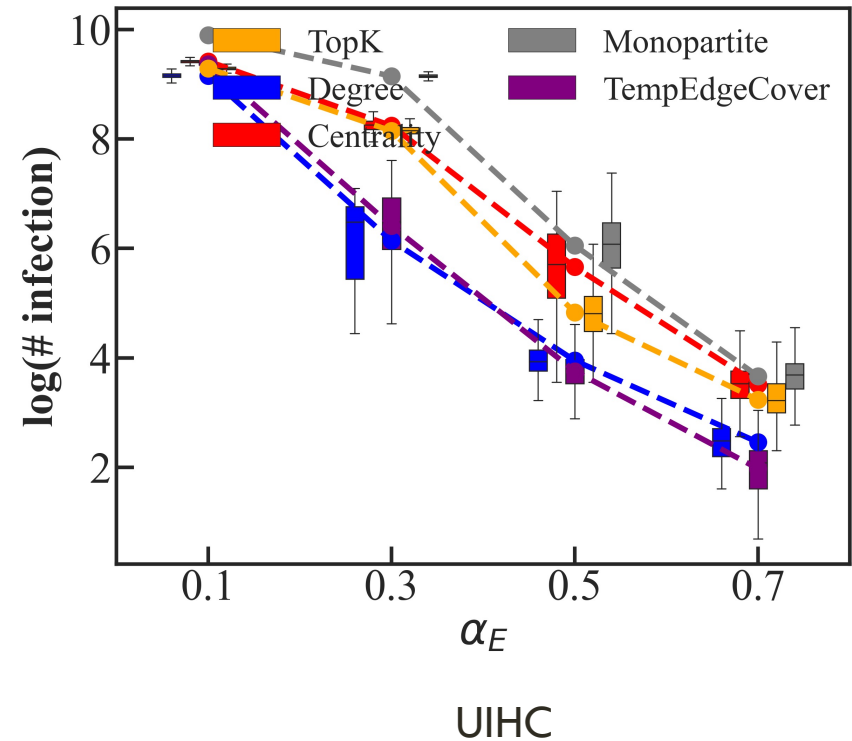
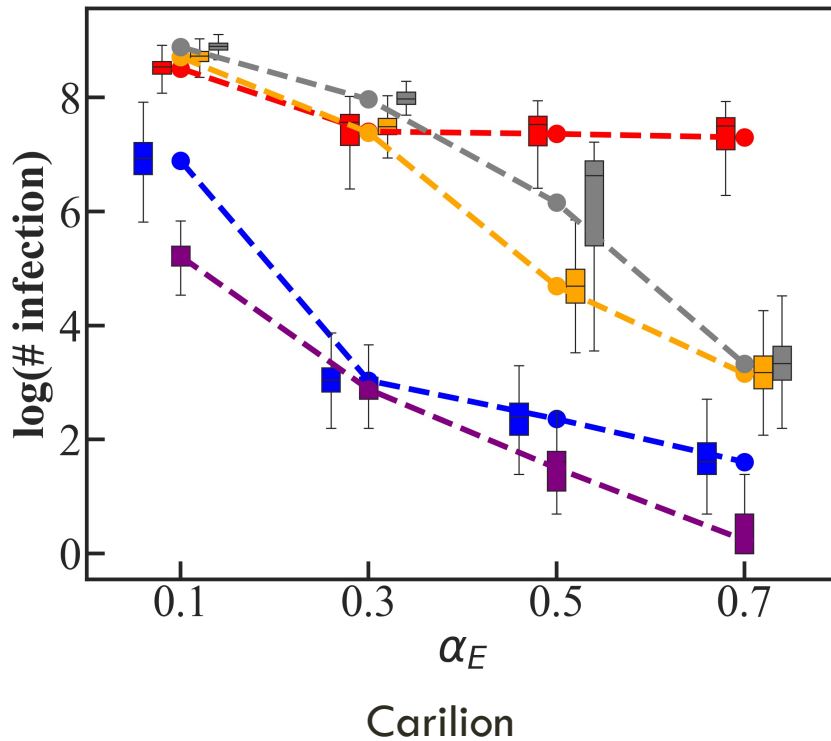


UIHC

Higher is better



# INFECTION CONTROL: BSIS



Our approach leads to improved infection control.